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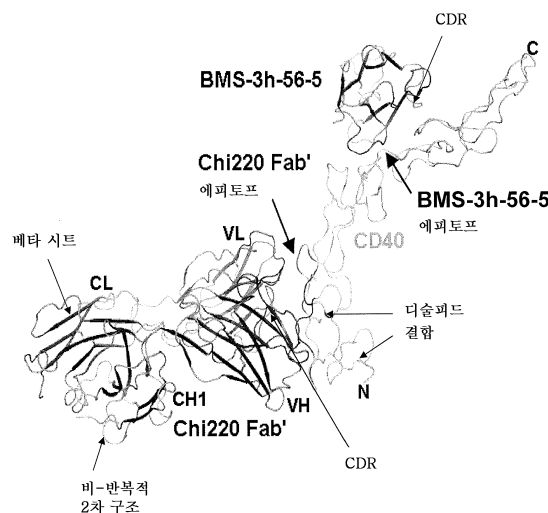
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(54) 발명의 명칭 CD40을 길항하는 항체 폴리펩티드

(57) 요약

인간 CD40의 신규 에피토프에 특이적으로 결합하는 항체 폴리펩티드가 제공된다. 이러한 항체 폴리펩티드는 CD40 효능제 활성을 나타내지 않는다. 이러한 항체 폴리펩티드는 CD40 활성화를 수반하는 질환, 예컨대 자가면역 질환의 치료에서 유용하다. 이러한 항체 폴리펩티드는 단일 V_L 또는 V_H 도메인을 포함하는 도메인 항체 (dAb)일 수 있다. 이러한 항체 폴리펩티드를 인간 혈청 알부민 (HSA)에 또한 결합할 수 있는 이중 특이적 시약이도록 변형함으로써 항체 폴리펩티드의 반감기를 증가시킬 수 있다.

대표도 - 도1



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명세서

청구범위

청구항 1

(a) BMS3h-56-269의 CDR1 영역을 포함하는 CDR1 영역 또는 BMS3h-56-269의 CDR1 영역과 2개 이하의 아미노산만큼 상이한 CDR1 영역, 여기서 BMS3h-56-269의 CDR1 영역은 서열 417의 아미노산 31 내지 35임;

(b) BMS3h-56-269의 CDR2 영역을 포함하는 CDR2 영역 또는 BMS3h-56-269의 CDR2 영역과 2개 이하의 아미노산만큼 상이한 CDR2 영역, 여기서 BMS3h-56-269의 CDR2 영역은 서열 417의 아미노산 50 내지 66임; 및

(c) BMS3h-56-269의 CDR3 영역을 포함하는 CDR3 영역 또는 BMS3h-56-269의 CDR3 영역과 2개 이하의 아미노산만큼 상이한 CDR3 영역, 여기서 BMS3h-56-269의 CDR3 영역은 서열 417의 아미노산 99 내지 105임

을 포함하는 제1 가변 도메인을 포함하고,

CD40에 결합하는 도메인 항체이고,

CD40에의 결합이 CD40을 길항하는(antagonize),

항체 폴리펩티드.

청구항 2

제1항에 있어서, 제1 가변 도메인이 서열 317, 서열 318, 서열 320, 서열 321, 서열 324, 서열 325, 서열 326, 서열 327, 서열 331, 서열 332, 서열 333, 서열 334, 서열 335, 서열 336, 서열 337, 서열 341, 서열 342, 서열 343, 서열 344, 서열 345, 서열 346, 서열 347, 서열 348, 서열 349, 서열 350, 서열 353, 서열 355, 서열 356, 서열 358, 서열 366, 서열 367, 서열 376, 서열 379, 서열 381, 서열 386, 서열 394, 서열 403, 서열 405, 서열 412, 서열 417, 및 서열 419로 이루어진 군으로부터 선택되는 BMS3h-56의 계통 군의 항체 폴리펩티드 중 하나의 아미노산 서열을 포함하는 것인 항체 폴리펩티드.

청구항 3

제1항에 있어서,

(a) CDR1 영역이 BMS3h-56-269의 CDR1 영역을 포함하고, 여기서 BMS3h-56-269의 CDR1 영역은 서열 417의 아미노산 31 내지 35이고,

(b) CDR2 영역이 BMS3h-56-269의 CDR2 영역을 포함하고, 여기서 BMS3h-56-269의 CDR2 영역은 서열 417의 아미노산 50 내지 66이고,

(c) CDR3 영역이 BMS3h-56-269의 CDR3 영역을 포함하고, 여기서 BMS3h-56-269의 CDR3 영역은 서열 417의 아미노산 99 내지 105인 것인

항체 폴리펩티드.

청구항 4

제1항에 있어서, 제1 가변 도메인이

(a) BMS3h-56-269의 FR1 영역을 포함하는 FR1 영역 또는 BMS3h-56-269의 FR1 영역과 2개 이하의 아미노산만큼 상이한 FR1 영역, 여기서 BMS3h-56-269의 FR1 영역은 서열 417의 아미노산 1 내지 30임,

(b) BMS3h-56-269의 FR2 영역을 포함하는 FR2 영역 또는 BMS3h-56-269의 FR2 영역과 2개 이하의 아미노산만큼 상이한 FR2 영역, 여기서 BMS3h-56-269의 FR2 영역은 서열 417의 아미노산 36 내지 49임,

(c) BMS3h-56-269의 FR3 영역을 포함하는 FR3 영역 또는 BMS3h-56-269의 FR3 영역과 2개 이하의 아미노산만큼 상이한 FR3 영역, 여기서 BMS3h-56-269의 FR3 영역은 서열 417의 아미노산 67 내지 98임, 및

(d) BMS3h-56-269의 FR4 영역을 포함하는 FR4 영역 또는 BMS3h-56-269의 FR4 영역과 2개 이하의 아미노산만큼

상이한 FR4 영역, 여기서 BMS3h-56-269의 FR4 영역은 서열 417의 아미노산 106 내지 116임을 포함하는 것인 항체 폴리펩티드.

청구항 5

제4항에 있어서,

- (a) FR1 영역이 BMS3h-56-269의 FR1 영역을 포함하고, 여기서 BMS3h-56-269의 FR1 영역은 서열 417의 아미노산 1 내지 30이고,
- (b) FR2 영역이 BMS3h-56-269의 FR2 영역을 포함하고, 여기서 BMS3h-56-269의 FR2 영역은 서열 417의 아미노산 36 내지 49이고,
- (c) FR3 영역이 BMS3h-56-269의 FR3 영역을 포함하고, 여기서 BMS3h-56-269의 FR3 영역은 서열 417의 아미노산 67 내지 98이고,
- (d) FR4 영역이 BMS3h-56-269의 FR4 영역을 포함하고, 여기서 BMS3h-56-269의 FR4 영역은 서열 417의 아미노산 106 내지 116인 것인 항체 폴리펩티드.

청구항 6

제1항에 있어서, 제1 가변 도메인이 서열 417인 BMS3h-56-269를 포함하는 것인 항체 폴리펩티드.

청구항 7

제1항에 있어서,

- (a) CDR1 영역이 서열 1274인 서열 X_1 -Tyr-Glu- Y_1 -Trp로 이루어지고, 여기서 X_1 은 Asp 또는 Gly이고, Y_1 은 Met 또는 Leu이고,
- (b) CDR2 영역이 서열 1275인 서열 Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 - Z_2 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly로 이루어지고, 여기서 X_2 는 Gln, Tyr, Pro, Trp, 또는 Ala이고, Y_2 는 Thr, Ser, Asn, Gly, Met, 또는 Gln이고, Z_2 는 Arg, Leu, Tyr, His, 또는 Phe이고, A_2 는 Lys 또는 Met이고,
- (c) CDR3 영역이 서열 1276인 서열 X_3 -Pro- Y_3 - Z_3 -Phe- A_3 - B_3 로 이루어지고, 여기서 X_3 은 Leu 또는 Pro이고, Y_3 은 Phe, Gln, Thr, 또는 Met이고, Z_3 은 Tyr, Pro, Leu, Thr, Ile, Phe, 또는 Met이고, A_3 은 Gln, His, Asp, Ser, Lys, Glu, 또는 Gly이고, B_3 은 Glu, Asp, 또는 Tyr인 것인 항체 폴리펩티드.

청구항 8

제4항에 있어서, 제1 가변 도메인이

- (a) 서열 1277인 서열 Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser- X_1 -Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe- Y_1 로 이루어진 FR1 영역, 여기서 X_1 은 Leu 또는 Arg이고, Y_1 은 Arg 또는 Ala임;
- (b) 서열 1278인 서열 Trp-Val-Arg- X_2 -Ala-Pro-Gly- Y_2 - Z_2 -Leu-Glu-Arg-Val-Ser로 이루어진 FR2 영역, 여기서 X_2 는 Gln 또는 Arg이고, Y_2 는 Lys 또는 Arg이고, Z_2 는 Gly 또는 Val임;
- (c) 서열 1279인 서열 Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn- X_3 -Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala- Y_3 -Asp-Thr- Z_3 -Val-Tyr- A_3 -Cys- B_3 -Lys로 이루어진 FR3 영역, 여기서 X_3 은 Thr 또는 Met이고, Y_3 은 Glu 또는 Asp이고, Z_3 은 Ala 또는 Ser이고, A_3 은 Tyr 또는 His이고, B_3 은 Ala 또는 Thr임; 및

(d) 서열 1280인 서열 X_4 -Gly- Y_4 -Gly-Thr-Leu-Val-Thr-Val-Ser- Z_4 로 이루어진 FR4 영역, 여기서 X_4 는 Trp 또는 Arg이고, Y_4 는 Gln 또는 Pro이고, Z_4 는 Ser 또는 Asn임

을 포함하는 것인 항체 폴리펩티드.

청구항 9

제1항에 있어서, 제1 가변 도메인 및 Fc 도메인을 포함하는 융합 폴리펩티드인 항체 폴리펩티드.

청구항 10

제9항에 있어서, 서열 1286인 BMS3h-56-269-IgG1* Fc 융합 폴리펩티드의 아미노산 서열로 이루어진 항체 폴리펩티드.

청구항 11

제9항에 있어서, 서열 1287인 BMS3h-56-269-IgG4 Fc 융합 폴리펩티드의 아미노산 서열로 이루어진 항체 폴리펩티드.

청구항 12

제1항 내지 제11항 중 어느 한 항에 있어서, 제2 항원에 특이적으로 결합하는 제2 가변 도메인을 추가로 포함하고, 여기서 제2 항원은 인간 CD40 이외의 항원인 항체 폴리펩티드.

청구항 13

제1항 내지 제11항 중 어느 한 항의 항체 폴리펩티드를 코딩하는 핵산.

청구항 14

제13항의 핵산을 포함하는 단리된 숙주 세포.

청구항 15

삭제

청구항 16

삭제

청구항 17

삭제

청구항 18

삭제

청구항 19

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청구항 31

삭제

청구항 32

삭제

발명의 설명

기술 분야

[0001] 기술 분야

[0002] CD40을 표적으로 하고 CD40 효능제 활성을 나타내지 않는 항체 및 이의 단편, 이를 포함하는 조성물, 및 CD40 활성 관련 질환의 치료를 위해 이를 사용하는 방법이 제공된다.

[0003] 관련 출원에 대한 상호 참조

[0004] 본 출원은 2011년 4월 21일자로 출원된 미국 가출원 번호 61/477,904를 우선권으로 청구하고, 이의 전체 내용은 본원에 참고로 포함된다.

[0005] 서열 목록

[0006] 본 출원은 ASCII 양식의 서열 목록을 포함하고, 전문이 본원에 참고로 포함된다. 2012년 4월 20일에 생성된 상기 ASCII 카피의 명칭은 200896W0.txt이고, 크기는 1,188,533 바이트이다.

배경 기술

[0007] CD40은 수지상 세포, B 세포 및 대식세포가 포함되는 항원 제시 세포 (APC) 상에 존재하는 종양 괴사 인자 (TNF) 수용체 슈퍼패밀리에 속하는 공동-자극 분자이다. CD40이 T_H 세포 상의 이의 리간드인 CD154 (CD40L)에

결합할 때 APC가 활성화된다. 시토카인 생산, 공동 자극 분자 (예컨대 CD86)의 상향-조절, 및 강화된 항원 제시 및 B 세포 증식이 포함되는 다양한 면역 반응에서 CD40-매개 APC 활성화가 수반된다. CD40은 내피 세포, 평활근 세포, 섬유모세포 및 상피 세포에 의해 또한 발현될 수 있다.

- [0008] 예를 들어 자가면역, 이식 거부 또는 알레르기 반응에 관련된 다양한 바람직하지 않은 T 세포 반응에서 CD40 활성화가 또한 수반된다. 바람직하지 않은 T 세포 반응을 제어하기 위한 한가지 전략은 CD40을 길항성 항체로 표적화하는 것이다. 예를 들어, 기존에 카이론(Chiron) 1212로 공지된 모노클로날 항체 HCD122 (루카투무맙 (Lucatumumab))가 현재 특정 CD40-매개 염증성 질환의 치료를 위해 임상 시험 중이다. 하이퍼텍스트 전송 프로토콜 clinicaltrialsfeeds.org/clinical-trials/show/NCT01275209 (최종 업데이트: 2011년 1월 11일)의 인터넷 상의 문헌 ["Study of HCD122 (Lucatumumab) and Bendamustine Combination Therapy in CD40⁺ Rituximab-Refractory Follicular Lymphoma", Clinical Trials Feeds] 참조. 그러나, 모노클로날 항체는 효능제 활성을 나타낼 수 있다. 예를 들어, 항-CD40 항체 Chi220의 유용성이 이의 약한 자극 잠재력에 의해 제한된다. 문헌 [Adams, et al., "Development of a chimeric anti-CD40 monoclonal antibody that synergizes with LEA29Y to prolong islet allograft survival", J. Immunol. 174: 542-50 (2005)] 참조.

발명의 내용

- [0009] 개요
- [0010] 부분적인 효능제 활성을 보유하지 않는 항-CD40 항체 길항제가 임상 환경에서 여전히 요구된다. 인간 CD40의 신규 에피토프에 특이적으로 결합하는 신규 항체 폴리펩티드가 제공된다. 이러한 CD40 에피토프는 경쟁 분석 및 항체 폴리펩티드와 CD40의 공동-결정화로부터 유래된 구조에 의해 제시되는 바와 같이 Chi220 에피토프와 중복되지 않는다. 이러한 항체 폴리펩티드는 유리하게는 CD40 효능제 활성을 나타내지 않는다. 이러한 항체 폴리펩티드는 자가면역 질환, 이식 거부, 및 알레르기 반응이 포함되는, CD40 활성화를 수반하는 질환의 치료에서 유용하다. 이러한 항체 폴리펩티드는 가변 도메인을 포함한다. 한 실시양태에서, 이러한 항체 폴리펩티드는 단일 가변 도메인을 함유하는 도메인 항체 (dAb)의 형태이다. 또 다른 실시양태에서, 이러한 dAb는 예를 들어 인간 혈청 알부민 (HSA)에 결합할 수 있는 제2 가변 도메인을 포함하는 이중특이적 시약이다.
- [0011] 제1 가변 도메인을 포함하는 항체 폴리펩티드로서, 상기 항체 폴리펩티드가 인간 CD40의 에피토프에 특이적으로 결합하며, 에피토프가 서열 1의 아미노산 서열을 포함하고, 상기 항체 폴리펩티드가 도메인 항체 (dAb) BMS3h-56-269 (서열 417)의 결합과 경쟁하며, 에피토프가 Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, 및 His162로 이루어진 군으로부터 선택된 하나 이상의 CD40 아미노산 잔기를 포함하는 것인, 항체 폴리펩티드가 제공된다.
- [0012] 제1 가변 도메인이 BMS3h-37, BMS3h-38, BMS3h-56, 및 BMS3h-198로 이루어진 계통 군으로부터 선택된 항체 폴리펩티드 중 하나의 아미노산 서열을 포함하고, 제1 가변 도메인의 겔보기 결합 상수가 1 pM 내지 100 nM인 항체 폴리펩티드가 추가로 제공된다. 제1 가변 도메인의 겔보기 결합 상수가 1 pM 내지 10 nM인 항체 폴리펩티드가 추가로 제공된다.
- [0013] 제1 가변 도메인의 아미노산 서열이 (a) BMS3h-56-269 (서열 417)의 CDR1 영역과 2개 이하의 아미노산만큼 상이한 CDR1 영역, (b) BMS3h-56-269 (서열 417)의 CDR2 영역과 2개 이하의 아미노산만큼 상이한 CDR2 영역, (c) BMS3h-56-269 (서열 417)의 CDR3 영역과 2개 이하의 아미노산만큼 상이한 CDR3 영역, (d) BMS3h-56-269 (서열 417)의 FR1 영역과 2개 이하의 아미노산만큼 상이한 FR1 영역, (e) BMS3h-56-269 (서열 417)의 FR2 영역과 2개 이하의 아미노산만큼 상이한 FR2 영역, (f) BMS3h-56-269 (서열 417)의 FR3 영역과 2개 이하의 아미노산만큼 상이한 FR3 영역, 및 (g) BMS3h-56-269 (서열 417)의 FR4 영역과 2개 이하의 아미노산만큼 상이한 FR4 영역을 포함하는 것인 항체 폴리펩티드가 또한 제공된다.
- [0014] 제1 가변 도메인의 아미노산 서열이 (a) BMS3h-56-269 (서열 417)의 CDR1 영역과 2개 이하의 아미노산만큼 상이한 CDR1 영역, (b) BMS3h-56-269 (서열 417)의 CDR2 영역과 2개 이하의 아미노산만큼 상이한 CDR2 영역, (c) BMS3h-56-269 (서열 417)의 CDR3 영역과 2개 이하의 아미노산만큼 상이한 CDR3 영역을 포함하는 것인 항체 폴리펩티드가 또한 제공된다.
- [0015] 제1 가변 도메인의 아미노산 서열이 BMS3h-56-258 (서열 10) 또는 BMS3h-56-269 (서열 417)의 아미노산 서열과 10개 이하의 아미노산만큼 상이한 것인 항체 폴리펩티드가 추가로 제공된다.
- [0016] 제1 가변 도메인의 아미노산 서열이 BMS3h-56-258 (서열 10) 또는 BMS3h-56-269 (서열 417)의 아미노산 서열과

5개 이하의 아미노산만큼 상이한 것인 항체 폴리펩티드가 추가로 제공된다.

- [0017] 제1 가변 도메인의 아미노산 서열이 BMS3h-56-258 (서열 10) 또는 BMS3h-56-269 (서열 417)의 아미노산 서열과 2개의 아미노산만큼 상이한 것인 항체 폴리펩티드가 추가로 제공된다.
- [0018] 제1 가변 도메인의 아미노산 서열이 BMS3h-56-258 (서열 10) 또는 BMS3h-56-269 (서열 417)의 아미노산 서열과 1개의 아미노산만큼 상이한 것인 항체 폴리펩티드가 추가로 제공된다.
- [0019] 항체 폴리펩티드가 BMS3h-56의 계통 군으로부터 선택되고, 제1 가변 도메인의 아미노산 서열이 (a) 서열 X_1 -Tyr-Glu- Y_1 -Trp (서열 1274) [식 중, X_1 은 Asp 또는 Gly이고, Y_1 은 Met 또는 Leu이다]을 갖는 CDR1 영역; (b) 서열 Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 - Z_2 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly (서열 1275) [식 중, X_2 는 Gln, Tyr, Pro, Trp, 또는 Ala이고, Y_2 는 Thr, Ser, Asn, Gly, Met, 또는 Gln이고, Z_2 는 Arg, Leu, Tyr, His, 또는 Phe이며, A_2 는 Lys 또는 Met이다]을 갖는 CDR2 영역; 및 (c) 서열 X_3 -Pro- Y_3 - Z_3 -Phe- A_3 - B_3 (서열 1276) [식 중, X_3 은 Leu 또는 Pro이고, Y_3 은 Phe, Gln, Thr, 또는 Met이고, Z_3 은 Tyr, Pro, Leu, Thr, Ile, Phe, 또는 Met이고, A_3 은 Gln, His, Asp, Ser, Lys, Glu, 또는 Gly이며, B_3 은 Glu, Asp, 또는 Tyr이다]을 갖는 CDR3 영역을 추가로 포함하는 것인 항체 폴리펩티드가 추가로 제공된다.
- [0020] 제1 가변 도메인의 아미노산 서열이 (a) 서열 Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly--Leu-Val-Gln-Pro-Gly-Gly-Ser- X_1 -Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe- Y_1 (서열 1277) [식 중, X_1 은 Leu 또는 Arg이고, Y_1 은 Arg 또는 Ala이다]을 갖는 FR1 영역; (b) 서열 Trp-Val-Arg- X_2 -Ala-Pro-Gly- Y_2 - Z_2 -Leu-Glu-Arg-Val-Ser (서열 1278) [식 중, X_2 는 Gln 또는 Arg이고, Y_2 는 Lys 또는 Arg이며, Z_2 는 Gly 또는 Val이다]을 갖는 FR2 영역; (c) 서열 Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn- X_3 -Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala- Y_3 -Asp-Thr- Z_3 -Val-Tyr- A_3 -Cys- B_3 -Lys (서열 1279) [식 중, X_3 은 Thr 또는 Met이고, Y_3 은 Glu 또는 Asp이고, Z_3 은 Ala 또는 Ser이고, A_3 은 Tyr 또는 His이며, B_3 은 Ala 또는 Thr이다]을 갖는 FR3 영역; 및 (d) 서열 X_4 -Gly- Y_4 -Gly-Thr-Leu-Val-Thr-Val-Ser- Z_4 (서열 1280) [식 중, X_4 는 Trp 또는 Arg이고, Y_4 는 Gln 또는 Pro이며, Z_4 는 Ser 또는 Asn이다]을 갖는 FR4 영역을 포함하는 것인 항체 폴리펩티드가 추가로 제공된다.
- [0021] 제1 가변 도메인이 BMS3h-56-258 (서열 10) 또는 BMS3h-56-269 (서열 417)의 아미노산 서열을 포함하는 것인 항체 폴리펩티드가 추가로 제공된다.
- [0022] 항체 폴리펩티드가 BMS3h-37의 계통 군으로부터 선택되고, 제1 가변 도메인이 서열
Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val- X_1 -Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-
Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Glu-Trp-Tyr-Glu-Met-Gln-Trp-Val-Arg-Arg-Ala-Pro-Gly-
Lys-Gly-Leu-Glu-Trp-Val-Ser-Ala-Ile-Ser-Gly-Asp-Gly-Tyr-Arg-Thr-Tyr-Tyr-Ala-Asp-Ser-
Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-
Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-Lys- Y_1 -Leu- Z_1 - A_1 -Phe-Asp-
Tyr- B_1 -Gly-Arg-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser
- [0023]
- [0024] (서열 1281) [식 중, X_1 은 Gln 또는 Arg이고; Y_1 은 Glu 또는 Gly이고; Z_1 은 Ala, Leu, 또는 Glu이고; A_1 은 Phe 또는 Tyr이며; B_1 은 Trp 또는 Arg이다]을 포함하는 것인 항체 폴리펩티드가 추가로 제공된다.
- [0025] 항체 폴리펩티드가 BMS3h-38의 계통 군으로부터 선택되고, 제1 가변 도메인이 서열
Glu-Val-Gln-Leu-Leu-Ala-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-
Cys-Ala-Ala-Ser-Gly-Phe- X_1 -Phe-Glu-Glu-Glu-Glu-Met-Ile-Trp-Val-Arg-Gln-Ala-Pro-Gly-
Lys-Gly-Leu-Glu-Trp-Val-Ser- Y_1 -Ile-Ser- Z_1 - A_1 -Gly- B_1 - C_1 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val-
Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-
Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Gly-Lys-Glu-Pro-Phe- D_1 -Tyr-Asp-Tyr-Trp-
Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser
- [0026]

- [0027] (서열 1282) [식 중, X₁은 Thr 또는 Pro이고; Y₁은 Ala 또는 Ser이고; Z₁은 Arg 또는 Gly이고; A₁은 Arg, Ser, Asn, Gln, Gly, His, 또는 Leu이고; B₁은 Tyr, Phe, Trp, 또는 Gly이고; C₁은 Ser 또는 Gly이며; D₁은 Arg, Met, 또는 Pro이다]을 포함하는 것인 항체 폴리펩티드가 또한 제공된다.
- [0028] 항체 폴리펩티드가 BMS3h-198의 계통 군으로부터 선택되고, 제1 가변 도메인이 서열
Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-
Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Ala-Gly-Trp-Glu-X₁-Trp-Trp-Y₁-Arg-Gln-Ala-Pro-Gly-
Lys-Gly-Leu-Glu-Arg-Val-Ser-Ala-Ile-Ser-Gly-Ser-Gly-Gly-Ser-Thr-Tyr-Tyr-Ala-Asp-Ser-
Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Z₁-A₁-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-
Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-B₁-Cys-Ala-C₁-D₁-Pro-Tyr-Ser-E₁-Asp-Tyr-F₁-
G₁-H₁-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser
- [0029]
- [0030] (서열 1283) [식 중, X₁은 Met 또는 Leu이고; Y₁은 Val 또는 Phe이고; Z₁은 Asp 또는 Asn이고; A₁은 Ser 또는 Thr이고; B₁은 Tyr 또는 His이고; C₁은 Lys 또는 Arg이고; D₁은 Asp 또는 Glu이고; E₁은 Tyr 또는 Phe이고; F₁은 Trp 또는 Arg이고; G₁은 Gly 또는 Arg이며; H₁은 Gln 또는 His이다]을 포함하는 것인 항체 폴리펩티드가 또한 제공된다.
- [0031] 도메인 항체 (dAb)인 항체 폴리펩티드가 추가로 제공된다.
- [0032] 가변 도메인이 Fc 도메인에 융합된 항체 폴리펩티드가 추가로 제공된다.
- [0033] 제2 항원에 특이적으로 결합하는 제2 가변 도메인을 추가로 포함하고, 여기서 제2 항원은 인간 CD40 이외의 항원인 항체 폴리펩티드가 추가로 제공된다.
- [0034] 제2 항원이 분화 클러스터 (CD) 분자 또는 주요 조직적합성 복합체 (MHC) 클래스 II 분자인 항체 폴리펩티드가 또한 제공된다.
- [0035] 제2 항원이 혈청 알부민 (SA)인 항체 폴리펩티드가 또한 제공된다.
- [0036] 본원에 개시된 항체 폴리펩티드를 코딩하는 핵산이 제공된다.
- [0037] 본원에 개시된 핵산을 포함하는 벡터가 또한 제공된다.
- [0038] 본원에 개시된 벡터를 포함하는 숙주 세포가 또한 제공된다.
- [0039] 치료 유효량의 본원에 개시된 항체 폴리펩티드 및 제약상 허용되는 담체를 포함하는 제약 조성물이 제공된다. 면역억제/면역조절제 및/또는 항염증제를 추가로 포함하는 제약 조성물이 또한 제공된다.
- [0040] 면역 질환의 치료를 필요로 하는 환자에게 치료 유효량의 본원에 개시된 제약 조성물을 투여하는 것을 포함하는, 상기 환자에서 면역 질환을 치료하는 방법이 제공된다. 이러한 제약 조성물을 면역억제/면역조절제 및/또는 항염증제와 조합하여 투여하는 방법이 또한 제공된다.
- [0041] 자가면역 질환 또는 이식-관련 질환인 면역 질환을 치료하는 방법이 제공된다. 애디슨병(Addison's disease), 알레르기, 강직성 척추염, 천식, 아테롬성동맥경화증, 귀의 자가면역 질환, 눈의 자가면역 질환, 자가면역 간염, 자가면역 이하선염, 결장염, 관상동맥 심장 질환, 크론병(Crohn's disease), 제1형 및/또는 제2형 당뇨병을 포함한 당뇨병, 부고환염, 사구체신염, 그레이브스병(Graves' disease), 길랑-바레 증후군(Guillain-Barre syndrome), 하시모토병(Hashimoto's disease), 용혈성 빈혈, 특발성 혈소판감소성 자반증, 염증성 장 질환, 재조합 약물 제품에 대한 면역 반응, 전신 홍반성 루푸스, 남성 불임증, 다발성 경화증, 중증 근무력증, 천포창, 건선, 류머티스성 열, 류머티스 관절염, 사르코이드증, 경피증, 쇼그렌 증후군(Sjogren's syndrome), 척추관절 병증, 갑상선염, 이식 거부, 혈관염, AIDS, 아토피성 알레르기, 기관지 천식, 습진, 나병, 정신분열병, 유전성 우울증, 조직 및 기관 이식, 만성 피로 증후군, 알츠하이머병(Alzheimer's disease), 파킨슨병(Parkinson's disease), 심근경색증, 졸증, 자폐증, 간질, 아르투스 현상(Arthus's phenomenon), 아나필락시스, 알콜 중독, 및 약물 중독으로 이루어진 군으로부터 선택되는 면역 질환을 치료하는 방법이 추가로 제공된다.
- [0042] 서열 1의 아미노산 서열을 포함하는 인간 CD40의 에피토프에 특이적으로 결합하는 제1 가변 도메인을 사용하여 CD40을 표적화하는 방법이며, 이때 항체 폴리펩티드가 도메인 항체 (dAb) BMS3h-56-269 (서열 417)의 결합과 경

쟁하는 것인 방법이 또한 제공된다.

[0043] 서열 1의 아미노산 서열을 포함하는 인간 CD40의 에피토프에 특이적으로 결합하는 제1 가변 도메인을 포함하고, 도메인 항체 (dAb) BMS3h-56-201 (서열 9)의 결합과 경쟁하는 항체 폴리펩티드 또는 이의 제약상 허용되는 염의 의학에서의 용도가 제공된다.

[0044] 서열 1의 아미노산 서열을 포함하는 인간 CD40의 에피토프에 특이적으로 결합하는 제1 가변 도메인을 포함하고, 도메인 항체 (dAb) BMS3h-56-201 (서열 9)의 결합과 경쟁하는 항체 폴리펩티드 또는 이의 제약상 허용되는 염의 면역 질환의 치료용 약제의 제조에서의 용도가 제공된다. 일부 실시양태에서, 이러한 제약 조성물은 면역억제/면역조절제 및/또는 항염증제와 조합되어 투여된다. 추가적인 실시양태에서, 면역 질환은 자가면역 질환 또는 이식-관련 질환이다. 추가적인 실시양태에서, 면역 질환은 에디슨병, 알레르기, 강직성 척추염, 천식, 아테롬성동맥경화증, 귀의 자가면역 질환, 눈의 자가면역 질환, 자가면역 간염, 자가면역 이하선염, 결장염, 관상동맥 심장 질환, 크론병, 제1형 및/또는 제2형 당뇨병을 포함한 당뇨병, 부고환염, 사구체신염, 그레이브스병, 길랑-바레 증후군, 하시모토병, 용혈성 빈혈, 특발성 혈소판감소성 자반증, 염증성 장 질환, 재조합 약물 제품에 대한 면역 반응, 전신 홍반성 루푸스, 남성 불임증, 다발성 경화증, 중증 근무력증, 천포창, 건선, 류머티스성 열, 류머티스 관절염, 사르코이드증, 경피증, 쇼그렌 증후군, 척추관절병증, 갑상선염, 이식 거부, 혈관염, AIDS, 아토피성 알레르기, 기관지 천식, 습진, 나병, 정신분열병, 유전성 우울증, 조직 및 기관 이식, 만성 피로 증후군, 알츠하이머병, 파킨슨병, 심근경색증, 졸중, 자폐증, 간질, 아르투스 현상, 아나필락시스, 알콜 중독, 및 약물 중독으로 이루어진 군으로부터 선택된다.

[0045] 면역 질환의 치료용 약제의 제조에서 사용하기 위한, 서열 1의 아미노산 서열을 포함하는 인간 CD40의 에피토프에 특이적으로 결합하는 제1 가변 도메인을 포함하고, 도메인 항체 (dAb) BMS3h-56-201 (서열 9)의 결합과 경쟁하는 항체 폴리펩티드 또는 이의 제약상 허용되는 염이 제공된다. 이러한 약제는, 예를 들어, 면역억제/면역조절제 및/또는 항염증제와 조합되어 투여될 수 있다. 면역 질환은, 예를 들어, 자가면역 질환 또는 이식-관련 질환일 수 있다. 면역 질환은 에디슨병, 알레르기, 강직성 척추염, 천식, 아테롬성동맥경화증, 귀의 자가면역 질환, 눈의 자가면역 질환, 자가면역 간염, 자가면역 이하선염, 결장염, 관상동맥 심장 질환, 크론병, 제1형 및/또는 제2형 당뇨병을 포함한 당뇨병, 부고환염, 사구체신염, 그레이브스병, 길랑-바레 증후군, 하시모토병, 용혈성 빈혈, 특발성 혈소판감소성 자반증, 염증성 장 질환, 재조합 약물 제품에 대한 면역 반응, 전신 홍반성 루푸스, 남성 불임증, 다발성 경화증, 중증 근무력증, 천포창, 건선, 류머티스성 열, 류머티스 관절염, 사르코이드증, 경피증, 쇼그렌 증후군, 척추관절병증, 갑상선염, 이식 거부, 혈관염, AIDS, 아토피성 알레르기, 기관지 천식, 습진, 나병, 정신분열병, 유전성 우울증, 조직 및 기관 이식, 만성 피로 증후군, 알츠하이머병, 파킨슨병, 심근경색증, 졸중, 자폐증, 간질, 아르투스 현상, 아나필락시스, 알콜 중독, 및 약물 중독으로 이루어진 군으로부터 또한 선택될 수 있다.

도면의 간단한 설명

[0046] 특허 또는 출원 파일은 하나 이상의 컬러 도면을 함유한다. 요청 및 필요한 비용의 지불 시 컬러 도면(들)이 있는 이러한 특허 또는 특허 출원 공보의 사본이 특허청에서 제공될 것이다.

도 1은, 하나는 dAb BMS3h-56-5 (서열 321)와의 것이고, 하나는 Chi220 항체의 Fab'와의 것인, 인간 CD40 (서열 1)의 2가지 상이한 공동-결정 구조의 결합 양식을 도해한다. β -가닥 (dAb에서 화살표로 표시됨) 및 비-반복적 2차 구조 (dAb에서 루프로 표시됨)와 함께 카툰으로서 BMS3h-56-5 및 Chi 220 Fab' 분자가 제시된다. 상보성 결정 영역 (CDR)이 또한 제시된다. 인간 CD40의 BMS3h-56-5 에피토프 잔기와 함께 카툰으로서 CD40이 또한 제시된다. Chi220 에피토프 잔기가 또한 제시된다. 디설피드 결합이 또한 제시된다. CD40의 N-말단 (N) 및 C-말단 (C)이 표시된다.

도 2는 인간 CD40 (서열 1)과 접촉 중인 BMS3h-56-5 (서열 321)의 공간 채움 모델을 도해하고, 이는 카툰으로 제시된다. CD40과 접촉한 dAb BMS3h-56-5의 표면 잔기가 제시된다. BMS3h-56-5 CDR3 영역 및 FR-2 잔기 Leu45, Arg47, Arg56 및 Phe99가 표시된다. 카바트(Kabat) 넘버링 (문헌 [Kabat et al., Sequences of Immunological Interest, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)])이 이러한 도식에서 사용되고, 이는 β -가닥의 잔기 넘버링을 동일하게 유지하기 위해 삽입 잔기가 사용된다는 점에서 순차적인 넘버링과 상이하다. 따라서, BMS3h-56-5에 대해, 순차적인 잔기 53이 잔기 52A가 되고, 순차적인 잔기 84, 85 및 86은 각각 82A, 82B, 82C이 되며, 카바트 잔기 번호 100이 없다 (이는 순차적인 잔기 103과 104 사이에 있을 것이다); 비-반복적 2차 구조 및 BMS3h-56-5 에피토프와 함께 카툰으로서 CD40이 또한 제시된다. 인

간과 마카카 파시쿨라리스(*Macaca fascicularis*) (시노몰구스(*cynomolgus*) 원숭이) 사이에 상이한 CD40 잔기인 Ala115, Phe99, Ser126, His162, Leu121, 및 Trp109는 막대 표시로 제시된다. BMS3h-56-5 에피토프의 일부인, 인간과 시노몰구스 원숭이 사이에 상이한 CD40 잔기는 Trp109, Leu121, 및 His162이다. CD40 잔기 Trp109 및 Leu121은 BMS3h-56-5 CDR3과 FR-2 사이의 틈새에 놓인다. Trp109의 돌연변이는 BMS3h-56-5 활성을 크게 감소 시키거나 또는 폐지시킨다.

도 3은 인간 및 영장류 종으로부터의 혈액 샘플 상에서의 PEG화 항-인간 CD40 dAb인 BMS3h38-2C-P40Br의 결합을 도해한다. 도 3A는 인간 및 시노몰구스 B 세포에 대한 BMS3h38-2C-P40Br 결합을 나타내고, 도 3B는 인간, 레서스(rhesus), 및 침팬지 B 세포에 대한 BMS3h38-2C-P40Br 결합을 나타낸다.

도 4, 도 5, 도 6, 및 도 7은 각각 BMS3h-56, BMS3h-37, BMS3h-38, 및 BMS3h-198 계통으로부터의 대표적인 도메인 항체 폴리펩티드들의 ClustalW2 정렬을 나타낸다.

발명을 실시하기 위한 구체적인 내용

- [0047] 인간 CD40에 특이적으로 결합하는 항체 폴리펩티드가 제공된다. 이러한 항체 폴리펩티드는 CD40 효능제 활성을 나타내지 않고, 이러한 항체 폴리펩티드는 CD40 활성화를 수반하는 질환, 예컨대 자가면역 질환의 치료에서 유용하다. 세포 결합 검정을 이용하는 1차 스크린에 이어지는 1회 이상의 오차-경향(error-prone) 또는 축중성 올리고뉴클레오티드-지향성 친화도 성숙 라운드를 사용하여 이러한 항체 폴리펩티드를 선별할 수 있다. 결과적으로, 단일 CD40 에피토프에 특이적으로 결합하는 항체 폴리펩티드 부류가 제공된다.
- [0048] "계통"은 하기 실시예에 개시된 바와 같이 오차-경향 또는 축중성 올리고뉴클레오티드-지향성 친화도 성숙에 의해 공통적인 전구물질로부터 제조되었고 동일한 CD40 에피토프에 결합할 것으로 예상되는 관련된 항체 폴리펩티드들의 세트이다. 다양한 계통을 지정하는데 항체 폴리펩티드의 호칭이 사용된다. 예를 들어, "BMS3h-56"라는 호칭은 인간 CD40에 대해 생성된, 계통 56의 항체 폴리펩티드들을 지칭한다. "계통 BMS3h-56" 항체 폴리펩티드는 BMS3h-56-1 내지 BMS3h-56-33, 및 BMS3h-56-202 내지 BMS3h-56-288을 포함한다.
- [0049] 따라서, 한 측면에서, 항체 폴리펩티드가 인간 CD40에 특이적으로 결합하는 가변 도메인을 포함하고, 이때 이러한 항체 폴리펩티드는 표 3에 열거된 도메인 항체 (dAb) 중 어느 하나의 결합과 경쟁한다. 예를 들어, 이러한 dAb는, 예를 들어 dAb BMS3h-56-5, BMS3h-56-201, 또는 BMS3h-56-258과 같이, BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198, 및 BMS3h-202로 이루어진 군으로부터 선택된 계통에 속할 수 있다. 또 다른 측면에서, 항체 폴리펩티드가 표 3에 열거된 dAb 중 어느 하나와 동일한 인간 CD40 에피토프에 특이적으로 결합한다. 예를 들어, 이러한 항체 폴리펩티드는 예를 들어 dAb BMS3h-56-5, BMS3h-56-201, 또는 BMS3h-56-258과 동일한 인간 CD40 에피토프에 특이적으로 결합하는 가변 도메인을 포함할 수 있다. 하기 개시된 바와 같이, 이러한 인간 CD40 에피토프는 예를 들어 서열 1의 아미노산 잔기 Trp109를 포함할 수 있다.
- [0050] 항체 폴리펩티드는 단일 가변 도메인을 함유하는 도메인 항체일 수 있다. 항체 폴리펩티드는 추가적인 도메인, 예컨대 Fc 도메인을 또한 포함할 수 있다. 예를 들어, 항체 폴리펩티드는 인간 혈청 알부민 (HSA)에 특이적으로 결합하는 제2 가변 도메인을 포함할 수 있다. 이같은 이중 특이적 항체 폴리펩티드는 예를 들어 반감기가 증가될 수 있다.
- [0051] 서열 목록에서, 서열 1은 인간 CD40의 아미노산 서열이고; 서열 2는 마카카 파시쿨라리스 CD40의 아미노산 서열이다. 도메인 항체 BMS3h-56-5의 아미노산 서열은 서열 321이다.
- [0052] 본원에서 사용된 바와 같이, "특이적 결합"은 예를 들어 표면 플라즈몬 공명으로 측정 시 약 1 μ M 이하의 해리 상수 (K_d)로 항체 폴리펩티드가 항원에 결합하는 것을 지칭한다. 적절한 검정 시스템에는 비아코어(BIAcore)TM 표면 플라즈몬 공명 시스템 및 비아코어TM 동역학 평가 소프트웨어 (예를 들어, 버전 2.1)가 포함된다. 특이적 결합 상호작용에 대한 친화도 또는 K_d 는 약 500 nM 이하 또는 약 300 nM 이하일 수 있다.
- [0053] 당업자는 "약"이라는 용어를 이해할 것이고, 이는 자신이 사용되는 문맥에 따라 어느 정도 변할 것이다. 일반적으로, 약은 언급된 값의 플러스/마이너스 10%인 값의 범위를 포함한다.
- [0054] 이러한 상세한 설명에 따라, 하기의 약어 및 정의가 적용된다. 본원에서 사용되는 경우에, 문맥적으로 명확하게 달리 지시되지 않는 한 단수형 형태 ("a", "an", 및 "the")가 복수의 지시 대상을 포함한다는 것을 주지하여야 한다. 따라서, 예를 들어, "항체(an antibody)"에 대한 언급은 다수의 이같은 항체를 포함하고, "투여량(the dosage)"에 대한 언급은 1회 이상의 투여량 및 당업자에게 공지된 이의 등가물에 대한 언급을 포함하는 것

등이다.

1. CD40 및 CD40 활성

인간 CD40에 결합하는 항체 폴리펩티드가 제공된다. CD40은 B-세포 표면 항원 CD40, Bp50, CD40L 수용체, CDw40, CDW40, MGC9013, p50, TNFRSF5, 및 중앙 피사 인자 수용체 슈퍼패밀리 구성원 5로 또한 공지되어 있다. 인간 CD40에 대한 관련된 구조 정보를, 예를 들어, 유니프롯(UniProt) 접속 번호 P25942, Q9BYU0, 및 Q53GN5에서 확인할 수 있다. "인간 CD40"은 하기 아미노산 서열을 포함하는 CD40을 지칭한다:

```
MVRLPLQCVL WGCLLTAVHP EPPTACREKQ YLINSQCCSL CQPGQKLVSD
CTEFTETECL PCGESEFLDT WNRETHCHQH KYCDNLGLR VQQKGTSETD
TICTCEEGWH CTSEACESCV LHRSCSPGFG VKQIATGVSD TICEPCPVGF
FSNVSSAFEK CHEWTSCEK DLVVQAGTN KTDVVCGPQD RLRALVVIPI
IFGILFAILL VLVFIKKVAK KPTNKAPHEK QEPQEINFPD DLPGSNTAAP
VQETLHGCQF VTQEDGKESR ISVQERQ (서열 1).
```

무스 무스쿨루스(*Mus musculus*), 수스 스크로파(*Sus scrofa*), 보스 타우루스(*Bos taurus*), 갈루스 갈루스(*Gallus gallus*), 카니스 파밀리아리스(*Canis familiaris*), 마카카 파시쿨라리스(시노몰구스 원숭이), 오비스 아리에스(*Ovis aries*), 에쿠우스 카발루스(*Equus caballus*), 및 라투스 노르베기쿠스(*Rattus norvegicus*)에서 또한 CD40의 서열을 분석할 수 있다.

본 발명의 항체 폴리펩티드가 CD40에 결합하는 것은 CD40 활성을 길항한다. "CD40 활성"에는 T 세포 활성화(예를 들어, T 세포 증식 또는 시토카인 분비의 유도), 대식세포 활성화(예를 들어, 대식 세포 내의 반응성 산소 종 및 산화질소의 유도), 및 B 세포 활성화(예를 들어, B 세포 증식, 항체 이소형(isotype) 전환, 또는 형질 세포로의 분화)가 포함되지만, 이에 한정되지는 않는다. 다른 분자와의 상호작용에 의해 CD40 활성이 매개될 수 있다. "CD40 활성"에는 CD40과 하기 분자들(괄호 안의 유니프롯 접속 번호로 확인됨) 사이의 기능성 상호작용이 포함된다:

CALR	(P27797);
ERP44	(Q9BS26);
FBL	(P22087);
POLR2H	(P52434);
RFC5	(P40937);
SGK1	(O00141);
SLC30A7	(Q8NEW0);
SLC39A7	(Q92504);
TRAF2	(Q5T1L5);
TRAF3	(Q13114);
TRAF6	(Q9Y4K3);
TXN	(Q5T937);
UGGT1	(Q9NYU2); 및
USP15	(Q9Y4E8).

예를 들어, TRAF2와의 상호작용이 CD40 "활성"에 포함된다. CD40/TRAF2 상호작용은 NF- κ B 및 JNK를 활성화시킨다. 문헌 [Davies et al., Mol. Cell Biol. 25: 9806-19 (2005)] 참조. 따라서, 이러한 CD40 활성화, 기준물과 비교하여, CD40-의존적 세포성 NF- κ B 및 JNK 활성화에 의해 결정될 수 있다.

본원에서 사용되는 바와 같이, "활성화한다", 및 "활성화된"이라는 용어는 기준물과 비교하여 적어도 10%, 예를 들어 적어도 10%, 25%, 50%, 75%, 또는 심지어 100%, 또는 이를 초과하는 값만큼의 소정의 측정가능한 CD40 활성의 증가를 지칭한다. 길항제의 부재와 비교하여 활성이 적어도 10% 만큼, 예시적인 실시양태의 경우 적어도 약 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, 또는 심지어 100% (즉, 검출가능한 활성이 없음) 만큼 감소되면, CD40 활성이 "길항된다". 예를 들어, 항체 폴리펩티드가 CD40 활성을 활성화하지 않으면서 일부 또는 모든 CD40 활성을 길항할 수 있다. 한 실시양태에서, 항체 폴리펩티드는 B 세포 증식을 활성화하지 않는다. 또 다른 실시양태에서, 항체 폴리펩티드는 IL-2, IL-6, IL-10, IL-13, TNF- α , IFN- γ 로 이루어진 군으로부터 선택된 하나 이상의 시토카인의 T 세포에 의한 분비를 활성화하지 않는다.

2. CD40 에피토프

인간 CD40 (서열 1)과 dAb BMS3h-56-5 (서열 321) 사이의 복합체의 X-선 결정학을 사용하여 본 개시내용의 항체 폴리펩티드가 인식하는 에피토프를 밝혀냈다. CD40 및 BMS3h-56-5의 구조 모델을 전자 밀도 데이터에 피팅(fitting)하여, 1개의 결정 형태의 결정학적으로 독립적인 복합체 3개 및 제2 결정 형태의 결정학적으로 독립적인 복합체 4개로부터 유래되는 CD40/BMS3h-56-5 복합체의 7개의 모델 또는 버전이 산출되었다. 이러한 버전들은 주쇄 원자에 대한 실제 공간 상관 계수가 약 0.92이고, 측쇄 원자에 대해서는 0.80이다. 7개의 버전에서 CD40 분자에 특정량의 유연성이 있지만, CD40/BMS3h-56-5 상호작용의 전반적인 성질이 모든 버전에서 유지된다. 이러한 버전들은 CD40 잔기 Trp109 및 BMS3h-56-5 Trp103 사이의 상호작용에서 상이하다 (카바트 넘버링, 하기

참조). 1개의 버전에서는 BMS3h-56-5 Trp103이 CD40 Trp109와 가장자리-대-면(edge-to-face) 상호작용을 형성하는 한편, 나머지 버전들에서는 전치 적층(displaced stacking) (즉, 면-대-면(face-to-face)) 상호작용을 형성한다.

[0065] 7가지 버전에 대한 형상 상보성 통계 (Sc)는 0.70 - 0.77 범위이고, 이는 전형적인 항체/항원 복합체보다 더 높은 정도의 형상 상보성을 나타낸다. 예를 들어, 이러한 값들은 4개의 프로테아제/단백질 억제제 복합체에 대한 0.71 - 0.76, 5개의 올리고머성 계면에 대한 0.70 - 0.74, 및 6개의 항체/항원 복합체에 대한 0.64 - 0.68의 범위에 필적한다. 문헌 [Lawrence et al., "Shape Complementarity at Protein/Protein Interfaces", J. Mol. Biol. 234: 946-950 (1993)] 참조.

[0066] 인간 CD40/BMS3H-56-5 복합체의 모델이 도 1에서 제시된다. 1개의 BMS3h-56-5 dAb가 1개의 CD40 분자에 결합한다. BMS3h-56-5 에피토프는 Chi220 Fab' 단편 에피토프와 중복되지 않는다. 모든 버전의 복합체에서 BMS3h-56-5와 접촉하는 CD40 잔기들의 세트가 규정된다: Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, 및 His162 (서열 1 기준). 복합체의 일부 버전에서 BMS3h-56-5와 접촉하는 CD40 잔기는 Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, 및 Lys160이다. Val154는 모든 버전에서 매립 CD40 잔기이다. 일부 버전에서의 매립된 기타 CD40 잔기는 Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, 및 Pro163이다.

[0067] 본원에서 사용된 바와 같이, "~와 접촉 중인"이라는 용어는 문헌 [Sheriff et al., J. Mol. Biol. 197: 273-296 (1987)] 및 [Sheriff, Immunomethods 3: 191-196 (1993)]에 의해 정의된 바와 같은 원자 유형 거리 의존성에 의해 최대값이 결정되는 원자간 거리를 지칭한다.

[0068] 본원에서 사용된 바와 같이, "매립"이라는 용어는 프로그램 MS (문헌 [Connolly, J. Appl. Crystallogr. 16: 548-558 (1983)])에 의해 정의되는 표면적, 1.7Å의 프로브 구체, 및 문헌 [Sheriff, Immunomethods 3: 191-196 (1993)]에 의해 정의된 바와 같은 원자 유형 의존적 반 데르 발스 직경의 원자가 1개 이상 있는 잔기를 지칭한다.

[0069] 도 2는 접촉 잔기 및 매립 잔기를 포함하는 BMS3h-56-5 (서열 321)의 표면을 나타낸다. 리본 도식으로 CD40 (서열 1)이 표시되고, 이때 주황색은 비-반복적 2차 구조를 나타내고, 마젠타색은 에피토프 잔기를 나타낸다. 제시된 CD40 잔기 Trp109, Ala115, Leu121, Ser126, 및 His162는 다양한 비-인간 영장류 서열에서 상이하다. CD40 잔기 Ala115 및 Ser126은 BMS3h-56-5 결합 부위의 반대쪽에 있다. BMS3h-56-5의 CDR3과 FR-2 (잔기 Leu45 및 Arg47) 사이에 놓인 틈새에서 Trp109 및 Leu121이 결합한다. His162는 BMS3h-56-5의 CDR2 내의 잔기들, 특히 Lys 56과 상호작용한다. 요약하면, 서열 1에서 사용된 넘버링을 참조로, 표 1에 열거된 하나 이상의 잔기를 CD40 에피토프가 포함한다.

표 1

BMS3h-56-5와 접촉하는 CD40 잔기:
Trp109, Leu121, His122, Ser124, Ser156,
Ala157, Phe158, Glu159, His162

[0070]

[0071] BMS3h-56-5를, 표 3에 열거된 다른 dAb들과 같이, 인간 CD40을 항원으로 사용하여 하기에 더욱 상세하게 기술된 스크리닝 및 친화도 성숙 방법에 의해 제조하였다. 공통적인 전구물질 dAb로부터 친화도 성숙에 의해 생성된 dAb들이 동일한 인간 CD40 에피토프에 결합할 것으로 예상된다. 예를 들어, 하기에 기술된 경쟁 연구는 공통적인 전구물질 dAb로부터 친화도 성숙에 의해 생성된 dAb들이 인간 CD40에 결합하는 것에 대해 서로 경쟁한다는 것을 나타낸다. 그러나, 이러한 dAb들이 적어도 Chi220 또는 G28-5 항체와는 경쟁하지 않는다는 것이 동일한 경쟁 연구에서 나타난다.

[0072] 3. 항체 폴리펩티드

[0073] 항체 폴리펩티드가 가변 도메인을 포함한다. 한 실시양태에서, 항체 폴리펩티드는 단일 가변 도메인을 함유하는 dAb 형태이다. 항체 폴리펩티드는 디설피드 결합에 의해 서로 연결된 2개의 중쇄 (H) 및 2개의 경쇄 (L)를 포함하는 전장 항-CD40 면역글로불린 분자일 수 있다. 이러한 실시양태에서, 각각의 사슬의 아미노 말단 부분은 내부에 함유된 상보성 결정 영역 (CDR)을 통해 항원 인식을 주로 담당하는 아미노산 약 100-110개의 가변 도

메인 (V_L 또는 V_H)을 포함한다. 각각의 중쇄의 카르복시-말단 "절반"은 이펙터 기능을 주로 담당하는 불변 영역 (Fc)을 규정한다.

[0074] 항체 폴리펩티드는 CD40에 특이적으로 결합하는 가변 도메인을 포함하는 전장 항-CD40 면역글로불린 분자의 일부분을 포함하는 "단편"일 수도 있다. 따라서, "항체 폴리펩티드"라는 용어에는, 예를 들어, 항원-결합 중쇄, 경쇄, 중쇄-경쇄 이량체, Fab 단편, $F(ab')_2$ 단편, Fv 단편, 단일쇄 Fv (scFv), 및 dAb가 포함된다. 따라서 "항체 폴리펩티드"라는 용어에는 제조합 조작 및 발현에 의해 제조된 폴리펩티드, 뿐만 아니라 하이브리도마 세포 클론에 의해 천연 제조합 및 분비에 의해 생산된 모노클로날 항체가 포함된다.

[0075] 업계에 공지된 바와 같이, 경쇄는 카파 (κ) 또는 람다 (λ)로 분류되고, 특정 불변 영역 C_L 을 특징으로 한다. 중쇄는 γ , μ , α , δ , 또는 ϵ 로 분류되고, 항체의 이소형을 각각 IgG, IgM, IgA, IgD, 또는 IgE로 규정한다. 중쇄 불변 영역은 IgG, IgD, 및 IgA의 경우에는 3개의 도메인 (CH1, CH2, 및 CH3)으로, IgM 및 IgE의 경우에는 4개의 도메인 (CH1, CH2, CH3, 및 CH4)으로 구성된다. 항-CD40 항체에는 임의의 면역글로불린 클래스 (IgA, IgD, IgG, IgM, 및 IgE)로부터 선택된 중쇄 불변 영역이 있을 수 있다.

[0076] 각각의 경쇄 가변 도메인 (V_L) 및 중쇄 가변 도메인 (V_H)은 아미노-말단에서 카르복시-말단으로 하기의 순서로 배열된 3개의 CDR 및 4개의 프레임워크 영역 (FR)으로 구성된다: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. 경쇄의 3개의 CDR은 "LCDR1, LCDR2, 및 LCDR3"으로 지칭되고, 중쇄의 3개의 CDR은 "HCDR1, HCDR2, 및 HCDR3"으로 지칭된다.

[0077] 본원에서 사용된 바와 같이, "Fc 도메인"이라는 용어는 문헌 [Kabat et al., Sequences of Immunological Interest, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)]에 따라 범위가 정해진 바와 같은 CH2 및 CH3 불변 도메인을 포함하는 불변 영역 항체 서열을 지칭한다. Fc 영역은, 예를 들어, IgG1 또는 IgG4 Fc 영역으로부터 유래될 수 있다. 가변 도메인이 Fc 도메인에 융합될 수 있다. 이러한 경우에, 가변 도메인 (dAb가 포함되는, V_L 또는 V_H 도메인)의 카르복실 말단이 Fc CH2 도메인의 아미노 말단에 연결 또는 융합될 수 있다. 대안적으로, 가변 도메인의 카르복실 말단이 CH1 도메인의 아미노 말단에 연결 또는 융합될 수 있고, CH1 도메인 자체는 Fc CH2 도메인에 융합된다. 단백질이 전체적으로 또는 부분적으로 CH1 도메인과 CH2 도메인 사이의 힌지(hinge) 영역을 포함할 수 있다.

[0078] CDR은 항원과의 특이적 상호작용을 형성하는 잔기의 대부분을 함유한다. 도 2에 제시된 바와 같이, 예를 들어, CDR2 및 CDR3 + FR4 잔기 Trp103이 CD40과 dAb BMS3h-56-5 사이의 접촉의 대부분을 형성한다. 예를 들어, 표 3에 열거된 dAb 중 하나의 CDR1, CDR2, 및 CDR3 영역과 아미노산 서열이 동일하거나 또는 각각 이러한 CDR1, CDR2, 및 CDR3 영역과 1개 또는 2개의 아미노산만큼 상이한 CDR1, CDR2, 및 CDR3 영역을 항체 폴리펩티드의 가변 도메인이 포함한다. 예를 들어, 항체 폴리펩티드가 예를 들어 BMS3h-56-5, BMS3h-56-258, 또는 BMS3h-56-201의 CDR1, CDR2, 및 CDR3 영역과 아미노산 서열이 동일한 CDR1, CDR2, 및 CDR3 영역을 포함할 수 있다.

[0079] "도메인 항체" (dAb)는 특이적으로 및 1가로 항원, 예컨대 CD40에 결합할 수 있는 단일 가변 (V_L 또는 V_H) 도메인을 포함한다. 예를 들어, dAb는 낙타류 dAb의 특성인 V_H 구조일 수 있다. 본원에서 사용된 바와 같은 " V_H 도메인"은 V_H 구조를 포함하도록 의도된다. 또 다른 실시양태에서, 본 발명의 V_H 도메인 (본원에서의 실시양태로서 제시된 모든 특색 및 특색들의 조합을 포함함)은 V_H 도메인 이외의 것이다. dAb는 용액 내에서 동종이량체 또는 이종이량체를 형성할 수 있다. 결합된 CD40 분자를 세포 표면 상에 가교시키는 능력으로 인해, 2가 항-CD40 항체는 효능제 활성을 나타낼 것으로 여겨진다. 임의의 특정 이론에 의해 제한되지 않으면서, 1가 dAb는 CD40을 활성화시키지 않는 것으로 여겨지는데, 이러한 dAb는 CD40을 가교시키지 않기 때문이다.

[0080] 본원에서 사용된 바와 같이, "가변 도메인"이라는 용어는 문헌 [Kabat et al., Sequences of Immunological Interest, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)]에서 정의된 면역글로불린 가변 도메인을 지칭한다. 가변 도메인 내의 CDR 아미노산 잔기의 넘버링 및 위치결정은 주지된 카바트 넘버링 합의에 따른다. 예를 들어, BMS3h-56-5 (서열 321)에 대한 카바트 넘버링이 표 2에서 순차적으로 넘버링된 동일한 서열에 비교된다. 카바트 넘버링에서, BMS3h-56-5는 삽입 잔기 52A, 82A, 82B, 82C가 있고, 잔기 100이 없다. 양쪽 넘버링 시스템에서, 발현 구축물의 일부본인 N-말단의 Ser 및 Thr은 음성 숫자로 제공된다.

변이체 가변 도메인이 하나 이상의 CDR 내에 1개 또는 2개의 아미노산 치환을 함유할 수 있다는 것이 추가로 제공된다. CD40에 특이적으로 결합하는 대표적인 가변 도메인이 표 3에서 열거된다.

[0088] BMS3h-56, BMS3h-37, BMS3h-38, 및 BMS3h-198 계통으로부터의 항체 폴리펩티드의 대표적인 가변 도메인들 간의 ClustalW2 정렬이 각각 도 4, 도 5, 도 6, 및 도 7에서 제시된다. 일반적인 규칙으로서, 관련된 단백질 서열들의 정렬에서 아미노산이 보존되는 정도는 단백질 기능에 대한 이러한 아미노산 위치의 상대적인 중요성에 비례한다. 즉, 모든 관련된 서열에서 공통적인 아미노산은 아마도 중요한 역할을 할 것이고, 쉽게 치환될 수 없다. 반면에, 서열들 간에 변하는 위치는 아마도 단백질의 활성을 유지하면서 다른 아미노산으로 치환될 수 있거나 또는 다른 방식으로 변형될 수 있다. 도 4, 도 5, 도 6, 및 도 7에 제시된 정렬 및 도 1 및 도 2로부터 규명되는 구조 관계는, 예를 들어, 서열 1의 아미노산 서열을 포함하는 인간 CD40의 에피토프에 특이적으로 결합하고, 이때 항체 폴리펩티드가 dAb BMS3h-56-201 (서열 9)의 결합과 경쟁하는 변이체 항체 폴리펩티드의 구축을 안내할 수 있다. 이같은 변이체 항체 폴리펩티드에는 표 3에 열거된 가변 도메인 중 임의의 것과 관련하여 치환, 삽입 또는 결실에 상응하는 아미노산 변형이 있는 것들이 포함되지만, 이에 한정되지는 않는다. 변이체 항체 폴리펩티드에는 표 3에 열거된 서열들 간에 보존되는 아미노산 변형에 상응하는 아미노산 변형이 있는 것들이 또한 포함된다.

[0089] 중쇄 및 경쇄 유전자의 V_L 또는 V_H 도메인의 경계에 관한 정보를 사용하여, CD40에 결합하는 것으로 공지된 항체 폴리펩티드를 코딩하는 클로닝된 중쇄 또는 경쇄 코딩 서열로부터 가변 도메인을 증폭하기 위한 PCR 프라이머를 디자인할 수 있다. 업계에 주지된 기술을 사용하여, 증폭된 가변 도메인을 적절한 발현 벡터, 예를 들어, pHEN-1 (문헌 [Hoogenboom et al. (1991) Nucleic Acids Res. 19:4133-4137]) 내로 삽입할 수 있고, 단독으로 또는 또 다른 폴리펩티드 서열과의 융합물로서 발현시킬 수 있다. 개시된 아미노산 및 폴리뉴클레오티드 서열을 기초로, 일상적인 방법인 기술을 사용하여 임의의 적절한 포유동물 숙주 세포주, 예컨대 CHO, 293, COS, NSO 등에 이어지는 단백질 A 친화도 크로마토그래피, 이온 교환, 역상 기술 등이 포함되는 방법 중 하나 또는 이의 조합을 사용하는 정제로 융합 단백질을 생산 및 정제할 수 있다.

[0090] 한 측면에서, 항체 폴리펩티드는 서열 1의 아미노산 서열을 포함하는 인간 CD40에 특이적으로 결합하는 제1 가변 도메인을 포함하는 "이중 특이적" 항체 폴리펩티드이다. 이중 특이적 항체 폴리펩티드는 인간 CD40 이외의 제2 항원에 특이적으로 결합하는 제2 가변 도메인을 포함한다.

[0091] 또 다른 실시양태에서, 예를 들어, 제2 항원은 면역 이펙터 세포의 세포 표면 분자, 또는 가용성 분자 예컨대 시토키닌일 수 있다. 이중 특이성 항체 폴리펩티드의 결합을 사용하여, CD40을 길항하고 제2 항원의 생물학적 활성을 길항할 수 있다. 면역 이펙터 세포의 세포 표면 분자에는 분화 클러스터 (CD) 분자가 포함된다. 대표적인 CD 마커들이 인터넷 하이퍼텍스트 전송 프로토콜 en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation (2012년 2월 22일에 최종적으로 수정됨)에서 열거되어 있다. 면역 이펙터 세포의 세포 표면 분자에는 주요 조직적합성 복합체 (MHC) 클래스 II 분자가 또한 포함된다. 이러한 세포 표면 분자들에 대한 항체가 업계에 공지되어 있고, 이중 특이적 항체 폴리펩티드를 구축하기 위한 가변 도메인의 공급원으로서 사용될 수 있다.

[0092] 한 실시양태에서, 이중 특이적 리간드의 항체 폴리펩티드들이 "아미노산 링커" 또는 "링커"에 의해 연결될 수 있다. 예를 들어, dAb가 아미노산 링커의 N-말단에 융합될 수 있고, 또 다른 dAb가 링커의 C-말단에 융합될 수 있다. 아미노산 링커가 임의의 길이일 수 있고, 임의의 아미노산 조합으로 이루어질 수 있지만, 연결된 도메인들 간의 상호작용을 감소시키도록 링커 길이가 비교적 짧을 수 있다 (예를 들어, 아미노산 5개 이하). 부피가 큰 아미노산 또는 2차 구조를 도입하기 쉬운 아미노산의 수를 감소시키도록 링커의 아미노산 조성이 또한 조정될 수 있다. 적절한 아미노산 링커에는 길이가 아미노산 3개, 4개, 5개, 6개, 7개, 10개, 15개, 20개, 또는 25개 이하인 것들이 포함된다. 대표적인 아미노산 링커 서열에는 (GGGGG)_n (서열 4) [식 중, n은 1 내지 5 사이의 임의의 정수일 수 있다]이 포함된다. AST (서열 5), TVAAPS (서열 6), TVA (서열 7), 및 ASTSGPS (서열 8)로 이루어지는 군으로부터 기타 적절한 링커 서열이 선택될 수 있다.

[0093] 제2 항원의 결합은 항체 폴리펩티드의 생체내 반감기를 증가시킬 수 있다. 예를 들어, 이중 특이적 항체 폴리펩티드의 제2 가변 도메인이 혈청 알부민 (SA), 예를 들어, 인간 혈청 알부민 (HSA)에 특이적으로 결합할 수 있다. HSA에 결합하도록 양식이 정해진 항체 폴리펩티드는 양식이 정해지지 않은 항체 폴리펩티드와 비교하여 생체내 t- α ("알과 반감기") 또는 t- β ("베타 반감기") 반감기가 증가될 수 있다. t- α 및 t- β 반감기는 얼마나 신속하게 물질이 신체 내에 분포되는지 및 신체로부터 제거되는지를 측정한다. HSA에 대한 연결은, 예를 들어, HSA에 특이적으로 결합할 수 있는 제2 가변 도메인과 항체 폴리펩티드의 융합에 의해 달성될 수 있다. 항-

인간 혈청 알부민 항체는 업계에 주지되어 있다. 예를 들어, 인터넷 하이퍼텍스트 전송 프로토콜 www.abcam.com/index.html에서 입수가 가능한 앵캠(Abcam)® (인간 혈청 알부민 항체) ab10241, ab2406, 및 ab8940, 또는 인터넷 하이퍼텍스트 전송 프로토콜 www.genwaybio.com에서 입수가 가능한 젠웨이(GenWay) (ALB 항체) 참조. HSA에 특이적으로 결합하는 가변 도메인을 임의의 이러한 항체로부터 수득한 후, 업계에 주지된 재조합 기술을 사용하여 본 개시내용의 항체 폴리펩티드에 융합시킬 수 있다.

[0094] 대안적으로, 항체 폴리펩티드를 HSA에 연결하는 것이 당업자에게 주지된 기술을 사용하여 항체 폴리펩티드 서열을 HSA 코딩 서열에 직접적으로 융합함으로써 달성될 수 있다. 예를 들어, 진뱅크(GenBank) 접속 번호 NM000477에서 입수가 가능한 cDNA 서열로부터 유래되는 프라이머를 사용하여 PCR에 의해 HSA 코딩 서열을 수득할 수 있다.

[0095] 한 실시양태에서, HSA-연결 도메인 항체 조성물의 $t\alpha$ -반감기가 10% 이상만큼 증가된다. 또 다른 실시양태에서, HSA-연결 도메인 항체 조성물의 $t\alpha$ -반감기는 0.25시간 내지 6시간 범위이다. 또 다른 실시양태에서, HSA-연결 도메인 항체 조성물의 $t\beta$ -반감기가 10% 이상만큼 증가된다. 또 다른 실시양태에서, HSA-연결 도메인 항체 조성물의 $t\beta$ -반감기는 12 내지 48시간 범위이다.

[0096] 또 다른 실시양태에서, PEG화에 의해 생체내 반감기가 증가되도록 항체 폴리펩티드의 양식이 정해질 수 있다. 한 실시양태에서, 공유결합으로 PEG가 연결된다. 또 다른 실시양태에서, 시스템인 또는 리신 잔기에서 PEG가 항체 폴리펩티드에 연결된다. 또 다른 실시양태에서, PEG-연결 항체 폴리펩티드는 유체역학적 크기가 24 kD 이상이다. 또 다른 실시양태에서, 총 PEG 크기는 20 내지 60 kD (경계 포함)이다. 또 다른 실시양태에서, PEG-연결 도메인 항체는 유체역학적 크기가 200 kD 이상이다.

[0097] N-히드록시숙신이미드 활성 에스테르, 숙신이미드 프로피오네이트, 말레이미드, 비닐 술폰 또는 티올을 포함하지만 이에 한정되지 않는 여러 PEG 부착 모이어티(moiety)를 사용하여 PEG화를 달성할 수 있다. 미리 정해진 위치에서 PEG 중합체를 항체 폴리펩티드에 연결시킬 수 있거나, 또는 이를 무작위로 도메인 항체 분자에 연결시킬 수 있다. 도메인 항체에 부착된 펩티드 링커를 통해 PEG화가 매개될 수도 있다. 즉, 항체 폴리펩티드에 융합된 펩티드 링커에 PEG 모이어티가 부착될 수 있고, 이때 링커가 PEG 부착을 위한 부위 (예를 들어, 유리 시스템인 또는 리신)를 제공한다. 예를 들어 문헌 [Chapman, et al., "PEGylated antibodies and antibody fragments for improved therapy: a review", Adv. Drug Deliv. Rev. 54(4):531-45 (2002)]에 개시된 바와 같이, 항체를 PEG화하는 방법이 업계에 주지되어 있다.

[0098] 이량체, 삼량체, 사량체 또는 기타 다량체를 형성하도록 항체 폴리펩티드가 디자인될 수도 있다. 융합 단백질로서의 다량체들의 발현, 다량체들 사이의 펩티드 링커를 통한 2개 이상의 다량체의 연결, 또는 번역 후에 다량체들을 서로 직접적으로, 또는 디설피드 결합에 의한 링커를 통해, 또는 2가, 3가 또는 다가 연결 모이어티 (예를 들어, 팔이 여러 개인 PEG)에의 연결에 의해 화학적으로 연결시키는 것을 포함하지만 이에 한정되지 않는 업계에 공지된 여러 방법에 의해 다량체를 형성하도록 항체 폴리펩티드들, 예를 들어, dAb들을 연결시킬 수 있다. 한 실시양태에서, 이러한 다량체가 CD40의 단일 분자에 결합할 수 있다.

[0099] 4. 제약 조성물 및 치료 방법

[0100] 제약 조성물은 치료 유효량의 하나 이상의 항체 폴리펩티드 및 임의로 제약상 허용되는 담체를 포함한다. 제약상 허용되는 담체에는, 예를 들어, 물, 염수, 포스페이트 완충 염수, 텍스트로스, 글리세롤, 에탄올 등, 뿐만 아니라 이의 조합물이 포함된다. 제약상 허용되는 담체는 융합 단백질의 보관 기관 또는 유효성을 강화하는 미량의 보조 물질, 예컨대 습윤화 또는 유화 작용제, 방부제 또는 완충제를 추가로 포함할 수 있다. 투여 후 활성 성분(들)의 신속 방출, 지속 방출 또는 지연 방출을 제공하도록 조성물이 제형될 수 있다. 적절한 제약 조성물 및 이의 제조 방법이 업계에 주지되어 있다. 예를 들어, 문헌 [Remington, THE SCIENCE AND PRACTICE OF PHARMACY, A. Gennaro, et al., eds., 21st ed., Mack Publishing Co. (2005)] 참조.

[0101] 제약 조성물은 면역억제/면역조절제 및/또는 항염증제를 추가로 포함할 수 있다. 면역 질환의 치료를 필요로 하는 환자에서 면역 질환을 치료하는 방법은 환자에게 치료 유효량의 제약 조성물을 투여하는 것을 포함할 수 있다. CD40-매개 T 세포 활성화를 길항하는 것은 예를 들어 자가면역, 이식 거부, 또는 알레르기 반응 동안 발생하는 원치 않는 T-세포 반응을 억제할 수 있다. CD40-매개 T 세포 활성화를 억제하는 것은 이러한 질환의 진행 및/또는 중증도를 완화할 수 있다.

[0102] 본원에서 사용된 바와 같이, "환자"는 동물, 예를 들어, 인간이 포함되는 포유동물을 의미한다. 환자가 면역 질환으로 진단될 수 있다. "치료" 또는 "치료하다" 또는 "치료하기"는 증상, 장애, 용태 또는 질환의 진행 또

는 중증도를 경감시키는 것을 수반하는 프로세스를 지칭한다. "면역 질환"은 세포성 및/또는 체액성 면역 반응이 포함되는 개체에서의 면역 반응의 발달과 연관되는 임의의 질환을 지칭한다. 면역 질환의 예로는 염증, 알레르기, 자가면역 질환, 또는 이식-관련 질환이 포함되지만, 이에 한정되지는 않는다. 자가면역 질환은 전신 홍반성 루푸스, 다발성 경화증, 류머티스 관절염, 당뇨병, 건선, 경피증, 아테롬성동맥경화증, 염증성 장 질환, 및 궤양성 결장염으로 이루어지는 군으로부터 선택될 수 있다.

[0103] 제약 조성물을 투여하는 것에 의해 치료될 수 있는 질환은 애디슨병, 알레르기, 감작성 척추염, 천식, 아테롬성 동맥경화증, 귀의 자가면역 질환, 눈의 자가면역 질환, 자가면역 간염, 자가면역 이하선염, 결장염, 관상동맥 심장 질환, 크론병, 제1형 및/또는 제2형 당뇨병을 포함한 당뇨병, 부고환염, 사구체신염, 그레이브스병, 길랑-바레 증후군, 하시모토병, 용혈성 빈혈, 특발성 혈소판감소성 자반증, 염증성 장 질환, 제조합 약물 제품 (예를 들어, 혈우병 환자에서의 인자 VII)에 대한 면역 반응, 전신 홍반성 루푸스, 남성 불임증, 다발성 경화증, 중증 근무력증, 천포창, 건선, 류머티스성 열, 류머티스 관절염, 사르코이드증, 경피증, 쇼그렌 증후군, 척추관절염, 갑상선염, 이식 거부, 및 혈관염으로 이루어진 군으로부터 선택될 수 있다. 자가면역-매개 용태에는 감염된 조직이 1차 표적이고, 일부 경우에는 2차 표적인 용태가 포함되지만, 이에 한정되지는 않는다. 이같은 용태에는 AIDS, 아토피성 알레르기, 기관지 천식, 습진, 나병, 정신분열병, 유전성 우울증, 조직 및 기관 이식, 만성 피로 증후군, 알츠하이머병, 파킨슨병, 심근경색증, 졸증, 자폐증, 간질, 아르투스 현상, 아나필락시스, 알콜 중독, 및 약물 중독이 포함되지만, 이에 한정되지는 않는다.

[0104] 제약 조성물은 단독으로, 또는 면역억제/면역조절제 및/또는 항염증제와의 조합 요법 (즉, 동시 요법 또는 순차 요법)으로 투여될 수 있다. 상이한 면역 질환들이 면역 질환을 치료하는데 유용한 특정한 보조 화합물의 사용을 필요로 할 수 있고, 이는 환자-대-환자를 기준으로 하여 결정될 수 있다. 예를 들어, 제약 조성물이 하나 이상의 적절한 아주반트(adjuvant), 예를 들어, 시토카인 (예를 들어, IL-10 및 IL-13) 또는 기타 면역 자극제, 예를 들어, 케모카인, 중앙-연관 항원, 및 펩티드와 조합되어 투여될 수 있다. 적절한 아주반트가 업계에 공지되어 있다.

[0105] 임의의 적절한 방법 또는 경로를 사용하여 항체 폴리펩티드 또는 제약 조성물을 투여할 수 있다. 투여 경로에는, 예를 들어, 경구, 정맥내, 복막내, 피하 또는 근육내 투여가 포함된다. 투여된 항체 폴리펩티드(들)의 치료적 유효 용량은 치료되는 면역 질환의 유형 및 중증도, 조합 요법의 사용, 항체 폴리펩티드(들) 또는 제약 조성물의 투여 경로, 및 환자의 체중이 예를 들어 포함되는 다수의 인자에 좌우된다. 도메인 항체의 치료 유효량에 대한 비제한적인 범위는 환자의 체중과 관련하여 0.1-20 mg/kg이고, 한 측면에서는 1-10 mg/kg이다. 질환 상태의 시험관내 및/또는 생체내 모델에서 CD40 길항작용에 필요한 항체 폴리펩티드(들)의 양이 항체 폴리펩티드(들)의 용량을 추가로 권고할 수 있다. 대표적인 모델이 하기 및 실시예에서 기술된다.

[0106] 5. 시험관내 및 생체내 모델

[0107] CD40을 길항하는 본 개시내용의 항체 폴리펩티드의 능력을 여러 이용가능한 시험관내 또는 생체내 모델 시스템에 중 하나에서 테스트할 수 있다. 적합한 동물 및 세포 모델 시스템이 하기에 기술된다. 추가적인 세포 검증 시스템이 실시예에서 기술된다.

[0108] 5.1. 염증성 장 질환 (IBD) 모델:

[0109] IBD는 병인이 불확실한 다인성 면역 장애이다. IBD와 유사한 점막 염증의 여러 마우스 모델이 정상적 및 병리학적 점막 기능 양쪽 모두를 관리하는 메커니즘에 대한 이해를 제공한다. IBD 모델은 문헌 [De Winter et al., Am. J. Physiol. 276: G1317-1321 (1999)]의 점막 면역 및 염증 시스템을 사용하는 것을 포함한다. 한 측면에서, CD4(+) T 림프구 하위집합인 CD4(+)CD45RBhigh 세포를 면역결핍 마우스에 주사하면 장의 염증을 일으킨다. 발병기전은 염증유발성 시토카인의 분비에 부분적으로 기인한다. 또 다른 CD4(+) 하위집단인 CD4(+)CD45RBlow T 세포의 공동-전달에 의해 결장염 유도를 방지할 수 있다. 이러한 집단은 활성화 마커의 취득 및 숙주 장으로의 귀소 면에서 CD4(+)CD45RBhigh 집단과 유사하게 행동한다. 그러나, 활성화되는 경우에 이들의 림포카인 프로파일은 상이하고, CD4(+)CD45RBlow T 세포에 의해 분비 및/또는 유도되는 항염증성 시토카인은 결장염을 방지한다. 드 윈터(De Winter) 등은 입양 전달 모델 및 결장염 발병기전을 촉진 및 방지하는 인자들의 설명을 제공한다.

[0110] 5.2. 자발적 관절염 모델:

[0111] 전신 자가면역에 의해 유발된 장기-특이적 질환의 모델이 문헌 [Kouskoff et al., Cell 87: 811-822 (1996)]에서 제공된다. 류머티스성 관절염 (RA)은 백혈구 침윤 및 윤활막세포 활성화에 이어지는 연골 및 골 파괴를 특

징으로 하는 만성 관절 질환이다. 쿠스코프(Kouskoff) 등은 T 세포 수용체 (TCR) 트랜스제닉(transgenic) 계통을 NOD 계통과 교배시킴으로써 생성된, RA의 자발적 마우스 모델을 개시하였다. 모든 후손에서 인간에서의 RA를 고도로 연상시키는 관절 질환이 발달된다. 이러한 무린 장애의 촉발은 트랜스제닉 TCR에 의한 NOD-유래 주요 조직적합성 복합체 (MHC) 클래스 II 분자의 기회 인식이다; 관절염으로의 진행은 CD4+ T, B, 및 아마도 골수 중 세포를 수반한다.

[0112] **5.3. 콜라겐-유도 관절염 (CIA) 모델:**

[0113] 콜라겐-유도 관절염의 마우스 모델이 문헌 [Brand et al., Methods Mol. Med. 102: 295-312 (2004)]에서 제공된다. 콜라겐-유도 관절염 (CIA)은 관절 연골의 주요 구성 단백질인 II형 콜라겐 (CII)으로의 면역화에 의해 감수성 계통의 설치류 (랫트 및 마우스) 및 비-인간 영장류에서 도출될 수 있는 자가면역 질환이다. 면역화 후에, RA와 여러 임상 및 조직학적 특색을 공유하는 자가면역 다발관절염이 동물에서 발달된다. 설치류에서의 CIA에 대한 감수성은 주요 조직적합성 복합체 (MHC)의 클래스 II 분자에 연관되고, CII에 대한 면역 반응은 콜라겐-특이적 T 세포의 자극 및 면역원 (이종성 CII) 및 자가항원 (마우스 CII) 양쪽 모두에 대해 특이적인 높은 역가의 항체의 생산 양쪽 모두를 특징으로 한다. 조직학적으로, 무린 CIA는 임상적인 관절염 개시에 상응하는 강한 윤활막염을 특징으로 한다. 이러한 실험 데이터는 CIA와 RA 사이의 병리학적 유사성으로 인해 CIA를 평가하는데 유용하다.

[0114] **5.4. 항원-유도 T 세포 증식 생체내 모델:**

[0115] T 세포 수용체 (TCR)-트랜스제닉 T 세포의 입양 전달을 사용하는 것은 항원-유도 T-세포 증식에 대한 생체내 모델을 제공한다. 문헌 [Pape et al., Immunol. Rev. 156: 67-78 (1997)]에는 공지된 펩티드/MHC 특이성의 확인 가능한 TCR을 균일하게 발현하는 TCR-트랜스제닉 T 세포의 입양 전달이 개시되어 있다. 이러한 모델은 항원-특이적 T 세포의 생체내 거동을 모니터링하는데 사용될 수 있다. 나이브(naive) T 세포가 먼저 2차 림프 조직의 T-세포 구역 내에서 활성화되어 B7-의존적 방식으로 증식된다. 이러한 기간 동안 아주반트 또는 염증성 시토카인이 존재하면, 강화된 개수의 T 세포가 축적되고, B-세포-풍부 소포 내로 이동하고, IFN- γ 를 생산하고 B 세포가 IgG2a를 생산하는 것을 돕는 능력을 획득한다. 염증이 효과적으로 길항되면, 대다수의 초기에 활성화된 항원-특이적 T 세포가 소포에 진입하지 않으면서 사라지고, 생존자는 IL-2 및 IFN- γ 를 불량하게 생산한다.

[0116] **실시예**

[0117] 표 3은 본 개시내용의 항체 폴리펩티드에 유용한 대표적인 항-인간 CD40 가변 도메인 아미노산 서열을 개시한다. 표 4는 표 3에 열거된 가변 도메인 서열을 코딩하는 대표적인 핵산을 개시한다. 업계에 주지된 바와 같이, 다중 코돈이 동일한 아미노산을 코딩할 수 있다. 따라서 단백질 서열을 코딩하는 핵산들은 코돈 축중성이 있는 핵산들을 포함한다. 표 3에 개시된 항체 폴리펩티드는 CD40에 특이적으로 결합하고, 하기 실시예에 기술된 반복적인 초기/1차 스크리닝 및 친화도 성숙 방법을 사용하여 제조되었다.

표 3

항-인간 CD40 가변 도메인 아미노산 서열

BMS3h-56-201
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVTVSS (서열 9)

BMS3h-56-258
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHENGQGT LVTVSS (서열 10)

BMS3h-37
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMHWVRQAPGKGLWVS AISDGYRYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYNGQGT LVTVSS (서열 11)

BMS3h-38
EVQLLESGGGLVQPGGSLRLSCAASGFTFEFEEMHWVRQAPGKGLWVS AISGGGSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKEPFRFDYNGQGT LVTVSS (서열 12)

BMS3h-41
EVQLLESGGGLVQPGGSLRLSCAASGFTFEYEMHWVRQAPGKGLWVS ISINGANTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKPLRFDYNGQGT LVTVSS (서열 13)

BMS3h-43
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLWVS GISRRGFTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKEPITYAMRYARFDYNGQGT LVTVSS (서열 14)

BMS3h-56
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKLPFIIFYNGQGT LVTVSS (서열 15)

BMS3h-106
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYHMQWVRQAPGKGLWVS MIDADGLGTYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGPQFGQFDYNGQGT LVTVSS (서열 16)

BMS3h-107
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYDMQWVRQAPGKGLWVS TISASGVFTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKYPNRFALNFDYNGQGT LVTVSS (서열 17)

[0118]

BMS3h-131
DIQMTQSPSSLSASVGDRTVITCRANSSILWALAWYQQKPKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAAGWPGTFGGGTKVEIKR (서열 18)

BMS3h-193
DIQMTQSPSSLSASVGDRTVITCRASQTIERRLNHWYQQKPKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYASPLTFGGGTKVEIKR (서열 19)

BMS3h-198
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWVRQAPGKGLERVS AISGGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYNGQGT LVTVSS (서열 20)

BMS3h-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMWVRQAPGKGLWVS ISASGGSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKEPVSYVATFDYNGQGT LVTVSS (서열 21)

BMS3h-217
DIQMTQSPSSLSASVGDRTVITCRASHFIGTLLSWYQQKPKAPKLLITYGSL LQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCGQVLWPATFGGGTKVEIKR (서열 22)

BMS3h-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFPKNEMTWVRQAPGKGLWVS AISDGGQATYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKNRIPDLVFDYNGQGT LVTVSS (서열 23)

BMS3h-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFDAGAMTWVRQAPGKGLWVS SIDKEGLSTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRIPGLVFDYNGQGT LVTVSS (서열 24)

BMS3h-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDAAMTWVRQAPGKGLWVS AIQPMGDGTYADSVKGRFTVSRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRIPTLQFDYNGQGT LVTVSS (서열 25)

BMS3h-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDSPMTWVRQAPGKGLWVS AITSNGYETYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRIPTLHFDDYNGQGT LVTVSS (서열 26)

BMS3h-5
EVQLLESGGGLVQPGGSLRLSCAASGTFDEHMSWVRQAPGKGLWVS RIGPDGFHTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRIPTLHFDDYNGQGT LVTVSS (서열 27)

BMS3h-6
EVQLLESGGGLVQPGGSLRLSCAASGTFGEYHMSWVRQAPGKGLWVS RITPLGTLTYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRIPSLTFDYNGQGT LVTVSS (서열 28)

BMS3h-7
EVQLLESGGGLVQPGGSLRLSCAASGTFGTNMSWVRQAPGKGLWVS RISPGGDYTYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRVPDLLFDYNGQGT LVTVSS (서열 29)

BMS3h-8
EVQLLESGGGLVQPGGSLRLSCAASGTFPSEEMSWVRQAPGKGLWVS RISADGANTYYADSVKGRFTISRDNSKNTL
YLQMNSLRAEDTAVYYCAKGRVPDLLFDYNGQGT LVTVSS (서열 30)

[0119]

BMS3h-9
EVQLLESGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRITAVDGDRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGKVP SLHFDYWGQGL LVTVSS (서열 31)

BMS3h-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFTMDMSWVRQAPGKGLEWVSRITGDMNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGL LVTVSS (서열 32)

BMS3h-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFERDDMTWVRQAPGKGLEWVSRINAGGVHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGL LVTVSS (서열 33)

BMS3h-12
EVQLLESGGGLVQPGGSLRLSCAASGFTFDDDSMTWVRQAPGKGLEWVSRISDGSASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGL LVTVSS (서열 34)

BMS3h-13
EVQLLESGGGLVQPGGSLRLSCAASGFTFTEEDMTWVRQAPGKGLEWVSRIDSVEGTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGL LVTVSS (서열 35)

BMS3h-14
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDSAMS WVRQAPGKGLEWVSRIDNPGQHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVPTLTFDYWGQGL LVTVSS (서열 36)

BMS3h-15
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHSMTWVRQAPGKGLEWVSRIDGGGNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGEVPLHFDYWGQGL LVTVSS (서열 37)

BMS3h-16
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQEPMTWVRQAPGKGLEWVSRITAYNGDYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGITPNLTFDYWGQGL LVTVSS (서열 38)

BMS3h-17
EVQLLESGGGLVQPGGSLRLSCAASGFTFENYPMWVRQAPGKGLEWVSRINATGSITYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVIPHLFDYWGQGL LVTVSS (서열 39)

BMS3h-18
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYDMSWVRQAPGKGLEWVSRITGTGNSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAQGVVPYLAFDYWGQGL LVTVSS (서열 40)

BMS3h-19
EVQLLESGGGLVQPGGSLRLSCAASGFTFEADMTWVRQAPGKGLEWVSRINVDGDRYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVPTLTFDYWGQGL LVTVSS (서열 41)

BMS3h-21
EVQLLESGGGLVQPGGSLRLSCAASGFTFDRADMTWVRQAPGKGLEWVSRISSEGKCTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGMVPLVFDYWGQGL LVTVSS (서열 42)

BMS3h-22
EVQLLESGGGLVQPGGSLRLSCAASGFTFHWEPMSWVRQAPGKGLEWVSRINSSGWDYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGMVPLVFDYWGQGL LVTVSS (서열 43)

BMS3h-24
EVQLLESGGGLVQPGGSLRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIPPEGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPNLTFDYWGQGL LVTVSS (서열 44)

BMS3h-26
EVQLLESGGGLVQPGGSLRLSCAASGFTFHHDMWVRQAPGKGLEWVSRISRGGLQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVIPDLHFDYWGQGL LVTVSS (서열 45)

BMS3h-27
EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYPMWVRQAPGKGLEWVSRINGDGANITYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGIIPMQFDYWGQGL LVTVSS (서열 46)

BMS3h-28
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDVPMWVRQAPGKGLEWVSRIDPYGSMNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGIMP SLTFDYWGQGL LVTVSS (서열 47)

BMS3h-29
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYDMSWVRQAPGKGLEWVSRISALGATTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGQLPALEFDYWGQGL LVTVSS (서열 48)

BMS3h-30
EVQLLESGGGLVQPGGSLRLSCAASGFTFKRYMYMTWVRQAPGKLEWVSGIVPSGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPDLHFDYWGQGL LVTVSS (서열 49)

BMS3h-31
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYDMTWVRQAPGKGLEWVSRISPTGGQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVIPYLSFSFDYWGQGL LVTVSS (서열 50)

BMS3h-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYMMGWARQAPGKGLEWVSSIDSHGAGTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGAPKFMTTYTFDYWGQGL LVTVSS (서열 51)

BMS3h-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFLSYPMHWVRQAPGKGLEWVSSIDSRGVTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGHSMTFDYWGQGL LVTVSS (서열 52)

BMS3h-34
EVQLLESGGGLVQPGGSLRLSCAASGFTFANSNMTWVRQAPGKGLEWVSRINPDGGSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAEGRIPTLHFDYWGQGL LVTVSS (서열 53)

BMS3h-35
EVQLLESGGGLVQPGGSLRLSCAASGFTFGPRRMGVRQAPGKGLEWVSSIDDIGRRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAEGAQGVLLFDYWGQGL LVTVSS (서열 54)

BMS3h-36
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDRYMMWVRQAPGKGLEWVSSIISTGELTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAETAGQFFDYWGQGL LVTVSS (서열 55)

[0120]

[0121]

BMS3h-39
EVQLLESGGGLVQPGGSLRLSCAASGFTTFPEYEMVWRQAPGKGLEWVSATISREGRATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVRFDYWGQGLTVTVSS (서열 56)

BMS3h-40
EVQLLESGGGLVQPGGSLRLSCAASGFTFSITYEMLWVRQAPGKGLEWVSISSSGNYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLMFYWGQGLTVTVSS (서열 57)

BMS3h-42
EVQLLESGGGLVQPGGSLRLSCAASGFTFDTEEMSWVRQAPGKGLEWVSISPNGAFTFYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPILFDYWGQGLTVTVSS (서열 58)

BMS3h-44
EVQLLESGGGLVQPGGSLRLSCAASGFTTFGHYDMWVRQAPGRGLEWVSTINGAGLNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQSASRIFDYWGQGLTVTVSS (서열 59)

BMS3h-45
EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYEMAWVRQAPGKGLEWVSISITLGTKTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQSSHTIFDYWGQGLTVTVSS (서열 60)

BMS3h-46
EVQLLESGGGLVQPGGSLRLSCAASGFTFIRYEMAWVRQAPGKGLEWVSISSSGWTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSDAHIFDYWGQGLTVTVSS (서열 61)

BMS3h-47
EVQLLESGGGLVQPGGSLRLSCAASGFTFYAYEMAWVRQAPGKGLEWVSSISDDGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDLQGQFDYWGQGLTVTVSS (서열 62)

BMS3h-48
EVQLLESGGGLVQPGGSLRLSCAASGFTFADHGMTWVRQAPGKGLEWVSGIGPSGEATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRIPNLFYWGQGLTVTVSS (서열 63)

BMS3h-49
EVQLLESGGGLVQPGGSLRLSCAASGFTFESQDMWVRQAPGKGLEWVSGISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRSDFDYWGQGLTVTVSS (서열 64)

BMS3h-50
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYDMWVRQAPGKGLEWVSRIHPGGVYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAVPKGFDYWGQGLTVTVSS (서열 65)

BMS3h-51
EVQLLESGGGLVQPGGSLRLSCAASGFTFRVYWMWVRQAPGKGLEWVSSIDPQGGMTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKARIPNLEFDYWGQGLTVTVSS (서열 66)

BMS3h-52
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYDMTWVRQAPGKGLEWVSRIINPTGSYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKARIPNLFYWGQGLTVTVSS (서열 67)

BMS3h-53
EVQLLESGGGLVQPGGSLRLSCAASGFTFADSEMMWVRQAPGKGLEWVSGIAHNGGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGHPQQTEAFDYWGQGLTVTVSS (서열 68)

BMS3h-54
EVQLLESGGGLVQPGGSLRLSCAASGFTFATYDMWVRQAPGKGLEWVSKISPNGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYQTHFDYWGQGLTVTVSS (서열 69)

BMS3h-55
EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYDMWVRQAPGKGLEWVSTISSSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYPKNFDYWGQGLTVTVSS (서열 70)

BMS3h-57
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHEDMTWVRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGLTVTVSS (서열 71)

BMS3h-58
EVQLLESGGGLVQPGGSLRLSCAASGFTFEKYIMGWARQAPGKGLEWVSTIDYWGQHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRSHLIPLQFDYWGQGLTVTVSS (서열 72)

BMS3h-59
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSTISYVGYTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKALRGEAFERFDYWGQGLTVTVSS (서열 73)

BMS3h-60
EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYMMHWVRQAPGKGLEWVSTIEVNGNRYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVGSKTSSDKSFDYWGQGLTVTVSS (서열 74)

BMS3h-61
EVQLLESGGGLVQPGGSLRLSCAASGFTFGTTEMAWVRQAPGKGLEWVSSISGSAGAWTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKIGGHPQGQFDYWGQGLTVTVSS (서열 75)

BMS3h-62
EVQLLESGGGLVQPGGSLRLSCAASGFTFPREWMWVRQAPGKGLEWVSSIQPMGQTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYSRNKGFDYWGQGLTVTVSS (서열 76)

BMS3h-63
EVQLLESGGGLVQPGGSLRLSCAASGFTFSEYMGWVRQAPGKGLEWVSSIQRVSGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKHESNWETFDYWGQGLTVTVSS (서열 77)

BMS3h-70
EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYSMQWVRQAPGKGLEWVSITPNGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTLGRGSYPGVDFDYWGQGLTVTVSS (서열 78)

BMS3h-71
EVQLLESGGGLVQPGGSLRLSCAASGFTFPSYAMTWVRQAPGKGLEWVSRIADGTVTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGSIPMLTFDYWGQGLTVTVSS (서열 79)

BMS3h-72
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYMIWVRQAPGKGLEWVSISPNGTGIZYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNQSVHVAFDYWGQGLTVTVSS (서열 80)

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BMS3h-73
EVQLLESGGGGLVQPGGSLRLSCAASGFTFENYEMTWVRQAPGKGLEWVSRIPAHGRLYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGQIPMLDFYWGQGLVTVSS (서열 81)

BMS3h-74
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSHYMMWVRQAPGKGLEWVSTISHFGDITYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNDMMKNGGFDYWGQGLVTVSS (서열 82)

BMS3h-75
EVQLLESGGGGLVQPGGSLRLSCAASGFTFERYDMSWVRQAPGKGLEWVSRIDSRGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLVPHLRFDYWGQGLVTVSS (서열 83)

BMS3h-76
EVQLLESGGGGLVQPGGSLRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRIDAMGDATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGKVPISIDYWGQGLVTVSS (서열 84)

BMS3h-77
EVQLLESGGGGLVQPGGSLRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRIDAMGDATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGVIPAFDYWGQGLVTVSS (서열 85)

BMS3h-78
EVQLLESGGGGLVQPGGSLRLSCAASGFTFQNDRMHWVRQAPGKGLEWVSSISATGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQTGTRNRFDYWGQGLVTVSS (서열 86)

BMS3h-79
EVQLLESGGGGLVQPGGSLRLSCAASGFTFNQPYMSWVRQAPGKGLEWVSSIDASGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAKDRIPNLVFDYWGQGLVTVSS (서열 87)

BMS3h-80
EVQLLESGGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRIDGGGNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGQVPELLFDYWGQGLVTVSS (서열 88)

BMS3h-81
EVQLLESGGGGLVQPGGSLRLSCAASGFTFVYSNMHTWVRQAPGKGLEWVSATISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPTLVFDYWGQGLVTVSS (서열 89)

BMS3h-82
EVQLLESGGGGLVQPGGSLRLSCAASGFTFVYSNMHTWVRQAPGKGLEWVSATISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRIPNLVFDYWGQGLVTVSS (서열 90)

BMS3h-83
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRINDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIPTLLEFDYWGQGLVTVSS (서열 91)

BMS3h-84
EVQLLESGGGGLVQPGGSLRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRIDGTGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLIPDLQFDYWGQGLVTVSS (서열 92)

BMS3h-85
EVQLLESGGGGLVQPGGSLRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRITGGGHETYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTIPLLEFDYWGQGLVTVSS (서열 93)

BMS3h-86
EVQLLESGGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRITERGDVTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTVPITLEFDYWGQGLVTVSS (서열 94)

BMS3h-87
EVQLLESGGGGLVQPGGSLRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRITGGGHETYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTVPITLEFDYWGQGLVTVSS (서열 95)

BMS3h-88
EVQLLESGGGGLVQPGGSLRLSCAASGFTFHEMTWVRQAPGKGLEWVSAINRLGQDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPGLVFDYWGQGLVTVSS (서열 96)

BMS3h-89
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRINDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGTVPITLEFDYWGQGLVTVSS (서열 97)

BMS3h-90
EVQLLESGGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRITERGDVTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPTLVFDYWGQGLVTVSS (서열 98)

BMS3h-91
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRINDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGLVTVSS (서열 99)

BMS3h-92
EVQLLESGGGGLVQPGGSLRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIPPEGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLIPDLQFDYWGQGLVTVSS (서열 100)

BMS3h-93
EVQLLESGGGGLVQPGGSLRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSAIAPGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRIPNLRFDYWGQGLVTVSS (서열 101)

BMS3h-94
EVQLLESGGGGLVQPGGSLRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRIDGTGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGQVPELLFDYWGQGLVTVSS (서열 102)

BMS3h-95
EVQLLESGGGGLVQPGGSLRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSAIAPGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDRIPNLRFDYWGQGLVTVSS (서열 103)

BMS3h-96
EVQLLESGGGGLVQPGGSLRLSCAAGFTFDLAEMTWVRQAPGKGLEWVSRIDEDGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAEGVIPSLTFDYWGQGLVTVSS (서열 104)

BMS3h-97
EVQLLESGGGGLVQPGGSLRLSCAASGFTFTDKHMSWVRQAPGKGLEWVSRISPDGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAEGVIPSLTFDYWGQGLVTVSS (서열 105)

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BMS3h-98
EVQLLESGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGKTPHLVFDYWGQGT LTVTSS (서열 106)

BMS3h-99
EVQLLESGGGLVQPGGSLRLSCAAAGTFDLAEMTWVRQAPGKGLEWVSRIDEDGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGQVPALVFDYWGQGT LTVTSS (서열 107)

BMS3h-100
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDSMMSWVRQAPGKGLEWVSRIIDPGGAQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LTVTSS (서열 108)

BMS3h-101
EVQLLESGGGLVQPGGSLRLSCAASGFTFEHADMSWVRQASGKGLEWVSRIIDNSGQSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LTVTSS (서열 109)

BMS3h-102
EVQLLESGGGLVQPGGSLRLSCAASGFTFSEAMNWVRQAPGKGLEWVSRIITDGDSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPTLHFDYWGQGT LTVTSS (서열 110)

BMS3h-103
EVQLLESGGGLVQPGGSLRLSCAASGFTFDDSDMTWVRQAPGKLEWVSIRGDDDETYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKNRIPDLVFDYWGQGT LTVTSS (서열 111)

BMS3h-108
EVQLLESGGGLVQPGGSLRLSCAASGFTFNVDMMQWVRQAPGKGLEWVSSIPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKHASTEGRPTAFDYWGQGT LTVTSS (서열 112)

BMS3h-109
EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYDMGWVRQAPGKGLEWVSWISAHGSFTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKMPYKFDYWGQGT LTVTSS (서열 113)

BMS3h-110
EVQLLESGGGLVQPGGSLRLSCAASGFTFGSGSMWVRQAPGKGLEWVSRIGSNGADTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGWVPNLVFDYWGQGT LTVTSS (서열 114)

BMS3h-111
EVQLLESGGGLVQPGGSLRLSCAASGFTFNRFDMTWVRQAPGKGLEWVVSATISGSGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRIPNLVFDYWGQGT LTVTSS (서열 115)

BMS3h-112
EVQLLESGGGLVQPGGSLRLSCAASGFTFGESDMKWVRQAPGKGLEWVSSIPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKSPSSRLKFDYWGQGT LTVTSS (서열 116)

BMS3h-139
EVQLLESGGGLVQPGGSLRLSCAASGFTFDSSMSWVRQAPGKGLEWVSIENQGATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRIPNLVFDYWGQGT LTVTSS (서열 117)

BMS3h-140
EVQLLESGGGLVQPGGSLRLSCAASGFTLDAYPMYVRQAPGKGLEWVSWIASGGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKRTKNFDYWGQGT LTVTSS (서열 118)

BMS3h-141
EVQLLESGGGLVQPGGSLRLSCAASGFTFMSYSMAWVRQAPGKGLEWVSGITSNGHRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKSTIGANSRNFYWGQGT LTVTSS (서열 119)

BMS3h-142
EVQLLESGGGLVQPGGSLRLSCAASGFTFEGYLSMWVRQAPGKGLEWVSSIAANGMQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKPRGIWGDFFDYWGQGT LTVTSS (서열 120)

BMS3h-143
EVQLLESGGGLVQPGGSLRLSCAASGFTFHESMTWVRQAPGKGLEWVSTIRHPGEFTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGLIPDLQFDYWGQGT LTVTSS (서열 121)

BMS3h-144
EVQLLESGGGLVQPGGSLRLSCAASGFTFAMYSMSWVRQAPGKGLEWVSSIAPPGGRTTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKQSLTGYSRFDYWGQGT LTVTSS (서열 122)

BMS3h-145
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQNPMSWVRHAPGKGLEWVSTIPANGRPTSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKYSQQPGRRFDYWGQGT LTVTSS (서열 123)

BMS3h-146
EVQLLESGGGLVQPGGSLRLSCAASGFTFANYHMTWVRQAPGKGLEWVSSIPDSGKQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPSLLFDYWGQGT LTVTSS (서열 124)

BMS3h-147
EVQLLESGGGLVQPGGSLRLSCAASGFTFAQYHMRWVRQAPGKGLEWVSTIINDIGSNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKVGGRGSFSDYWGQGT LTVTSS (서열 125)

BMS3h-148
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMKWVRQAPGKGLEWVSTISASGVFTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKREHAGQPPFDYWGQGT LTVTSS (서열 126)

BMS3h-149
EVQLLESGGGLVQPGGSLRLSCAASGFTFNGYAMSWVRQAPGKGLEWVSTINANGKYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKKLTLASNYFDYWGQGT LTVTSS (서열 127)

BMS3h-150
EVQLLESGGGLVQPGGSLRLSCAASGFTFMDYDMKWVRQAPGKGLEWVSSITALKGKTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDSVKYPLNFDYWGQGT LTVTSS (서열 128)

BMS3h-151
EVQLLESGGGLVQPGGSLRLSCAASGFTFPHYTMAWVRQAPGKGLEWVSSIQSPGWRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKYGDGLPLTFDYWGQGT LTVTSS (서열 129)

BMS3h-167
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGTPMSWVRQAPGKGLEWVSRIQDEGQETYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LTVTSS (서열 130)

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BMS3h-168
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSMSWVRQAPGKGLEWVSAIGSDGPSYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIP TLHFDYWGQGT LVTVSS (서열 131)

BMS3h-169
EVQLLESGGGLVQPGGSLRLSCAASGFTFNP GEMTWVRQAPGKGLEWVSSIDGSGSSYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIP TLHFDYWGQGT LVTVSS (서열 132)

BMS3h-170
EVQLLESGGGLVQPGGSLRLSCAASGFTFPESMMGWVRQAPGKGLEWVSSIGVPGATTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGGSRDNDYWGQGT LVTVSS (서열 133)

BMS3h-171
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHSMMHWVRQAPGKGLEWVSSISVPGPKTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSLRDLRPGDSKSF DYWGQGT LVTVSS (서열 134)

BMS3h-197
EVQLLESGGGLVQPGGSLRLSCAASGFTFGSAAMDWVRQAPGKGLEWVSSINDMGSNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQGRFDYWGQGT LVTVSS (서열 135)

BMS3h-199
EVQLLESGGGLVQPGGSLRLSCAASGFTFGYDRMAHWVRQAPGKGLEWVSSIDGPGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEGRRVPDFDYWGQGT LVTVSS (서열 136)

BMS3h-200
EVQLLESGGGLVQPGGSLRLSCAASGFTFGEYEMTWVRQAPGKGLEWVSRIDPFGSETYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEGVVPDLNFDYWGQGT LVTVSS (서열 137)

BMS3h-201
EVQLLESGGGLVQPGGSLRLSCAASGFTFDKYVMGWVRQAPGKGLEWVSTIGSYGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRLT LSA TKFDYWGQGT LVTVSS (서열 138)

BMS3h-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYVMGWVRQAPGKGLEWVSTIAHRGDITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRRRLSDYRFDYWGQGT LVTVSS (서열 139)

BMS3h-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQFDMYVRQAPGKGLEWVSAISPAGTGYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGDRSSLFDYRGQGT LVTVSS (서열 140)

BMS3h-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFKD TGMTWVRQAPGKGLEWVSSISYGRDYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDA AVYYCAKLNALGFDYWGQGT LVTVSS (서열 141)

BMS3h-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYPMWVRQAPGKGLEWVSGINAPGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQQMSSGVFDYWGQGT LVTVSS (서열 142)

BMS3h-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNQDMTWVRQAPGKGLEWVSSIDSSGQLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVKS LARFDYWGQGT LVTVSS (서열 143)

BMS3h-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFPESDMKIWRQAPGKGLEWVSSISPNGMDTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPAQVLFDYWGQGT LVTVSS (서열 144)

BMS3h-209
EVQLLESGGGLVQPGGSLRLSCAASGFTFEQYVMGWVRQAPGKGLEWVSTIGTSKGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQRRLSTRVHFDYWGQGT LVTVSS (서열 145)

BMS3h-210
EVQLLESGGGLVQPGGSLRLSCAASGFTFGEHMSWVRQAPGKGLEWVSAITGDGDRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTVSWNGRFDYWGQGT LVTVSS (서열 146)

BMS3h-211
EVQLLESGGGLVQPGGSLRLSCAASGFTFAWYMMGWVRQAPGKGLEWVSR IAPSGIITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLRGKFDYWGQGT LVTVSS (서열 147)

BMS3h-212
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYEMRWVRQAPGKGLEWVSSISAGTDITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQSLNFDYWGQGT LVTVSS (서열 148)

BMS3h-213
EVQLLESGGGLVQPGGSLRLSCV ASGFTFDEEPMTWVRQAPGKGLEWVSIIDPGGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSNMFDYWGQGT LVTVSS (서열 149)

BMS3h-214
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYPMHWVRQAPGKGLEWVSSIASSGITTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKFTRLHFPAQFDYWGQGT LVTVSS (서열 150)

BMS3h-215
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYAMGWVRQAPGKGLEWVSRISPEGSRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLRPYASKFDYWGQGT LVTVSS (서열 151)

BMS3h-230
EVQLLESGGGLVQPGGSLRLSCAASGFTFRPYDMGWVRQAPGKGLEWVSTISHQGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVSHHFDYWGQGT LVTVSS (서열 152)

BMS3h-231
EVQLLESGGGLVQPGGSLRLSCAASGFTFSAYNMWVRQAPGKGLEWVSWINSTSGSRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNWHRGRFDYWGQGT LVTVSS (서열 153)

BMS3h-232
EVQLLESGGGLVQPGGSLRLSCAASGFTFDRYRMGWVRQAPGKGLEWVSTINRLGQSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVKKHFDYWGQGT LVTVSS (서열 154)

BMS3h-233
EVQLLESGGGLVQPGGSLRLSCAASGFTFAHYNMWVRQAPGKGLEWVSTITKTGRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGQDFDYWGQGT LVTVSS (서열 155)

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BMS3h-234
EVQLLESGGGGLVQPGGSLRLSCAASGFTFYPYSHMWRQAPGKGLEWVSTIDGSGMFTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAEDSLKASFDYWGQGLTLTVSS (서열 156)

BMS3h-235
EVQLLESGGGGLVQPGGSLRLSCAASGFTFPLPYGMWVRQAPGKGLEWVSIGPYGHGHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKRRKKFDYWGQGLTLTVSS (서열 157)

BMS3h-236
EVQLLESGGGGLVQPGGSLRLSCAASGFTFPRYRMSWVRQAPGKGLEWVSITPYGAHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKYGKWFDYWGQGLTLTVSS (서열 158)

BMS3h-237
EVQLLESGGGGLVQPGGSLRLSCAASGFTFNEYAMRWVRQAPGKGLEWVSTIDRLGLHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGLTLTVSS (서열 159)

BMS3h-238
EVQLLESGGGGLVQPGGSLRLSCAASGFTFERYNMRWVRQAPGKGLEWVSTIDRLGLATYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKGSWSFDYWGQGLTLTVSS (서열 160)

BMS3h-239
EVQLLESGGGGLVQPGGSLRLSCAASGFTFGIYDMKWVRQAPGKGLEWVSTISSSGHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKYPQYPFDYWGQGLTLTVSS (서열 161)

BMS3h-240
EVQLLESGGGGLVQPGGSLRLSCAASGFTFWVYDMRWVRQAPGKGLEWVSTISATGVHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKYPAGRFDYWGQGLTLTVSS (서열 162)

BMS3h-241
EVQLLESGGGGLVQPGGSLRLSCAASGFTFTYDMIWVRQAPGKGLEWVSATSPNGTGTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKPPQVNTFFDYRGQGLTLTVSS (서열 163)

BMS3h-243
EVQLLESGGGGLVQPGGSLRLSCAASGFTFEKEDMGWVRQAPGKGLEWVSHISPNGYATYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKWSFSFDYWGQGLTLTVSS (서열 164)

BMS3h-244
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSATPMWARQAPGKGLEWVSTISESGYSTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKWNSTTGFDYWGQGLTLTVSS (서열 165)

BMS3h-245
EVQLLESGGGGLVQPGGSLRLSCAASGFTFNTVDMEWVRQAPGKGLEWVSISPNGWDTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAEAPHRAFDYWGQGLTLTVSS (서열 166)

BMS3h-246
EVQLLESGGGGLVQPGGSLRLSCAASGFTFEDKEMSWVRQAPGKGLEWVSRIDALGDSTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAEGMVPRLKFDYWGQGLTLTVSS (서열 167)

BMS3h-247
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSDHSMWVRQAPGKGLEWVSIDIEPHGVHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCANPTFDYWGQGLTLTVSS (서열 168)

BMS3h-248
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSPHTMHWVRQAPGKGLEWVSGIGPDGTTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKRSYSDRWGTFDYWGQGLTLTVSS (서열 169)

BMS3h-249
EVQLLESGGGGLVQPGGSLRLSCAASGFTFYASDMKWVRQAPGKGLEWVSISPNGWDTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKADYTHSFYWGQGLTLTVSS (서열 170)

BMS3h-250
EVQLLESGGGGLVQPGGSLRLSCAASGFTFAHYNMRWVRQAPGKGLEWVSTITKGFRTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKAGQFDFDYWGQGLTLTVSS (서열 171)

BMS3h-251
EVQLLESGGGGLVQPGGSLRLSCAASGFTFSHYHMGWARQAPGKGLEWVSVIGPRGISTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKSPSRHFRFDYWGQGLTLTVSS (서열 172)

BMS3h-252
EVQLLESGGGGLVQPGGSLRLSCAASGFTFNEYAMRWVRQAPGKGLEWVSTIDRLGLHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGLTLTVSS (서열 173)

BMS3h-253
EVQLLESGGGGLVQPGGSLRLSCAASGFTFGNYSMKWARQAPGKGLEWVSTITPDGWYTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKVGDAVNWIGGFDYWGQGLTLTVSS (서열 174)

BMS3h-254
EVQLLESGGGGLVQPGGSLRLSCAASGFTFGDYGMKWVRQAPGKGLEWVSAITSNQDFTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKSLYKFDYWGQGLTLTVSS (서열 175)

BMS3h-255
EVQLLESGGGGLVQPGGSLRLSCAASGFTFPTYKMGWVRQAPGKGLEWVSFDYWGWRYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKSPYSWTHDSPHFDYWGQGLTLTVSS (서열 176)

BMS3h-256
EVQLLESGGGGLVQPGGSLRLSCAASGFTFRPYTMCAWRQAPGKGLEWVSCISDAGSFYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKRMSSFDYWGQGLTLTVSS (서열 177)

BMS3h-257
EVQLLESGGGGLVQPGGSLRLSCAASGFTFQNYQMAWVRQAPGKGLEWVSTISGTGKNTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKTPQNYFSVRRFDYWGQGLTLTVSS (서열 178)

BMS3h-258
EVQLLESGGGGLVQPGGSLRLSCAASGFTFGAYTMGWVRQAPGKGLEWVSKISTSGGQTYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKPLNHWAFDYWGQGLTLTVSS (서열 179)

BMS3h-272
EVQLLESGGGGLVQPGGSLRLSCAASGFTFNAYPMTWVRQAPGKGLEWVSRIDGVRHTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYYCAKIIPNFDYWGQGLTLTVSS (서열 180)

BMS3h-273
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAVDMTWVRQAPGKGLEWVSAISPSGSATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRVPDLGFDYWGQGT LVTVSS (서열 181)

BMS3h-274
EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYAMGWARQAPGKGLEWVSIAGAKGLSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAARGKFDYWGQGT LVTVSS (서열 182)

BMS3h-275
EVQLLESGGGLVQPGGSLRLSCAASGFTFTRYQMGWVRQAPGKGLEWVSVINWVGSYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKMSGKFAYWGQGT LVTVSS (서열 183)

BMS3h-276
EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMMWVRQAPGKGLEWVSTIIPAGTSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPSIRLFDYWGQGT LVTVSS (서열 184)

BMS3h-279
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYDMGWVRQAPGKGLEWVSWISPNGYDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGGVKFDYWGQGT LVTVSS (서열 185)

BMS3h-282
EVQLLESGGGLVQPGGSLRLSCAASGFTFVWYMAWVRQAPGKGLEWVSTIQADGEQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKASYALVYPPEEFDYWGQGT LVTVSS (서열 186)

BMS3h-287
EVQLLESGGGLVQPGGSLRLSCAASGFTFNYSMWVRQAPGKGLEWVSAIDDLGVSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKWRLKNSQPTDFDYWGQGT LVTVSS (서열 187)

BMS3h-292
EVQLLESGGGLVQPGGSLRLSCAASGFTDQAHMMWVRQAPGKGLEWVSFINPSGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPSLSSSFYWGQGT LVTVSS (서열 188)

BMS3h-293
EVQLLESGGGLVQPGGSLRLSCAASGFTFETGQMWARQAPGKGLEWVSNIDGSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSTQNYRFDYWGQGT LVTVSS (서열 189)

BMS3h-296
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYPHYWVRQAPGKGLEWVSIHKDRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQGTVPDGFYWGQGT LVTVSS (서열 190)

BMS3h-297
EVQLLESGGGLVQPGGSLRLSCAASGFTFPDEGMTWVRQAPGKGLEWVSTIETGGTVTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKMDGSGTWTQTFDYWGQGT LVTVSS (서열 191)

BMS3h-298
EVQLLESGGGLVQPGGSLRLSCAASGFTFDSLGMWARQAPGKGLEWVSIRAEAGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYLADSDYWGQGT LVTVSS (서열 192)

BMS3h-299
EVQLLESGGGLVQPGGSLRLSCAASGFTFSESYMEWVRQAPGKGLEWVSGIDHIGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDDRGGSMFYWGQGT LVTVSS (서열 193)

BMS3h-300
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGGYMMWVRQAPGKGLEWVSSIGASGAYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTGGRLDYWGQGT LVTVSS (서열 194)

BMS3h-301
EVQLLESGGGLVQPGGSLRLSCAASGFTFDEGHMGWVRQAPGKDLWVSYIGSLGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKREFSNGGFDYWGQGT LVTVSS (서열 195)

BMS3h-302
EVQLLESGGGLVQPGGSLRLSCAASGFTFKTSPHYWVRQAPGKGLEWVSSIDRTGGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQALLTDAKRFDYWGQGT LVTVSS (서열 196)

BMS3h-303
EVQLLESGGGLVQPGGSLRLSCAASGFTFDGRDMWVRQAPGKGLEWVSAISPSGLDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAERPQMLVTNFDYWGQGT LVTVSS (서열 197)

BMS3h-304
EVQLLESGGGLVQPGGSLRLSCAASGFTFGNDPMSWVRQAPGKGLEWVSGIGREGDSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDSMRHQPFYWGQGT LVTVSS (서열 198)

BMS3h-305
EVQLLESGGGLVQPGGSLRLSCAASGFTFDETYMKWVRQAPGKGLEWVSAIGASGADTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKFTHLNGRFDYWGQGT LVTVSS (서열 199)

BMS3h-306
EVQLLESGGGLVQPGGSLRLSCAASGFTFGGWPMGWVRQAPGKGLEWVSGIDIDGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGQGT LVTVSS (서열 200)

BMS3h-307
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDQAMWVRQAPGKGLEWVSTIQDGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPSKPFYWGQGT LVTVSS (서열 201)

BMS3h-308
EVQLLESGGGLVQPGGSLRLSCAASGFTFETGQMWARQAPGKGLEWVSNIDGSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAVRNFAFDYWGQGT LVTVSS (서열 202)

BMS3h-309
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGHDMWVRQAPGKGLEWVSAISPHGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIRGWIGHDTQPFYWGQGT LVTVSS (서열 203)

BMS3h-310
EVQLLESGGGLVQPGGSLRLSCAASGFTFESKDMWVRQAPGKGLEWVSSISSDGTHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQELGGSWQFDYWGQGT LVTVSS (서열 204)

BMS3h-311
EVQLLESGGGLVQPGGSLRLSCAASGFTFADRDMWVRQAPGKGLEWVSGIGASGTSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAKGGTGPTDLWDFDYWGQGT LVTVSS (서열 205)

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BMS3h-312
EVQLLESGGGLVQPGGSLRLSCAASGFTFDDEKMLWVRQAPGKGLEWVSSISVSLHITYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEEAGSWSFYWGQGLTVTVSS (서열 206)

BMS3h-313
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQERMiWVRQAPGKGLEWVSDISASGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEEAGSWSFYWGQGLTVTVSS (서열 207)

BMS3h-37-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 208)

BMS3h-37-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 209)

BMS3h-37-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRQGLTVTVSS (서열 210)

BMS3h-37-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 211)

BMS3h-37-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWISAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRQGLTVTVSS (서열 212)

BMS3h-37-6
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 213)

BMS3h-37-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 214)

BMS3h-37-8
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFHYRGRGLTVTVSS (서열 215)

BMS3h-37-9
EVQLLESGGGLVQPGGSLRLSCVASGFTFEWYEMQWVRQAPGKGLEWISAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 216)

BMS3h-37-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLLMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 217)

BMS3h-37-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 218)

BMS3h-37-12
EVQLLESGGGLVQPGGSMRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 219)

BMS3h-37-201
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSMISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 220)

BMS3h-37-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGWRYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 221)

BMS3h-37-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELLYFDYRGRGLTVTVSS (서열 222)

BMS3h-37-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 223)

BMS3h-37-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 224)

BMS3h-37-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELGYFDYRGRGLTVTVSS (서열 225)

BMS3h-37-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELAFDYRGRGLTVTVSS (서열 226)

BMS3h-37-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELLYFDYRGRGLTVTVSS (서열 227)

BMS3h-37-209
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELFFDYRGRGLTVTVSS (서열 228)

BMS3h-37-210
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELQFDYRGRGLTVTVSS (서열 229)

BMS3h-37-211
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELFFDYRGRGLTVTVSS (서열 230)

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BMS3h-37-212
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWWSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEFFDYWGRTLVTVSS (서열 231)

BMS3h-37-213
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWWSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELLFFDYWGRTLVTVSS (서열 232)

BMS3h-37-214
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWWSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNLEFFDYWGRTLVTVSS (서열 233)

BMS3h-37-215
EVRLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWWSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEFFDYWGRTLVTVSS (서열 234)

BMS3h-38-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCSKEPFRFDYWGGTLVTVSS (서열 235)

BMS3h-38-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTVSS (서열 236)

BMS3h-38-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTVSS (서열 237)

BMS3h-38-4
EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWWSISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTVSS (서열 238)

BMS3h-38-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTVSS (서열 239)

BMS3h-38-6
EVQLLEPGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLLMNSLRAEDTAVYYCSKEPFRFDYWQGALVTVSS (서열 240)

BMS3h-38-7
EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWWSISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQTLVTVSS (서열 241)

BMS3h-38-8
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTIHRDN SKNTL
YLQMNSLRAEDTAVYYCSKEPFRFDYRGLTTLTVSS (서열 242)

BMS3h-38-9
EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWWSISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQTLVTVSS (서열 243)

BMS3h-38-10
EVQLIDSGGGFVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPFRFDYWGGTLVTVSS (서열 244)

BMS3h-38-11
EVQLLDPGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGREPFRFDYWGGTLVTVSS (서열 245)

BMS3h-38-12
EVRLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTVSS (서열 246)

BMS3h-38-13
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTVSS (서열 247)

BMS3h-38-201
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQTLVTVSS (서열 248)

BMS3h-38-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQTLVTVSS (서열 249)

BMS3h-38-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQTLVTVSS (서열 250)

BMS3h-38-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFPQEEEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQTLVTVSS (서열 251)

BMS3h-38-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFAAEMIWVRQAPGKGLEWWSAISGSGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQTLVTVSS (서열 252)

BMS3h-38-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISRPGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQTLVTVSS (서열 253)

BMS3h-38-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISRMGFSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQTLVTVSS (서열 254)

BMS3h-38-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWWSAISRWGHSYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQTLVTVSS (서열 255)

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BMS3h-38-209
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRIGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 256)

BMS3h-38-210
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRWGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 257)

BMS3h-38-211
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRQGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 258)

BMS3h-38-212
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISVGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 259)

BMS3h-38-213
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRWGWSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 260)

BMS3h-38-214
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRNGLSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 261)

BMS3h-38-215
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGLGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 262)

BMS3h-38-216
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISALGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 263)

BMS3h-38-217
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRRGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 264)

BMS3h-38-218
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRHGWSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 265)

BMS3h-38-219
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 266)

BMS3h-38-220
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRIGNSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 267)

BMS3h-38-221
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGHGWSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 268)

BMS3h-38-222
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRWGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 269)

BMS3h-38-223
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFMYDYGQGT LVTVSS (서열 270)

BMS3h-38-224
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFYDYGQGT LVTVSS (서열 271)

BMS3h-38-225
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 272)

BMS3h-38-226
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPLYDYDYGQGT LVTVSS (서열 273)

BMS3h-38-227
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFMYDYDYGQGT LVTVSS (서열 274)

BMS3h-38-228
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRNGFSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 275)

BMS3h-38-229
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRTGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 276)

BMS3h-38-230
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISREGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 277)

BMS3h-38-231
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRQGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 278)

BMS3h-38-232
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRGGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 279)

BMS3h-38-233
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEMIWVRQAPGKGLEWWSAISRTGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 280)

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BMS3h-38-234
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRNGRSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 281)

BMS3h-38-235
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 282)

BMS3h-38-236
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRKGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 283)

BMS3h-38-237
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRGGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 284)

BMS3h-38-238
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRGSYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 285)

BMS3h-38-239
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRNGMSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 286)

BMS3h-38-240
EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEIMWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (서열 287)

BMS3h-41-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFTEHEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRPEDTAVYYCAKEPLRFDYWGQGT LVTVSS (서열 288)

BMS3h-41-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFEYEMIWVRQAPGKGLEWISSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYRGQGT LVTVSS (서열 289)

BMS3h-41-3
EVQLLEPGGGLVQPGGSLRLSCAASGFTFEYEMIWVRKAPGKMEWVSSISGNANTYYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKEPLRFYGYWGQGT LVTVSS (서열 290)

BMS3h-41-4
EVQLLDGGGLVQPGGSLRLSCAASGFTFEYEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGRT LVTVSS (서열 291)

BMS3h-41-5
EVQLLGGGGGLVQPGGSLRLSCAASGFTFEYEMIWVRQAPGKSLWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRYDDWGQGT LVTVSS (서열 292)

BMS3h-41-6
EVQPLESGGGGLVQPGGSLRLSCASGFTFNEYEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGT LVTVSS (서열 293)

BMS3h-41-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFAEYEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGT LVTVSS (서열 294)

BMS3h-41-8
EVQLDPPGGGLVQPGGSLRLSCAASGFTFTESEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGT LVTVSS (서열 295)

BMS3h-41-9
EVQLLEPGGGLVQPGGSLRLSCAASGFTFEYEMIWVRKAPGKMEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRPEDTAVYYCAKEPLRFDDWGQGT LVTVSS (서열 296)

BMS3h-41-10
EVQLLESRGGLVQPGGSLRLSCAASGFTFEYEMIWVRKAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDNWGQGT LVTVSS (서열 297)

BMS3h-41-11
EVQLLESRGGLVQPGGSLRLSCAASGFTFTEHEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFSVRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGT LVTVSS (서열 298)

BMS3h-41-12
EVQPLESGGGGLVQPGGSLRLSCAASGFTFEYEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGT LVTVSS (서열 299)

BMS3h-41-13
EVQLLESAGGLVQPGGSLRLSCAASGFTFAEYEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQALVTVSS (서열 300)

BMS3h-41-14
EVQLLEPGGGLVQPGGSLRLSCAASGFTFEYEMIWVRQAPGKGLEWVSSISGNANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDNWGQGT LVTVSS (서열 301)

BMS3h-43-1
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYYEMSWVRQAPGKGLEWVSGISRRGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGT LVTVSS (서열 302)

BMS3h-43-2
EEQLLESGGGLVQPGGSLRLSCTASGFTFNMYYEMSWVRQAPGKGLEWVSGISRRGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYATRYARFDYWGQGT LVTVSS (서열 303)

BMS3h-43-3
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYYEMSWVRQAPGKGLEWVSGISRRGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYGGQGT LVTVSS (서열 304)

BMS3h-43-4
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYYEMSWVRQAPGKGLEWVSGISRRGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDNWGQGT LVTVSN (서열 305)

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BMS3h-43-5
EVQLLESGGGLVQPGGSLRLSCTASGFTFNTYEMSWVRQAPGKLEWVSGIGRRGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGLTVTVSS (서열 306)

BMS3h-43-6
EVQLMESGGGLVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRTLVTVSS (서열 307)

BMS3h-43-7
EVQLLESGGGLVQPGGSLRLSCTASGFAFNMYEMSWVRQAPGKLEWVSGISR HGFTTYYADSVKGRFTVSRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARSDYWGQGLTVTVSS (서열 308)

BMS3h-43-8
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYFCAKEPITYDMRYARSDYWGQGLTVTVSS (서열 309)

BMS3h-43-9
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYSMRYARFDYGLGTMVTVSS (서열 310)

BMS3h-43-10
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYSGQGLTVTVSS (서열 311)

BMS3h-43-11
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRKAPGKLEWVSGISR HGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGQGLTVTVSS (서열 312)

BMS3h-43-12
EVQLFESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRTLVTVSS (서열 313)

BMS3h-43-13
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRTLVTVSS (서열 314)

BMS3h-43-14
EVQLLESGGGVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGQGLTVTVSS (서열 315)

BMS3h-43-15
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRKAPGKLEWVSGISR RGFTTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGQGLTVTVSS (서열 316)

BMS3h-56-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFTFDWQGGLTVTVSS (서열 317)

BMS3h-56-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFTFDWQGGLTVTVSS (서열 318)

BMS3h-56-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCTKL PFI FEYWGQGLTVTVSS (서열 319)

BMS3h-56-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFMFDRQGGLTVTVSS (서열 320)

BMS3h-56-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFTFDWQGGLTVTVSS (서열 321)

BMS3h-56-6
EVQLLESGGGLVQPGGSLRLSCAASGFSFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFI FDNRGQGLTVTVSS (서열 322)

BMS3h-56-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTSVYHCAKPPFI FGDWGPGTLTVTVSS (서열 323)

BMS3h-56-8
EVQLLESGGGLVQPGGSRRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFTFDWQGGLTVTVSS (서열 324)

BMS3h-56-9
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFMFDRQGGLTVTVSS (서열 325)

BMS3h-56-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKL PFMFDRQGGLTVTVSS (서열 326)

BMS3h-56-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFMFDRQGGLTVTVSS (서열 327)

BMS3h-56-12
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCLKL PFI FDYWGQGLTVTVSS (서열 328)

BMS3h-56-13
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCTKL PFI FDYWGQGLTVTVSS (서열 329)

BMS3h-56-14
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGMVLERVSAINPQGTRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKL PFF FDSRGQGLTVTVSS (서열 330)

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BMS3h-56-15
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (서열 331)

BMS3h-56-16
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (서열 332)

BMS3h-56-17
EVQLLESGGGLVQPGGSLRLSCAASGFSFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (서열 333)

BMS3h-56-18
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKVLERVSAINPQGTRITYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (서열 334)

BMS3h-56-19
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCALPFTFEDWGQGLTVTVSS (서열 335)

BMS3h-56-20
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCTKLPFTFEDWGQGLTVTVSS (서열 336)

BMS3h-56-21
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCLKLPFTFEDWGQGLTVTVSS (서열 337)

BMS3h-56-22
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRADDTAVYHCKLPFTFEYWQGLTVTVSS (서열 338)

BMS3h-56-23
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPYSYDWSGQGLTVTVSS (서열 339)

BMS3h-56-24
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCAKEPYSYDWSGQGLTVTVSS (서열 340)

BMS3h-56-25
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (서열 341)

BMS3h-56-26
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGGQGLTVTVSS (서열 342)

BMS3h-56-27
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDWGQGLTVTVSS (서열 343)

BMS3h-56-28
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELMWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (서열 344)

BMS3h-56-29
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELMWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGGQGLTVTVSS (서열 345)

BMS3h-56-30
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (서열 346)

BMS3h-56-31
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWVRQAPGKGLERVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGGQGLTVTVSS (서열 347)

BMS3h-56-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLWVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLTVTVSS (서열 348)

BMS3h-56-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLWVSAINPQGTRITYADSVMGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDDRGGQGLTVTVSS (서열 349)

BMS3h-56-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTYFSDRGQGLTVTVSS (서열 350)

BMS3h-56-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPPFFFEWGQGLTVTVSS (서열 351)

BMS3h-56-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTYFKDWGQGLTVTVSS (서열 352)

BMS3h-56-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPHYFSEWGQGLTVTVSS (서열 353)

BMS3h-56-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCALPMHFFEDWGQGLTVTVSN (서열 354)

BMS3h-56-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMHWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPPFFSEWGQGLTVTVSS (서열 355)

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BMS3h-56-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFSEWGQGLVTVSS (서열 356)

BMS3h-56-209
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPYGNLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 357)

BMS3h-56-210
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPPGTLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDRGQGLVTVSS (서열 358)

BMS3h-56-211
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 359)

BMS3h-56-212
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPMGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 360)

BMS3h-56-213
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGSHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 361)

BMS3h-56-214
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPSGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDRGQGLVTVSS (서열 362)

BMS3h-56-215
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPHGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 363)

BMS3h-56-216
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPAGRLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 364)

BMS3h-56-217
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 365)

BMS3h-56-218
EVQLLESGGGLVQPGGSLRLSCAASGFTFDYEMMWVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 366)

BMS3h-56-219
EVQLLESGGGLVQPGGSLRLSCADS GFTFPPVEMMWVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 367)

BMS3h-56-220

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 368)

BMS3h-56-221
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPNHNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 369)

BMS3h-56-222
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPHGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 370)

BMS3h-56-223
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGRGLERVSAINPPGMLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 371)

BMS3h-56-224
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGQLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 372)

BMS3h-56-225
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 373)

BMS3h-56-226
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPSGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 374)

BMS3h-56-227
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPSGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 375)

BMS3h-56-228
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPSGTLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 376)

BMS3h-56-229
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPYGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 377)

BMS3h-56-230
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 378)

BMS3h-56-231
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLVTVSS (서열 379)

BMS3h-56-232
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGSHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (서열 380)

[0146]

[0147]

BMS3h-56-233
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWGTLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 381)

BMS3h-56-234
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPNRGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFADWGQGT LVTVSS (서열 382)

BMS3h-56-235
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWQLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 383)

BMS3h-56-236
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPHGGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 384)

BMS3h-56-237
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPAGMLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 385)

BMS3h-56-238
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPHGTLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 386)

BMS3h-56-239
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 387)

BMS3h-56-240
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 388)

BMS3h-56-241
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPAGFLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 389)

BMS3h-56-242
EVQLLESGGGLVRPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 390)

BMS3h-56-243
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 391)

BMS3h-56-244
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 392)

BMS3h-56-245
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 393)

BMS3h-56-246
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWGTLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 394)

BMS3h-56-247
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPWGGYTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGRGT LVTVSS (서열 395)

BMS3h-56-248
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPYGNLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 396)

BMS3h-56-249
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPHGGFTYYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 397)

BMS3h-56-250
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPAGFYTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 398)

BMS3h-56-251
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPAGGLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 399)

BMS3h-56-252
EVQLLESGGGLVQPGGSLRLSCAASGAFRDYEMWMVRQAPGKGLERVSAINPHGSLTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (서열 400)

BMS3h-56-253
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPAGGYTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYCAKLPFTFDDWGQGT LVTVSS (서열 401)

BMS3h-56-254
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFWFTEWGQGT LVTVSS (서열 402)

BMS3h-56-255
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFMFSDRGQGT LVTVSS (서열 403)

BMS3h-56-256
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPFLFQEWGQGT LVTVSS (서열 404)

BMS3h-56-257
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWMVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YMQMNSLRAEDTAVYYCAKLPTRFDDWGQGT LVTVSS (서열 405)

BMS3h-56-258

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[0149]

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLTVTVSS (서열 406)

BMS3h-56-259
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRDYMGQGLTVTVSS (서열 407)

BMS3h-56-260
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFKDWGQGLTVTVSS (서열 408)

BMS3h-56-261
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFQEWGQGLTVTVSS (서열 409)

BMS3h-56-262
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPQLFHDRGQGLTVTVSS (서열 410)

BMS3h-56-263
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPQLFEDWGQGLTVTVSS (서열 411)

BMS3h-56-264
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHC AKLPFGFSEWGQGLTVTVSS (서열 412)

BMS3h-56-265
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPQLFQDWGQGLTVTVSS (서열 413)

BMS3h-56-266
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFFHEWGQGLTVTVSS (서열 414)

BMS3h-56-267
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPHYFKDWGQGLTVTVSS (서열 415)

BMS3h-56-268
EVQLLESGGGLVQSGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFEWGQGLTVTVSS (서열 416)

BMS3h-56-269
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFRFSDRGQGLTVTVSS (서열 417)

BMS3h-56-270
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLP L FQDWGQGLTVTVSS (서열 418)

BMS3h-56-271
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFSEWGQGLTVTVSN (서열 419)

BMS3h-56-272
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPQGRTRYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFWFQEWGQGLTVTVSS (서열 420)

BMS3h-56-273
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLTVTVSS (서열 421)

BMS3h-56-274
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHC AKLPWFEDWGQGLTVTVSN (서열 422)

BMS3h-56-275
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLTVTVSS (서열 423)

BMS3h-56-276
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFFQEWGQGLTVTVSS (서열 424)

BMS3h-56-277
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFFHEWGQGLTVTVSS (서열 425)

BMS3h-56-278
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLTVTVSS (서열 426)

BMS3h-56-279
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHC AKLPMFFEDWGQGLTVTVSN (서열 427)

BMS3h-56-280
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLTVTVSS (서열 428)

BMS3h-56-281
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFFQEWGQGLTVTVSS (서열 429)

BMS3h-56-282
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFFHEWGQGLTVTVSS (서열 430)

BMS3h-56-283
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMMVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLTVTVSS (서열 431)

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[0151]

[0153]

BMS3h-193-2
DIQMTQSPSSLSASVGSVITITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYASPLTFGQGTNVEIKR (서열 457)

BMS3h-193-3
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFAAYYCHQYESPPLTFGQGTKVEIKR (서열 458)

BMS3h-193-4
DIQMTQSPSSLSASVGDRVTITCRASRTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 459)

BMS3h-193-5
DIQMTQSPSSLSASVGERVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISNLQ
PEDSATYYCHQYASPLTLGQGTKVEIKR (서열 460)

BMS3h-193-6
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYASPLTLGQGTKVEIKR (서열 461)

BMS3h-193-7
DIQITQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKDPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 462)

BMS3h-193-8
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKW (서열 463)

BMS3h-193-9
DIQLTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSEFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 464)

BMS3h-193-10
DIQMSQSPSTLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 465)

BMS3h-193-11
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKDPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 466)

BMS3h-193-12
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 467)

BMS3h-193-13
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 468)

BMS3h-193-14
DIQMTQYSPSSLSASVGDRVTITCRASQSIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 469)

BMS3h-193-15
DIQMTQSPSSLSASVGDRVTITCRASRTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHPYESPPLTFGQGTKVEIKR (서열 470)

BMS3h-193-16
DIQMTQSPSSLSASVGDRVTITCRASQAIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYASPLTLGQGTKVEIKR (서열 471)

BMS3h-193-17
NIQMTQSPSSLSASVGDRVTITCRASQAIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 472)

BMS3h-193-18
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 473)

BMS3h-193-19
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTEFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 474)

BMS3h-193-20
DIQMTQTPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVKEIKR (서열 475)

BMS3h-193-21
DIQMTQSPSSLSASVGSVITITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 476)

BMS3h-193-22
HIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 477)

BMS3h-193-23
DVQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLTSRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYASPLTFGQGTKVEIKR (서열 478)

BMS3h-193-24
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVVIKR (서열 479)

BMS3h-193-25
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 480)

BMS3h-193-26
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 481)

BMS3h-193-27

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[0155]

DIQMTQSPSSLSASVGDRTTITCRASQTIGRRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 482)

BMS3h-193-28
DIQMTQSPSSLSASVGDRTTITCRASQSIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIIR (서열 483)

BMS3h-193-29
DIQMTQSPSSLSASVGDRTTITCRASQTIERRLNWYQQKPGKAPKLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 484)

BMS3h-193-30
DIQMTQSPSSLSASVGDRTTITCRASQSIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 485)

BMS3h-193-2501
DIQMTQSPSSLSASVGDRTTITCRASQTIERRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQFEHPLTFGQGTKVEIKR (서열 486)

BMS3h-193-2502
DIQMTQSPSSLSASVGDRTTITCRASFPIIDRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 487)

BMS3h-193-2503
DIQMTQSPSSLSASVGDRTTITCRASSTIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 488)

BMS3h-193-2504
DIQMTQSPSSLSASVGDRTTITCRASSQIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 489)

BMS3h-193-2505
DIQMTQSPSSLSASVGDRTTITCRASERIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 490)

BMS3h-193-2506
DIQMTQSPSSLSASVGDRTTITCRASQQIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 491)

BMS3h-193-2507
DIQMTQSPSSLSASVGDRTTITCRASQPIARRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 492)

BMS3h-193-2508
DIQMTQSPSSLSASVGDRTTITCRASGNIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 493)

BMS3h-193-2509
DIQMTQSPSSLSASVGDRTTITCRASRNIDRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 494)

BMS3h-193-2510
DIQMTQSPSSLSASVGDRTTITCRASQSTGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 495)

BMS3h-193-2511
DIQMTQSPSSLSASVGDRTTITCRASQNIIGRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 496)

BMS3h-193-2512
DIQMTQSPSSLSASVGDRTTITCRASEVIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 497)

BMS3h-193-2513
DIQMTQSPSSLSASVGDRTTITCRASEATIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 498)

BMS3h-193-2514
DIQMTQSPSSLSASVGDRTTITCRASTIARRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 499)

BMS3h-193-2515
DIQMTQSPSSLSASVGDRTTITCRASLNIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 500)

BMS3h-193-2516
DIQMTQSPSSLSASVGDRTTITCRASQTIERRLNWYQQKPGKAPRLLIYLSKQLSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (서열 501)

BMS3h-198-1
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMMWVRQAPGKGLERVSATISGSGGSYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSFDYWGQGLTVTVSS (서열 502)

BMS3h-198-2
EVQPLESGGGLVQPGGSLRLSCAASGFTFAGYEMMWVRQAPGKGLERISATISGSGGSYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSFDYWGQGLTVTVSS (서열 503)

BMS3h-198-3
EVQLLESGGGSVQPGGSLRLSCAATGSTFAGYEMMWVRQAPGKGLERVSATISGSGGSYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSYDYWGQGLTVSVSS (서열 504)

BMS3h-198-4
EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMMWVRQAPGKGLERVSATISGSGGSYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYHCARDPYSFDYWGQGLTVTVSS (서열 505)

BMS3h-198-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMMWVRQAPGKGLERVSATISGSGGSYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYHCAKEPYSYDYWGQGLTVTVSS (서열 506)

BMS3h-198-6
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMMWVRQAPGKGLERVSATISGSGGSYYADSVKGRFTISRDDSKNTL
YLQMNSLR PETA VYYCVKDPYSFDYWGQGLTVTVSS (서열 507)

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[0157]

BMS3h-198-7
EVQLLESGGGLVQPGGSLRLSCAASGSTIAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 508)

BMS3h-198-8
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGLVTVSS (서열 509)

BMS3h-198-9
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGLVTVSS (서열 510)

BMS3h-198-10
EVQLLESGGGLVQPGGSLRLSCAASGSTIAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGLVTVSS (서열 511)

BMS3h-198-11
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVSVSS (서열 512)

BMS3h-198-12
EVQLLESGGGLVQPGGSLRLSCAASGFTIAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGLVTVSS (서열 513)

BMS3h-198-13
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGLVTVSS (서열 514)

BMS3h-198-14
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDTKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGLVTVSS (서열 515)

BMS3h-198-15
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 516)

BMS3h-198-16
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGQGLVTVSS (서열 517)

BMS3h-198-17
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 518)

BMS3h-198-18
EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWVRQAPGKGLERVAATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 519)

BMS3h-198-19

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EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 520)

BMS3h-198-20
EVQLLESGGGLVQPGGSLRLSCAAPGFTLAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGLVTVSS (서열 521)

BMS3h-198-21
EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 522)

BMS3h-198-22
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYWGQGLVTVSS (서열 523)

BMS3h-198-23
EVQPLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGNTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTGVYYCARDPYSFDYWGQGLVTVSS (서열 524)

BMS3h-198-24
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGQGLVTVSS (서열 525)

BMS3h-198-25
EAQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 526)

BMS3h-198-26
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDHWGQGLVTVSS (서열 527)

BMS3h-198-27
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (서열 528)

BMS3h-198-28
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGQGLVTVSS (서열 529)

BMS3h-198-29
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDHRGQGLVTVSS (서열 530)

BMS3h-198-30
EVQLLESGGGLVQPGGSLRLSCAASGYTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYWGQGLVTVSS (서열 531)

BMS3h-198-31
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDNKNTL
YLQMNSLRAEDTAVYHCAKEPYSYDYWGQGLVTVSS (서열 532)

[0159]

BMS3h-198-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNMGGTLVTVSS (서열 533)

BMS3h-198-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYMGQGLVTVSS (서열 534)

BMS3h-198-34
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNMGGTLVTVSS (서열 535)

BMS3h-198-35
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWFRQAPGKGLEHVS AISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYMGQGLVTVSS (서열 536)

BMS3h-198-36
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMHWFRQAPGKGLEHVS AISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNMGGTLVTVSS (서열 537)

BMS3h-198-37
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELHWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYRGQGLVTVSS (서열 538)

BMS3h-198-38
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELHWFRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYMGQGLVTVSS (서열 539)

BMS3h-202-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGQGLVTVSS (서열 540)

BMS3h-202-2
EVQLLVSGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGP EHVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGQGLVTVSS (서열 541)

BMS3h-202-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRKAPGMGLEHVS SISASGGYTYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGQGLVTVSS (서열 542)

BMS3h-202-4
EVQLLVSGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRQAPGKGLEHVS SISASGGSTYYADSVKGRFSISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGHGALVTVSS (서열 543)

BMS3h-202-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGQGLVTVSS (서열 544)

BMS3h-202-6
EAQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRQAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
YLQNLRLRAEDTAVYYCAKEPYSYVATFDYMGRTLVTVSS (서열 545)

BMS3h-202-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKSTL
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGPGALVTVSS (서열 546)

BMS3h-202-8
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
FLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGQGLVTVSS (서열 547)

BMS3h-202-9
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPYSYVATFDYMGPGALVTVSS (서열 548)

BMS3h-202-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVYVATFDYMGQGLVTVSS (서열 549)

BMS3h-202-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEHVS SISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDAAVYYCAKEPYSYVATFDYMGQGLVTVSS (서열 550)

BMS3h-217-1
NIQMTQSPSSLSASVGDRTVITCRASHFIGTLLTWYQHKGKAPKLLITYGSL LQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 551)

BMS3h-217-2
DIQMTQSPSSLSASVGDRTVITCRASHFIGTLLSWYQQKPRKAPKLLITYGSL LQSGVPSRFSGSGSGDTFTLTISSLH
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 552)

BMS3h-217-3
DIQMTQSPSSLSASVGDRTVITCRASHFIGTLLSWYQQKPGKAPKLLVTVGSL LQSGVPSRFSGSGSGDTFTLTISNLQ
PEDFATYYCGQGVLPPTFGQGTRVENIR (서열 553)

BMS3h-217-4
DIQMTQSPSSLSASVGDRTVITCRASHFIATLLSWYQQKPGKAPKLLITYGSL LQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 554)

BMS3h-217-5
DIQMTQSPSFLSASVGDRTVITCRASHFIATLLSWYQQKPGKAPKLLITYGSL LQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 555)

BMS3h-217-6
DIQMTQSPSSLSASVGDRTVITCRASHFIGTLLSWYQQKPGKATKLLITYGSL LQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 556)

BMS3h-217-7
DIQMTQSPSSLSASVGDRTVITCRASHFIGLLSWYQHKGKAPKLLITYGSL LQSGVPSRFSGSGSGDTFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 557)

BMS3h-217-8

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[0161]

DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 558)

BMS3h-217-9
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSMQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 559)

BMS3h-217-10
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGGTEFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 560)

BMS3h-217-11
DIQMTQSPSSLTASVGDRTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGGTEFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 561)

BMS3h-217-12
NIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 562)

BMS3h-217-13
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 563)

BMS3h-217-14
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 564)

BMS3h-217-15
DIQMTQSPSSLSASVGDRTITCRVSHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKQ (서열 565)

BMS3h-217-16
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPRKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 566)

BMS3h-217-17
DIQTIQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (서열 567)

BMS3h-217-18
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 568)

BMS3h-217-19
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVENR (서열 569)

BMS3h-217-20
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 570)

BMS3h-217-21
DIQMTQAPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVENR (서열 571)

BMS3h-217-22
DIQMTQSPSSLSASVGDRTITCRASHFIGSLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 572)

BMS3h-217-23
DIQMTQSPSSLSASVGDRTITCRASHFIGSLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTIVEIKR (서열 573)

BMS3h-217-24
DITLMTQSPSSLSASVGDRTITCRASHFIGSLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 574)

BMS3h-217-25
DIQMTQSPSSLSASVGDRTITCRASHFIGTLVSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATYGGGTKVEIKR (서열 575)

BMS3h-217-26
DIQMTQSPSSLSASVGDRTITCRASHFIGTLVSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVENR (서열 576)

BMS3h-217-27
DIKMTQSPSSLSASVGDRTITCRASHFIGTLVSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 577)

BMS3h-217-28
DIQMTQSPSSLSASVGDRTITQASHFIGTLVSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 578)

BMS3h-217-29
DIQMTQSPSSLSASVGDRTITCRASHFIGTLVSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 579)

BMS3h-217-30
DIQMTQSPSSLSASVGDRTITCRASHFIGTLVSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 580)

BMS3h-217-31
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (서열 581)

BMS3h-217-32
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDLATYYCGQEVLPATFGQGTKVEIKR (서열 582)

BMS3h-217-33
DIQMTQSPSSLSASVGDRTITCQASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFTLTISSLQ
PEDFATYYCGQEVLPATFGQGTKVEIKR (서열 583)

[0162]

[0163]

BMS3h-217-34
DIQMTQSPSSLSASVGDRTIITCRASHFIGTLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTFTLTIGSLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 584)

BMS3h-217-35
DIQMTQSPSSLSASVGDRTIITCRASHFIGTLLSWYQKPGKATKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPPTFGQGTVEIKR (서열 585)

BMS3h-217-2301
DIQMTQSPSSLSASVGDRTIITCRASHFIASLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 586)

BMS3h-217-2302
DIQMTQSPSSLSASVGDRTIITCRASHFIGLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 587)

BMS3h-217-2303
DIQMTQSPSSLSASVGDRTIITCRASHFIGLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIRR (서열 588)

BMS3h-217-2304
DIQMTQSPSSLSASVGDRTIITCRASHYIASLLSWYQKPGKAPKLLITYGSLLSQSGAPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 589)

BMS3h-217-2305
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWASYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 590)

BMS3h-217-2306
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWSSYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 591)

BMS3h-217-2307
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWSSYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 592)

BMS3h-217-2308
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWGSWLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 593)

BMS3h-217-2309
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWASWLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 594)

BMS3h-217-2310
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWSSWLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 595)

BMS3h-217-2311

DIQMTQSPSSLSASVGDRTIITCRASHMIAQLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 596)

BMS3h-217-2312
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLRWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 597)

BMS3h-217-2313
DIQMTQSPSSLSASVGDRTIITCRASHRIAQLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 598)

BMS3h-217-2314
DIQMTQSPSSLSASVGDRTIITCRASHYIASLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 599)

BMS3h-217-2315
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLIRFGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 600)

BMS3h-217-2316
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITYKSYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 601)

BMS3h-217-2317
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITWGSYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 602)

BMS3h-217-2318
DIQMTQSPSSLSASVGDRTIITCRASHFIGPLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDSATYYCGQVLWLPATFGQGTVEIKR (서열 603)

BMS3h-217-2319
DIQMTQSPSSLSASVGDRTIITCRASHMIAQLLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 604)

BMS3h-217-2320
DIQMTQSPSSLSASVGDRTIITCRASHFIGPLSWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 605)

BMS3h-217-2321
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLMWYQKPGKAPKLLITYGSLLSQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 606)

BMS3h-217-2322
DIQMTQSPSSLSASVGDRTIITCRASHFIGSLLSWYQKPGKAPKLLITYGSLWQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQVLWLPATFGQGTVEIKR (서열 607)

[0164]

[0165]

표 4

인간 항-CD40 가변 도메인을 코딩하는 뉴클레오타이드 서열

[0166]

BMS3h-56-201	GAGGTGCAGCTGTTGGAGTCCGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT TCACCTTTCCGGATTATGAGATGTGGTGGGTCGGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC GCAGGGTACGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAACTTCCGTTTTACTTTACAGGAGT GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 608)
BMS3h-56-258	GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT TCACCTTTCCGGATTATGAGATGTGGTGGGTCGGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAAATCC GCAGGGTACGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAACTTCCGTTTTACTTTACAGGAGT GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 609)
BMS3h-37	GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT TCACCTTTGAGTGATGAGATGCAATGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCGG TGATGGTTATCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACT GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 610)
BMS3h-38	GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTG TAGTGGTGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGTAATTACTGTGCGAAAGAGCGTTTCGTTTGTACTACT GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 611)
BMS3h-41	GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT TCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCATCTATTTCGG TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAAGAGCGCTTGGGTATTTTGACTACT GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 612)
BMS3h-43	GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTACAGCCTCCGGAT TCACCTTTAATATGTATGAGATGTCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG GCGTGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGTAATTACTGTGCGAAAGAGCGATTACGTATGCTATGA GGTATGCGCGTTTGTACTACTGGGTACGGGAACCTGGTCAACCTCTCGAGC (서열 613)
BMS3h-56	GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT TCACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC GCAGGGTACGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGTAATTACTGTGCGAAACTTCCGTTTTATTTTGACTACT GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 614)

BMS3h-106
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGACTTATCATATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCAATGATTGATGC
GGATGGCTTTGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAACCGGTCGCACTTTGTCAGT
TTGACTACTGGGTACGGGAACCTGCTCACCCTCTCGAGC (서열 615)

BMS3h-107
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCTTCCGGAT
TCACCTTTTCGGGTATGATATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCGGGTGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCACTCTCCC GCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAATATCCTAATCGTTTTCGCTTA
ATAATTGTACTACTGGGTACGGGAACCTTGGTCAACCTCTCGAGC (서열 616)

BMS3h-131
GACATCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACCGTGTCAACATCACTTGCCGGGCAATA
TTCTTATTTTGTGGGCTTAGCTTGGTACCAGCAGAAACAGGGAAGGCCCTTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAATGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAGTCTGCAA
CCTGAAGATTTTGTACTGTACTGTCTCAGAAATGCGGTTGGCTTGTACTGTGCGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 617)

BMS3h-193
GACATCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACCGTGTCAACATCACTTGCCGGGCAAGTC
AGACGATTAAGCGTCTGTTAAATTGGTATCAGCAGAAACAGGGAAGGCCCTTAAGCTCCTGATCTATCTTGCCTCCCG
TTTGCAAAATGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAGTCTGCAA
CCTGAAGATTTTGTACTGTACTGTCTATCAGATGCGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 618)

BMS3h-198
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCCTGATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCAGCAGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGTAATTACTGTGCGAAAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAAACCTGCTCACCCTCTCGAGC (서열 619)

BMS3h-202
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGACTGCTGAGATGTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGGC
TAGTGGTGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC GCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGTAATTACTGTGCGAAAGAGCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGTACGGGAACCTGCTCACCCTCTCGAGC (서열 620)

BMS3h-217
GACATCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACCGTGTCAACATCACTTGCCGGGCAAGTC
ATTTTATTTGACTCTGTATCTTGGTACCAGCAGAAACAGGGAAGGCCCTTAAGCTCCTGATCACTTATGTTCCCTT
GTTGCAAAATGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAACATCAGCAGTCTGCAA
CCTGAAGATTTTGTACTGTACTGTGTGTCAGGGGTGCTGTGGCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 621)

BMS3h-1

[0167]

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGAAGATAGAGTAGACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGAGTC
GGATGGTCAGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCCGCGGTATATTACTGTGCGAAAATCGGATTCTGACTTTGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 622)

BMS3h-2
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGTGGGGTATGACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAA
GGAGGGTCTGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGATACCGCGGTATATTACTGTGCGAAAGGTAGGATTCTGGGCTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 623)

BMS3h-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTATGAGCATGATAGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGAGC
TATGGGTGATGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCGTCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTTACTCTTCAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 624)

BMS3h-4
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTCGCTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACTTC
GAATGGTTATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 625)

BMS3h-5
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTATGAGCATGATAGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCATTTGGTCC
GGATGGTTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 626)

BMS3h-6
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTATGAGTATCATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTACCTC
TCTTGGTACGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTTCTGCTTACGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 627)

BMS3h-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTATGAGATGCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTGCC
GGGTGGTATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGATACCGCGGTATATTACTGTGCGAAAGGGCGTGTCCGGATCTGCTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 628)

BMS3h-8
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGTCTGAGGAGATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCCGC

[0168]

TGATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTGTTCGGATCTGCTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 629)

BMS3h-9
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTATGAGGATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGCGGT
TGATGGTATGAGATCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGTAAAGGTTCCTCTTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 630)

BMS3h-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGACGATGGATATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACGGG
TGATGGTATGAAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 631)

BMS3h-11
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGCGTGATGATATGACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAAATGC
TGGGGGTGTGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGATACCGCGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 632)

BMS3h-12
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGATGATTCTATGACGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTGAG
TGATGGTGCAGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 633)

BMS3h-13
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTACTGAGGAGGATATGACGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATAG
TGTGGTGAAGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGACACCGCGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 634)

BMS3h-14
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATTGCGGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATAA
TCCTGGTCAGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCAGGATACCGCGGTATATTACTGTGCGAAAGGTACTGTCTTACGTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 635)

BMS3h-15
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGACGATAGTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATGG
TGGGGGTATATACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG

[0169]

TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAGGTTCCCTCGTCTTCATT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 636)

BMS3h-16
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTACAGGACCTATGACTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGCGTA
TAATGGTGGTATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCTAAATTGACTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 637)

BMS3h-17
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAATTATCCGATGTCTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAAATGC
TACGGGTTCTATTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATTCTCATTTGATGT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 638)

BMS3h-18
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGTGATTATGATATGAGTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGG
TACTGGTAATAGTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTGGTGCCGATTCTTGCTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 639)

BMS3h-19
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGCTGATGCGATGACGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAAATGT
GGATGGTGATCGACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTACTGTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 640)

BMS3h-21
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATCGGGCGGATATGACGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCGGG
GGAGGGTAAGTGTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCTCAATTGGTTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 641)

BMS3h-22
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCAITGGGGCGATGTCTTGGGTCGCGCAGGCTCCGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAAATTC
TTCTGGTTGGGTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCTCAATTGGTTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 642)

BMS3h-24
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGTGATGAGCGATGACTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTCTCTCC
TGAGGGTGCTCCGACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCTAAATTGACTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 643)

BMS3h-26
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATATAATCATGATATGTCTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTCG
GGGTGGTCTTCAGACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTGTGCGGATCGCATT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 644)

BMS3h-27
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAATGAGTATCTATGTGCTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAAATGG
GGATGGTGTATATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATTCTCGGCTATGAGT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 645)

BMS3h-28
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGGATATGCTATGTCTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATCC
TTATGGTTCTATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATGCTAGTCTTACTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 646)

BMS3h-29
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGGATATGATATGTCTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTTCGGC
GCTTGGTGCTACTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTACTTCCGGCTTGGAGT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 647)

BMS3h-30
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAAGCGTATTATATGACTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGTCC
TTCTGGTAATAGACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCGATCTGCATT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 648)

BMS3h-31
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCATATGATATGACTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTCTCC
GACGGGTGGGACACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGTTATCCGTATTGTCTT
TTTCTCCGTTTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 649)

BMS3h-32
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTAAGTATTGGATGGGTTGGGCTCCGACAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGATTGATTCC
GCAATGGTCTGGTATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGCTCTAAGTTTATGACTA
CGTATACGTTTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 650)

BMS3h-33

[0170]

[0171]

GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTTCGCTTATCCGATGCATTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTCTC
GAGGGGTTCGGTTACATACCTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCTAGTTGGAGCTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 651)

BMS3h-34
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTGCGAATAGTAAATGACTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTATATCC
GGATGGTGGGTCTACATACCTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTATTCCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 652)

BMS3h-35
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTGGGCCGAGGAGGATGGGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGA
TATTGGTCGTAGGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGCGCAGGGGTGTGTGTGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 653)

BMS3h-36
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTGAGGATTATAGGATGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCTAC
TTCTGGTAGGTCGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGTTCTGTTGACTACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 654)

BMS3h-39
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTCCGGAGTATAGATGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCAGCGATTTCGCG
TGAGGGTCGGGCTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAACCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCTGTTCTGTTGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 655)

BMS3h-40
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTGACCTTATGAGATGCTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATTTCTTCTC
TTCTGGTAATTATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTGATGTTTACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 656)

BMS3h-42
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTGATCTGAGGAGATGAGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCC
TAATGGTGGCTTTTACATTCTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCTATTCTGTTGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 657)

BMS3h-44
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTGGTCATTATGATATGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTATATGG

TGCTGGTCTGAATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTAGTGTATTGTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 658)

BMS3h-45
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTAGGAGTTATGAGATGGCTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTATGATC
TCTGGGTACGAAGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTCTTCTACTATATTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 659)

BMS3h-46
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTATAGTATGAGATGGCTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTGTC
GTC TGGTTGAGACACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGTGTATTTTACTACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 660)

BMS3h-47
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTATGCTTATGAGATGGCTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTGGA
TGATGGTACGCGGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTATTTTACTACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 661)

BMS3h-48
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTGCTGATCATGGGATGACGTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTGGTCC
GTCTGGTGAGGCGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGATTTCCTAATCTGTGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 662)

BMS3h-49
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTGGATCTCAGGATATGCTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTAGTCC
GAA1GGTTGGATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATAGGTCTGATTTTACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 663)

BMS3h-50
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTGGGATTATGATATGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTCTGTA
TCCGGGTGGTGTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCGAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGTTCTAAGGGTTTACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 664)

BMS3h-51
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGG6GGTCCCTGCCTCTCCTGTGTCAGCCTCCGGAT
TCACCTTTTGGGTTATTGGATGACTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATCC
GCAGGGTGGGATGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCTCTCGGACAATTCGAAGAACACGCTG

[0172]

[0173]

TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCGGTATTCTCTAATTTGGAGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 665)

BMS3h-52
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGAGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGCCTATGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGCGCA
GACGGGTTCTTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTAAGATTCCGAATTTGGTTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 666)

BMS3h-53
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGGATAGTGAGATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGCGCA
TAATGGTGGGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGTCACTCTCAGCAGACTG
AGGCTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 667)

BMS3h-54
GAGATGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCTACTTATGATATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGATTTTCTCC
GAATGGTTGGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAGACGCAATTTGACTACT
GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 668)

BMS3h-55
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGTTTATGATATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTTC
TTGGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAAGAAATTTTGACTACT
GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 669)

BMS3h-57
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTCATGAGGATAGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTACTAGGAGTAAGTTTGACT
ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 670)

BMS3h-58
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAGAAGTATATTATGGGTTGGGCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTGATTA
TTGGGGTCAGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTAGTCACTCTATTCTCTGC
AGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 671)

BMS3h-59
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATTATGCGATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAACGATTTCTGTA
TGTGGGTATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCTCTGCGGGGGGAGGCGT
TTACGGAGCGTTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 672)

BMS3h-60
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCCGTATATGATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGGT
TAATGGTAATAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGGTTGGTTCGAAGACGTCGT
CGGATAAGGATTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 673)

BMS3h-61
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTACGACGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTAG
TGCTGGTGTCTGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATTTGGTGGGCATCTCAGGGTTC
AGTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 674)

BMS3h-62
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGCTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCTAGGGAGTGGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGACGC
TATGGGTGAGACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATTCTCGGAATAAGGGGTTTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 675)

BMS3h-63
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTACGAGTGAGTATATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACAG
GTATGGTAGTACGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACATGAGTCTAAATTGGGAGACTT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 676)

BMS3h-70
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGTGTATAGTATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACTCC
TAATGGTACTCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTCTTGGTCGGGGTCTTATC
CTGGTGTGATTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 677)

BMS3h-71
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGAGTTATGCTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAGGTATTACGGC
GGATGGTACTGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTCTATTCCGATGCTTACGT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 678)

BMS3h-72
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCATCTATGATATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTCTTCC
TAATGGTACTGGTATATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATCAGAGTGTTCATCATGCTG
TTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (서열 679)

BMS3h-73

[0174]

[0175]

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGAGAATTATGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTGCGCC
GCATGGTCGGCTTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCCGGGTATATTACTGTGCGAAAGGTGAGATTCCGATGCTTGATT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 680)

BMS3h-74
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTTCGAATTATGATGATGATGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TTTTGGTGATATTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCCGGGTATATTACTGTGCGAAAAATGATATGGTGATGAAGAATG
GGGGGTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 681)

BMS3h-75
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGAGAGGTATGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTGATTC
CGGGGGTTGGTCTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGGGTATATTACTGTGCGAAAGGGTTGGTGCCGATCTGAGGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 682)

BMS3h-76
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TATGGGTGATGCTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGGGTATATTACTGTGCGAAAGGTGATTTCCGAGATTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 683)

BMS3h-77
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TATGGGTGATGCTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCCGGGTATATTACTGTGCGAAAGGTGATTTCCGCGCTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 684)

BMS3h-78
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGAGAATGATCGGATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGATTCTGCG
TACTGGTGGTGATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCCGGGTATATTACTGTGCGAAAGGTGATTTCCGAGATTGTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 685)

BMS3h-79
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTAATCAGCCTTATATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTGATGC
TTCGGGTGGTACTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGGGTATATTACTGTGCGAAAGGTGATTTCCATCTTGTGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 686)

BMS3h-80
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTGATGG

TGGGGTTATAATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGGGTATATTACTGTGCGAAAGGGCAGGTCTCTGAGCTGCTGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 687)

BMS3h-81
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTTGTTTCGTGCAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTATGCGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCCGGGTATATTACTGTGCGAAAGGTGCGATTCTCAGCTTGGTGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 688)

BMS3h-82
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGTTTCGTGCAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTATGCGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCCGGGTATATTACTGTGCGAAAGGTGATTTCTTCTTGTGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 689)

BMS3h-83
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTTGATGATTCGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTAAATGA
TGCTGGTAGTCTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCCGGGTATATTACTGTGCGAAAGGTACTATTCTCTTCTGAGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 690)

BMS3h-84
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGTTTCGGAATACTAGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTGATGG
GACTGGTGGTGATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGGGGACACCCGGGTATATTACTGTGCGAAAGGGCTTATTCTGATCTCAGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 691)

BMS3h-85
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTATTGG
TGTTGGTCAATGAGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCCGGGTATATTACTGTGCGAAAGGTACTATTCTCTTCTGAGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 692)

BMS3h-86
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCACGATTACTGA
GAGGGGTGATGTGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCCGGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 693)

BMS3h-87
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTATTGG
TGGTGGTCAATGAGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG

[0176]

[0177]

TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 694)

BMS3h-88
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTTCATGAGACGGAGATGACGTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTAAATCG
GCTGGGTCAGGATACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCTGGGCTGGTTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 695)

BMS3h-89
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTTTCGATGATTGATGAGTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTAAATGA
TGCTGGTAGTCTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 696)

BMS3h-90
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTGATTAATGAGATATGACTTGGGTCGCGCAGGCTCCAGGGAAAGGATCTAGAGTGGGTCTCAGGATTACTGA
GAGGGGTGATGTGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGAATTCCTACGTTGGTGT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 697)

BMS3h-91
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTTTCGATGATTGATGAGTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTAAATGA
TGCTGGTAGTCTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCTAATTGTGACTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 698)

BMS3h-92
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTGCTGATGAGCGATGACTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTCTCC
TGAGGGTGCTCCGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCCTGATCTTCACT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 699)

BMS3h-93
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTTCAGGATAGTGATATGACGTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGC
GCCTGGTGGTAGTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCTTAATCTTAGGT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 700)

BMS3h-94
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGGATACTATGAGTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGATGG
GACTGGTGGTGATACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAGGTTCTTGAGCTGCTGT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 701)

BMS3h-95
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTTCAGGATAGTGATATGACGTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGC
GCCTGGTGGTAGTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCGTATTCTTAATCTTGTGT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 702)

BMS3h-96
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCGCCGGAT
TCACCTTTGATCTGGCGGAGATGACTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
GGATGGTGTCTCTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGTGTTATTCGCTCTGACTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 703)

BMS3h-97
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTACTGATAGCATATGAGTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGGATTTGCGCC
TGATGGTAGCTATACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGTGTTATTCGCTCTGACTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 704)

BMS3h-98
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTGCTGAGGATGATATGACTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
TGATGGTAGTCGGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTACCGAGGACGCCGCGGTATATTACTGTGCGAAAGGGTAGCTCCGATTGACTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 705)

BMS3h-99
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCGCCGGAT
TCACCTTTGATCTGGCGGAGATGACTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
GGATGGTGTCTCTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGAGGTCTTGTGTTGTTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 706)

BMS3h-100
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTCGATGATGTCGTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGGATTGATCC
TGGGGGTGCTCAGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTAGCTCCGATTGACTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 707)

BMS3h-101
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCGTGTGCAGCCTCCGGAT
TCACCTTTGAGCATCGGATATGAGTTGGGTCGCGCAGGCTCCAGGGAAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
TAGTGGTAGTCTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTAGCTCCGATTGACTT
TTGACTACTGGGGTCAGGGAAACCTTGTCACCGTCTCGAGC (서열 708)

BMS3h-102

[0178]

[0179]

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTAGTGAGGCGGAGATGAATTGGTCCGCCAGGCTCCAGGGGAAGGGTCTAGAGTGGGTCTCACGATTTACGAC
GGATGGTGATCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCGTATTCTACTCTTCATT
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 709)

BMS3h-103
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCAGGAT
TCACCTTTTGAATAGTGATATGACTTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCATATATTGGGG
TGATGATGATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTCGGATTCTTGTTGT
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 710)

BMS3h-108
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTAATGGCGGATATGCACTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGCTCTACGAGGGGGCGA
CTGCTTTTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 711)

BMS3h-109
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGGGCGTATGATATGGGTTGGTCCGCCAGGCTCCAGGGGAAGGTCTGGAGTGGGTCTCATGATTTCG
TACTGGTTCTGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGCTCTATAAGTTTGACTACT
GGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 712)

BMS3h-110
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGGGAGTGGGTCTAGTGAATTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCACGGATTGGTAG
TAATGGTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGATGGTTCCATATTTGGTTT
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 713)

BMS3h-111
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTAATCTGTTTGAATGACGTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGATTCTCTAATTCTGTG
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 714)

BMS3h-112
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGGGAGAGTGATATGAAGTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCTTCTCTGCTCTAAGT
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 715)

BMS3h-139
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGATAGTAGTGAGATGAGTTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCATCGATTGAGAA

[0180]

TCAGGGTGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCGATTCTTAATCTTGTT
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 716)

BMS3h-140
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGATGCGTATCTATGATTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCATGATTGCTTC
GGGTGGTGGTGGCATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTACAGGAATTTTGACTACT
GGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 717)

BMS3h-141
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTATGAGTATTCTATGGCTTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAGGGATTACTTC
TAATGGTAATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATCGACTGGGGCTAATAGTAGGA
ATTTTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 718)

BMS3h-142
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGAGGGTATCTGATGTCGTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAAGTATTGCGGC
TAATGGTATGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGAGGGGTATTTGGGATG
GGGATTTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 719)

BMS3h-143
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTATGAGTCTACGATGACGTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAACTATTCGGCA
TCGGGTGAGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCTGATCTTCAGT
TTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 720)

BMS3h-144
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGGGATGATAGTATGAGTTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCATCTGATTGCGCC
GCGGGTGGTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACAGTCTGTCAGCGGGTATAGTA
GGTCTTTTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 721)

BMS3h-145
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCGAGAAATCCGATGTCGTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCAACGATTCTGCG
GAATGGTCTCTACATCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATAGTCAGCAGCCGGTCTGCT
GGTTTGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 722)

BMS3h-146
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGTGAATTATCATATGACGTGGTCCGCCAGGCTCCAGGGGAAGGTCTAGAGTGGGTCTCATCTGATTCTGA
TAGTGGTAAGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG

[0181]

TATCTCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCGCTCTCTTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 723)

BMS3h-147
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCGCGAGTATCATATGCGTTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGA
TATTGGTAGTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTGGGGGGCGGGGAGTTTTT
CTTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 724)

BMS3h-148
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATATGATATGAAGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCTGGTGTGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGTAGTGTAAAGTATCCTCTTA
ATTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 725)

BMS3h-149
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTAAGTATTATGATATGAGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTATATGC
TAATGGTAAGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTGACTCTTGCTCTTAAT
ATTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 726)

BMS3h-150
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTATGGATTATGATATGAAGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTATGCG
GCTTGGTAAGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTATGTTAAAGTATCCTCTTA
ATCTTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 727)

BMS3h-151
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTCCGCAATTATACATGATGGCGTGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTCACTG
CCCTGGTTGGCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATATGGGATGGTCTCTTTGA
CTTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 728)

BMS3h-167
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAGTGGTACGCCGATGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTGGGGA
TGAGGGTCAGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGGTACTCCGGATTGACTT
TGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 729)

BMS3h-168
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAGTAGTAGTTGATGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGGTG
TGATGGTCCGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGGGTATTTCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 730)

BMS3h-169
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAATCTGGTGAGATGACGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGG
GTCTGGTTCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGATGACACCGCGGTATATTACTGTGCGAAAAGGGTATTTCTACTCTCTCATT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 731)

BMS3h-170
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTCTGAGTCTATGATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGATTGGGTA
TCTGGTGCTACTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGGTGTAAGTGATGATAATT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 732)

BMS3h-171
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGGTCAGCATAGTATGCTATGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGT
TCCGGGTCCGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTCTTAGGGATTTCGTCCCG
GTGATAGTAAGAGTTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 733)

BMS3h-197
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGGTCTCGTGCTATGGATTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGA
TATGGGTCTTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGGTGGTGGTTTGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 734)

BMS3h-199
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGGTTATGATAGGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGATTGATGG
TCCYGGTGGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGGAGGAGGGTTCCCTGATTTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 735)

BMS3h-200
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGGTAGTATGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGSATTGATCC
GTTTGGTCTTGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGTGTGGTTCCTGATTGAATT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 736)

BMS3h-201
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGTAAAGTATGTTATGGGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGGTAG
TTATGGTGGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGCTTACTCTTAGTGCGGACTA
AGTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 737)

[0182]

[0183]

BMS3h-203
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAGGATTATGTGATGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTTCAG
TCGGGGTGATATTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAGGCGTCTTAGTGATTATC
GGTTTGACTACTGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (서열 738)

BMS3h-204
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGGAGTTTGATATGTATTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCC
GGCTGGTACTGGTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGATCGGTCTAGTCTTT
TTGACTACAGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (서열 739)

BMS3h-205
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGTACGGGTATGACGTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTTCAG
TTATGGTCGTGATACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTGAATGCGGCGTGGGTTTG
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 740)

BMS3h-206
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTCGTATCCGATGAGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATGCG
GCCGGGTACGAGGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACAGATGTCTAGTGGGGTTTTCG
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 741)

BMS3h-207
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAATCAGGATATGACTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTGATAG
TTCTGGTCAGCTTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTAAGTCTCTTGCGCGGTTTG
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 742)

BMS3h-208
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
TCACCTTTCTGAGTCTGATATGAAGTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAAGTCC
GAATGGTTGGGATACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACAGATGTCTAGTGGGGTTTTCG
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 743)

BMS3h-209
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGTATGTGATGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGTAC
GTCCGGTAAGTATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACAGTGGTCTCTGACTCGGGTTTC
ATTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 744)

BMS3h-210
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTGGAGCATATGAGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACGGG
TGATGGTGATCGTACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACAGGTTTCGTGGAAATGTCGTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 745)

BMS3h-211
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTGGTATAAATAGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCAAGGATTGCTCC
GTCTGGTATTATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTGCGTGGAATTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 746)

BMS3h-212
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAATATGAGATGAGGTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCTTC
GGCTGGTACTGATACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGTCGCTTAATTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 747)

BMS3h-213
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGTAGCTCCGGAT
TCACCTTTTGAAGGAGCCGATGACTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAATTAATTGATCC
GGGTGGTGGGGGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTAATAGTATGTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 748)

BMS3h-214
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTTCGCTATCCATGCAATTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTTC
TTCGGGTATTACGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTACTCGGCTGCATTTTCCTG
CGCAGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 749)

BMS3h-215
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTTCGATTATGCAATGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCCTC
TGAGGGTTCTAGGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTCGCGCCGATGCGTCGAAAT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 750)

BMS3h-230
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGCCGTATGATATGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCCTC
TCAGGGTAAATCGGACATACTACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTCTCATCATTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 751)

[0184]

[0185]

BMS3h-231
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGTAGGTATCGGATGGGGTGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAAGATTAAATTC
GACTGGTTCTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAAATTGGCATCGGGGAGGTTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 752)

BMS3h-232
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGTAGGTATCGGATGGGGTGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACGATTACGAA
GACTGGTTTCTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTGAAGAAGCATAAGTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 753)

BMS3h-233
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGCAATTATAATATGCGGTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACGATTACGAA
GACTGGTTTCTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGCGGGCAGTTTGATTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 754)

BMS3h-234
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTAGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATCTTATAGTATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACTATTGATGG
TAGTGGTATGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGATTCTCTGAAGGCTCTTTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 755)

BMS3h-235
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGCTTTATGGGATGTTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCATATATTGGGCC
TTATGGTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAAAGCGGAAGAAGTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 756)

BMS3h-236
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTAGGTATCGGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAAGTATTACTCC
GTATGGTGCTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATATGGTAAGTGGTATTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 757)

BMS3h-237
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATGAGTATGCGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACGATTGATCG
TCGGGTCTTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTGGGCTTTTACGTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 758)

BMS3h-238
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAGCGGTATAATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACGATTGATCG
GCTGGGTCTTGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGCGGGTTCGTGGTCTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 759)

BMS3h-239
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTATTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACGATTTCGTC
GTGCGGTACTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATATCCTCAGCCTTATCTCTTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 760)

BMS3h-240
GAGGTGCAGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGGTGATATGATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACGATTTCGTC
GACTGGTGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATATCCTCAGCCTTATCTCTTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 761)

BMS3h-241
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCAGTTATGATATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAGCTATTTCTCC
TAATGGTACTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACCTCCGAGGTGAATGATGAGT
TTGACTACCGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 762)

BMS3h-243
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGGAGGATATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCATATTTCCGCC
GAATGGTTATGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTGGTCTAGTTTGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 763)

BMS3h-244
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGTACTCCGATGGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAACTATTTCTGA
GAGTGGTTATAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATCGAATTCGACTACTGTTTGTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 764)

BMS3h-245
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAAATCGGTGATATGGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTCCGCATCGGGCGTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 765)

[0186]

[0187]

BMS3h-246
GAGGTGCAGCTGTTGGAGTCTGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGATCATTGATGATGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATGC
TTTGGGTGATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGATGGTTCTCTCTGTAAGT
TTGACTACTGGGTGAGGAAACCTTGTCACCGTCTCGAGC (서열 766)

BMS3h-247
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAGTGATCATTGATGATGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATGCC
GCATGGTGTTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATCCTACTTTTGACTACTGGGTCT
AGGGAACCTTGTCACCGTCTCGAGC (서열 767)

BMS3h-248
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCCGCATATGATGATGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATGCC
GGATGGTACTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACGTTTCGTATAGTTGGGATCGTG
GGTGGACGTTTGACTACTGGGTGAGGAAACCTTGTCACCGTCTCGAGC (서열 768)

BMS3h-249
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAGTCTTCGGATGAAGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGCTGATTATATCTATCTT
TTGACTACTGGGTGAGGAAACCTTGTCACCGTCTCGAGC (서열 769)

BMS3h-250
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCCGATATATAATATGCGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTCA
GACTGGTTTTCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGTGAACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGCGGGCAGTTTGATTGTTGACT
ACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 770)

BMS3h-251
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCCGATATCATATGGGTTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTGGGCT
GAGGGGATTATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATCGCCTTCGCGTATAGGTTTG
ACTACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 771)

BMS3h-252
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAATGAGTATGCGATGAGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCG
TCTGGGTCTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTGGGCTTTTACGTTTGACT
ACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 772)

BMS3h-253
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTAATTATAGTATGAAGTGGGCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCC
TGATGGTTGGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTGGGGGATGCTGTTTGGGGGT
GGAATTGTTGGGTTGACTACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 773)

BMS3h-254
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGGGATTATGATGATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTACGTC
TAATGGTGATTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATCTTTGATAAGTTTGACTACT
GGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 774)

BMS3h-255
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGGCTCCGGAT
TCACCTTTTCCACTATATAAGATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAATTATGATTA
TTGGGGTTGGCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTCCGATTCTTGACTCATG
ATAGTCTCAATTTTACTACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 775)

BMS3h-256
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTAGGCCCTATACGATGTGTGGGCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGTATTAGTGA
TGCTGGTTCTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGGATGTTCTTTTGACTACT
GGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 776)

BMS3h-257
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCAGAAATATCAGATGGCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTAGTGG
GACTGGTAAGAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACCTCTCAGAAATATTTTAGTG
TGCTGCGTTTGACTACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 777)

BMS3h-258
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGGGCTATACTATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGATTTCGAC
GTCTGGTGGGACATATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACCTTTGAAATGGTGGGCGTTTG
ACTACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 778)

BMS3h-272
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGCGTACTATGACTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGATTGATGG
TTATGGTGGGACATATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGATATTCTCAATTTTGACT
ACTGGGTGAGGGAACCTTGTCACCGTCTCGAGC (서열 779)

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[0189]

BMS3h-273
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGGGGCGGTGATATGACGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCCGC
TAGTGGTTCTGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTGTCGGGATCTTGTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 780)

BMS3h-274
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGATAGTTATGCGATGGGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGGGGC
TAAGGGTTTGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCTAGGGTAAGTTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 781)

BMS3h-275
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTACTCGGTATCAGATGGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTAATGT
TTGGGGTTCGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGTCTGGGAAGTTTGCTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 782)

BMS3h-276
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTTCTCTGTGCAGCTCCGGAT
TCACCTTTGGGAATTATAGTATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTATTC
TGCTGGTACGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTGATTAGGTTGTTGACT
ACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 783)

BMS3h-279
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGGTGGGTATGATATGGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGATTCTCC
GAATGGTTATGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGGTGAAGTTTGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 784)

BMS3h-282
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGTTGGTATGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGGC
TGATGGTGAGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTTCGTATGCTCTTGTTGATC
CTCTGAGGAGTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 785)

BMS3h-287
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTACGAATTATAGGATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
TCTGGGTGTGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAA1TGGAGGCTTAAGAATAGTCAGC
CGACGGAATTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 786)

BMS3h-292
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGCATCAGGCTCATATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATTATTAATCC
TTGCGGTTATATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACCTTGCCTAGTCGCTCTCTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 787)

BMS3h-293
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGAGACTGGTCAGATGGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAAATATTGATGG
GTCGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTACGAGAATATCGGTTTG
ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 788)

BMS3h-296
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGCTGCTATTCCGATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTATCAA
GGA1TGTAGGATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACAGGGTACGCCGTTGATGGT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 789)

BMS3h-297
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTCCGATGAGGGTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGAC
TGGTGGTACGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGATGGGTCTGATACATGCG
AGAGCTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 790)

BMS3h-298
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGATAGTCTGGGATGGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATATATTGCGGC
TGAAGGGTCTTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATGATGGTCTGTTGAGTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 791)

BMS3h-299
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTAGTGAGTCTGATATGAGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTGATCA
TATTGGTGGTGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGATGGTCTGTTGGGTCTA
TGTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 792)

BMS3h-300
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCTCCGGAT
TCACCTTTGCTGGTGGGTATATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGGGC
TAGTGGTGGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGGGTGAAGTTAGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (서열 793)

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[0191]

BMS3h-301
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGAGGGGCATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCATATATTGGGAG
TCTGGGTTTGATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGGAGTTTAGTAATGGGGGGT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 794)

BMS3h-302
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAAGACTAGTCCCTATGTATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATCG
GACTGGTGGGCATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGCTCTGCTTACTGATGCGA
AGCGTTTGTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 795)

BMS3h-303
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGGTCCGGATATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTATTATCG
GAGTGGTCTGGATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTCCTCAGATGCTGGTTACTA
ATTTTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 796)

BMS3h-304
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTAATGATCCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTGGTCG
GGAGGGTGATCTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATTCTATGCGGCATCAGCCGT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 797)

BMS3h-305
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTGAAGACTTATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGGGC
GTCGGGTGCTGATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTACGCATCTGAATGGTCGGT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 798)

BMS3h-306
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGGGTGGCTATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATAT
TGATGGTGCTCCGACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGCGGGTCTTGSTCTT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 799)

BMS3h-307
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTGAAGACTTATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTTCAGGG
TGATGGTGCTCCGACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTAGTAAGCGTTTGACTACT
GGGGTCAGGGAACCTGTCACCGTCTCGAGC (서열 800)

BMS3h-308
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGCTGTCAGATGGGTGGGGCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAATATTGATGG
TCTGGTACGTATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGTGCGGAATTTGCTTTTG
ACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 801)

BMS3h-309
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTGAAGACTTATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTATGCC
TCATGGTACGTATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGATTAGGGGTGGATTGGTCT
ATGATACGCAGCCTTTGACTACTGGGGTCAGGGAACCTGTCACCGTCTCGAGC (서열 802)

BMS3h-310
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGTAAAGATATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGTC
GGATGGTACTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAGAGCTGGGTGGGTCTTGGCAGT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 803)

BMS3h-311
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGGATCGTATATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGGGC
GTCCGGTACGCTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGGAGGCTCTACTGATT
TGTGGGATTTGACTACTGGGGTCAGGGAACCTGTCACCGTCTCGAGC (서열 804)

BMS3h-312
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGATGAGAAGATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGT
GAGTGGTCTGATACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGCGGGTCTTGSTCTT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 805)

BMS3h-313
GAGGTGCAGCTGTTGGAGTCCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGAGGAGAGGATGATTTGGGTCCGCCAGGCTCTGGGAAGGGTCTAGAGTGGGTCTCAGATATTTCGGC
TTCGGTGGGACTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGCGGGTCTTGSTCTT
TTGACTACTGGGGTCAGGGAACCTTGTCACCGTCTCGAGC (서열 806)

BMS3h-37-1
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCGG
TGATGGTTATCTACATACCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAAATCCAATGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGATTTTGACTACA
GGGGTCGGGGAACCTTGTCACCGTCTCGAGC (서열 807)

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[0193]

BMS3h-37-203

GAGGTGCAGCTGTTGGAGCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCTCTGTGCAGCCTCCGGAT
TACCTTTGGGTGGTATGAGTACAGTGGGTCCGCCGGGCTCAGGGAAAGGAAGT AGAGTGGGTCTACAGCATTTCTGG
TGATGGTATCTGACATACATACGCAGACTCCGTGAAGGCGGGTTCACCATCTCCCGCACAATTCGAAGAACACGCTG
TATCTGCAAAATGAACACCTGCTGCGGACGAGCCGGTATATTACTGTGCGAAGAGCTCTACTTTGACTACT
GGGTCGGGGAACCTGGTCAACGCTGTCAGAC (서열 821)

BMS38-37-204

GAGGTGACAGCTCTGGAGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
CTACTTTTGGATGGTATGAGATGCACTGGGTGCCGGGCTCAGGGAAGGGACTAGAGTGGGCTCAGCAATTTCTG6
TGATGGTTATCTGACATACTACGACGACTCGTGAAGGACGGTTACCATCTCCCGACAAATTCAGAAACACGCTG
TCTGACAAATGAACACGCTGCTGCGCGAGGACACCCGGTATTACTCTGCGAAGAGCTGGGGTCTTTGACTACT
GGGTCGGGGAACCTGCTGACCTGACGCTG (seq. 822)

BMS3h-37-205
GAGGTGCGACCTGTGGAGTCTGGGGGAGGCTTGTACAGCCTGGGGGGTCCCTGCCTCTCTCTGTGCAGCCTCCGGAT
TCAACCTTGGAGTGGTATGAGATGCAAGTGGGTCCGCGGGCTCCAGGGAAGGAGCTAGAGTGGGTCTCAGCAATTCGG
TGATGGTTATCGTACATACTACGCAAGACTCCGTGAAGGCCGGTTCACCATCTCCCGCGCAAAATCCAGAACAACGGT
TATCTGCAAAATGAACACAGCTCGCTGCTCGGAGCAACCGGTATATTACTGTGCGAAGAGTGGAGTATTTTGACTACT
GGGGTGGGAGCTCCGTGCTGAGGAGC (서열 223)

BMS3h-37-206
GAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTCTGTCAGCCCTCCGGAT
TCACTTTTAGTGGTATGAGATGCAAGTGGGTCCGCGGGCTCAGGGGAAGGAGCTAGAGTGGGTCTCAGCAATTTCTGG
TGATGGTTATCGTACATACTACGACAGACTCCGTGAAAGCCGGTTTCAACATCTCCCGCACAATTCAGAAACACAGCTG
TATCTGCAAAAGAACAGCTCGCTGCTCCGAGATACCGGCTATATTACTGTGCGAAGGGTGGAGTATTTTGACTACT
GGGGTCTGGGATCTGGTCACTGACGAGTCTGAGAGC (서열 824)

BMS 3h- 37-207

GAGGTGGCATCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTTGGATCGGAC
TACCTTTTGTAGTGGTTATGAGATGTCAGTGGGTCCGCGGGTCTCAGGAGAGGAGTAAAGTGGGTTCTACAGATTTCTGTG
TGATGGTTATGCTACATACTACGCACTCTCGTGAAGGCGGGTTACACATCTCCCGGACAATTCCAGAAACACGCTG
TATCTGCAAAATGAACCGATCTGCTGCGGAGGACACGCGGGTATATTCTGCGAAAGAGCTGGCCTTCTGTGACTACT
GGGGTGGGGGACATGCTGCTGACGCTCTCGAC (서열 825)

BMS3h-37-208

GAGGTGACAGCTGTGGAGTCTGGGGGAGGCTTGTACAGCTGGGGGTCCCTGCCTCTCTGTGACGCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAAGTGGGTCCGCGGGCTCAGGGAAGGACTAGAGTGGGTCTCAGCAATTCG
TGATGGTTATCGTACATACTACGACAGCTCGTGAAGGCGGTTCCACATTCTCCCGGCAATTCAGGAACACGCT
TATCTGCAAAAGAACACAGCTGCTGCTCGGAGGACGCGGTATTAATTACTGTGCGAAGAGCGCTTGTACTTTGACTACT
GGGGTCGGGGCTCCGCTGGTCCAGCTCTCTGAGC (서영 826)

BMS3h-37-209

GAGGTGCGATCTCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGATG
TACACCTTGGTGGTATGAGTACAGTGGGTCCGCGGGCTTCAGGGAAGGAGTAAAGTGGGTCTCAGCAATTTCTGG
TGATGGTTATCGTACATACTACGACAGACTCGTGAAGGCGGGTTCACATCTCCCGGACAATTCAGAAACACGCTG
TATCTGCAAAATGAACACGCTGCTGCGGAGGACACCCGGTATTACTCTGCGAAGAGTGGAGTTCTGTGACTACT
GGGGTGGGGGACCTGCTGCTGCTGCTGCGAGC (sister 827)

BMS3h-37-210

GAGGTGACGATCTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTGTGACGCTCCGGAT
TCACCTTTAGTGGTATGAGATGCAGTGGGTCCGCGGGCTCCAGGGAAGGAGTAGAGTGGGTCTACGCAATTCGTG
TGATGTTATCTGACATACTACGACAGCTCGTGAAGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCT
TATCTGCAAAATGAACACGCTCGCTGCGGACGAGCTCGGGTATATTACTTGCAGGAAGAGCTGCAGTTCTTTGACTACT
GGGGTCCGGGGAAGCTGGTCACTGCTGCTGCTGAGC (서형 828)

BMS3h-37-211

GAGGCTGAGCTGTGGAGCTCGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTGTGACCACTCCGGAT
TCCACTTTCAGTGGTATGAGATGAGCTGGTGGCTGCCGGGCTCAGGGAAGGAGCTAGATGGGCTCAGCATTCTCG
TGATGGTTATCGTACATACCGAGACTCCGTGAAGGCGGGTTCACCATCTCCCGCAGCAATTCCAAGAACAGCTG
TATCTCAAAATGACAGCTGTGCTGCCGAGGATACCGGGGATATTACTTGCGAAGAGCTGCTCTCTTGGACTAT
GGGCTCGGGGAGCACTGGCTCAGCTTCGAGC (sequence 829)

BMS3h-37-212

TGACCTGCAGCTGTGGAGCTCGGGGAGGCTTGGTAGCGCTGGGGGGTCCCTGCCTCTCTGTGCAGCCTCCGGAT
CAGGTTTGAAGTGGTAGAGTAGAGTGGTGGCCGGGCTCAGGAAGAAGCATAGAGTGGTCTCAGCATTCTCGG
TGATGGTTATCTGACATACACGAGACTCCGTGAAAGGCGGTTTCAACATTCTCCCGACCAATTCCAAGAACACGCTG
TATCTCAAAATGAACAGCTGTGTCGCCGAGCTTCCCGGATATATTACTTGCGAAAGAGTTGGAGTTCTTGGACTAG
GGGCTGCGGAGCCCTGGTCACTGCTCGAGC (서형 838)

BMS3h-37-213

GAGGTGCACGTTCTGGAGCTCGGGGGAGGCTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACAGCTCCGGAT
TACCTTTGAAGTGGTATGAGATGACAGTGGGTCCGCGGGCTCAGGGAAGAGCATAGATGGGTCTCAGCATTTCTGG
TGATGGTTATCGTACATACTACGACAGATCCGTGAAAGGCGGGTTCACCATCTCCCGGCACAATTCCAAAGACACGCTG
TCTGTCAGAAATGACAGCTGTGCTGCCGAGGACACCGGATATTACTTGTGCGAAGAGTTGCTCTCTTTGACTACC
GGGCTGAGGACCACTTGGTCATCGGCTCGGCTCAGGCT (서명 831)

BMS3h-37-214

CGAGTCAGCAGCTGTGGAGTCTGGGGGAGGCTGGTACAGCTGGGGGGTCCCTGCTCTCTCTGTCAGCACTCCGGAT
TGATTTTGAAGGGTATGAGATGACAGTGGTCCGGCTCAGGGAAGGACATAGAGTGGGTCTCAGCATTTCTGG
TGATGGTTATCGTACATACTACGAGACTCCGTGAAAGGCGGTTCACCATCTCCCGACCAATTCCAAGAACACGCTG
TCTGCTCAAAATGAACAGCTGCGTCCGAGGATACCGCGGTATATTACTTGCGAAAACTGGAGATTTTGACTACT
GGGTCGGGGAGCACTGGTCACTGGAGCTGAGC (sage 832)

BMS3h-37-215
GAGGTGCGCGTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAAGCTCCGGAT
TACCTTTTGAAGTGATAGATGTCAGTGGTGCCTGGGCTCAGAGGAAGGACTAGAGTGGGTCTACGCATTTCGTGG
TGATGTTATCGTACATACACGAGACTCCGTGAAGGCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTGT
TATCTGCAATGAACAGCTGCTGGCAGGACACCCGGTATATTACTGTGCGAAAGATGTCAGTTCTTTGACTACT
GGGTGCTGGGGAACCTGGTCACGCTGACCG (서열 833)

BMS3h-38-1
GAGGTGCAGCTGTTGGGGCTGGGGGAGGCTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TACCTTTTGGAGGAGGAGAGATGATTTGGGTGCGCAGGCTCAGAGGAAGGGTCTAGAGTGGGTCTACGATTAAAGTG
TAGTGGTGTAGCACATACTACGACAGCTCGTGAAGGGCGGGTTCACCATCTCCGCGCAAAATCCAAAGAACAGCTG
TATCTGCAAAAGAACAGCTGCTGCGCAGGATACGCCGGATATTAATCTGTCGAAAGAGCGTTCTGTTTGTACTAC
GGGGTCAGGGAACCTGTGACCGTCTCGAGC (서열 834)

BMS3h-38-2
GAGGTGCAGCTGTTGGCTCTGGGGAGGCTTGGTACAGCTCTGGGGGTCCTGCGTCTCTCTGCGCAGCTCCGGAT
TACCTTTTGGAGGAGGAGAGATGATTTGGGTTCGTACGGCTCAGGGAAGGGTCTAGAGTGGGTCTACGATTAGTGG
TAGTGGTGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAATTCCAAGAACACGCTG
TATTGCAAAATGAACAGCTCGCTGCCAGAGCTACCCGGTATATTACTGTGGGAAGAGCGGTTTCGCTATGACTACT
GGGTGCGAAATCCTGGTCACTCCGTCTGAGAC (서열 835)

BMS3h-38-203
GAGGTGCAGCTCTTGGCGCTCTGGGGGAGGCTTGTCAGCGCTGGGGGGTCCCTGCCTCTCTCTCGCAGCCCTCCGGAT
TACCTTTTGAAGGAAGAGATGATTTGGTCGTCAGGCTTCAGGGAAGGGTCTAGAAGGGCTCTACGTAATTAGTGG
TAGTGGTGTGACACATACTACGAGACTCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCACGAACACGCTG
TATCTGCAATGAACAGCTGCGTCGGAGGACCTCCGGTATATTACTGTGGGAAGAGCGCTTCTCTACGACTACT
GGGGTCAGGGAACCTGCTGACCGTCTGAGC (서열 849)

BMS38-3h-218
TACGCTGCAGCTGTGGCGCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCTCCGGAT
GACCTTTGAGGAGGAGGAGATGATTGGTTCGTGAGCTTCAGGAGAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GCACGGTTGGAGCAATACATCCAGCAGCTCTGGAAGGCGGGTTCACATCTCCCGCACAATTCAAGAAACAGCGTG
TACTCTGAAATGACAGCTGCTGCGGAGGATACCGCGGATATTACTGTGGGAAGAGCCGTTTCTGTTATGACTACT
GGGTGCGAGAACCTTGGTCACCGCTCTCGAG (서열 864)

BMS38-3h-219
 TGGCTGCAGCTGTGGCTGCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTCGCGCAGCTCCGGAT
 TCACCTTTGAGGAGGAGAGATGATTGGTCCGACAGCTCAGGAGAGGGTTCTAGAGTGGGTTCTCAGCATTAAGCAG
 GATGGTGTGATGACATACCTACCGACAGCTCGTGAGAGCCGGGTACATCTCCCGCGACAATTCAAGAAACAGCTG
 TAGTTCGAATAGAGCAGCTGCTGCGAGGATACCGCGGATTAATCTGTTGGGAAAGACCGCTTTCGTTATGACTACT
 GGGGTGCGAGAACCTGGTCACCGCTCTCGAGC (서열 865)

BMS3h-38-220
TACGCTGCAGCTGTGGCTGTGGGGAGAGGCTTGGTACAGCCTGGGGGGTCTCTCGTCTCTCTGCGCAGCTCCGGAT
TGACCTTTGAGGAGGAGGAGATGATTTGGTCCGACAGCTCCAGGAGAGGGTCTAGAGTGGGTCTCAGCTATTATGTCG
TACGCTGATACAGCACAATACGACAGACTCGGTGACGGGGCGGGTTACATCTCCCGCGACAATTCAGAAACAGCGTG
TATCTGCAAAATGACAGCTGCTGTCGCGAGCAAGCTGCGGTATATTCTTGGGAAAGACGCGTTCGTATTGACTACT
GGGGTCAGGGAACCTGGTCACCGCTCTCAGC (사별 866)

BMS3h-38-221

TGGTGTGCAGCTGTGGCTGTGGGGGAGGCTTGTGACAGCTGGGGGGTCCCTGCGTCTCTCTCGGCAGCCTCCGGAT
TCACCTTTGAGGAGGAGAGATGATTGGTCCGACAGCTCCAGGAGAGGCTTAGAAGTGGGTCACAGTATTAGTAGT
GCACGGTTGGAGCACAATACGCGAGACTCGTAGGGGCGGTTACCATCTCCCGGACAAATCCAGAAACACGCTG
TGTTCAGAAATGAACAGCTGCGTCCGAGGATACCGCGGAGTATTACTGTGGGAAAGACCGTTCGTATGACTACT
GATGTCGGAACACCTGCGCACCTGTCGAGG (시퀀스 867)

BMS3h-38-222
GAGGTGCAGCTGTGTGGCGTCTGGGGGAGGCTTGTGACAGCTGGGGGGTCCCTGCCTCTCTCTGCGCAGCTCCGGAT
TACCTTTTGAGGAGGAGGAGATGATTTGGTCCGCGAGCTTCAAGGAAGGCTAGAGTGGGCTCAGCTATTTGAG
GTGGGTTGTAGCACATACTAGCAGACTCCTGGAAGGGCGGTTACCATCTCCCGGCAATTCAGAAACACGCTG
TATCTGCAATGAACAGCTCGCTCGGAGGATACCGGTTATATTACTTGGGAAGAGGTTCTGTTATGACTACT
GGGTCAGGATCCCTGCTGACCTGTGGAG (서열 868)

BMS38-3h-223

TGACCTGCACGTGTGGCTGTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGGCGAGCCTCCGGAT
CAGCTTGTGAGGAGGAGAGATGATTGGTCCGTGAGCTCAGAGGAAGGCTTAGAGTGGGTCTACAGTATTATGTG
TAGTGTGGTGTAGCACATACGCGAGACTCTGTGAAGGGCGGTTCACATCTCCCGCGACAACTCCAGAAACACGCTG
TATCTGCAAAAGAACAGCTGCTGCGGGAGATGAGGATATTAATCTGTGGGAAGAGCCGTTCTGATGATCGACT
GGGATCGGACCTGCTGGTCCCTGTACGAC (서형 869)

BMS3h-38-224
GAGGTGCAGCTGTGGTGGCTGTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTCCGCGACGCTCCGGAT
TCACTTTTGGAGGAGGAGAGATGATTTGGTCCGTCAAGCTCCAGGGAAGGCTAGAGTGGGCTCAGCTATTAGTGG
TAGTGGTGTGACACATACTACGAGACTCGTGAAGGGCGGTTCAACATCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAATGAACACGCTGCGTCCGAGGACTACCGGTTATATTCTGTGGGAAGAGCGTTCCTCCGCTACGACTACT
GGGGTCAGGACACTGGTCAACCGTTCAGG (서열 870)

BM3h-38-225
GAGGTCGACGCTGTGGCGTCTGGGGAGGCTTGGTCAGCCTGGGGGGTCCCTGCGTCTCTCTGCGAGCCTCCGGAAT
TACCTTTGAGGAGGAGAGATGATTTGGTCCGTGACGCTCAGGGAAGGGTTAGAGTGGGTTCTCAGCTATTGATGG
TAGTGGTGGTGGCACAATACCGACAGCTCGTGAAGGGCCGGTTCACATCTCCCGGACAATTCCAAGAACACCGTG
TATCTGCAAAATGAACACGCTGCGTCCGAGGATACCCGGTATATTACTGTGGGAAGAGCCGTTCTGTTATGACTGCT
GGGCTACCGGACCACTGTGCTCATCTCGAGC (서열 871)

BMS3h-38-226

TACGCTGCACGTGTGGCGTCTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCGCGACCTCCGGAT
GAGGTTCTTGGAGAGAGAGAGATGATTGGGTCCTGACGGTCAAGGAAGAGGTCTAGAGTGGGTCTCACTATTATGGG
TAGTGGTGGTACACATACCGACAGCTCGTGAAGGGCGGGTTCACATCTCCCGACAATTCGAAGAACACGCTG
TATCTCGAAATGAACACGCTGCTGCGGAGATACCGCGGTATTACTTCTGGGAAGACCGCTGTACTACTGACTACT
GGGCTACCAAGCTTGGTCACTGCTGCTGCTGACG (size 872)

BM53h-38-227
GAGCTGCAGCTGTGGCGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGAGCCTCCGGAT
TACCTTGTGAGGAGAGAGAGATGATTGGTCCGTGAGGCTCAGGGAAGGGTTAGAGTGGGTCTCAGCTATAGTGG
TAGTGGTGTAGCACAATACGAGACCTGCTGAAGGGCCGGTTACCATCTCCCGACAAATCCAAGAACACGGT
TATCTGCAAAATGAACAGCTGCGTCCGAGATACCCGGTATATTAAGTGTGGGAAGAGCCCATGTACTATGACTACT
GGGCTGAGGCTACAGCCTTGGTCACTGCTGTCGAGC (region 873)

BMS3h - 38 - 228
GAGGTGCACGCTGTGGCGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCTCGCGAGCCTCGGAT
TACCTTTTGAGGAGGAGGAGATGATTGGTCCGCGAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTAGCTATTAGTAG
GAACGGTTTCAGCACAATACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCGAAGAACAGCTG
TATCTGCAAATGAACAGCTGCGTCCGAGGATACCCGGCTATATTACTGTGGGAAGAGGGCTCTGTTATGACTACT
GCGGTCAGGGAACCTGTGACCGCTCGAGC (seq. 874)

BNS3h-38-229

TAGCTGTACAGTCTTGGCTGTGGGGAGGCTTGGTACAGCTGCGGGGTCCTTGCCTCTCTCTGCGCAGCTCCGGAT
GACCTTGTGTGGAGGAGGAGATGATTTGGTCCGCCAGGCTCAGGGAAGGGTTAGAGTGGGTCTCAAGTATTAGTCG
CACGGTGGGAGCACATACCTACGAGACTCGTAGGGGGCGGTTACCATCTCCCGCACAATTTCGAAGAACACGTG
TATCTGCAATGAACAGCTGCTGCCGAGGATACCGGGTATTACTGTGGGAAGAGCGCTTTCGTTATAGGCTACCTG
GGGCTAGGCTACCACTTGGTCACTGGAGCAGG (sage 875)

BMS3h-28-230

TAGCTGCACGCTTGTGGCTGTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTCGCAGCCTCCGGAT
GACGCTTTGAGGAGAGAGAGATAGTTTGGGTGCCAGGCTCAGGGAAGGGTTAGAGTGGGTCTCAAGCTATTAGTCG
GGAGGGTGGGACACATACCTACGCAGACTCGTAGAGGGCGGGTTCACCATCTCCCGCACAATTTCAGAACAACGCTG
TATCTGCAATGAACAGCCTGCTGCCGAGATACCGCGGTATTACTTGTGGGAAGAGCGCTTCTGTTATGACTACT
GGGGTCAAGCCCTGGTCACTGCTGACGCTCGACG (서열 876)

BMS3h - 38 - 231

GAGGTGTCAGCTGTGTGGCTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCTGCGACGCTCCGGGT
TCCCTTCTGAGGAGAGGAGATGATTTGGTTCGCGAGGCTCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTAGTCG
GCAGGGTTGGAGCACATACTACGACAGACTCGTGAAGGGCCGGTTACCACTTCTCCCGCACAATTCGAAGAACGCTG
TATTCGAAATGAACACGCTGCTGCCAGGATACCCGGTATATTACTCGTGGGAAGAGCGCTTCTGTTATGACTACT
GGGTCAGGTCAGGCTCCCTGTGACCGCTCTCGAGC (서열 877)

BMS3h-38-232
GAGGTTCAGCTTTGTCGCTGCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
GAGGTTCGATGAGGAGGAGGATGATTGGTCCGCAGGCTCAGGGAAGGCTTAGAGTGGGTCACGATTATAGTAG
GGGCGGTGGGAGCACAATACGCAAGCTCTGGAAGGGCCGGTTCACATCTCCCGGACAATTCAGAAACAGCGTG
TATTCAGAAATGAACAGCGCTGCGTGGCGAGATACCGGCTGTTATCTAGTGGGAAGAGCGCTTGTTGTTAGCATCT
GGGTTCAGGAAAGCTTGATCCGCTCTCGAG (시퀀스 878)

BM53h-3n-233

GAGGTCTGACCTTTGGCGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGCTCTCTCGCGCAGCCCTCCGGAT
TACACTTTCGAGGAGGAGGATGATTGGGTCGCGAGCTCCAGGAGAGGCTTAGAGTGGGTTACAGCTATTAGTCG
CACGGGTTACAGCACATACGCGACACTCGTGAGAGGGGGGTTTCACTATCTCCGCGCAAACTCCAGAAACAGCGTG
TATCTGCAAAATGAACAGCGTCGCTGCGAGATACCGGGGTTATATTCTGGGAAAGAGCGTTTGGTTATGACTACT
GGGTCGCACTCTGGTCCGCGCTCGGAGC (서형 879)

BMS3h-38-234

GAGGTCTGAGGCTTGTGGCTGTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTCGCGCAGCTCCGGAT
TCCACTTTCAGGAGGAGGAGATGATTGGTCCGCCAGGCTCCAGGAGAGGTTTAGAGTGGGTCTCAGCTATTAGTAG
GAACGGTAGGAGCACAATACGCAAGCATCGTGAAGGGCCGGTTTACCATCTCCCGGACAAATCCAGAAACAGCCGT
TCTCTCAAAATGCAAGCTGCGTCCGCGGAGATACCGGGGTATTAATCTGGGGAAGAGCCGTTTCGTTATGACTACT
GGGTGATGGAACCGGTCGTCAGCTCTCGAGC (서열 880)

BMS3h-38-235
GAGGTGCAGCTGTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCTGCGCAGCTCCGGAT
TCACCTTTTGAAGGAGGAGAGATGATTTGGTCCGCGAGGCTCAGGGAAGGGCTAGAGTGGGTCTCAGCTATTAGTAG
GAACGGTTACAGCACATACTACGAGACTCGTGGAAGGGCCGTTACACATCTCCCGACAATCCAAGAACACGCTG
TATCTGCAATGAACACGCTGCGTCCGAGACACCGGTAATTACTGTGGGAAGAGGTTTCTGTTATGACTACT
GGGTCAGGGAACCTGGTCCAGCGTCTGACG (서열 881)

BMS3h-38-236
GAGGTGCAGCTTGTGGCTCTGGGGGAGGCTTGTGACAGCTGGGGGGTCCCTGCCTCTCTCCGCGACGCTCCGGAT
TACCTTTTGAAGGAGGAGAGATGATTTGGGTCGCGAGGCTCAGGGAAGGGTCTAGAGTGGGCTCAGCTATTAGTAG
GAAGGGTAGCAGCACATACTACGAGACTCGTGGAAGGGCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACACGCTGCGTCGGAGGATACCGGGTATATTAAGTCTGGGAAGAGCGGTTCTGGTATGACTACT
GGGGTCAGGCTCCGTGTGACCTGCTCAGC(서열 882)

BMS3h-38-237

GAGGTGCTTCTTGGCTCTGGGGAGGACCTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
TACACTTGGAGGAGGAGGATATTTGGTTCGCGAGCCTCAGGAGAGGGTCTAGAGTGGGTCTCAGCTATTATGTGC
GGCGGTTGGAGCACAATACGCGAGACTCGTGAGGGCGGGTTACACATCTCCGCGACAATTCAGAAACACGCTG
TATCTCGAAATGAACACGCTGGTGGCGAGGATACCGGGATATTAATCTGCGGGAAGAGCGGTTCTGGTATTGACTACT
GGTTCGAGGAACCTGGTCACTGCTCGAGC (서열 883)

BMS3h-38-238
GAGGTGCAGCTCTGGTGGCTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCTCTCGCAGCCTCCGGAT
TCACTTCTAGGAGGAGGAGATGATTTGGTCCGCGAGGCTCAGGGAAGGGCTAGAGTGGGTCACTATTAGTCG
CTCGGTTACAGCACATACTACGAGACTCGGTGAAGGGCGGTTACACATCTCCGCGACAATTCAAGAACACAGCTG
TATTCGAAATGAACACGCTGCGCGGACATACCGGTAATTACTGTGGGAAGAGCTTCTGTTATGACTACT
GGGGTCAGGCTCGTGTCACTGCTCAGC (사영 884)

BMS3h-38-239

TAGGCTGCAGCTGTGGCTCTCGGGGAGCGCTGGTACAGCTGGGGGGTCCCTGCCTCTCTCGCGAGCCTCCGGAT
CGACCTGTGAGGAGGAGAGATGATTGGTCCCGCAGCGTCCAGGGAAGGCTAGAGTGGGCTCAGCTATTAGTAG
GAACGGTATGAGCACATACCGAGACTCCGTGAAGGGCGGTTACCATCTCCCGGACAAATCCGAAGAACAGCGTG
TATCTGCAAAATGAACACGCTCGCTGCCGAGAGCCCGGTATATTACTGTGGGAAGAGCGGTTTCGTATGCTACT
GGGGTGCAGGACCTGGTCAGCTCTCGAGC (서열 885)

BMS38-38-240

TGACCTGCAGCTGTGGAGCTCGGGGAGGCTGGTACAGCTGGGGGGTCCCTGCCTCTCTCGCGAGCCTCCGGAT
GAGGCTTGTGAGGAGGAGAGATGATTTGGTCCGCCAGCGTCCAGGGAAGGCTAGAGTGGGTCTCAGCTATTAGTAG
GAACGGTTACAGACATACTACGACAGCTCGGTGAAGGGCGGTTACCATCTCCCGCAACAATCCGAAGAACACGCTG
TATCTGCAATGAACACGCTCGCTGCGGAGCCGAGTACCGGATATTACTGTGGGAAGAGCGGTTGCTATG

GGGGTCAGGAGACCTGTCGACCTCTGAGC (ATCC 876)

BMS3h-41-1
GAGGTCTTACCTTGATGGACTCTGGGGAAGCGTGGTACAGCTGGGGGGTCCCTGCCTCTCTCTGTGCAGCCTCCGGAT
CTGACCTTCAGTACGATAGAGATGATTGGGTCCGCAGCGCTCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTCCGG
TAATGGTGTAAATACATACATACCGAGACTCTGCGTAAGGAGCGGTTCACATCTCCCGGACAAATCCAGAAGACAGCTG
TATCTCGAAATGAACACGCTGCGTCCGAGAGAGCCGGTATATTACTGTGCGAAGAGCGCGCTAGGTTGGTCTACTACT
GGGACTCAGGAACCTTGTCATGCTCTCTGTGAGC (sacII 877)

BM53h-41-2
GAGGTGCTAGCTGTTGGAGCTCGGGGGAGCGTTGGTACAGCCTGGGGGGTCCCTGCGTCTCCTGTGCAGCCTCCGGAT
CACCCATTCTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCAGGGAAAGGTTGAGTGGATCTCATCTATTTCGGG
TAATGTGCTAATACATACACGACACCTCGTGAAGGGCGGGTTCACATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAAGAACACCTGCGTGGCGGAGGACCCGGTATATTCTGTGCGAAAGAGCGGCTTAGGTTTGACTACA
GGGTCAGGGAACCTGGTCAACGCTCTGACG (서형 888)

BMS3h-41-13

GAGGTGCGACGTCTTGGACCTCGGGGAGGCTTGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACAGCTCCGGAT
TCACCTTCTACTGAGTATGAGATGATTTTGGTCCGACAGGCTCCAGGGAAGGTATGGATGGGTCTCATCTATTTCGGG
TAATGTGCTAATACATACTACGACAGCTCCGTGAAGGCGCGTTCACCATCTCCCGGACAAATCCAAGAACATGCTG
TATCTGCAAAATGAACAGCTCGCTGCCGAGGAGCCGGTATTACTTACCTGCGGAAGAGCCGCTAGGTTTGGCTACT
GGGTGCGGACACTTGTGCTGACCTTCTGACG (서열 389)

BMS3h-41-49
GAGGTGCAAGCTGTTGGATTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCACTGCGTCTCTCTGTGCAGCCTCCGGAT
TACCTTCTACTGAGTATGAGATATTTGGGTCCGCCAGGCTCAGGGAAGGGTCTGGATGGGTTCATCATTTATTCGGG
TAATGGTGCTAATACATACTACGACAGCTCGTGAAGGGCGGGTTCACCATCTCCCGGACAATTCCAAGAACAGCTG
TATCTACAAATGAACCAAGCTCGCTGCCGAGGACACCGGGTATATTACTGTGCGAAGAGAGGGTCTAGGTTTGACTACT
GGGCTCGGGGACCTGGTACAGCTCTCGAGC (서열 898)

BMS3h-41-5
GAGGTGCAGCTGTGGGTCAGGGGAGGCTTGTACAGCTGGGGGGTCCCTGCCTCTCTGTGACCTCGGAT
TCACCTTTACTGAGTAGAGATGATTGGGTCCCGCAGCGTCCAGGGAAGAGTGTGAGTGGGTCAATCATTTTCGG
TAATGGTCTAATACATACTACGACAGACTCGTGAAGGCGCGTTACCATCTCCCGACCAATCCAGAAGACAGCTG
TATCTGCAATGAACAGACTTCGCTGCTGAGACACCGGCTATTACTTGTGCGAAGAGCGGCTTAGGTATGACGAG
GGGTCAGGGAAGCTTGTGACCTGTCCGAG (서열 891)

BMS3h-56-5
GAGGTGCACCTGATTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCCTGTGACAGCCTCCGGAT
TGATCTCTTCGGGATATAGAGTGTGTGGGTCCGCAGGCTCAGAGGAAGGCTGTAGAGCGGGTCTACGCTATTAATCC
GACGGGTACGGCTACATACACGACAGCTCTGTGATGGGCGGGTTCACATCTCCCGGACAATTCCAGAAACACGCTG
TATGCTAAAGTAAGACCGCTGCGTGGGAGATACCGGCTATTAATCTGTGCGAAATCCGGTTACTTTTACGACCT
GGGTCAGGAGAGCTGGTCCAGCTCTCGAC (928 nt)

BM53h-56-6
GAGGTGACACTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCTGTGCAAGCCTCCGGAT
CTCTCCATTTCGGGATTATGAGATGTGGTACCGCAAGCTCCAGGAGAGGGTCTAGAGCGGGTCTACGTTATTAATCC
GCAAGGTACGCTACATATCCGCAAGCTTCGTGAAGGGCGGGTTCACATCTCCCGACAATCTCAGAAACACGCTG
TCTGCAAAATGAACCGCTCCGGAGATACCGGGGATATTAATCTGCGAAATCTCGTTTATTTTGAACAACC
GGGTGACGGAAGCACTGGTCCCGCTCGGAGT (서열 921)

BMS3h-56-7
GAGCTGCACCTGTGGAGTCTGGGGGAAGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCCTGTGCAGCCTCCGGAT
TGAGTTCTCGGAGATTAGAAGTGTGTGGGTCCGCAGAGCTCAGAGGAAGGGTCTAGAGCGGGTCTACGCTATTAATCC
GCAAGGATACGGCTACATACACGACAGCTTCGTGAAGGGCCGGTTACACATCTCCCGACAAATCTCAAGAACACCGTG
TATTCGAAACCAAGCAGCCTGGCTGCGGAGAGTACCTGGTATATCTGTCGAAACCTCGTTATTTTTGGCGACT
GGGCTCCGGGAAGACCTGGTCCAGCTGCTGGAT (서열 922)

BMS3h-56-C8
GAGGTGCTGAGCTTTGGAGTCTGGGGGAAGGCTTGGTACAGCCTGGGGGGTCCGCGCTCTCTCTGTGACAGCCTCCGGAT
TCAACCTTTCCGGATTATAGAGTTGTTGGGTCGCGAAGCTCCGGGGAAGGCTTAGAGCGGGTCTACGATATTAATCC
GCAAGGTACAGCTACATACACGCAAGCTTCGTGAAGGGCGGTTACGATCTCCCGACAATTCAGAAACACGCTG
TATCTCGAAATGAACAGCCTGGCTCGGAGATACCGGGTATTAATTCTGCGAAATTCGTTTACTTTT1GAGGACT
GGGTGCTGAAGGCTGGTCCGCTCGGAGT (seq. 923)

BMS35h-56
GAGGTGACGACTGTGGAGTTCAGGAGGAGGCTTGGTACGACCTGGGGGGTCCCTGCGTCTACTCTGTGCAGCCTCCGGAT
TACACTTTCGGGATATAGAGTGTGGTGGGTCCGACAGCTCCAGGAGGAGGCTTAGAGCGGGTCTACGCTATTAATCC
GCAAGGTACGCGTACATACCTACGCAAGCTCCGTGATGGGCGGGTTCACATCTCCCGCAAACTCCAGAAACACCGTG
TATGCTCAAAATGACGCTGGCTGCCGAGGATACGCGGTATTAATTCTGTGCAAACTCCGTTTATGTTTGACGACC
GAGGTTCAGGAGCAACCTGCTCCGCGGACGCTC (서형 924)

BMS3h-56-10
GAGGTGCTGATCTGGAGATCTGGGAGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGACCTCCGGAT
TCAACCTTCGGGATTATAGAGTATGGTGGGTGCGCAGAGTCCAGGAGAAGTGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAAGGTACAGCTACATACACGCAAGATCTCGTGAAGGGCCGGTTACCATCTCCCGCAAAATTCAGAAACATCTGT
TATGTCAAGTAAGACAGCTGCGTGCACGAGGATACGCGGTATTAATTCTGTCGCAAACTCCGCTTTATGTTGGACGACC
TGAGTCGAGGAGACCTTGTCACCGCTGACGCT (A) (CH 925)

BMS3h-56-11
GAGGTGCACGTCTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCTCTCCTGTGCAGCCTCCGGAT
TGGTCTTCGGGATTATGAGATGTGGTGGGTCCGCAGCTCCAGGAGAGGGTTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCTACATACGCAGACTCGTGAAGGGCCGGTTACCATCTCCCGGCAGAACTCCAGAACACGCTG
TATCTGCAAAATGAACCGCTGCGAGCGAGAGTACGCGGTATATTACTTGTGCGAAACTCCGGTATTGTTGCGACC
GGGCTGCGGGAGAGGCTGGTCAAGCTGCTGAGC (A) (Seq 926)

BMS3h-56-12
GAGGTTCAGCTCTGGTGGAGTCTGGGGGAGGCTGTATACAGCACTGGGGGGCTCCCTGCGTCTCTCTGTGCAAGCCTCCGGAT
GAGTTCCTTCGGGATATGAGATGTGTGGGTCCGCAGGCTCAGGGAAGGGTTAGAGCGGGTCTCAGCTATTAAATCC
GCAAGGTACCGGTATCACTACGACAGCTCGTGGAAGGGCCGGTTACATCTCCCGGACAATTCCAGAAACACGCTG
TATCTGCAAAATGAACCAAGCTGCGTCCGAGGATACCCGGTATATTACTGTGTGAAACTTCGGTTATTTTCGACTACT
GAGCTCAGGGAAGCTGGTCAAGCTCTCGAGC (서열 927)

BMS3h-56-13

GAGGTGCACCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTACTCTGTGCAAGCCTCCGGAT
TGGATCTTCGGGATATGAGATGTGGTGGCTCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGACTTAAACCC
GCAGGGTACCGTACATACTATGCAGACTCGTGGAAGGGCGGGTACCATCTCCCGGACAACTCCAGAAACACGCTG
TACTTGCAAATGAACACGCTCGCTGGTGATAGCCGGGATATCACTGTACGAAGAACTCCGTTTATTTTGGACTACT
GGGTCAGGGGAAGCTCGTCACTCGTCCGATGAC (서열 98)

BMS3h-56-14
GAGGTGGTCTTGGAGTCTGGGGGAGGCTTGGTACAGCTCGGGGGCCCTCGCTCTCTCTGTAGCGCTCCGGAT
TCACCTTCTGGGATTATGAGATGTGGTGGGCTCGCAGGCTCCAGGAGGTGGTCTAGAGCGGGTCTCAGCTATTAACTC
GCAGGGTACCGGTACATACTACGACAGACTCGTGGAAGGGCGGTTCACATCTCCCGGACAACTCCAGAAACAGCTA
TATCTCAGAAATGAACACAGCTGCGTGGCGGAGATACCGGGTATTATCTGTCGCAAACTTCGGTTTGTGTGACTCA
GGGTGCGAAGAGACCTGGTCAACCTCTCGAGC (서열 1219)

BMS3h-56-15
GAGGTGGTGGATCTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGATCGAT
TACACCTTCTGGGATTATGAGATGTGTGGGTCTCGCGGGTCTCAGGAGGAAGGTCTAGAGCGGGTCTACAGTTATTAATCC
GCAGGGTACCGTACATACTACGACAGACTGTGTGAAGGGCGGGTTACACTTCCCGACAATTCAGAAACACCGTGT
TATCTGCAAAATGAACCGAGTGGCGTCCGAGGATACCCGGTATTAATTACTGCGAAACTCTGGTTACTTTGAGGACT
GAGGTGCGGGAGGCTCGTTCGACCTCTCGAC (서열 15)

BMS3h-56-16
GAGGTGGTCACTTTGGAGTCTGGGGGAGGCTTGGTACAAGCTCGGGGGCTCCCTGCGTCTCCTGTGACGCTCCGATGAC
TCAACCTTTCGGGATATGAGATGTGTGGGTCTCGACAGGCTCCAGGAGAGGGTCTAGAGCGGGTCTCAAGCTATTAAATCC
GCAGGGTACCGGTACATACTACGACAGACTCGGTAGGGCGGTTCACATCTCCCGACAATTCACGAACACCGTCT
TGTTCGAAATGAACGACTCGCTGCTCGGAGACACCCGGATATTACTGTGCGAAACTCCGTTTACTTTGAGGACT
GAGGTGAGGAGGACCTGGTCAAGCTCTCGAGC (서열 16)

BMS3h-56-17
GAGGTGCTGAGCTTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TCTTCCTTCTGGGATTTAGATATGTGTGGTACGCGAGGCTCAGGAGGAAGGTCTAGAGCGGGTCTACAGTTAATATC
GCAGGGTACGGTACATATTACGACAGCTCCGTGAAGGGCGGGTTCACATCTCCCGACAATTCACGAACACGCTG
TATCTGCAATGAACACGCTGCTGGCCGAGGACCCGGATATTAAGTGTGCGAAATCCGTTTACTTTTGGAGCT
GAGGTGAGGGAAGAGCTGGTCAAGGCTCTCGACG (서열)

BMS3h-56-18
GAGGTCTGAGTCTTGGAGTCTGGGGAGGCTTGGTACAGCTCGGGGGCTCCCTGCGTCTCTCCTGTGCAGCTCCGGAT
TCACCTTCTGGGATATGAGATGTGTGGGTCCGCAGGCTCAGGGAAGGTCTAGAGCGGGTCTCAGCTATTAACTC
GCAGGGTACGCTACATACGACAGACTCGTGAAGGCGGGTTCACCATCTCCCGGACAATTCGAAGAACATGCTG
TATCTCAAAATGAACGCTGCTGCGGACGAGACACGCGGATATTAATCTGCGAAACTCCGTTACTTTTGGAGAT
GGGGTCAGGGAAGCTGGTCACTGCTCGAGC (서열 933)

BMS3h-56-19
TACGTCGACGCTGTGGAGCTGTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCGTGCAGCCTCCGGAT
GAGGTTCTCGGGATTATAGATGTGGTGGGTCGCAGGCTCCAGGAGGGGCTAGAGGGGGTCTACGATTATTAATCC
GCAGGGATACAGCTACATACACGAGCACTCGTGAAGGGGGGTTACATCTCCCGGACAATTCCAGAAACACCGTGT
TCTCTGCAATTGACAGCCTGCGTCGGGAGGATACCGGATATCACTGTGCGAAATCTCGTTACTTCTTGTAGGACT
GGGTGCAAGGCAACCTGGTCCCGCTCTCGAGC (서형 934)

BMS3h-56-20

TACGTTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTCAGCAGCTCCGGAT
GAGGTTCTCGGGATTATGAGATGTGGTGGTCCGCAAGCTCCAGGAGAGGGTCTAGAGGGGTCTACGATTATTAATCC
GCAGGGTACAGCTACATACACGACGCTCTGTCAGGGGGGGTTCACATCTCCCGACAAATCCAGAAACAGCTG
TATCTGCAAAATGAACAGCTGCTGCGCCGAGGATACCGAGGATATTAATCTACGAAATCTCGTTACTTCTTGGAGACT
GGGTGGAGGACCGCTGGCTCCCTCTCGAGC (서형 935)

BMS3h-56-21
 TACGCTGCAGCTGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTCAGCAGCTCCCGGAT
 GAGGTTCTCGGGATTATAGAGTTGGTGGTCCGCAGGCTCCAGGAGAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCTGACATACACGACGACCTCGTGAGAGGGCCGGTTCACATCTCCCGGCAAACTTCAGAAACAGCGTG
 TACTTCGAATACAGCAGCTGCTGCGCGAGGATACGCGGTGATATCTGTTGAAACTCCGTTTACTTCTTAGGACT
 GGGTGCAGGGAGACCTGGTCCCGCTCTCGAGC (서열 936)

BMS3h-56-22

TGAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTACTCTGTGCAGCCCTCGGAT
CACCCTTTCGGGATATAGAGTGTGTGGTCCGCAAGCTCCAGGAGGAGGCTGTAGAGCGGGTCTCAGCTATTAACCC
GCAGGGTACGCTACATATGTGCAAGCTCGTAGGGGGCGGTTCACATCTCCCGGACAAATCCAGAAACAGCGTG
TCTGCAAAATGAACAGCTGCTGCGGATATACCCGGGTATCATCTACGAAATCTCCGTTATTTTGAATACT
GGGTGCAAGCAACCTGGTCCGCTGCGAGT (서형 937)

BMS3h-56-23
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTCTGTGCAGCCTCCGGAT
TCACTTTTCGGGATATAGAGATGGTGGGTCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGCTCAGCTATTAATACC
GCAGGGTACGCGTACATACTACGAGACTCCGATGGCGGGTTCACCATCTCCGCGACAATTCAGAAGAACACGCTG
TATCTGCAAAATGAACACGCTGCCTGCGGAGACACCGGGTATTATTCTGTCGGAAGAAACCTTATAGTTTGTACTCT
GGGCTACGGGAACTCGTGCACCGTCTGCAGC (서열 938)

[illegible]

BMS3h-56-25
GAGGTGCGAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTCCGTGCGAGCTCCGGAT
TCACTTTCCTGGGATTATGAGATGTGGTGGTGCCTGGGGTCCAGGGAAGGGTCTAGAGCGGGCTCAGCTATTAATCC
GCAAGGTACGCGTACATACTACGAGACTCCGATGATGGCCGGTTCACCATCTCCCGGACAATTCAAGAACACGCTG
TATCTGCAAAATGAACACGCTGCGTCGGAGGATACCGGGTATTATTACTGTGGCAAACTTCGGTTTCTTTGACGACT
GGGGTCAGGGAACCTGGTCAACCGTCTCGAC (서열 940)

BM53h-56-26

GTGGAGTCAGCTTGTGGAGCTCTGGGGGAGGCTTGGTAGACCTGGGGGGTCCCTGCGTCTACTCTGCGACGCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGTGGTGGTCCGCGGGCTCAGAGGAAGGTTCTAGAGCGGGTCTCAGCTATTATATCC
GCAGGGTACCGCTACATACTACGCAGACTCCGTGATGGGCGGGTTCACCATCTCCCGACAAATCCAAGAACACGGTG
TATCTCGAAATGACCGCTGTGGCTGCGGACGACTCGGGTATTAATCTGTGCGAAATCTCGCTTGTATGTTGCGACCC
GGGCTCAGGAAGCCCTGGTCAAGCTCGAGG (sacchar. 941)

BMS3h-56-27
 GTGAGTCGACGCTGTGGAGCTCGGGGAGGAGCTTG1TGG1ACAGCCTGGGGGGTCCCTGCTGCTACTCTGTGCACGCTCCGGAT
 TCACCTTTCCGGGATTATGAGATGTGGTGGTGGTCCGACGGCTCAGAGGAGGGTCTAGAGCGGGTCTCAGCTAATTAATCC
 GCAGGGTACGCTACATACCTACGCAGACTCTGATGGGCGGGTTCACCATCTCCCGACAAATTCGAAGAACACGGTG
 TATCTGCAAATGAACACGCTGCGTGCACGAGCTCGGTGATTAATCTGTGCGAAATCTCGTTTATGTTTGGGACT
 TGGGCTCAGGGAACCTGGTGCAGCTCGGAG (서열 942)

BMS36-5h-28
GAGGTGACCTGCTTGGAGCTCTGGGGAGGAGGCTTGGTACAGCCTGGGGGGCTCTGCTGCTCTCTGTGACAGCCTCCGGAT
TACCTTTTCTGGGTATGAGTTGGTGGTGGTCCGACGGCTCAGAGGAAGGGTTAGAGCGGGTTACAGCTATTATATCC
GCAGGGTACGCTACATACCTACGACAGCTCTGTTAGTGGCGGGTTCACCATCTCCCGACAAATCCAGAAACACGGTG
TATCTGCAATGAAGTACGCTGGGTGCGAGGATACCGGGTATTAATTGTGCGAAACTTCGTTACTTTACTTTGGACACT
GGGCTGACGAAACCTGGCTGCTCAGCGTCTCGAGG (sequence 943)

BM53h-56-29
GAGGTGCGACCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACTTTCGTGGGTATGAGTGTGGTGGGTCGCGAGGCTCAGGGAAGGTTATAGAGCGGGTCTCAGCTATTATATCC
GCAGGGTACGGCTACATACTACGCACTCTCGTATGGGCGGGTTCACCATCTCCCGCAGCAATTCACAGAACACGGTG
TATCTCAGAAATGAACAGCTTGGCTCGGAGGAGCTCGGGTATTAATTCTGCGAAACTTCGTTTATGTTTGCGACCC
GGGCTGCGAAACCTGGCTGCTCACGCTGACGCG (sartre 944)

BMS36-5h-30

GAGGTGCACGCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGCTCTGCCTCTCTGTGCAGCCTCCGGAT
TCACTTTCGTGGGTATGAGATGTGGTGGTCCGCAGGCTCAGGGAAGGGTTAGAGCGGGTCTCAGCTATTATAC
GCAGGGTACGGCTACATACCTACGCAGACTCGTGTAGTGGCGGGTTCACCATCTCCCGACAAATTCGAAGAACACGCTG
TATCTGCAAAATGACGAGCTGGGTGCCGAGATACCGGGTATTAATTCTGCGAAACTTCGTTCATTTTGGGACT
GGGCT

(nt 945)

BMS3h-56-31

TGACGTGCAGCTGTGGAGTCTGGGGGAGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCCTGTGCAGCCTCCGGAT
CAGGCTTTCGTGGGTATGAGATGTGGTGGTTCGCGAGGCTCAGGGAAGGGTTAGAGCGGGTCTCAGCTATTATATCC
GCAGGGTACGGCTACATACACGAGACTCGTATGGGCGGGTTCACCATCTCCCGGACAATTCGAAGAACACCGTG
TATCTGCAATGAACAGCCTGCGTCGGAGGATACTCGGGTATTAATTCTGCGAAACTCCGTTTATGTTGACACCC
GGGGCTGAGCAACCTGGCTGACGCTGCGG (서형 946)

BMS3h-56-32

TGACCTGCAGCTGTGGAGCTCGGGGGAGCTTGGTAGCAGCTGGGGGGTCCCTGCGTCTCCTGTGCAGCTCCGGAT
CAGGTTTCGGGATATAGAGATGTGGTGGTCCGCAAGCTCAGGGAAGGGTCTAGAGTGGGTCTCAGCATTAATACC
GCAGGGTACGGCTACATACACGAGACTCGTGAATGGGCGGGTACCATCTCCCGCAGCAATTCGACAGAACACGGTG
TATCTGCAAAAGAACAGCTGCGCTGCCGAGATACCGCGGTATTAATCTGTGCGAAATCCGTTTACTTTGGACACT
GGGCTGAGCAATCCGCTGCTGCGCGGAGC (서열 947)

BMS3h-56-214
GAGGTGTCAGCTGTGGAGTCTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGCTCTCTCTGTCAGCCCTCCGGAT
TCACTTTCCGGGATATAGAGTGTGGTGGTCCGCGAGCTTCAGGGAAGGGCTAGAGCGGGCTTCAGCTATTAATCC
GTCCGGTGGGTGACATACTACGACGACTCGTGAAGGGCGGGTTCACCATCTCCCGCAAAATCCAAGAACAACGCTG
TATCTGCAAAAGAACAGCTGCGTGGCGGAGGATACCGGGTATATTACTGTGCGAAATCTGTTTACTTTTGACGACG
GGGCTCCGGTCAACTGGTCAACCGTCTGCAGC (서열 961)

BMS3h-56-215
GAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGTGACAGCCTGGGGGGTCCCTGCGCTCTCTCTGTGCAGCCTCCGGAT
TACCTTCTCGGGATATAGAGTGTGGTGGTCCGAGGCTCAGAGGAAGGCTGTAGAGCGGTCTCAGCTATTAATCC
GCACGGTCTGTGACATACACGACAGCTCCGTGAAGGGCCGGTTCACATCTCCCGACAATTCTCAAGAACACGGT
TGTCTCAAAATGAACAGCTGCTGCGGAGATACCGGAGTATTAATTGTGCAAACTCGCTTTACTTTTGTGACGACT
GAGGTGAGGACCACTGGTGCCTGCTGAGC (서열 962)

BMS3h-56-216
TACGCTGCAGCTATTGGAGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCTGTGCAGCCTCCGGAT
CGAGTTTCGGGATATAGAGTGTGGTGGTCCGAGCCTCAGAGGAAGGTTTAGAGCGGGTCTCAGCTATTAATCC
GGCCGGTCGGTGCATACACTACGACAGCTCCGTGACAGCCGGTTCACATCTCCCGACAATTCTCAAGAACACCGTG
TATCTCAAAATGAAGACAGCTGCTGCCGGATACCGGGATATACTTGTGCGAAATTCGTTTACTTTTGGAGCT
GGGTGCGAGGCAACCTGGTCACTGCTCGAGC (서열 963)

BMS3h-56-217

TGAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCTCCGGAT
CAGCTTTCGGGATATAGAGTGTGGTGGTCCGACAGGCTCAGGAAGAGGTTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTAGCTTGACATACCTGCAGACGACCTCGTAGAGGGCGGTTACCATCTCCCGACAAATTCAAGAACACGGCTG
TATCTCGAAATGACAGCTGCTGCTGCGAGGAATCGCGGATATACTGTGCGAAACTTCGTTTACTTTTGGAGACT
TGAGCTCAGGGAACCTTGGTCACCGCTCTCGAG (서열 964)

BM53h-56-218
GAGGTGACAGTTGTTGGAGTCTGGGGGAGGCTTGACGACGCTGGGGGGTCCCTGCGTCTCCTGTGACGACCTCCGGAT
TGCTTCCTCCGACTACAGAGTGTGGTGGTCCGACAGGCTCAGAGGAGAGGTCTAGAGCGGGTCTACGATTAATATCC
GCAAGGTACGCTACATACATACGACAGATCCGTGAAGGGCCGGTTCACATCTCCCGACAATTCTCAAGAACACGGTG
TATTCAGAAATGAACAGCTGCGCTCGGAGATACCCGGATATCATCTGTGCGAAATCTCCGTTTACTTTTGACGACT
GGTTCGAGGACCACTTGGTCACGCTGTGGG (사형 965)

BNS3h-56-219
GAGGTGGACGTCTTGGAGTCTGGGGGAGCTTGGTACAGCCTGGGGGGCTCGTCTCTCTTGCAGACATCCGGAT
TCACTTTCCTCCGCGGAGGATGTGGTGGTCCGACAGCTCAGAGGAGGGGTAGAGGGGGTCTCAGCTATTAATCC
GCAAGGATACGGCTACATACTACGCAGACTCTCGTAGAGGGCGGTTACCATCTCCCGGACAAATTCAGAAACACGGTG
TATCTGCAATGAAGACAGCTCGCTGCCGAGGATACCGGGATTAATTACTGTGGAGAACTTCGGTTACTTTTGGAGCT
GGGGTACGGGACCACTGGTGCACGTGGAGCG (서열 966)

BMS3h-56-220
GAGGTGCAGCTTGTGGAGTCTGGGGGAGCTTGGTACAGCCTGGGGGGTCTCGTCTCTCTTGCAGCATCCGGAT
TACCTTTCCGGATTATAGATGTGGTGGTCCGAGGCTCAGAGGAAGGTTAGAGCGGGTTCAGCATTAATACC
GTACGGTGGGTGACATACAGCAGACTCCGTGAGAGGGCCGGTTCACATCTCCCGCAGCAATTCAGAAACAGCGTG
TATCTGCAATGAAGACAGCTGCGTCCCGAGGATACCGGGTAAATTAATCTGTGCGAAATTCGGTTACTTTTGGCAGCT
GGGCTCAGGAAGCACTGGTGCACGTGCGAGG (서형 967)

BMS3h-56-221
GAGGTGCACGTGTGGAGTCTGGGGGAGGCTTGTTACAGCCTGGGGGGTCTCGTCTCTCTGTGCAGCATCCGGAT
TACCTTTTCGGGATATAGAGTGTGGTGGTCCGACAGCTCAGAGGAAGGGTTAGAGCGGGTCTACGCTATTAATCC
GTGGGGTAAACACACATACCTACGCAGACTCCGTGAAGGGCGGGTACCATCTCCCGCAGCAATTCAGAAACACGCTG
TATGTCGAATGACAGCTCGCTGCCGAGGATACCCGGGTATTAATCTGTGCAGAACTTCGGTTTCTTTGAGGACT
GGGCTCAGGGAACCTGGTCACGCTGACGCG (시퀀스 968)

BMS3h-56-222
GAGGTGCACCTCTGTGGAGTCGTGGGGAGGACCTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCCTCCGGAT
GATCTCTTCGGGATATAGAGTATGTGGGTCTCCGAGGCTCAGGAGGAAGGCTAGAGCGGGTCTCAGCATTAATTC
GCACGGTGGCTACACATACTACGACAGCTCGTGGAAGGGCGGGTTCACATCTCCCGACAACTCCAGAAACACGGTCT
TATGCTCAAAATGAACGACCTCGTGGCGAGGATACCGGGTATTATTAATCTGCGAAACTTCGGTTACTTTGAGGACT
GGGTCAGGAGAACCTGGTCAGCTCTCGAGC (서열 969)

BMS3h-56-223
GAGGTGACCTCTGTGGAGTCTGGGGGAGGACCTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TACCATTTCTGGGATATGAGATGTGTGGGTCTCCAGGACCTCTCAGGAGGGGCTAGAGCGGGTCTCAGCTATTAAATCC
GCCCGTATGCTCACATACACGACGACTCGGTGAAGGGCCGGTTACACATCTCCCGACAAATTCAGAAACACGCTGT
TATTCGAAATGAACACGCTGCTGGCGAGGATACCCGGGTATATTCTGCGAAACTCCGTTTATTTGACGACT
GGGCTCAGGGAACCTGGTCACTGCTCCGAC (서열 978)

BMS3h-56-224

GAGGTGACGACCTGTTGGAGTCTGGGGGAGCCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TCCATCTTCCGGATATATGAGATGTGTGGGTGCGCCAGGCTCCAGGAGAGGCTTAGAGCGGGTCTCAGCTATTAATCC
GTGGGTCAAGTGACATACACGACGACCTCGTGAGGGCGGGTTCACATCTTCCCGACAATTCAGAAACACGCTG
TATCTGCAATGAACACGCTGCGTCCGAGGATACCGCGGTATTAATCTGCGAAACTCTCGTATCTTTAGAGACT
GGGTGACGGGAACTGGTCAAGCTCTCGAC (서열 971)

BMS3h-56-225
GAGGTGCACCTCTGGAGTCTGGGGGAG6CCTGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCCTCCGGAT
GAGCTCTCTGGGATTAAGAATGTGTGGGTCCGACAGGCTCAGGGAAGGGTCTAGAGCGGGTCTACAGTTATTAATCT
GTGGGGTGGTACACATACAGCAGACTCCGTGAAGGGCCGGATCACATCTCTCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAAGAACACGCTGCGTGGCAGGATACCGGGTATTAATCTGCGGAACTCCGTTACTTTTACGACACT
GAGCTGAGGGAACCTGGTCAAGGATAC (c.977)

BMS3h-56-226

GAGGTGACAGTCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGATGTCATCTTCGGGATATAGAGTATGTTGGGTCTCGCAGGCTCTCAGGGAAGGCTTAGAGCGGGTCTCAGACTTAAATCTGTGGTGGGCTGACATACACGACAGACTCCGTGAAGGGCCGGTTACACATCTCCCGGACAATTCAGAAACACGCTGATTCGCAAAATGAACCGCTCGCTGGCGAGGATACCGGGTATATTACTGCGGAAACTCCGTTATCTTGGAGACTTGGTCCGGAAGACCTGGTCCGCTGCTCGAC (서열 973)

BMS3h-56-227
GAGCTGCAGCTGTTGGAGTCTGCGGGAGGACCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TACTCTTCCGGATATATGAGATGTGTGGGTCTCGCAGGCTCTCAGGAGAGGGCTTAGAGCGGGTCTCAGCATTAATCT
GTCCGGTGGGTGACATACAGCAGACCTCGTGAGGGCGGGTTCACATCTTCCCGACAACTCCAGAAACACGGTCT
TATCTGCAAAAGAACACGCTGGCTGGCGAGGATACCGGGATTAATTACTGTGCGAAACTTCGTTACTTCTTTCAGCACT
GGGTCAGGGAACCTGGTCAAGGCTCTCGAGC (서형 974)

BMS3h-56-228
GAGGTGCTGCTTGGAGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TACACTTCTGGGATATGAGATGTGTTGGTCTCGCAGGCTCTCAGGGAAGGCTTACAGCGGGTCTCAGATTATTAATC
GTGGGTACGCTCACATACTACGACAGACTCGTGAAAGGCGGGTTACACATCTCCCGGCAATTCAGAAACACGCTG
TATCTCGAAATGAACGACCTGCTGCGGAGGATACCGGGTATATTACTGTGCGAAACTCCGTTACTTTTGGAGACT
GGGTCAGGGAAGCTGCTGCTGCTCTCGAGC (see 975)

BMS3h-56-229
GAGGTGCACCTTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCAGTCTTCGGGATTATGAGATGTGTGGGTCCGCAAGCTCCAGGAGGAGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GTACGGTTCTGTCACATACACGACACTCTGTGAAGCGGGTTCACCATCTCCCGGACAAATCCAGAAACACCGTG
TATCTCAGAAATGAACAGCCTGCGTCCGAGGATACCCGGGATTAATTACTGTGCGAAATCCGTTTACTTTTGTGACGACT
GGGCTCAGGAGGACCTTGCTGGCCGTCTGGC (서형 976)

BM53h-56-230
GAGGTCTACCTTTGTTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TGACATTTCCGGATTATAGATGTGTGGTCCGCAGCTCCAGGAGAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGTACACATACCTACGCAAGCTCCGTGAAGGGCGGTTACCATCTCCCGGACAATTCCAGAACACCGTGT
TATCTGCAAATGAACCGCTGGCTGCGGAGGATACCCGGGTATTACTGTGCGAAATCTCGTTTACTTTTGGGAACT
GGGGTCAGGGAACAGCTGGTCCCGCTCTGAGC (977)

BMS3h-56-231

TGAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGTGACAGCCTGGGGGGTCCCTGCGCTCTCTCTGTGCAGCCTCCGGAT
CAGCTTTCGGGATTATGAGTGTGTGGTCCGACAGCTCAGGAGGAGGGTCTAGAGGGGGTCTCAGCTATTAATCC
CAGGGTGGGTGCACATCTGCACGACCTCGTAGGGGGCGGTTACCATCTCCCGCGACAATTCAAGAACACGCTG
TATCTCAAAATGAACACCTGCTCGCGAGGATACCGAGGCTATTACTGTGCGAAATCCGTTTACTTTTGAAGACT
GGGGTGAAGAACCTTGGTACCCTCTCGAGC (서철 978)

[illegible]

BMS3h-56-233
GAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTCTCTGTGCAAGCTCCGGAT
TACCTTTCCGGGATTAGAGATGTGGTGGTCCGCAGGCTCCAGGGAAGGGCTAGAGCGGGCTCAGCTATTAATACC
GTGGGGTACCTTGACATACTACGACAGACTCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAGGAACACGCTG
TATGTGCAAAAGAACACCTGCGCTCGGAGGATACCCGGTATATTACTGTCCGAACCTCCGTTTATCTTTGACGACT
GGGCTACGGGAACCTGCTGACCGTCTCGAG (서열 980)

BMS3h-56-234
GAGGTGCACGTTGTTGAGTCTGGGGGACGCTTGGTACGACCTGGGGGGTCCCTGCGCTCTCTCTGTGACGACCTCCGGAT
GCTGTTTCGGGATATTAGAGTGTGGTGGTCCGCAGAGCTCAGAGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GAACGGTGGCTGACATACACGACAGCTCCGTGAAGGGCCGGTTACACATCTCCCGACGAATTCAGAAACACGCTG
TATCTCAGAAATGAACGACCTGCGTCCGCGAGGATACCCGGGTATTACTGTGCGAAACTTCGGTTACTTTCTGGGACCT
GGGTCAGGAACCCCTGGTCCAGCTGACGCG (서열 981)

BMS3h-56-235
GAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGTGACAGCTGGGGGGTCCCTGCCTCTCTCTGTGCAGCTCCGGAT
TCACTTCTCGGGATTATGAGATGTGGTGGTGCAGCTCCAGGAGGAGGCTAGAGCGGGCTCAGCTATTATTAAC
GTGGGGTCAGCTGACATACACGAGACTCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCAGAACACAGCTG
TATGTCAAATGAACAGCTGCGTCCGAGGATACCGGCTATTACTGTGCAGAACTCCGTTTACCTTTTGACGACT
GGGTTCAGGACTCCGTGACACCGTCTGCGC (서열 982)

BM53h-56-236
GAGGTGCACCTTTGGTAGTCTGGGGGAGGCTTGGTACGACCTGGGGGGTCCCTGCGCTCTCTCTGTGCAGGCTCCGGAT
TCCATTTCCGGATTATGAGATGTGGTGGGTCGCCAGGCTCAGAGGAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GCACGGTGGCTCACATACACGACAGCTCTGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAGAAACACGGT
TATCTGCAATTGAACGCTCGCTGGCGGAGATACC CGGGTATTAATTCTGCGGAAATCCGTTTACTTTTCCGACGACT
GGGCTGCGGGAGACCTCGGTGACCGCTGCTGACG (서형 983)

BMS3h-56-237

GAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCCTGCGCTCTCCTGTGACAGCCTCCGGAT

TACCTTTCGGGATATAGAGTGTGGTGGTCCGACAGCTCAGAGGAGGGTCTGGAGCGGGTCTACAGTATTAATCT

GCCGGGTATGTTGACATCTACGACAGCTCGTAGAGGGCCGGTTCACATCTCCCGGCAATTCAGAAACACCGTGT

TGCTGCAGAAATGACAGCTCGCTGCCGAGGATACCCGGGTATTAATCTGTGCGAAATCCGTTTACTTTTGGACACT

GATGTCAGGAGAACCTCGTCCAGCTGCGC (시퀀스 984)

BM53h-56-238
GAGGTGCTGATTTGGAGTCTGGGGGAGGCTTGGTACGAGCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGGCTCCGGAGT
TCCACTTTCGGGATATAGAGTGTGGTGGGTCGCCAGGCTCAGGAAGAGGCTTAGAGCGGGTCTCAGCTATTAAATCC
GCACGGTACTTTGACATACACGACAGCTTCGTGAAGGGCGGGTTACCATCTCCCGACAAATTCAGAAACACCGGT
TATGCTCAAGTAAGACGAGCTGCGTCCGAGGATACCCGGGTATTACTGTGCGAAATTCGGTTTACTTTGAGGACT
GGGTCGAGGAAACCTGGTCACCGCTCCGAGC (서형 985)

BM53h-56-239

TGACCTGCAGCTTGTTGGAGTCTGGGGGAGGCTTGGTCAGACCTGGGGGGTCCCTGCGCTCTCTCTGTGCAGCCTCCGGAT
CAGCTTTCGGGATATAGAGTGTGGTGGTCCGCAGGCTCAGGAGGAGGCTTAGAGCGGGTCTCAGCTATTAATCT
GTGGGGTTCGTTGACATACACGACAGCTCCGTGAAGGGCCGGTTACACATCTCCCGACAAATTCAGAAACACGCT
TATCTCAGTAAGAACCGCTGCTGCGCCGAGGATACCCGGGTATTAATCTGTGCGAAATCTCGTTTACTTTTGACGACT
TGGCTCAGGAAAGCCCTGGTCGCTCCGCTGACG (서형 986)

BM53h-56-240
GAGGTCTGACCTTTGGTGAAGTCTGGGGGAGGCTTGGTACGACCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TACCTTTCGGGATATTAGAGTATGGTGGGTCCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTACGATTATTAATCT
GTACGGTGGCTGACATCATACGCAAGCTTCGTGAAGGGCGGGTTACCATCTCCCGGACAATTCAGAAACACGCTG
TATCTGCAATGAAGACCGCTGCGTCCCGAGGATACCCGGGTATTAATTCTGTGCGAACTTCGGTTACTTTTGGAGACT
TGGGTCAGGAAAGCCCTGGTCCGCTGACCGTGGAGC (서형 987)

BMS3h-56-241
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCTCTCTGCAGCCTCCGGAT
TCACTTCTCGGGATACAGAGATGTGGTGGTCCGCGAGCTCCAGGGAAGGGCTAGAGCGGGTCTCAGCTATTAATCC
GGCCGGTTCTTGACATACTACGACAGACTCGTGAAGGGCCGGTTCACATCTCCCGCACAATTCACGAACAACGCTG
TATCTGCAATGAACACAGCTGCGTCCGAGGATACCCGGTATATTAAGTCTGCGCAAACTTCGTTTACCTTTTGAGGACT
GGGGTCAAGGGAACCTGGTCAAGCTCTCGAC (access 988)

BMS3h-56-242

TGAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTCAGCCCTGGGGGGTCCCTGCCTCTCTGTGACGCCCTCCGAT
TCACCTTCTCGGATATTAGAGTATGGTGGGTCCGCAGGCTCAGGAGAGGGTCTGGAGCGGCTACAGTATTAAATC
GTACGGTGGCTGACATACTACGACAGCTCGTAGAGGGGCGGTTACATCTCCCGACAAATCCAGAACACCGT
TATTCGAAATGAACACGCTGTGTCGAGGATACCCGGTATTACTGTGCGAAATCCGGTTACTTTTGGAGCT
GGGGTCAGAAAGCTGTCGACCGCTGCG (987-989)

BMS3h-56-243

GAGGTGACCTGCTTGGAGTCTGGGGGAGGCTTGGTCAGCCTGGGGGGTCCCTGCGCTCTCTCTGTGCAAGCCTCCGGAT
TCCATCTTCGGGATATAGAGTGTGGTGGGTCGCCAGGCTCCAGGAGAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GTGGGGTGGGTCTACATACATCCGCAAGCTCCGTGAAGGGCGGGTCTCACATCTCCCGCGACAATTCAGAAACACGCTG
TATTCGAAATGAACACGCTGCTGCGGAGATGCGCGGATATATCTGTGCGAAATCCGTTTACTTTTGAAGACT
GGGTGACGGGAGCTGGTCCCGCTCTGAGC (서열 998)

BMS3h-56-244

GAGGTGACCTTTGTTGAGCTGTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCCTGCGCTCTCTCTGTGACGCTCCGG6AT
TACACTTTCGGGATTATGAGATGTGTTGGGTCGCCAGGCTCAGGAGAGGGTCTAGAGCGGGTCTACGATTTAATCC
GTGGGGTGGGTTGACATACACGACGACTCGTGAAGGGGGTCTCACATCTCCCGGACAAATCCAGAAGACACGCTG
TATCTGCAAAATGACAGCTCTGCTGCCGAGATGCGGGGATTAATCTGTGCGAAATTCGTTTACTTTTGTGACGACT
GTGGTCAGGGAACCTTGGTCACCGCTCTGACG (서열 991)

BMS3h-56-245
GAGGTGACAGCTTTGGAGCTGCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTCGTGACGCTCCGGAT
TGCTTCATTTCGGGATTATGAGATTGTTGGTCCGCAGCTCCAGGAGAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GTACCGTGGGTCGACATACATCGACAGCACTCTGGAAGGGCGGTTACATCTCCCGGCACAATTCAGAAACACGCTG
TATTCGAAAGGACAGCCCTGCTGCGAGGATACACGGGTATTAATCTGTCGAAATCTCGTTTACTTTTGTAGGACT
TGGCTCAGGGAACCTGGTCACCCCTCTCGAGC (서열 992)

BMS3h-56-246

TGAGCTGCAGCTTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCTGTGCAGCCCTCCGGAT
CACCCTTTCGGGATTATAGAGTTGTTGGTCCGCAAGCTC CAGGAGAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTACGTTGCATACACGACGACTCGTGAAGGCGGGTTCACATCTCCCGGACAATTCAGAAACACGCTG
TCTGCAAAATGAACAGCCTGCTGCTCGGAGATACCGGAGGTTATTACTGTGCGAAATTCGTTTACTTTTGAAGACT
GGGGTGCAGGAACCTGGT CACCGCTCTGAGC (서철 993)

BMS3h-56-247

GAGGTGCTTGGATTTGGAGTGGGAGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCCTGTGACGCTCCGGAT
TACACTTTCGGGATATAGAGTGTGGTGGTCCGCAGAGTCCAGGGAAGGGCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGCTACACATACACGACAGCTCCGTGAAGGGGGGGTTACCATCTCCCGGCAAAATCCAGAAACACCGTG
TATCTGCAAAATGACAGCTGCGTCCGAGGATACCCGGGTATATTACTGTGCGAAATCCGTTTACTTTTGGAGACT
GGGGTCGGGGAACCTGGTCCGCGGCTAGC (cyt 994)

BMS3h-56-248
GAGGTGACCTTTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TACATCTTCGGGATATAGAGTGTGGTGGTCCGCAGGCTCCAGGAGAGGCTTAGAGCGGGTCTCAGCTATTAAATCC
GTACGGTAACCTGACATACCTACGCAGACTCTCGTAGAGGGGCGGTTACCATCTCCCGCACAATTCAGAGAACACCGTG
TATCTGCAAGTAAGACAGCTGCGTGCCGAGGATACCCGGGTATTACTGTGCGAAATCTCGGTTACTTTCTGGAGACT
GGGCTCAGGAGCACTCGGTGACCGCTGACGAGC (서열 995)

BMS3h-56-249
GAGCTGCACGTGTGGAGTGGTGGTGGTGGTGCACGCTGGGGGGTCCCTGCGCTCTCTCCTGTGCAGCCTCCGGAT
TACCTTTCGGGATTATAGAGTGTGGTGGTCCGCAGGCTCCAGGAGAGGCTTAGAGCGGGTCTCAGCTATTAATCC
GCACGGTGGGTACACATACGCAGACCTCGTGAAGGGGGGGTTCACATCTCCCGCACAATTCAGAAACACCGTG
TATGTCAGAAAGAACGCTGCGTCCCGAGGATACCCGGGTATTAATCTGTGCGAAATTCGGTTTACTTTGAGGACT
GGGCGGAGAACCCGTGCTCAGCGGCGAGCT (서형 996)

BMS3H-56-250
GAGGTGACCGTCTGGAGCTCGGGGAGGCTGGTACAGCCTGGGGGGTCCCTCGCTCTCTCTGCGAGCTCCGGAT
TGCTCTCCGGATATAGAGTGTGGTGGTCCGCGAGGCTCAGGGAAGGTTAGAGCGGGTTCAGCTATTATATCC
GGCCGGTTCTACACATATACGAGACTCTCGGAAGGCGGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGAGGAATGAACACGCTCGCTGCCGAGGATCCGCGGTATATTACTGTCGAAACCTCCGTTTACTTCTCGAGCT
GGGCTCAGGAAGACTGGTCACTGCTGCTGAGC (sequence 997)

BMS3h-56-251
GAGCTGCACGCTTGTGGACTCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TACCTTCTCCGGATTTAGAGATGTGGTGGTTCGCCGAGGCTCAGGGAAAGGGTTAGAGACGGGTCTCAGCTATTATACCTC
GGCGGTGGCTCACAATACTACGAGACTCTGGTGAAGGGCGGGTTACCATCTCCCGCAACATTCGAAGAACACGGTG
TATCTGCAAAATGAACACGCTGCTGCGGACGATACCGGGTATATTAAGTGTGCGAAACCTCCGTTTACTTTTGGACGACT
GGGGTCAAGAACTCCGTGCTGCTGCTGCGACTCTGAGG (zone 998)

BMS3h-56-252

TGGCTGCAGCTCTTGGAGCTCGGGGAGGCTTGGTACAGCTGCGGGGGTCCCTCGCTCTCTCTGTCAGCATCCGGAT
GAGGCTCTCCGGATATTAGAGATTGGTGGTTCGCCAGGCTCAGGGAAGGTTAGAGACGGGTCTCAGCATTAATAC
GCACGGTTCCTACATACCTACGCAGACTCTGGAAAGGCGGGTTCACCATCTCCCGACAAATTCGAAGAACAGCGTG
TATTCTGCAATGAACAGCTCGCTGCCAGGATACCGGGATTAATTACTGTGCAAACTCCGTTTACTTTTGGAGCT
GGGGTCAGGGAAGCTTGGTCAGCTCTCTCGAGC (서열 999)

BMS35h-56-253

TGAGCTGCAGCTTGTTGGACTCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGACAGCTCCGGAT
CAGCTCTCGTGATTAGAGATGTGGTGGTTCGCGCAGGCTCAGGGAAGGCTGTAGAGCGGCTCAGCATTAATACCC
GGCCGGTGGGTACACATACCTACGAGACTCTCGTGAAGGGCGGTTACCATCTCCCGCAACAATCCAAAGAACACGGTG
TATCTGCAAAATGAACACGCTGCGTCCGAGGATACCGGATATACACTGTGCGAACTTCGGTTACTTTCCTGAGACT
GGGGTCAAGAGACTCTGGTCACTCTCTGAGG (서열 1000)

BMS35h-56-254

TGAGCTGCACCTCTGGAGCTCTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACAGCTCCGGAT
CAACCTCTCCGGATATTAGAGTGTGGTGGTCCCGACGGCTCAGGGAAGGGTTAGAGCGGGTCTCAGCTATTAAATCC
GCAGGGTACGGTACATACCTACGCAGACTCTGGTGAAGGGCCGGTTCACATCTCCCGACAAATTCCAAGAACACGGTG
TATCTGCAAAATGAACACGCTGCGTCCGAGGACACCGGGTATTAATCTGCGAAACTCCGTTTGGTTATCCGGAGT
GGGGTCAAGAACTCTGGTCACTCTCTGAGC (서열 101)

BMS3h-56-255
GAGGTCTGACCTCTGGAGCTCTGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACAGCTCCGGAT
CTACCATCTCCGGATATAGAGATGTGGTGGTCCCGCAGGCTCAGGGAAGGGTTAGAGCGGGTCTCAGCATTAATACC
GCAGGGTACCGGTACATACCTACGCAGACTCTCGGAAGGGCGGGTTACCATCTCCCGACAAATTCGAAGACACCGTG
TATCTGAGGAATGAACACGCTCGCTGCCGAGGATCCCGGGTATATTACTGTGCAAACTTCGTCATGCTTTCCGACC
GGGGTCAAGGAACCTGGTCACTGTCTGTCGAGC (서열 1002)

BMS3H-56-256
GAGGTCTGACCTTTGGAGCTCTGGGGAGGCTTGGTAGCACTGGGGGGTCCCTGCGTCTCTCTGACGACCTCCGGAT
TAGCTCTCCGGATATAGAGTGTGGTGGTCCGACAGGCTCAGGGAGAGGTCTAGAGCGGGTCTCAGCTATTATACC
CGAGGGTACCGCTACATACCTACGAGACTCTCGTAGGGGCGGGTTCACCATCTCCGCGACATATCCAAGAACACGCGTG
TATCTGCAATGAACACGCTGCGTCCGACGACACCCGGTATATTACTTGCGAACTTCGGTTTTGTCTCAGGAGT
GGGGTACGGAACACTGGTCACTCTCTGCGAC (서열 1003)

[0223]

BMS3h-56-270
GAGGTGCACGCTGTGGAGTCTGGGGAGGCTTGGTACAGCTCGGGGGTCCCTGCCTCTCTCTGTCAGCCTCCGGAT
TCACTTCTCCGGATATGAGATGTGGTGGTTCGCGAGGCTCAGGGAAGGGCTAGAGCGGGCTCAGCTATTATACCG
GCAGGTCACGCTACATACGACGAGACTCGTGAAGGGCGGTTCAACATCTCCCGGACAAATTCAGAAACACGCTG
TATTCGAAATGAACAGACTTCGCTGCCGAGGACACCGGATATTACTGTGCGAAATCCGACGCTGTTTCAGGACT
GGGTCAGGGGAACCTGGTCAACGCTTCGACG (서열 1817)

BMS3h-56-284
GAGGTGCAGCTTGTGGAGTCTGGGGGAGGCTTGTACAGCCTGGGGGGTCCCTGCCTCTCTCTGTGCAGCTCCGGAT
TACCTTTTCGGGATTATAGATGTGGTGGGTCGCCAGCCTCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGGTGACATACTACGAGACTCGGTGAAGGGCGGTTCACCATCTCCCGCACAATCCAAGAACAACGCTG
TATCTGCAAAATGAACAGCTTGCCTCGGAGGACCTCGGGTATATCACTGTGCGAAATCCCATGTTCTTTGAGGACT
GGGGTCAGGAGCTGCTGTTCCAGCTCTGCAAC (서열 1031)

BMS3h-56-285
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GTGGGGTGGGTTGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAACTCCGTTTCTTTACGAGT
GGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1032)

BMS3h-56-286
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GTGGGGTGGGTTGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAACTCCGTTTCTTTACGAGT
GGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1033)

BMS3h-56-287
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
GTGGGGTGGGTTGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAACTCCGTTTCTTTACGAGT
GGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1034)

BMS3h-56-288
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCC
CGAGGGTACGCGTACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAACTCCGATGTTCTTTGAGGACT
GGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1035)

BMS3h-106-1
GAGGTGCAGCTGTTGGAGACTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGACTTATACATATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGTCTCAATGATTGATGC
GGATGGTCTTGGGACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAGCTCCGAGTGGTTCAGT
TTGACTACTTTGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1036)

BMS3h-106-2
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGACTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGACTTATACATATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGTCTCAATGATTGATGC
GGATGGTCTTGGGAACTACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAGCTCCGAGTGGTTCAGT
ATGACTACTGGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1037)

BMS3h-107-1
GAGGTGCAGCTGTTGGAGTCAAGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGGGATTATGATATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGTCTCAACGATTAGTGC
GTGCGGGTGTATACATACACGAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTGCGAAGTATCTAACTGTTTGCCTTA
ATAGTTTTGACTACAGGGGTCGGGGAACCTTGGTACCCTCTCGAGC (서열 1038)

BMS3h-107-2
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCSTCTCTCTGTGCAAGCTCCGGAT
TCACCTTTCGGGATTATGATATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGTCTCAACGATTAGTGC
GTGCGGGTGTATACATACATACAGACTCCGTGAAGGGCCGGTTACCATCTCCCAGGACAATTCCAAGAACACGCTG
TATCTGCAAA1GAACAGCCTGCGTGCCGAGGATACCCGCGTATATTACTGTACGAAATATCCAAATCGTTTTCGCGTA
ATAATTTTGACTACTGGGTCAGGGAACCTTGGTACCCTCTCGAGC (서열 1039)

BMS3h-131-1
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAATA
GTTCTAATTTTGGGCGTTAGCTTGGTACGACAGAAACAGGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAAGTGGGTCCTACACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGTTAGAAATGCGGTTTGGCTTGTACGTTTCAGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 1040)

BMS3h-131-2
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGACAGCA
GTTCTAATTTTGGGCGTTAGCTTGGTACGACAGAAACAGGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAAGTGGGTCCTACACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGTTAGAAATGCGGTTTGGCTTGTACGTTTCAGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 1041)

BMS3h-131-3
GACATCCAGATGACCGTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGACAGATA
GTTCTAATTTTGGGCGTTAGCTTGGTACGACAGAAACAGGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAAGTGGGTCCTACACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGTTAGAAATGCGGTTTGGCTTGTACGTTTCAGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 1042)

BMS3h-131-4
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAATA
GTTCTAATTTTGGGCGTTAGCTTGGTACGACAGAAACAGGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAAGTGGGTCCTACACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGTTAGAAATGCGGTTTGGCTTGTACGTTTCAGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 1043)

BMS3h-131-5
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAATA
GTTCTAATTTTGGGCGTTAGCTTGGTACGACAGAAACAGGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTACCGG
TTTGCAAAAGTGGGTCCTACACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGTTAGAAATGCGGTTTGGCTTGTACGTTTCAGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 1044)

BMS3h-131-6
GACATCCAGATGACCGTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAATA
GTTCTAATTTTGGGCGTTAGCTTGGTACGACAGAAACAGGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
ATTGCAAAAGCGGGTCCTACACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGTTAGAAATGCGGTTTGGCTTGTACGTTTCAGGCAAGGGACCAAGGTGGAAA
TCAAACGG (서열 1045)

[0226]

[0227]

BMS3h-131-7
GACATCCAGATACCCAGTCTCCATCTCCTGTCTGCATCTGAGGAACCGTGTACCATCACTTGCGGGGAGATA
GTCTTATTTCTTGGGGCTAGCTTGTGACAGCAGAAACGAGGAAGCCCTAAGCTCTGATGAGAGTCTTTCGGG
TTTCAAAAGTGGGTCCATCACGTTTCAGTGGCAGTGGAATCTGGGACAGATTCACTCTACCATCAGCAGTCTGCAA
CTCAGAGATTCTGACTGACTACTGTGTTGAGAATCGGTTTGGCTGGTACGTTGACCAAGGACCAAGGTGGAAAT
TCAAAAGC (서열 1046)

BMS3h-131-18
GATCCAGATGACCCAGTCTCCATCTCACTGTGTCATCTGTAGGAGACCGTGTCCATCACTTGCCTGGGCAAAAT
GTCTATTATTGTGGGGCTAGTCTTGTCACAGCAGAAACAGGGGAAGACCCCTGAGCTCTCGATCGAGAGTTCTTCCTGG
TCTGCAAAATGGGGTCCCATCAGTTCAGTGTGACATGCGATGGATCTGGGACAGATTCACTCTCAACATCAGCAGTCTGCA
CATCGAAGGATTCTGACTACTACTGTGTGAGAAATGCGGTTTGGCCCTGGTACGTTGCGGCACAGGACCAAGTGGGAAA
TCAAAGG (서열 1047)

BMS3h-131-9
GACATCCAGATGCCACCGAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTCCATCACTTGCCTGGGCGAATA
TGCTCTAATATTTGGGGGCTTGGCTTGGTACAGCAGAAACAGGGGAAAGCCCTAAGCTCTGATCGAGAGTTCTTCCTGG
TTTGCAAAAGTGGGGTCCATACAGTTCTCAGTGCAGTGGATCTGGGACAGATTTCATCTTCACCATCAGCAGTCTGCAA
CTCGAAGGATTTGCTAGCTACTACTGTGTTCAAGATCGCGTTTGGCTGGTACGTTCTGGCCAGGAGCAAGGTGGAA
ACAACAAAG (서열 1048)

BM53h-131-10
GACATCCAGATGCCACCGATCCATCTCTCTGTCTGCATCTGTAGGAGACCGTGCACCATCACTTGCGGGCAAAAT
GTCTTATCTTGTGGGGCTAGCTTGGTACAGCAGCAAACTGGGAAAGCCCTAAGCTCTGTATGAGAGATCTTCTCGG
TTTGCAAAAGTGGGGTCCCATCAGCTTTCAGTGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCAA
CCCGAAGGATTTGCTACGATCTACTGTGTTAGAAATGCGGTTTGGCTGGTACGTTGGCGCAAGGACCAAGGTGGAA
TCAACAGG (서열 1049)

BMS3h-131-11
GACATCCAGATGCCACCACTCCATCTCCCTGTCTGCTCTGTGAGGACCGTGTCCACATCACTTGCCGGGCAATA
TGCTATTATTGTGGGGCTAGCTTGTGACACGACGAACAACAGGGAAGCCCTAAGCTCTGATGAGAGTTCTTCGGG
TTTGCAAAAGTGGATCCCATCAGCTTCAGTGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCA
CATCGAAGATTCTGACTGACTACTCTGTGTCAGAAATCGGTTTGGCTTGGTACGTTGGCGCAAGGCAACAGGTGGAA
TCCAAAGCG (서열 1058)

BMS3h-131-12

GACATCCAGATGCCCAAGTCTCCATCCTCCTGTCTGCATCTGTGGAGACCGTGTACCATCACTTGC CGGGCAAAAT
TGCTTAAATTGTGGGGGTAGTCTTGTAACAGCAGAAACAGGGAAGCCCTAAGCTCTGTATGAGAGATTCTTCGGG
ATTGCAAAAGCGGGTCCCATCACTGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTTCACCATCAGCAGTCTGCAA
CTCAGAGATTTGCTTACTGACTACTGTGTTGAGAAATCGGTTTGGCTTGTACGTTCGGCAAGGACCAAGGTGGAAAT
TCAAGACG (서열 1851)

BMS3h-131-13)
GACATCTCTTGTACCCAGTCTCCATCTCTCTGCTGCATCTGTAGGAGACCGTGCACCATCACTTGC CGGGCAAAAT
TGCTTAAATTTGTGGGGCTAGCTTGTGACACAGCAAAACAGGGAAGCCCTAAGCTCTGATCGAGAGTTCTTCGGG
TTTGCAAAATGGGGTCCCATCAGCTTCTCAGTGGCAGTGGATCTGGGACAGATTTCATCTTCACCATCAGCAGTCTGCAA
CTCGAAGATTTGCTAGCTACTACTGTGTTCAAGATCGGTTTGGCCTGGTACTGTTGGCCAGGACCAAGGTGGAAAT
TCAGAACG (서열 1052)

BMS3h-131-14
GACATCCAGATGACCGAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACACTCTGCCGGGCAAAAT
GTCTTAATTTCTTGGGGCGTTAGCTTGTGACAGCAGAAACAGGGAAGCCCTAAGCTCTGATCGAGAGTTCTTCGG
TTTGCAAAATGGGGTCCATCAGCTTTGACGTGAAGTGGAACTGGGACAGATTTCATCTTCACCATCAGCGGTCTGCAA
TCCAGGATTTTCTAGCTACTACTGTGTCAGAAATCGCGTTTGGCTGTGACTTCGACAAAGGACCAAGGTGGAA
TCAAACGG (서열 1053)

BMS13h-131-15
GACATCTAGTACGACCGAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGGTGTACCATCCCTTGC CGGGCAAAAT
GTCTCAATTTGTGGGGGTAGTCTTGGTACAGCAGAAACAGGGAAAGCCCTAAGCTTCTGATCGAGATGTCTTCGG
TTTGCAAAAGTGGGTCCCATCAGTTTTCAGTGGCAGTGCATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCA
ACTCGAAGATTTTGCTACTACTCTGTGTTCAGAAATCGGTTTGGCTTGGTACTGTGGCACAAGGCAACGAGTGGGAA
TCAAAAGT (cyt 1854)

BMS3h-193-1
GACATCAGATGGCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATCACTTGCGGGGCAAGTC
AGACATATAGCGCTCGT1TAAATTGGTATCAGACAGAAACAGGGAAAGCCCTAAGCTCTGATCTATCTGCTCCCG
TTTGCAAGTGGGGTCCATCAGGTTTCAAGTGGCAGTGGATCTGGGACAGATTTCATCTTCACCATCAGCAGTCTGCA
ATCTCGAAGTATGTGTCAGTACTCTGTCATCAGTATGCCAGTCCACCTTTGACCTTAGGCCAAGGACCAAGTGGAA
TCAAACGG (서원 1955)

BMS3h-193-2
GACATCAGATGACGACCGACTTCCATCTCCCTGTCTGCATCTGTAGGAGACAGTGCACCATCACTTGCGGGGCAAGTC
AGACATATGAGCGTCGTTTAAATTTGGTATCAGAGAAACAGGGGGAAGCCCTAAGCTCTCGATTATCTTGTCTCCCG
TTTGCAAAAGTGGGTCCCATCAGCTTTCAGTGGCAGTGGAATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCAA
CTCGAAGATTTTGTCTACGTACTACTGCCATCAGTATGCGAGTCCACCTTTGACGTCTGGCCAGAGGCAACATGTGGAAA
TCAAAGCG (서원 1856)

BMS3h-193-3
GACATCAGATGACCCAGTCTCCATCTCCCTATCTGCATCTGTAGGAGACCGTGTCACCATCACTTGCGGGGCAAGTC
AGACATATAGCGCTCGTTTAAATTTGGTATCAGCAAAACAGGGAAAGCCCTAAGCTCTGATCTATCTTCTCTCCG
TTTGCAAAATGGGGTCCATCAGGTTTCAAGTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGGAA
CTCAGGAATTTTGGTCGCTCATCTACTGTCATCAGTACGAGAGTCCACCTTTGACCTTTGGCCAAAGGCAACAAATGGGAA
TCAAACG (서열 1857)

BMS3h-193-4
GCACATCAGATGACCGACAGTCTCCATCTCCCTGCTGCATCTGTAGGAGACCGTGTACCATCACTTGCGGGGCAAGTC
GGATATATGAGCGTCGT1TAAAT1GGTATCAGAGAAACAGGGAAAGCCCTAAGCTCTGATCTATCT1GCTTCGGC
TTTGCAAAAGTGGGGTCCATCAGGTTTCAAGTGGCAGTGGATCTGGGACAGATTTCATCT1CACCATCAGCAGTCTGCAA
CTCGAAGATTCTCTTACGTACTCTGTCATCAGTATGAGAGTCACCTT1TGAAGTCGGCCAAAGGGACAAAGTGGAA
TCAAAGG (서열 1058)

BMS3h-19-35
GACATCAGATGACGCCAGTCTCCATCTCCCTGCTGCATCTGTAGGGAAGCGTGCACCATCACTTGCGGGCAAGTC
AGACATTTAGGCGTCGTTTAAATTTGGTATCAGCAAGAAACAGGGAAGACCCCTAAGCTCTGATCTATCTTCTCCCG
TTTGCAAAAGGGGTCCTATCAGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCATCTCACCATACGAATCTGGAA
CTCAGGAAGTCTCGCTACGTACTCTGATCAGTATGCGAGTCCACCTTTGACGTAGGCGAAGGCAAGATGGGAA
TCAAAGG (서열 1859)

BMS3h-193-6
GACATCCAGATGCCACCGAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACCGTGTCCATCACTTGC CGGGCAGCC
AGACTGTTGAGCTCGTTTAAATTGGTATCAGCAGAAACAGGGAAGGCCCTAAGCTCTGATCTATCTGTGTTCCCG
TTTGCAAAATGGGGTCCATCAGGTTTCAGTGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAA
CTCAAGAGTTTGTCTACGTACTCTGTCATCAGTATGCGAGTCCACCTTTGACGTAGGCCAAGGACCAAGTGGAA
CCTGGAGC (서열 1860)

BM53h-193-7
GACATCCAGAAATCCACCGAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCCTGTGCACCATCACTATGCCGGGCAAGTC
AGACATTTGAGCGTCGTTTAAATTGGTATCAGCAAGAAACAGGGAAGACCTTAAGCTCTGATCTATCTGTCTTCCCG
TTTGCAAAAGTGGGGTCCCATCAGGTTCTAGTGGCAGTTGATCTGGGACAGATTTCACCTTCACCATCAGCAGTCTGCAA
CTCAGAGATTCTTCTACGTACTACTGTATCAGTAGAGAGTCTCCTTTGACGTTCCGGCAAGGGCAAGATGGAA
TCAAAGC (서열 162)

BMS3h-193-8
GACATCCAGATGACCCAGCTCCATCTCCCTGTCGTGCACTCTGAGGAGACCGTGTCCACCATCACTTCCGGGGCAAGTC
AGACATTTGAGCTCGTTTAAATTGGTATCAGCAGAAACAGGGGAAGCCCTAAGCTCTGATCTATCTTGCTTCCCG
TTTCAAAAGTGGGGTCCCATCAGCTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAA
CTCAAGATTTCTTGACTACTACTCTATCAGTATGAGAGTCCACCTTTCAGCTTCTGGCCAAAGGGCAAAAGTGAA
TCAAAATG (서열 1062)

BMS3h-193-9
GACATCCAGTGTACCCAGTCTCCATCTCTCTGTGTCATCTGTAGGAGACCAGATCACCATCACTTGC GGGGCAAGT
GAGATCTGTAGCGTCGTTTAAATTTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCTGATCTATCTTGCTTCCG
TTTGAAGAATGGGGTCCATCACGTTTTCAGTGGCAGTGGATCTGGGACGAATTCACCTTCACCATCAGCAGTCTGCAA
CTCAAGAGTTTCTTACGTACTCATCTGTCATCAGTATGAGAGTCACCTTTGACGTTTCGGCAGGGGACAAAGTGGAAA
TCCAAAGG (서열 1063)

BM53h-193-10
GACATCCAGATGTCCTCCAGTCTCCATCACCCTGTCTGCATCTGTAGGAGACCGTGTCCACATCACTTCCGGGGCAAGTC
AGACATTTGAGCGTCGTTTAAATTTGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCTGATCTATCTGTCTTCCG
CTTGCAAAAGTGGGGTCCATCAGCTTCTAGTGGCAGTGGATCTGGCAGATTCTCACTTCACCATCAGCAGTCTGCAA
CTCAAGGATTTTGGCTAGCTACTATCTATCAGTATGAGAGTCCACCTTTGATGTTCCGCCAAGGGCAAGATGGAAA
TCAAAGG (서열 1064)

BMS3h-193-11
GACATCCAGATGCCCAAGTCTCCATCTCTCTGTGTCATCTGTAGGACCGTGTACCAATTACTTCCGGGGCAAGT
GACATCTTGGAGTCGT1TTAAAT1GGTATCAGCGAAGAACGAGGAAAGACCTTAAGCTCTGATCTATCTGTCTCCCG
TTTGCAAAAGTGGGGTCCCATCAGCT1TTCAGTGGCAGTGGATCTGGGACGATT1CACTCTCCATCATGCAAGTCTGCAA
CCAGAAGAG1TCTGACGTACTACTGTATCAGTATGAGAGTCCACCT1TTCAGCTTCCGCAAGGACCAAGTGGGAA
TCAACGG (서벌 1065)

BMS3h-193-12
GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCCGTAGGAGACCGTGCACCATCACTTGCGGGGCAAGTC
AGACATTTGAGCGTCGTTAAACTGGTATCAGCAGAAGACAGGGAAAGCCCTAAGCTCTGATCTATCTGTCTCCCG
TTTGCAAAAGTGGGGTCCATACAGTTCTCAGTGGCAGTGGATCTGGGACAGATTTCACCTTCACCATCAGCAGTCTGCAA
CTCAGAGATTTCTGACTAGTACTGTCTATCAGTATGAGAGTCACCTTTTACGTTTGGCCAGGGGACAAAGTGGAAA
TCAAAGG (서열 1066)

BMS3h-193-13
GACATCAGATGACCCAGTCTCCATCTCCCTGTGTGCATCTGAGGGACCGTGTACCATCACTTGCGGGGCAAGT
AGACATTTGAGCGTCGTTAAATTGTGATCAGCAGAAACAGGGAAAGCCCTAAGCTCTGATCTATCTGTCTCC
TTTGCAAAAGGGGGCCATCAGCTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCATTACAGAGCTGTGCA
CTCAGAGGATTTGCTAGCTACTACTCTGATCAGTATGAGAGTCACCTTTGACGTTTCGGCCAAAGGACCAGAGTGAA
TCCAAAGG (서열 1067)

BMS3h-193-14
GACATCCAGTACCGACCCAGTATCCATCTCTGGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGGCGGGCAAGT
AGTCAGATTGAGCGTCGT11TAATTGGTATCAGCAAGAACAGGGGAAGCGCC1TAAGCTCCTGATCTATCTGTGCTCC
TTTGCAAAATGGGGTCCCATCAGCTTTCAGTGGCAGTGGATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCAAC
CTCAGAAGATTTCGATCACTACTCTGATCAGTATGAGAGTCCACCT11TACGCTTCGGCCAAAGGACTAAAGTGGAA
TCAAAGCG (서열 1068)

BMS3h-193-15

GACATCCAGATGACCCAGTCTCCATCTCTGCTCTGCATCTGTAGGAGACCGTGTACCACTACTTCCGGGGCAAGTGGACATCTTAGCGTCGT1TAAATGGTATCAGCAAGAACAGGGAAAGCCCTAAGCTCCTGATCTATCTTGTCTGGCTTTGCAAAATGGGGTCCCATCAGCTTCAGTGGCAGTGGATCTGGGACAGATTCTACTCCACATCAGCAGTCTGCAACCTCGAAGATTCTGACTGATCTGTCATCCGTATGAGAATCCACCTTTGAGCTTCCGGCAAGGGACCAAGGTTGGAATCAACAAGC (서열 1869)

BMS3h-193-136

CCAGTCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCGGGGCAAGT
AGGCATTTGAGCGTCGTTAAATGTGATCAGCAAGAAACAGGGAAGGCCCTAAGCTCCTGATCTATCTTGTCTCCG
TTTGCAAAATGGGGTCCCATCTCGTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGAGCTGTGCAC
CCAGAAGGTTTCTGACTACTCTACTGTATCAGTAGTGGCAGTCCACTTTCAGCGCTCGGCAAGGGACCAAGGTTGGAA
TCAACAGG (서열 1878)

BMS3h-193-17
ACCATCAGATGACCGACGTCCTCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCGGGGCAAGT
AAGCTATTGAGCGTCGTTTAAATTGGTATCAGCAAGAAACAGGGAAGGCCCTTAAGCTCCTGATCTATCTTGTCTTC
TTTGCAAAATGGGGTCCATACAGTTTCTAGTGCAGTGGAATCTGGGACAGATTCACTCTACCATCAGCAGTCTGCA
CCTGAAGATTTCGATCACTACTGTCATCAGTATGAGAGTCCACCTTTGAGCTTCGGCCAAAGGACCACCAAGTGGAA
TCAAGAC (서열 1871)

BMS3h-193-18
GACATCAGATGACCCAGTCTCCATCTCTCGTCTGCATCTGAGGACCGTGTACCATCACTTCCGGGGCAAGT
AGACATTTGGGGTCGTTTAAATTGGTATCAGCAAGAAACAGGGAAGCCCTAAGCTCTGATCTATCTTGTCTTCC
TTTGCAAAATGGGGTCCATACAGTTCTCAGTGGCAGTGGATCTGGTGAGATTCACTCTACCATCAGCAGTCTGCA
CTCAGGAAGTTTCTGACTAGTACTGTCATCAGTAGAGATCCACCTTTGAGCTTCGGCCAAGGGACCAAGATGGAA
CTTCAAGG (서열 1872)

BM53h-19-19
GACATCCAGATGACCCAGTCTCCATCTCCCTTTTCGATCTGTAGGAGACCCTGTACCATCACTTGGCAGCAAGT
AGACATTTGAGCGTCGTTTAAATTTGGTATCAGCAGAAACAGGGAAGGCCCTAAGCTCCTGATCTATCTTGTCTCC
TTTGCAAAATGGGGTCCCATACGTTCTCAGTGCAGTGGATCTGGGACAGAAATTACTCTCACCATCAGCAGTCTGCA
CCTGAAGATTTTCTAGCTACTACTGTCTATCAGTATGAGAGCTCACCTTTGACGTCGGCCAGGGCAAGCTGGAA
TCAAAAGC (서열 1073)

BMS3h-193-20
GACATCCAGATGACCCAGACTCCATCTCCCTGCTGCATCTGTAGGAGACCCTGTCCACCATCACTTCCGGGGCAAGTC
AGACCTGTGAGCGTCGTTTAAATTTGGTATCAGCAGAACACGGGGAAGCCCTAAGCTCTGATCTATCTTGCTTCCGC
TTTGCAAGATGGGGTCCCATCAGGTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAA
CTCGAAGATTTTGCCACGTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGCAAGATGGAAAT
TCAAACGG (서열 1074)

BMS3h-193-21
 GACATCCAGATGACCCAGTCTCCATCTCTGCTTGTGCAATCTGTAGGAGACAGTGTCCATCACTTGCCTGGGCGAAGT
 AGACATCTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCTGATCTATCTGTGTTCCCG
 TTTCGAAGATGGGGTCCATCAGCTTGTAGTGGCAGTGATCTGGGACAGATTCTCACTTCACCATCAGCAGTCTGCAA
 CCGGAAGGTTCTTACTGACTCATCTGTCATCAGTATGAGAGTCCACCTTGTGACGTCTCGCCCAAGGCGCAAAAGTGAAA
 TCAAAGG (서열 1875)

BMS3h-193-22

ACACCTCCAGATGACCAGCTGCTCCATCCCTCTGCTGCATCTGTAGGAGACCCTGTGCCACCTCACTTCCGGGGCAAGTC
AGACATTTGAGCGTCGT1TAATTTGGTATCAGCGAAACACGGGAAGCCCTAAGCTCTGATCTATCT1GCTTCCG
TTTGCAAGTGGGGTCCCATCAGGTTTCAAGTGCAGTGATCTGGGACAGATTTCACCTTCACCATCAGCAGT1CTGCAA
CTCGAAGATTTTCTACGTACTGCTGCATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGACCAAAAGTGGAAA
TCAAACGG (1876)

BM53h-193-23
GACGTCCAGATGACCCAGCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTCCACATCACTTGCCGGGCAAGTC
AGACAGTTCGAGCGTCGTTAAATGGTATCAGCAGAAACAGGGGAAGCCCCAAGCTCTGATCTATCTTACTTCCCG
TTTGAAGAAGCGGGGCCCATCACTGTTTCAAGTGGATGGATCTGGGACAGATTTCACTTCACATCAGCAGCTCTGCAA
CTGAAGAATTTGCTACGTACTACTGCCATCAGTATGCGAGTCCACCTTTGACGTTTCGGCAAGGGACCAAGGTGAAAA
CCTAAAGG (sequence 1077)

BMS3h-193-24
GACATCCAGATGACCCAGTGCCTACTCTCCCTGTCTGCATCTGTAGGAGACCGTGTCCCATCACTTGCCGGGCAAGTG
AGACGATTTGAGCGCTGTTAAATGGTATCAGCAGAAACCAAGGAAAGCCCTCAAGCTCTGATCTATCTTGCTTCCCG
TTTGCAAGTGGGGTCCCATCAGCTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTTCCACATCAGCAGTCTGCAA
CTGAAGATTTTCTACGTACTACTGTGCACCATGTAGAGTCCACCTTTGACGTTTCGGCAAGGGACCAAGTGGTAA
CCTAAAGG (sequence 1878)

BMS3h-19n-125

GACATCCAGATGACCCAGTCTCCATCTCCTGTCTGCATCTGTAGGAGACCCAGTCCACATCACTTGCCTGGGCGAAGTC
AGCATCTTAGGCGTCGTTAAATTTGGTATCAGCAGAAACCTGGGGAAGCCCTAGGCTCTGATCTATCTTGCATCCCG
TTTGCAAAATGGGGTCCCATCAGCGTCTAGTGGCAGTGGATCTGGGACAGATTCACTCTACCATCAGCAGTCTGCAA
CTCGAAGATTCTCTAGCTACTGCTCATCAGTATGAGAGTCCACTTTGACGTCGCGCAAGGCGCAAATGGGAA
TCCAAAGC (서열 197)

BMS3h-193-26
GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTCCCATCACTTGCCGGGCAAGTC
AGCCGATTGAGCGCTGTTTAAATTGGTATCAGCAGAAGCCAGGGAAGCCCTAAGCTCTGATCATCTTGTCTCCCG
TTTGCAAAGTGGGGTCCCATCAGTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACATCAGCAGTCTGCAA
CTCAAGATTTTGTCTACATACTACTGTCACTCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAAGGACCAGGTGGAAA
TCAAAGG (sequence 1080)

[0232]

BMS3h-193-27
GACATCTCAGATGACCAGTCTTCATCTCCCTGCTGCATCTGTAGGAGACCGTGTCACCATCACTTGCGGGGCAAGTC
AGACATCTGGGGCTGTTTAAATGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCTGATCTATCTTGTCTCCG
TTTGCAAGTGGGGCCCATCAGCTTTCAGTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCGAA
CCTGAAGTATTCTACGTACTACTGTCATCAGTATGAGAGTCCATCTTGGACTTCGGCCAGGGGCAAGATGGGAA
TCAAACG (서형 1081)

BMS3h-193-28
GACATCCAGTGAATGACCCAGTCTTCATCTCCCTGTCGTCATCTGTAGGAGACCGTGTCACCATCACTTGCCGGGCAAGTC
GATCTGATGAGCGCCGTTAAATGGTATCAGCAGAAACAGGGAAGACCCCTAAGCTCTCGATCTATCTGTCCTCCG
TTTGCAAGTGGGGCCCATCAGCTTTCAGTGGCAGTGGATCTGGGACAGATTTCATCTCAGCATCAGCAGTCTGCAC
CTGAAGGTTTCTAGCTACTCTGTCATCAGTAGAGATCTCTTGGACCTCGGCACAGGGCAACAAATGGAAT
CCGAGG (서현 1982)

BMS13-193-29
GACATCCAGATGACCCAGTCTTCATCCCTCCCTGTCTGCATCTGTAGGAGACCAGTCACCATCACTTCCGGGGACAGTC
AGACATCTTGGAGCTGTTTAAATTTGGTATCAGCAGAAACCTGGGAAAGCCCTAAGCTCTGCATCTATCTTCATCCG
TTTGCAAGTGGGGTCCCATCAGCTCTGAGTGGCAGTGGATCTGGGACAGATTTCATCTTCACTACAGCATCTGCGAA
CTCGAAGGTTTCTAGCTACTCTGTCATCAGTATGAGAGTCCATCTTTGACGTTCGGCACAAGGCAAACTGGGAA
TCAACAGG (서형 1083)

BMS13h-19h-30
GACATCTCAGATGACCGACCTGCTCCATCTCCCTGTCTGCATCTGTAGGACAGCGTGTCCACATCACTTGCCGGGCAAGTC
TGATCTTGATGAGCGCGCTTAAATTTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCTGATCTATCTTGCTTCCG
TTTGCAAGTGGGGTCCCATCAGCTTTTCAAGTGGCAGTGGATCTGGGACAGATTTCATCTTCACTACGAGCTTGCAC
CTCGAAGATTGCTACTGACTACTGCTCATCAGTATGAGAGTCCTCTTGACGTTCCGGCAAGGACCAAGTGGAA
TCAACCG (서철 1084)

BMS3h-193-2501
GACATCCAGGATGACCACGTCCATCCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCTGGGCAAGTC
AGACGATTCAGATCGCTCTTTAAATTGGTATCAGCAGAAACCTGGGAAGCCCTTAGCTCTGATCTATCTTGTACCCG
TTTGCAAAGTGGGGTCCCATCAGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTTCACATCAGCAGTCTGCAAC
TCTGAAGATTTTGCTACGTACTACTGTCAATGTTCTGAGCACCACCTTTGACGTTCTGGCAAGGACCAAGTGGAAA
TCAAAGG (서열 1085)

BHS3h-193-2582

TCCATCCAGATGACCTTCATCTCCATCTCCCTGCTGCATCTGTAGGACGACCGAGTACCATCACTTCGCCGGCAAGTT
GCCATTCGATCGCTGTCTAAATTTGGTATCAGCAAGAACTGGGAAAGCCCTAGBCTCTGTATCTATCTGTGATCCCG
TTTGCAAGTGGGGTCCCATCAGCTCTCAGTGGCAGTGGATCTGGGACAGATTTCATCTTACCATCAGCAGTCTGCAA
CTCGAAGGTTGCTACGTACTACTGCTCATAGTATGAGAGTCCACTTTGACGTTCGGCAAGGCGCAAGGTGGAA
TCAAACGG (서형 1086)

BMS3h-193-2503
GACATCCAGATGCCACCACTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCACATCTTGCCGGGCAAGT
CACCATTGCTCCCTGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTTAGGCTCTGATCTATCTTGCTACCGG
TTTGAAAGTGGGGTCCCATCCGCTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTCGCAA
CTCGAAGATTTTGCTACGCTACTGTCTCATGATATGAGAGTCCACCTTTGACGTTCTGGCAAGGCAAGGTGGAAA
TCAAACGG (서연 1087)

[0233]

BMS3h-193-2504
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTTACCATCACTTGCCGGGCAAGTT
CCAGATTTGGCGTCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1088)

BMS3h-193-2505
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTG
AGCGGATTTGGCGTCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1089)

BMS3h-193-2506
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
AGCAGATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1090)

BMS3h-193-2507
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
AGCGGATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1091)

BMS3h-193-2508
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTG
GGAACATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAAGCG (서열 1092)

BMS3h-193-2509
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
GGAACATTTAGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1093)

BMS3h-193-2510
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
AGAGCATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1094)

[0234]

BMS3h-193-2511
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
AGAACATTTGGGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1095)

BMS3h-193-2512
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTG
AGGTCATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1096)

BMS3h-193-2513
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTG
AGGCGATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1097)

BMS3h-193-2514
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTA
CCAGCATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1098)

BMS3h-193-2515
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTT
TGAACATTTGGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTACCCG
TTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1099)

BMS3h-193-2516
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
AGACGATTTAGCGCTGTTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCTTAGGCTCCTGATCTATCTTGTGCGAA
GTTGCAAAAGTGGGTCCTATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCTGGCCAAGGGACCAAAGTGAAAA
TCAACGG (서열 1100)

BMS3h-198-1
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTTACGCTGGGGGTCCTGCGTCTCTCTGTCAGCTCTCCGGAT
CCACATTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGCGTGTCTCAGCTATTAGTGG
TAGTGGTGTAGCACATACTACGACACTCCGTGAAGGGCCGTTTACCATCTCCGAGACGATTCCAAGAACACGCTG
TATCTGCAATGAACGCTGCGTGCAGGATACCCGCTATATCTGTGCGAGAGATCTTATAGTTTTCAGTACT
GGGTCAGGGAACCTGGTCACCGTCTCGAGC (서열 1101)

[0235]

BMS3h-198-2
GAGGTGACGACCTGGTAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCCTGTGACGCTCCGGATG
CTACTTTTCGTGGGTATAGATGATGTGGTGGTCCGCAGCTCCAGGGAAGGCTCTAGAGCGGATCTCAGCTATTAGCGC
TAGTGGTGTAGCACATACTACGCAAGCTCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAGGAACACGCTG
TATCTCGAAATGAACCGCTGCTGCGGAGGATACCGGGTATTACTTGTGCGAGAGACCTTATAGTTTGTGACTACT
GGGTCAGGAGAGCTGGTCCGCTGTCTGAGC (사형 1182)

BMS3h-198-3
GAGCTTGACGACTGTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCCACCGGAT
CAGGCTTTTCTGGGTATAGATGTGGTGGTCCGACAGGCTCAGGGAAGGCTGTAGAGCGGGTCTACGATTATAGTGG
TAGTGGTGGTAGACACATACTACCGAGACTCGTGGAAGGGCCGGTTACCATCTCTCCGACGAGTTACAGAAACACGCTG
TACTGCAAAITGAACACGCTGCTGCGGAGACATCCGGGTATATTACTTGTGCGAGAGAGCTCTTACAGTTATGACTACT
GGGGTCAAGGGAACCTGAGTCTCCGCTCGGCT (seq. 1183)

BMS3h-198-4
GAGGTGCAGCTGTGGAGTCTGGGGAGGCTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAC
TACCCTTTCTGGGTATGAGATGTGGTGGTCCGCGAGCACGAGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGTAGCACATACTACGACAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGATTCGAAGAACACGCTG
TATCTGCAAAATGAACACGCTGCGTCCGAGGATACCGAGTATCACTGTGCGAGAGATCCTTATGATTTTGACTACT
GGGGTCAGGACACTGGTCTGACCGTCTGACG (서열 1104)

BMS3h-198-5
GAGGTTCACATCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCCTGCGTCTCCTGTGACGCTCCGGAT
TGCTTTCCTTGGGTATAGAGTGTGGTGGGCTCGCAGGCTCAGGGAAGGCTGTAGAGCGGGTCTCAGCATTAGTGG
TAGTGGTGGTAGCACAATACTACGCACTCTGTGAAGGGGCGGTTACCATCTCCCGACGATTCGAAGAACACGCTG
TATCTCGAAATGAACCGCTGGTGTGCGGAGATACCGCGGTATCATCTGTGCGAAGAAACCTTATGATTGTACTACT
GGGGTCAGGGGAAGCTGGTCCAGCTGTGACG (서형 1185)

BM53h-198-6
GAGGTGCAGCTTGTTGAGCTCGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCCTCTCTGTCAGCCTCCGGAT
CCACCTTTCTGGGATAGAGATGTGGTGGTCCGCGAGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGTAGCACATACTACGCGAGACTCCGTGAAGGGCCGGTTACCATTCTCCGCGCAGATTCCAAGAACACGCTG
TATTCGAAATGAACACAGCTGCGTCCCGAGGATACCCGGGTATATTACTGTGAAAGACTCTTATAGTTTGTACTACT
GGGGTCAGGGAAGCTTGCTCAGCGTTCGACG (서열 1106)

BMS3h-198-7
 CAGGATGCACGATCTGGAGTCTGGAGTGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
 CACCATATCCCGGGTATGAGATCTGGTGGGTCCGCAGGCTCCGGGGAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACAATACTACGACAGCTCCGTGAAGGGGCGGTTACCATCTCCCGACGAGTTCAAGAACACGCTG
 TATCTGCAAAATGACCGCTGCGTCGGAGATACCGCGGATATTATCTGCGAGAGAGTCTTATAGTTTGGTACTAT
 GGGGTGAGGGGAACCCGCTGACCGCTCTGAGC (서현 1197)

BMS3h-198-8

CGAGTGCAGCTGTGAGAGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCCTGTGCAGCCTCCGAGTAC
CCACCTTTCTGGGTATGAGATGTGGTGGTACCCAGCAGCTCCAGGGAAGGCTTACAGAGCGGCTTCAGCTATTATGTGG
AAGTGTGAGAAGCACATACCTACGCAGACTCCTGAAAGGGCCGGTTACCATCTCCCGACGAGTTCCAAGAACACGCTG
TATCTCGAAATGAACCGCTGGTGCAGGATACCGCGGATATTACTTGCAGGAAGACTCTTATAGTTTGTGACTACT
GGGGTCAGGGGAACCTGGTCACTGCTCAGGC (서형 1188)

BMS3h-198-9
 TACCTGCACGTGCTGGAGCTCTGGGGGAGGCTTGTCAGACCTGGGGGGTCCCTCGCTCTCTCTGTGACGCCTCCGGAT
 GACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTACGCTATTAGTGG
 TAGTGGTGTAGCAGCTACTACGACAGCTCTGTAAGGGCCGGTTACCATCTCCCGCCAGCATTCAGAAACACGCTG
 TATCTGCAAAATGGAACGCTGCTGCTGCCGAGGATACGCGCATATTACTGTGCGAAGAACCTATTAGTTTGGACTACT
 GATTCAGTGAAGCACTGGTCACGCTCTCGAGC (서형 1189)

BMS3h-19h-10

BMS3h-198-111

BMS3h-198-112

TGACCTGACCTGTGGAGCTCTGGGGGAGCTTGGTACGAGCTCGGGGGCTCGCTCTCTCCTGTGCAGCCTCCGGAT
 CAGATTCTGGTGGGTATGAGATGTGGTGGGTCGCGAGGCTCCAGAGGAGGGGTCTAGAGCGGGTCTCCGATTATGTGG
 TAGTGGTGTAGCACAATACGCGGACTCTCGTAGAGGGCGGGTACCATCTCCCGGACGATTCCAGAAACACGCTG
 TATCTCCAAATGAGACAGCTGTGGTGGCGGAGATACCGGGTATTAATTCTGCGAAGATCCTTATAGTTTGGCTACT
 GGGGCTAGGAGCAACCTGGTGCAGCTTTTCAGG (시퀀스 1112)

BMS3h-198-13
GAGGTGCACGTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTCTCCTGTGCAGCCTCCGGAT
TCACTTCTCTGGGTATAGATGTGGTGGTGCAGCGCTTCAGGGAAGGCTCAGAGCGTGTCCAGCTATTAGTGG
TAGTGGTGTAGCATACTACGACAGACTCCGTGAAGGGCCGGTTACCATACCCGCGCAGATTCCAAGAACACGCTG
TATCTGCAAAAGAACAGCCTGCTGGTGCAGGAGATACCCGGGTATATTACTGTGCGAAGAGCGCTTATAGTTTGCATCT
GGGCTCAGGGAACCTGTGACCGCTTCAGCG (서열 1113)

BNS3h-198-14

GAGGTGACAGCTGTGGAGTCTCCGGGAGGCTTGGTACAGCTGGGGGCTCTCGTCTCTCGTACGCTCCGGAT
TCACCTTTCTGGGTATGAGATGTGGTGTGTCGCGAGCTCAGGAGAGGCTGTAGAGCGGGTCTCAGCTATTAGTG
TAGTGGTGTAGCACATACGACAGACTCGTAGAGGGCGGGTTCACCATCTCCGCGACGATACCAAGAACACGCTG
TATCTCAAAAGAACAGCTGCTGCTCCGAGGATACCGGCTGATTATTAATCTGGGAGAAAGTCTTATAGTTTGTGACTCT
GGCATGAGGAAACCTTGTCACGGCTCTCGAGC (서열 1114)

BMS3h-19-15

BMS3h-198-16
CAGCTTCGACGCTGTGGAGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTCGCTCTCTCTGTCGAGCCTCCGGAT
CGACCTTTCTGGGTATAGAGTGTGGTGGTCCGACAGCTCCAGGAGAGGCTTAGAGCGGATCTACGCTATTAGTGG
TAGTGGTGGTAGCACATACGCGACGCTCGTGGAGAGCGGGTTCACATCTCCCGCGACGATTCCAGAAACAGCGTG
TACTGAAAATGCAACGCTGGCTGCGGAGATACCGCGGTTATTACTGTGCAAGAGATCTTATAGTTTGACTACT
GGGTGAGGAGCAAGCTGGTCCCGCTTCGAGC (서열 1116)

BMS3h-198-17
GAGGTGTCAGCTTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCCTCCGGA
TCACTTTTCTGGGTATAGAGTTGGTGGGTCGCCAGGCTCCAGGAGAGGCTTATAGAGCGGGTCTCAGCTATTATGATGG
TAGTGGTGGTAGCACATACAGCAGACTCTCGAAGGAGCCGGTTACCATCTCCCGCAGAGTCCAGAAACACGGCTG
TCTCAAGAAACAGCCTGCGTGGCGAGGATACCGGGATATATTACTGTGCAGAGATCCTTATAGTTTGACTACT
GGGCTGAGGAGCAAGCTGGTCACCGCTCTCGAGC (서열 1117)

BMS3h-198-18
TACGTCGACGCTGTGGAGCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAC
GAGGTTCTGCTGGGTATAGAGTTGTTGGGTCGCCGGGCTCAGGAGAGGTTATAGAGCGGTGCAGACTATTATGAG
TAGTGGTGAGTACACATACGTACGAGACCTCGTGAAGACGGGTTTACCATCTCCCGCAGAGTTCAGAAACACGCTG
TCTGCAAAATCAACGCTCTGCTGCAGAGATACCGGCTATTAATTCTGCGAGAGATCTTATAGTTTTGACTACT
GGGTCAGGAGGACCTGGTCCCGCTCTCGAGC (서열 1118)

BMS3h-198C-1T
GAGGTGCAAGCTGTTGGAGTCTGGGGGAGGCTTGTGACAGCCTGGGGGGTCCCTGCGCTCTCTCCGTGCGACCTCCGGAT
TCACTTTCCTGGGATAGTGTGGTGGTCCGCGAGGCCCGAGGGAAGGCTAGAGCGGGCTCAGCTATTAGTGG
AAGTGGTGGTAGCACATACTACGAGACTCGGTGAAGGGCCGGTTCACATCTCCCGCAGCATTCACGAACACGCTG
TATCTGCAATGAACACGCTGCGTCCGGAGGATCCGGGTATATTACTGTGCGAGAGATCTTATTAGTTTGACTACC
GGGCTCAGGGAACCTGGTCAACCGTCTCAGC (서열 1119)

BMS3h-198-20
GAGGTGTCAGCTCTGGTAGTCTGGGGAGGCTTGTGACAGCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCCCGGAT
TACACTTACCTGGGTATAGAGATGTGGTGGGTCGCGCAGGCTCAGGGAAGGGCTAGAGCGGGCTCAGCTATTATGTGG
TAGTGGTGTAGCACATACTACGACAGACTCGGTGAAGGGCGGTTCACATCTCCCGCAGATTCCAGGAACACGCTG
TATCTGCAAAAGAACAGCTGCTGCCGAGATACCGGGTATATTACTGTGCAAGAAAGATATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (서원 1129)

BMS3h-198-21
GAGGTGACGACTCTTGAAGTCTGGGAGCAAGGCTTGGTACAGCTCGGGGGTCCCTGCGCTCTCTCTGTGCAAGCTCCGGCAG
TACCTTCCTTGTGGGTATGAGATGTGGTGGGTCTCGTCCGGTCTCAGGAGGAAGGTCTAGAGCGGGTCTACGATTATAGTGG
TAGTGTGGTATGACATACATACGCAAGCTCCGTGAGAGGCGGGTTCACCACTCCCGCAGGATTCAGAAACAGCGCTG
TATCTCGCAAAATGAACAGCTGCGTCCGAGATACCGGGTATATTACCTGCGGAGAGACTCTTATAGTTTGTGACTACT
GGACTCGGGAGAGCTTGGTCAAGGCTCTCGAGC (사염 1121)

BMS3h-198-22
GAGGTGACAGCTTTGGAGTCTGGGGAGGCTGTACAGACCCCGGGGGTCCCTGCGTCTCTCTGTCCGCCCTCCGGATG
CTACCTTTCTTGGGTATGAGATGTGTTGGTCTCGCAGGCTCTCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTATGTGG
TAGCGGTGGTACACATATACGCAACTCTCGTAGGGCGGGTTCACCATCTCCCGGACGATTCCAGAAACACGCTGTCT
TGCTGCAATGAACACGCTGTCTCGCGAGGATACCGCGTATTACTGTGCGAAGAACCTTAGTATTGACTACT
GGGCTGTGAGCTCTGGTATTGCTCTCGAGC (서열 1122)

BMS3h-198-23
GAGGTGACACGCTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
CAGCTTTTCGTGGGTATAGAGTGTGGTGGGTGCGCAGGCTCAGGGAAGGGTCTAGAGCGGGTCTCAGCATTTAGTGG
TAGTGGTGGTTAACACATACACGAGACTCGTGAAGGGCCGGTTACCACATCTCCCGGACGATTCCAAGAACACGCTG
TATCTGCAAAATGACACGCTGGCTGCGAGGAACCGGGGTATTAATCTGCGGAGAGACCTTATAGTTTGTGACTACT
GGGGTCAGGGTACCTTGGTCACCGCTCTGAGC (서현 1123)

BMS3h-198-24
TACAGTGCACGTCTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCCCTGCGTCTCCTGTGACGCTCCGGAT
GCACCTTTCTGGGTATAGAGTATGGTGGGTTCGCCAGGCTCAGGGAAGGGCTTAGAGCGGGTCTCAGCTATTATGAGG
TAGTGGTGGTACACATACCTACGCAGACTCCGTGAAGGGCGGTTACCATTCTCCCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACACGCTGCTGCGGAGATACCCGGCTATATTACTTCTGCGAAGAACCTTATAGTTTGTACTCT
GGGCTCAGGGGAACCTGGTCCAGCTCTGAGC (서형 1124)

BMS138-19h-25
 TAAGCCGACGATCTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
 GACCTTCGCTGGGTATAGAGTATGGTGGGTGCGCAGGCTCCAGGAGAGGGTCTAGAGCGCGTCTCAGCTATTATGAGG
 TAGTGGCGGTAGCACATACCTACGAGACTCGTGAAGGCGCGGTTCACATCTCCGCGACGATTCCAGAAACACCGTG
 TATCTGCAAAAGAACACGCTGCGTGCAGGATACCGCGGTATTAATTCTGCGGAGAGATCTTATGTTTGGTGACT
 GGGGCTGGGCTCTGGT (서형 1125)

BM538-19h-26
GAGCTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCCCTGCGTCTCTCTGTGACGCCCTCCGAT
CACCATTTCCTGGGTATGAGATGTGGTGGTCCGCAGGCTCAGAGGAGGGTCTAGAGCGGGTCTCAGCATATTAGTGG
TAGTGGTGTAGCACATACCTACGCAGACTCTGTGAAGGGCCGGTTCCTCATCTCCCGACGAGATTCAGAAACACCGT
TATCTGCAAATGAACCAAGCTGTGGCTCGAGGATACCCGGGTATTACTTGTCGGGAAGAACCTTATAGTTTGGACCACT
GGCTGACGGGACCACTGGTCCGCTGCGAGG (서형 1126)

BMS3h-198-27
GAGGTGCACGTGTGGAGTCTGGGGGAGGCTTGGTCAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCGAGCCTCGGGAT
CACCATTTCCTGGGTATAGAGTGTGGTGGTTCGCGAGGCTCAGGAGGAGGTTAGAGCGGGTCTACGACTATTAGTGG
TAGTGGTGATGACACATACACGAGACTCCGTGAAGGGGCGGTTACCATCTCCCGGACGATTCAGAAACACGCTG
TATCTGCAATGAACGACCTGCTGCCGAGGATACCCGGGTATTAATTCTGCGGAGAGATCTTATAGTTTGGACTACT
GGGACTGAGGACCTCGGTGACCGCTCGC (시퀀스 1127)

BMS3h-198-28
GAGGTGCACCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
GAGCTTCTGCTGGGTATGAGATGTGGTGTTCGCGACAGCTCAGGAGGAGGCTTAGAGCGGGTCTACGATATTAGTGG
TAGTGGTGTGATGACATACACGACAGCTCCGTGAAGGGCCGGTTCACATCTCCCGCAGGATTCAGAAACACCGTGT
TATTCGAAATGAACAGCCTGCTGCGCCGAGATACCCGGGTATATTACTGTGCGAAGATCTCTATAGTTTGAACACT
GGGTGACCAAGCACTGGTCACTGCTCCAGC (size 1128)

BMS138-198-29

GTGAGTCGACGATCTTGGAGTCTGGGGGAGGCTTGGTAGAGCCTGGGGGGCTCCCTGCTCTCTGTGACGCCCTCCGGAT
TCACCTTTCTGGGTATGAGATGTGGTGGGTCCGCAGAGCTCAGAGGAGGGGTAGAGCGGGTCTACGATATTATGTGG
TAGTGGTGTGACACATACACTACGACAGTCCGTGAGAGGGCCGGTTCACATCTCCCGGACGATTCACAGAAACACGCTG
TATGCTCAGAAATGAACACGCTGGCTGCGGAGTACCCGGGTATTACTGTGCGAAGAACCTTATAGTTTGTACACCC
GGGTCGAGGAAAGCTGGTCCAGCTCTCAGC (서형 1129)

BMS3h-198-30
GAGGTCTGAGCTTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
ACACCTTTTCGTGGGTATGAGATGTGTGGGTCCGCAAGCTCCAGGAGGAGGTCTAGAGCGGGTCTACGATTATAGTGG
TAGTGGTGGTAGACACATACGCGAGACTCTGTGAGAGGGGGGGTTCACATCTCCCGGACGATTCAGAAACACCGTGT
TATCTGCAAAAGAACAGCTGCGTGGCGAGATACCGGGGTATATTACTGTGCGAAGAAGACCTATAGTTTGGTACCACC
GGGACCTGAGCAACCTGGTCCCGCTCCGAGG (서열 1130)

BMS3h-198-31
TACGCTGCAGCTGGTGGAGTCTGGGGGAAGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAAGCCTCCGG6AT
GCAGCTTTCGTGGGTATAGATGTGTGGGTCCGCAAGCTCCAGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGACACATACGCAAGCTCTGTGAAGGGCGGTTACCATCTCCCGACAATTCAGAAACACCGTG
TATGCTCAAAAGCAAGCTGCTGCGGAGGATCGGAGTATCTACTGTGCGAAGAACCGCTTATAGTTATGACTACT
GGGTCGGAAGACCTGGTCACCGCTGACGCC (397 nt 1131)

BMS3h-19h-32

TGACCTGCACGTGTGGTAGCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
CAGGTTTCTGGGTATGAGATGTGGTGTTCGCGAGCTCCAGGAGAGGCTTAGAGAGGGGTCTACGATATTAGTGG
TAGTGGTGTAGGACATACACGAGACTCCGTGAAGGGGGCGGTTCACATCTCCCGGACAATTCAGAAACACCGTG
TCTCTCAAAATGAACAGCTCTGCTGCGAGATACCGGGTATATTACTGTGCGAAGATCTTATAGTTTGTGACAACT
GGGTCAGGCAAGCTTGGTCCGCTGACGAG (seq. 1132)

BMS19h-38-19-33

TGACCTGCAGCTGTGGAGTCTGGGGGAGGCTTGTGACAGCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
CAGGTTTCGTGGGTATGAGATGTGGTGGTCCGAGCTCAGGAAGAGGCTTAGAGGGGGTCTCAGCTATATGTAGG
TAGTGGTGTAGCACAATCTGCGAGACTTGTGAAGGGCCGGTTACACATCTCCCGGACGATTCAGAAACAGCGTG
TATCTCGAAATCAACAGCTACGCTCGGAGGATACCGGCTATATCTGTGCAAGAAACCTTATAGTTATGACTACT
GGGTCGAGCAAGCACTGTGCTGCTCTCGAGC (서열 1133)

BM53h-198-34

BMS3h-19h-35

TGACCTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCTGTCTCCTGTGCAGCCTCCGGAT
CAGGTTTCGTGGGTATGAGATGTGGTGGTCCGACAGCTCCAGGAGAGGCTGTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGTATGACATACTACGACAGCTCTGTGAAGGGCCGGTTACCATTCTCCCGACGATTCCAGAAACACGCTG
TATCTCAAAATGAACAGCTTGGTGGCAGAGATACCCGGTATCATCTGTGCGAAAGAACCTTATAGTTATGACTACT
GGGCTGAAAGGACCTGGTCCGCTCGGAG (서열 1135)

BMS3h-19h-36

GAGGTGCACGTTCTGGAGTCTCGGCGAGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCTCCTGTGACGCTCCGGAT
TACCTTTTCGTGGGTATGAGATGTGGTGTGTCGCAGGCTCCAGGAGAGGGCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGTAGCACATACAGCGACATCCGTGAAGGGCCGGTTACCATCTCCCGACGATTCAGAAACACCGTG
TATGCTCAAATGAACAGCTGGGTGCGGAGATACCCGGTATATTACTGCGGAAAGACTCTTATGTTTGAACACT
GGGTCACCAACCTGGTCAAGGCGAGC (서현 1136)

BMS3h-198-37
 GAGGTGCACGCTCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGCGTCTCTCTGTGACGCTCCGGAT
 TCACCTTTGCTGGGTATGAGTTGTGTGGGTCTGACCGACCTCAGGGAAGGCTTAGAGCGGGTCTCAGCTATTAGTGG
 AAGTGTGGTGTAGCACATACTACCGACACTCGTGAGGGCGGGTTCACCATCTCCCGGACGATTCAGAAACACGCTG
 TATCTCGCAAAATGAACACGCTGCTGCCGAGGATACCGGGGTATTACTCTGCGCAAGAACCTTATAGTTTGTGACTACC
 GGGCTCAGGGAAGCTGCTGACCTGCTCGCTCGAGC (서열 1137)

BMS3h-198-38
 GAGCTGCACCTGTCTGGAGTCTGCGGGAGAGCCTGGTACAGCCTGGGGGGCTCCCTGCGTCTCTCTGTGACGCTCCGGAT
 TACCTTTTCCTGGGTATGAGTTGTGTGGGTCTCGCAGGCGCCAGGAGAGGTTCTAGAGCGGGTCTCAGCTTATGATGG
 AAGTGGTGGTAGCACATACTACGCGACATCGTGAAGGCGCGTTACCATCTCCCGGACGATTCAGAGAACACGCTG
 TATCTCGAAATGAACACGCTGCTGCGGAGGATACCGGGATATTAATCTGTGCGAGAGACCTTATAGTTTGTGACTCT
 GGGCTCAGGAGACCTGCTGCGGCTCTGAGC (서열 1138)

BNS3h-202-1
GAGGTGCACGCTGTGGAGTCTGGGGGGGGCTGGTACAGCTGGGGGGCCCTGCGTCTCCTGTGCAGCCTCCGAT
TACCTTTTCGACGCTGTGAGATCTGTGGGTGCGAAGCTCTCAGGAGAAGGTCTAGAGTGGGTCTCATCTATTTCGGC
TAGTGGTGGTCTACATACTACGACAGCTCGTGAAGGGCCGGTTACCATCTCTCCGCGACAATTCAGAAACACGCTG
TATTCGCAAAATGAGGCTCGGCGCGAGGACACCGGATATTCTGTGCGAAGACGGTGAGTTATGTGGGCA
TGCTTGACATCTGGGCTCAGGGAACCTCGGTACCGCTCTGAGC

BMS3h-202-2
GAGGTTCACCTTCTGGTGCTGGGGGAGGCTTGGTACAGCCTGGGGGGCTCCCTGCCTCTCTGTGCAAGCCTCCGAT
TAGCTATTTCCGACGCTGAGATGTCTGGGTGCGCCAGGCTCAGGAGAGGGTCCAGAGTGGGTCTCATCAATTTCTGGC
TAGTGGTGGTCTACATACTATGCAAGCTCGTGAGAGGCGGGTTCACATCTTCCCGACAATTCAGAGAACACGCTG
CATTCGCAAAATGACGAGGCGCTCGCGAGGACACCGCGGTATATTCTGTGCGAAGAGCCGGTGAGTTATGTGGGCA
GTTTGGACTACTGGGGTCAGGAGGCTGGTCCAGCTCTCGAC (s. text 1148)

BMS3h - 202 : 3
GAGGTGCTGAGTCTGGAGTCTGGGGGAGGCTGGTACAGCTGGGGGGCCCTGCGTCTCTGCTGTGCAAGCTCCGGAT
TACACTTTCGACGTCGAGATGGTGTGGGTCCGAAGCTCAGGAGTAGGTCTAGAGTGGGTCTCATATTTCGCG
TAGTGGTGGTATACATACGACGACCTCGTGAAGGCGCGGTCCACATCTCCCGGACAATTCCAGAACTATGCTG
CTGTCGCAAAATGAGGCTGCGTCCGCGAGGACCGCGGTATATCTGCTGCGAAGGACCGGTGAGTTATGTGGCAG
CATTTGACATCGGGCTACGGGACGGTCCGTCACCTCGCAGGCT (scaffold 1141)

BMS3h-202-4
GAGGTGCTGCTTGGTGCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGGAT
TACCTTTCCGACTGCTAGATGCTGGGTCCGACAGGCTCAGGGAAGGCTAGAGTGGGTCTCATATTTCGCG
TAGTGGTGGTCTACATACCTACGACACTCGTGACGGCCGGTCTCCATTCTCCCGACGATTCAGAAACACGCTG
CATCTGCAAAATGAGGCTGCTGCGCCGAGGACACGGCGTATTACTTCTGCGAAAGACGGTGAGTTATGTGGCA
CGTTTGACTGACTGGGCTATGGAGGCTGACCGTCTGACG (size 1142)

BMS3h-202-5
GAGGTGCGATGTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGACGCTCCGATG
TCACATTTCCGACGCTGTAGATGTTGGTGGTCTGCCAGGCTCTCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGGC
TAGTGGTGGTCTACATACTACGCACTCGTGAAGGGCGGTTACCATCTCCCGGACAAITCCAAGAACACGCTG
TATCTCGAAATGACGCTGAGGACCGGAGGACACCGGGATATATCTGTGCGAAGAACCGGTGAGTTATGTGGCAAC
CGTTTGACCTAGGGGTGACGGCAACCTGGTCCAGCTGTGACG (서열 1143)

BMS3h-202-6
GAGGCGCAGCTGTTGGAGTCTGGGGGTGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGATCTCATCTATTTCCGC
TAGTGGTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC CGCGACAA TTC AAGAACACGCTG
TATCTGCAATTGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCGGGAACCTTGGTCACCGTCTCGAGC (서열 1144)

BMS3h-202-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGC
TAGTGGTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC CGCGACAA TTC AAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGAGCCCTGGTCACCGTCTCGAGC (서열 1145)

BMS3h-202-8
GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGC
TAGTGGTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC CGCGACAA TTC AAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGGAACCTTGGTCACCGTCTCGAGC (서열 1146)

BMS3h-202-9
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGC
TAGTGGTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC CGCGACAA TTC AAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGGAACCTTGGTCACCGTCTCGAGC (서열 1147)

BMS3h-202-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGC
TAGTGGTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC CGCGACAA TTC AAGAACACGCTG
TATTTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGGAACCTTGGTCACCGTCTCGAGC (서열 1148)

BMS3h-202-11
GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGC
TAGTGGTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCC CGCGACAA TTC AAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGGAACCTTGGTCACCGTCTCGAGC (서열 1149)

BMS3h-217-1
AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTAATTTGGTACCAGCATAAACCAGGGAAGGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTTCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAACCGG (서열 1150)

BMS3h-217-2
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAAT
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTCCGACGTTCGGTCAAGGGACCAAGGTGGAAA
TCAACCGG (서열 1151)

BMS3h-217-3
GACATCCAGATGACCCAGTCTCCGTCTCCCTGACTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTCTCTACGTTCGGCCAAGGGACCAAGGTGGAAA
ACATACCGG (서열 1152)

BMS3h-217-4
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTCCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAACCGG (서열 1153)

BMS3h-217-5
GACATCCAGATGACCCAGTCTCCATCCTTCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTCCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAACCGG (서열 1154)

BMS3h-217-6
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGACTTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCCCCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAACGCT (서열 1155)

BMS3h-217-7
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTTCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAACCGG (서열 1156)

BMS3h-217-8
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTTGGTACTCTGTTATCTTGGTACCAGCATAAACCAGGGAAGGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGGTACGGGGGTGCTGTGGCTTCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAACCGG (서열 1157)

[0242]

[0243]

BM53h-217-22
GACATCATAGGATGACCAGCTCCATCTCTCGTCTGCATCTGTAGGAGACCGTGCACCATCACTTCCGGGGCAAGCT
ATTCTTTGGTTCTCTGTATCTTGGTACGACGAAACAGGGAAAGCCCCAAGCTCTCGATCACTTATGGTTCCT
GTTCGAAGATGGGGTCCATCAGTTTCAAGTGGCAGTGGATCTGGGACAGATTTCGCTTCACCATCAGCAGTCTGCAA
CTCGAAGATTCTCTAGCTACTCTGTGGTCAGGGGGTCTGTGGCTGCGACGTTTCGGCCAAAGGACCAAGGTGGA
TCAAAGG (서열 117)

BMS3h-217-2301

ACATCCAGATGACCGACCGAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGGTGCACCATCACTTGC CGGGCAAGTC
GCTCTATTGCCAGCTGTGTATCTTGTACCAAGTGAACACGGGAAAGCCCTAAGCTCTGCATCAGCTTATGGTCTCT
GTTGCAAGGTGGGGTCCCATCAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGC AA
CTCAGAGATTTCTGCTACTACTCTGTGTGTCAGGGGTGCTGTGGCTGCACGATCTCGGCAAGGGACAACGGTGGAA
TCAACAAAG (시퀀스 1185)

[0249]

BMS3h-217-2316
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTACAAAGTCCTA
CTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1200)

BMS3h-217-2317
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
CTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1201)

BMS3h-217-2318
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGGGCCCTTATCTTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1202)

BMS3h-217-2319
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTGGATTGCACCCCTGTTATCTTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1203)

BMS3h-217-2320
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGGGCCCTTATCTTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1204)

BMS3h-217-2321
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTTTAACTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1205)

BMS3h-217-2322
GGCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAAGTGAACAGGGAAAGCCCTAAGCTCCTGATCACTTACGGGTCCTG
GTTGCAAAAGTGGGTCCTACACGTTTTCAGTGGCAGTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTGTCAGGGGGTGTCTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAA
TCAAACGG (서열 1206)

[0250]

[0251]

[0252]

[0253]

실시예 1

인간 항-CD40 가변 도메인 BMS3h-1 내지 BMS3h-225의 생성

하기의 실시예는 BMS3h-1 내지 BMS3h-225로 지정된 일련의 항-인간 CD40 가변 도메인의 생성을 기술한다. 파지 표면 상에서의 단일 면역글로불린 가변 도메인 레퍼토리의 재조합 발현에 이어서, 파지 레퍼토리를 고정된 표적 항원과 접촉시키고, 미결합 파지를 제거하고, 결합된 파지를 증식시키는 것에 의해 선별을 수행한다. 이러한 프로세스는 종종 "패닝(panning)"으로 지칭된다. 이는 단일 면역글로불린 가변 도메인의 스크리닝, 뿐만 아니라 디스플레이 라이브러리에서 발현될 수 있는 다른 항체 단편, 예를 들어, scFv, Fab, 및 Fab'에 적용가능하다. 대안적으로, 폴딩된 구성원에만 결합하는 고정된 포괄적 리간드 (예를 들어, 단백질 A 또는 단백질 L)에 대해 패닝하는 것에 의해 적합하게 폴딩(folding)된 구성원 변이체의 발현에 대해 파지를 예비-선별할 수 있다. 이는 기능성이지 않은 구성원의 비율을 감소시킴으로써 표적 항원에 결합할 가능성이 있는 구성원의 비율을 증가시키는 장점이 있다. 예를 들어, WO 99/20749에 포괄적 리간드로의 예비-선별이 교시되어 있다. 예를 들어, 문헌 [Harrison et al., Meth. Enzymol. 267: 83-109 (1996)]에 파지 항체 라이브러리의 선별이 일반적으로 기술되어 있다.

[0254]

통상적으로, 고체 지지체, 예를 들어, 플라스틱 튜브 또는 웰 상에, 또는 크로마토그래피 매트릭스, 예를 들어 세파로스(Sepharese)TM (파마시아(Pharmacia)) 상에 고정된 정제된 항원을 사용하여 스크리닝을 수행한다. 복합 항원, 예컨대 세포 표면 상에서 스크리닝 또는 선별을 또한 수행할 수 있다 (문헌 [Marks et al., BioTechnology 11: 1145 (1993)]; [de Kruif et al., Proc. Natl. Acad. Sci. USA 92: 3938 (1995)]). 또 다른 별법은 용액 내의 비오틴화 항원에 결합하는 것에 이어지는 스트렙타비딘이 코팅된 비드 상에서의 포획에 의한 선별을 수반한다.

[0255]

클론 BMS3h-1 내지 BMS3h-69:

[0256]

감소되는 농도의 항원 (라운드 1의 100 nM; 라운드 2의 10 nM; 라운드 3의 1 nM)을 사용하는 3회의 선별 라운드를 비오틴화 인간 CD40 단량체 (BMS가 공급함, CD40 1 몰 당 1.5 몰 비오틴) 및 비오틴화 인간 CD40-Ig (BMS가 공급함, CD40-Ig 1 몰 당 3.3 몰 비오틴) 양쪽 모두에 대해 병행하여 수행하였다. 나이브 4G 및 6G 도만티스(Domantis) dAb 라이브러리로부터의 파지를 선별을 시작하기 전에 하기와 같이 조합하였다:

[0257]

1) 아미노산 7-9개 길이의 4G + 6G VH CDR3.

[0258]

2) 아미노산 10-12개 길이의 4G + 6G VH CDR3.

- [0259] 3) 아미노산 13-15개 길이의 4G + 6G VH CDR3.
- [0260] 4) 4G VK
- [0261] 5) 6G VK
- [0262] 각각의 선별 라운드는 원하는 농도의 항원을 750 μ l의 나이브 라이브러리 풀 또는 후속 선별에서 산출된 파지와 750 μ l의 PBS + 2% 마블(Marvel) (2% (w/v) 마블을 함유하는 포스페이트 완충 염수 [프리미어 푸드(Premier Foods), 영국])의 혼합물에 첨가하는 단계 및 엔드-오버-엔드(end-over-end) 혼합에 의해 실온에서 1시간 동안 인큐베이션하는 단계를 수반하였다. 그 후, 100 μ l의 재현탁된 다이나비즈(Dynabeads)® M-280 스트렙타비딘 [인비트로젠(Invitrogen), 영국]을 첨가함으로써 비오틴화 항원 파지 복합체를 포획하고, 실온에서 엔드-오버-엔드로 혼합하면서 5분 동안 인큐베이션하였다. 그 후, 킹피셔(KingFisher) 자기 분리기 [써모 피셔 사이언티픽(Thermo Fisher Scientific), 영국]를 사용하여 다이나비즈®를 회수하고, 7 $\times$ 1 ml PBS + 0.1% 트윈(Tween) 20 (0.1% (v/v) 폴리옥시에틸렌소르비탄 모노라우레이트 [시그마-알드리치(Sigma-Aldrich), 영국]를 함유하는 PBS, PBST)에 이어서 1 $\times$ 1 ml PBS로 세정하였다. 세정된 다이나비즈® 상에서 유지된 결합된 파지를 500 μ l의 트립신-PBS (PBS 450 μ l에 첨가된 50 mM 트리스(Tris)-HCl pH 7.4, 1 mM CaCl₂에 용해된 10 mg/ml 트립신 50 μ l [시그마-알드리치, 영국])와 함께 인큐베이션하는 것에 의해 용출시켰다. 파지-함유 용액을 회수하고, 250 μ l를 사용하여 30분 동안 37°C에서 1.75 ml의 지수 성장기 이. 콜라이(*E. coli*) TG1 (OD₆₀₀ 0.4)에 감염시켰다. 이. 콜라이 TG1 파지 감염 배지를 1분 동안 마이크로 원심분리기에서 11,600 g에서 원심분리하였다. 생성된 세포 펠릿을 1 ml 2 $\times$ TY (1리터 내의 16 g 트립톤, 10 g 효모 추출물 및 5 g NaCl)에 재현탁시키고, (121°C에서 15분 동안 오토클레이빙(autoclaving)하고,) 15 μ g/ml 테트라사이클린이 보충된 TY를 함유하는 9 cm 페트리 접시 상에 플레이팅하였다. 플레이트를 37°C에서 밤새 인큐베이션하였다. 그 후, 15% 글리세롤이 보충된 2 $\times$ TY 2 ml를 각각의 플레이트에 첨가하고, 세포를 유리 스프레더(spreeder)로 느슨하게 하고, 철저히 혼합하였다. 급어낸 박테리아 50 μ l를 사용하여 15 μ g/ml 테트라사이클린이 보충된 2 $\times$ TY 50 ml에 접종하고, 250 rpm에서 진탕시키면서 37°C에서 밤새 성장시켰다. 밤새 배양물을 3,300 g에서 15분 동안 원심분리하여 박테리아를 펠릿화시켰다. 파지를 침전시키기 위해, 10 ml의 PEG/NaCl (20% 폴리에틸렌 글리콜 8000, 2.5 M NaCl)을 40 ml 상청액에 첨가하였다. 파지/PEG 용액을 혼합하고, 얼음 상에서 1시간 동안 방치한 후, 3,300 g에서 30분 동안 4°C에서 회전시키고, 상청액을 폐기하였다. 펠릿을 2 ml PBS에 재현탁시키고, 마이크로 원심분리기에서 11,600 g에서 10분 동안 회전시켜, 나머지 박테리아 잔해물을 제거하였다. 그 후, 파지를 함유하는 생성된 상청액을 적합한 비오틴화 CD40 항원에 대한 다음 선별 라운드에 사용하였다.
- [0263] 선별 라운드 2 및 3에 이어서 모노클로날 파지 ELISA를 수행하였다. 3회의 250 μ l PBST 세정에 이어지는 3회의 250 μ l PBS 세정을 사용하여 모든 세정을 수행하였다. 플레이트를 밤새 4°C에서 50 μ l/웰의 0.2 M 카르보네이트-바이카르보네이트 완충제, pH 9.4 내의 1 μ g/ml 뉴트라비딘(NutrAvidin) (써모 사이언티픽(Thermo Scientific), 영국)으로 코팅하였다. 플레이트를 세정한 후, 2% MPBS (PBS 내의 2% w/v 마블 탈지유 분말 [프리미어 푸드])로 1시간 동안 실온에서 차단하였다. 그 후, 플레이트를 세정하고, 50 μ l/웰의 2% MPBS 내의 0.7 μ g/ml 비오틴화 인간 CD40과 함께 인큐베이션하였다. 플레이트를 세정하고, 파지 상청액을 동일한 부피의 2% MPBS에 첨가하였다. 그 후, 플레이트를 1시간 동안 실온에서 인큐베이션하였다. 플레이트를 세정하고, 결합된 파지를 2% MPBS에서 1:5000 희석된 항-M13-HRP 접합체 (GE 헬스케어(GE Healthcare), 영국)으로 검출하고, 1시간 동안 실온에서 인큐베이션하였다. 플레이트를 세정하고, ELISA를 슈어블루 1-컴포넌트 TMB 마이크로웰 퍼옥시다제(SureBlue 1-Component TMB MicroWell Peroxidase) 용액 (KPL 인크(KPL Inc), 미국)을 사용하여 발색시켰다. 뉴트라비딘으로 코팅되었지만 비오틴화 CD40으로는 코팅되지 않은 플레이트와의 비교에 의해 특이적 파지를 확인하였다. 미디프렙(MidiPrep)을 사용하여 pDOM4 (도만티스) 라운드 2 및 라운드 3 산출물로부터 dAb V-유전자를 분리하고, pDOM5 (도만티스) 내로 클로닝하였다. WO 2007/085815에 개시된 pDOM4는 유전자 III 신호 펩티드 서열이 효모 당지질-고정(anchored) 표면 단백질 (GAS) 신호 펩티드 (WO 2005/093074)로 교체된 Fd 파지 벡터의 유도체이다. pDOM4는 리더 서열과 유전자 III 사이의 c-myc 태그(tag)를 또한 함유하고, 이는 유전자 III을 다시 프레임 내에 놓는다.
- [0264] 결합 dAb를 하기와 같이 확인하였다. 96개의 개별적인 콜로니들 (pDOM5 내)을 각각의 산출물로부터 오토크베이션(OnEx Autoinduction) 배지 (노바젠(Novagen), 영국)를 함유하는 터리픽 브로스(Terrific Broth) 200 μ l 내로 코스타 96웰 셀 컬처 클러스터(Costar 96 Well Cell Culture Clusters) (코닝 인코포레이티드(Corning Incorporated), 미국)에서 250 rpm에서 진탕시키면서 37°C에서 밤새 채집하였다. 배양물을 원심분리하여 세포를 펠릿화하고, 상청액을 CD40 결합 dAb에 대해 항원 결합 ELISA에 의해 검정하였다. 맥시소프

(MaxiSorp) 96웰 면역플레이트 (눈크(Nunc), 미국)를 밤새 4℃에서 50 μl /웰의 0.2 M 카르보네이트-바이카르보네이트 완충제, pH 9.4 내의 1 $\mu\text{g}/\text{ml}$ 뉴트라비딘으로 코팅하였다. 모든 세정은 파지 ELISA에 대해 기술된 바와 같았다. 플레이트를 1시간 동안 실온에서 200 μl 의 1% 트윈 20을 함유하는 PBS로 차단하였다. 그 후, 플레이트를 세정하고, 50 μl /웰의 0.1% PBST 내의 0.7 $\mu\text{g}/\text{ml}$ 비오티닐화 인간 CD40과 함께 인큐베이션하였다. 청정화된 dAb-함유 배양 상청액을 등가 부피의 0.1% PBST와 함께 ELISA 플레이트에 첨가하였다. 플레이트를 1시간 동안 실온에서 인큐베이션한 후, 세정하였다. 결합된 dAb를 2단계 공정을 사용하여 검출하였다: 먼저, 0.1% PBST에 1:2000 희석된 9E10 (항-myc IgG, 시그마-알드리치, 영국)을 1시간 동안 실온에서 첨가한 후, 세정하고, 이어서 0.1% PBST에 1:2000 희석된 항-마우스 Fc-HRP (시그마-알드리치, 영국)를 1시간 동안 실온에서 첨가하였다. 플레이트를 세정하고, ELISA를 슈어블루 1-컴포넌트 TMB 마이크로웰 퍼옥시다제 용액 (KPL 인크, 미국)을 사용하여 발색시켰다. 색을 발색시켰고, 등가 부피의 1 M HCl을 첨가하여 색측정 반응을 정지시켰다. ELISA 플레이트를 450 nm에서 판독하였다. 뉴트라비딘으로 코팅되었지만 비오티닐화 CD40으로는 코팅되지 않은 플레이트와의 비교에 의해 특이적 파지를 확인하였다.

[0265] CD40에 대해 특이적인 클론을 비드- 또는 ELISA-기반 수용체-결합 검정 (RBA)으로 테스트하여, CD40 리간드 결합의 억제력을 평가하였다. RBA에서 억제력을 나타낸 도메인 항체를 B-세포 증식 검정에서 테스트한 후, 다양한 다른 시험관내 검정에서 테스트하였다. 이러한 검정들이 하기에서 더욱 상세하게 기술된다.

[0266] **BMS3h-106 내지 -225:**

[0267] BMS3h-1 내지 BMS3h-69에 기술된 바와 같이, 그러나 하기와 같이 변형하여, BMS3h-106 내지 -225를 비오티닐화 CD40 또는 비오티닐화 CD40-Fc에 대한 선별로부터 단리하였다. 나이브 4G 및 6G 라이브러리로부터의 파지를 선별을 시작하기 전에 하기와 같이 조합하였다:

[0268] 6) 아미노산 7-9개 길이의 4G VH CDR3.

[0269] 7) 아미노산 10-12개 길이의 4G VH CDR3.

[0270] 8) 아미노산 13-15개 길이의 4G VH CDR3.

[0271] 9) 아미노산 7-9개 길이의 6G VH CDR3.

[0272] 10) 아미노산 10-12개 길이의 6G VH CDR3.

[0273] 11) 아미노산 13-15개 길이의 6G VH CDR3.

[0274] 12) 4G VK

[0275] 13) 6G VK

[0276] CD40-Fc의 경우 160 nM 및 CD40의 경우 100 nM의 항원 농도에서 라운드 1을 수행하였다. 산출물 역가는 2.0×10^4 내지 9.0×10^7 TU/ml (기능성 바이러스 역가) 범위였다.

[0277] 라운드 2를 위해, 라운드 1로부터의 강화된 파지를 쌍으로 조합한 후 선별에서 사용하였다:

[0278] 1) 아미노산 7-9개 길이의 4G + 6G VH CDR3 (라운드 1로부터의 풀 1 + 4).

[0279] 2) 아미노산 10-12개 길이의 4G + 6G VH CDR3 (라운드 1로부터의 2 + 5).

[0280] 3) 아미노산 13-15개 길이의 4G + 6G VH CDR3 (라운드 1로부터의 3 + 6).

[0281] 4) 4G + 6G VK (라운드 1로부터의 풀 7 + 8)

[0282] 100 nM의 항원 농도에서 선별을 수행하였고, 항원-파지 복합체를 뉴트라비딘 (써모 피셔 사이언티픽, 영국)과 커플링된 M-280 토실-활성화 다이아비즈® (인비트로젠)를 사용하여 포획하였다. 산출물 역가는 6.5×10^7 내지 7.5×10^8 TU/ml 범위였다.

[0283] 20 nM의 항원 농도에서 라운드 3을 수행하였고, CD40-Fc 선별의 경우에는 6.7 μM 유리 인간 Fc 꼬리 (BMS)의 존재하에 수행하였다. 산출물 역가는 4.3×10^7 내지 1.6×10^9 TU/ml 범위였다.

[0284] 라운드 2에 대해 기술된 바와 같이, 그러나 2 nM의 항원 농도에서, 그리고 500배 과량의 미표지 CD40-Fc의 존재 및 부재 하에 라운드 4를 수행하였다. 파지를 비오티닐화 항원과 함께 처음 1시간 동안 인큐베이션한 후에 이

러한 경쟁자를 첨가하였고, 그 후 혼합물을 전과 같이 밤새 인큐베이션하였다. 이러한 경쟁 단계는 오프(off) 속도가 더 낮은 dAb의 선별을 강화하기 위한 목적으로 포함되었다. 산출물 역가는 경쟁 부재 시에는 1.8×10^7 내지 4.4×10^7 , 경쟁 존재 시에는 1.8×10^6 내지 2.3×10^7 TU/ml 범위였다.

[0285] 선별 진행을 모니터링하기 위해, 모노클로날 파지 ELISA를 라운드 2 및 3 후에 수행하였다. BMS3h-1 내지 BMS3h-69에 대해 기술된 바와 같이 이를 수행하였다. VK 라이브러리 스크리닝의 경우 단백질 L이 $0.8 \mu\text{g/ml}$ 의 최종 농도로 포함된 것을 제외하고는 BMS3h-1 내지 BMS3h-69에 대해 기술된 바와 같이 결합 dAb를 확인하였다. 단백질 L의 첨가는 dAb 가교에 의해 신호 강도를 증가시켰다.

[0286] **BMS3h-70 내지 -105:**

[0287] BMS3h-70 내지 -105를 면역튜브에 수동적으로 흡착된 항원에 대한 선별로부터 분리하였다. 나이브 4G 및 6G 도만티스 dAb 라이브러리로부터의 파지를 선별을 시작하기 전에 하기와 같이 조합하였다:

[0288] 1) 아미노산 7-9개 길이의 4G VH CDR3.

[0289] 2) 아미노산 10-12개 길이의 4G VH CDR3.

[0290] 3) 아미노산 13-15개 길이의 4G VH CDR3.

[0291] 4) 아미노산 7-9개 길이의 6G VH CDR3.

[0292] 5) 아미노산 10-12개 길이의 6G VH CDR3.

[0293] 6) 아미노산 13-15개 길이의 6G VH CDR3.

[0294] 7) 4G VK

[0295] 8) 6G VK

[0296] 제1 선별 라운드를 위해, 0.2 M 카르보네이트-바이카르보네이트 완충제, pH 9.4 내의 $10 \mu\text{g/ml}$ 인간 CD40-Fc 용합물 (BMS) 1 ml를 눈크의 맥시소프(MaxiSorp) 면역튜브에 첨가한 후, 롤링(rolling)하면서 4°C 에서 밤새 인큐베이션하였다. 그 후, 튜브를 비우고, 포스페이트 완충 염수 (PBS)로 3회 세정하였다. 그 후, MPBS를 가득 채우고 1시간 동안 실온에서 인큐베이션함으로써 튜브를 차단하였다. 그 후, 튜브를 비우고 PBS로 3회 세정하였다. 4 ml MPBS 내의 라이브러리 파지를 튜브에 첨가하고, 실온에서 엔드-오버-엔드로 회전시키면서 1시간 동안 인큐베이션하였다.

[0297] 튜브를 비우고, PBST (PBS + 0.1% (v/v) 트윈 20)로 10회 세정하였다. 세정된 튜브 상에서 유지된 결합된 파지를 $500 \mu\text{l}$ 의 트립신-PBS (PBS $450 \mu\text{l}$ 에 첨가된 50 mM 트리스-HCl pH 7.4, 1 mM CaCl_2 에 용해된 10 mg/ml 트립신 $50 \mu\text{l}$ [시그마-알드리치, 영국])와 함께 10분 동안 실온에서 엔드-오버-엔드로 회전시키면서 인큐베이션하는 것에 의해 용출시켰다. 파지-함유 용액을 회수하고, $250 \mu\text{l}$ 를 사용하여 30분 동안 37°C 에서 1.75 ml의 지수 성장기 이. 콜라이 TG1 (OD₆₀₀ 0.4)에 감염시켰다. 이. 콜라이 TG1 파지 감염 배지를 1분 동안 마이크로 원심분리기에서 11,600 g에서 원심분리하고, 생성된 세포 펠렛을 1 ml 2×TY (1리터 내의 16 g 트립톤, 10 g 효모 추출물 및 5 g NaCl)에 재현탁시켰고 (현탁액을 121°C 에서 15분 동안 오토클레이빙함), $15 \mu\text{g/ml}$ 테트라사이클린이 보충된 LB 한천을 함유하는 9 cm 페트리 접시 상에 플레이팅하였다. 플레이트를 37°C 에서 밤새 인큐베이션하였다. 그 후, 15% 글리세롤이 보충된 2×TY 2 ml를 각각의 플레이트에 첨가하고, 세포를 유리 스프레더로 느슨하게 하고, 철저히 혼합하였다.

[0298] 급어낸 박테리아 $50 \mu\text{l}$ 를 사용하여 $15 \mu\text{g/ml}$ 테트라사이클린이 보충된 2×TY 50 ml에 접종하고, 250 rpm에서 진탕시키면서 37°C 에서 밤새 성장시켰다. 밤새 배양물을 3,300 g에서 15분 동안 원심분리하여 박테리아를 펠렛화시켰다. 파지를 침전시키기 위해, 10 ml의 PEG/NaCl (20% 폴리에틸렌 글리콜 8000, 2.5 M NaCl)을 40 ml 상청액에 첨가하였다. 파지/PEG 용액을 혼합하고, 얼음 상에서 1시간 동안 방치하였다. 그 후, 용액을 3,300 g에서 30분 동안 4°C 에서 회전시키고, 상청액을 폐기하였다. 펠렛을 2 ml PBS에 재현탁시키고, 마이크로 원심분리기에서 11,600 g에서 10분 동안 회전시켜, 나머지 박테리아 잔해물을 제거하였다. 그 후, 파지를 함유하는 생성된 상청액을 CD40-Fc 항원에 대한 다음 선별 라운드에 사용하였다. 라운드 1로부터의 산출물 역가는 7.5×10^4 내지 1.5×10^7 TU/ml (형질전환 단위/ml) 범위였다.

[0299] 제1 선별 라운드로부터 회수된 강화된 파지를 사용하여 제2 선별 라운드를 수행하였다. 정확하게 상기 기술된

바와 같이 이를 수행하였고, 산출물 역가는 2.5×10^7 내지 1.2×10^8 TU/ml 범위였다.

[0300] 제2 선별 라운드로부터 회수된 강화된 파지를 사용하여 제3 선별 라운드를 수행하였다. 상기 기술된 바와 같이, 그러나 $1 \mu\text{g/ml}$ 의 항원 농도로 이를 수행하였다. 산출물 역가는 5.1×10^7 내지 7.5×10^8 TU/ml 범위였다.

[0301] 선별 진행을 모니터링하기 위해, 모노클로날 파지 ELISA를 라운드 2 및 3 후에 수행하였다. 개별적인 콜로니들의 샘플을 $15 \mu\text{g/ml}$ 테트라사이클린이 보충된 $2 \times \text{TY } 200 \mu\text{l}$ 내로 채집하고, 코스타 96웰 셀 컬처 클러스터 (코닝 인코포레이티드, 미국)에서 250 rpm에서 진탕시키면서 37°C 에서 밤새 인큐베이션하였다. 배양물을 원심분리하여 세포를 펠릿화하고, 상청액을 CD40-결합 파지 dAb에 대해 항원 결합 ELISA에 의해 검정하였다. 3회의 $250 \mu\text{l}$ PBST 세정에 이어지는 3회의 $250 \mu\text{l}$ PBS 세정을 사용하여 모든 세정을 수행하였다. 맥시소프 96웰 면역플레이트 (눈크, 미국)를 밤새 4°C 에서 $50 \mu\text{l}/\text{웰}$ 의 0.2 M 카르보네이트-바이카르보네이트 완충제, pH 9.4 내의 $0.5 \mu\text{g/ml}$ CD40-Fc (BMS)로 코팅하였다. 플레이트를 세정한 후, $250 \mu\text{l}$ 의 2% MPBS로 1시간 동안 실온에서 차단하였다. 플레이트를 세정하고, 파지 상청액을 등가 부피의 2% MPBS에 첨가하고, 1시간 동안 실온에서 인큐베이션하였다. 플레이트를 세정하고, 결합된 파지를 2% MPBS에서 1:5000 희석된 항-M13-HRP 접합체 (GE 헬스케어, 영국)으로 검출하고, 1시간 동안 실온에서 인큐베이션하였다. 플레이트를 세정하고, ELISA를 슈어블루 1-컴포넌트 TMB 마이크로웰 퍼옥시다제 용액 (KPL 인크, 미국)을 사용하여 발색시켰다. 유리 Fc로 코팅된 플레이트와의 비교에 의해 특이적 파지 dAb를 확인하였다.

[0302] 상기 라운드 2 및 3 선별 산출물 각각으로부터의 dAb 유전자 풀(pool)로서 대장균 균주 HB2151 내의 가용성 발현 벡터 pDOM5 내로 서브클로닝하였다. 이러한 벡터는 대장균에서의 c-myc 태그 (로슈 디아그노스틱스 게엠베하(Roche Diagnostics GmbH))가 있는 유리 dAb의 발현 및 상청액으로의 분리를 허용하였다.

[0303] 수동 선별로부터의 CD40-결합 dAb를 하기와 같이 확인하였다. 96개의 개별적인 콜로니들 (pDOM5 내)을 각각의 산출물로부터 오넥스 오토인큐베이션 배지 (노바젠, 영국)를 함유하는 터리픽 브로스 $200 \mu\text{l}$ 내로 코스타 96웰 셀 컬처 클러스터 (코닝 인코포레이티드, 미국)에서 250 rpm에서 진탕시키면서 37°C 에서 밤새 채집하였다. 배양물을 원심분리하여 세포를 펠릿화하고, 상청액을 CD40 결합 dAb에 대해 항원 결합 ELISA에 의해 검정하였다. 맥시소프 96웰 면역플레이트 (눈크, 미국)를 밤새 4°C 에서 $50 \mu\text{l}/\text{웰}$ 의 0.2 M 카르보네이트-바이카르보네이트 완충제, pH 9.4 내의 $0.5 \mu\text{g/ml}$ CD40-Fc (BMS)로 코팅하였다. 모든 세정은 파지 ELISA에 대해 기술된 바와 같았다. 플레이트를 1시간 동안 실온에서 $250 \mu\text{l}$ 의 1% 트윈 20을 함유하는 PBS (PBST)로 차단하였다. 청정화된 dAb-함유 배양 상청액을 등가 부피의 0.1% PBST와 함께 ELISA 플레이트에 첨가하였다. 플레이트를 1시간 동안 실온에서 인큐베이션한 후, 세정하였다. 결합된 dAb를 2단계 공정을 사용하여 검출하였다: 먼저, 0.1% PBST에 1:2000 희석된 비오티닐화 9E10 (항-myc IgG, 시그마-알드리치, 영국)을 1시간 동안 실온에서 첨가한 후, 세정하고, 이어서 0.1% PBST에 1:5000 희석된 스트렙타비딘-HRP (벤더 메드시스템즈(Bender MedSystems), 오스트리아)를 1시간 동안 실온에서 첨가하였다. 플레이트를 세정하고, ELISA를 슈어블루 1-컴포넌트 TMB를 사용하여 발색시켰다. 유리 Fc로 코팅된 플레이트와의 비교에 의해 특이적 파지 dAb를 확인하였다.

[0304] CD40에 대해 특이적인 클론들을 비드- 또는 ELISA-기반 수용체-결합 검정 (RBA)으로 테스트하여, CD40 리간드 결합의 억제력을 평가하였다. RBA로부터 수득된 효능 측정치가 표 5에서 제공된다 (1차 스크리닝 시도). RBA에서 억제를 나타낸 도메인 항체를 B-세포 증식 검정에서 테스트한 후, 다양한 다른 시험관내 세포 검정에서 테스트하였다.

[0305] **BMS3h-210 내지 -225**

[0306] BMS3h-210 내지 -225를 전체 세포에 대한 선별로부터 단리하였다. 나이브 4G 및 6G 도만티스 dAb 라이브러리로부터의 파지를 선별을 시작하기 전에 하기와 같이 조합하였다:

[0307] 1) 아미노산 7-9개 길이의 4G + 6G VH CDR3.

[0308] 2) 아미노산 10-12개 길이의 4G + 6G VH CDR3.

[0309] 3) 아미노산 13-15개 길이의 4G + 6G VH CDR3.

[0310] 4) 4G 및 6G VK

[0311] 라운드 1을 위해, 세포 표면에서 발현된 인간 CD40 (BMS가 공급함)으로 안정적으로 형질감염된 DG44 CHO 세포주를 항원으로 사용하였다. 이러한 세포에 대한 선별 전에, 상기에 개요된 라이브러리 풀을 형질감염되지 않은 CHO 세포와 함께 인큐베이션하여, CD40 이외의 세포 표면 항원에 대해 특이적인 dAb를 디스플레이하는 파지들

이들로부터 고갈시켰다. 양쪽 유형의 세포를 베르센(Versene) (인비트로젠)과의 인큐베이션에 의해 수확한 후 생육력에 대해 평가하였다. 6백만개의 형질감염되지 않은 생육성 CHO 세포를 4 ml PBS + 2% (w/v) BSA (PBS/BSA)에 재현탁시키고, 4℃에서 1시간 동안 엔드-오버-엔드로 회전시켜 차단하였다. 달리 언급되지 않는 한 모든 후속 단계를 4℃에서 수행하였다. 세포를 185g에서 5분 동안 원심분리하고, 고갈된 라이브러리 파지를 함유하는 상청액을 신선한 튜브로 옮겼다. 여기에 1 ml PBS/BSA 내의 6×10^6 개의 생육성 CHO-CD40 세포를 첨가하고, 혼합물을 1시간 동안 회전시켰다. 그 후, 185g에서 5분 동안 원심분리하고 10 ml PBS/BSA에 재현탁시키는 것에 의해 세포를 5회 세정하였다. 최종 세정 후, 세포를 이전과 같이 펠릿화하고 나서, 5 mM 트리스-HCl pH 7.4, 0.1 mM CaCl_2 가 보충된 PBS 내의 1 mg/ml의 소 채장으로부터의 XIII형 트립신 (시그마 알드리치, 영국) 0.5 ml에 재현탁시키고, 마이크로 원심분리기 튜브로 옮겼다. 세포를 실온에서 10분 동안 회전시킨 후, 5분 동안 16000g에서 원심분리하였다. 상청액 내의 용출된 파지를 사용하여 이. 콜라이를 감염시켰고, 산출물 파지 역가는 5.1×10^5 내지 2.7×10^6 TU/ml (형질전환 단위/ml)인 것으로 결정되었다.

[0312] 제1 선별 라운드로부터 회수된 강화된 파지를 사용하여 제2 선별 라운드를 수행하였다. 상기 기술된 바와 같이, 그러나 초기 고갈 (선별 해제) 단계 없이, 그리고 CHO-CD40 대신 RAMOS 인간 B 세포 (ATCC)를 사용하여 이를 수행하였다. 산출물 역가는 2.3×10^5 내지 7.5×10^5 TU/ml 범위였다.

[0313] 제2 라운드에 대한 것과 같이 제3 선별 라운드를 수행하였다. 산출물 역가는 1.9×10^8 내지 3.5×10^8 TU/ml 범위였다.

[0314] 상기 라운드 2 및 3 선별 산출물 각각으로부터의 dAb 유전자를 풀로서 대장균 균주 HB2151 내의 가용성 발현 벡터 pDOM5 내로 서브클로닝하였다. 이러한 벡터는 대장균에서의 c-myc 태그가 있는 유리 dAb의 발현 및 상청액으로의 분비를 허용하였다.

[0315] CD40에 대해 특이적인 클론을 CHO 세포 수용체-결합 검정 (RBA)으로 테스트하여, CD40 리간드 결합의 억제를 평가하였다. RBA에서 억제를 나타낸 도메인 항체를 B-세포 증식 검정에서 테스트한 후, 다양한 다른 시험관내 세포 검정에서 테스트하였다.

[0316] **오차-경향 PCR에 의한 친화도 성숙**

[0317] 하기 실시예 6에서 기술된 B-세포 증식 검정에서 중화 활성을 나타낸 13개의 BMS3h dAb에 대해 오차-경향 파지 라이브러리를 구축하였다 (표 17 참조). 뮤타자임(Mutazyme) II 중합효소 (애질런트 테크놀로지스(Agilent Technologies)로부터의 진모프(GeneMorph) II 키트의 일부분)를 사용하여 중합효소 연쇄 반응 (PCR)에 의한 증폭 동안 dAb 유전자 내로 무작위로 오차를 도입하는 것에 의해 이를 수행하였다. 돌연변이된 dAb 유전자를 pDOM4 벡터 내에 GAS1 리더 서열의 제어 하에 fd 파지 유전자 III 단백질과의 유전자 융합물로서 클로닝하였고, 이는 감염성 파지 입자를 생성시키는데 필요한 모든 fd 유전자를 함유하였다. 이러한 라이브러리는 크기가 약 1×10^8 CFU (콜로니 형성 단위)였고, 이때 오차율은 dAb 유전자 당 아미노산 2-5개였다.

[0318] 이러한 라이브러리로부터 생성된 파지를 가용성 비오틴화 인간 CD40에 대한 3회의 선별 라운드에 적용하였다. 파지 라이브러리를 2% MPBS (2% (w/v) 마블 건조 탈지유 분말이 보충된 포스페이트 완충 염수)와 예비혼합하고, 비오틴화 인간 CD40 (BMS)를 1 ml의 최종 부피로 20 nM의 최종 농도로 첨가함으로써 제1 파지 선별 라운드를 수행하였다. 엔드-오버-엔드로 혼합하면서 혼합물을 1시간 이상 동안 실온에서 인큐베이션하였다. 그 후, 항원-파지 복합체를 50 μl 의 M-280 스트렙타비딘 다이아비즈® (인비트로젠)로 포획하고, 1 ml PBST로 7회 세정한 후, 1 ml PBS로 1회 세정하였다. 세정된 파지를 5 mM 트리스-HCl pH 7.4, 0.1 mM CaCl_2 가 보충된 PBS 내의 1 mg/ml의 소 채장으로부터의 XIII형 트립신 (시그마 알드리치, 영국) 0.5 ml와 함께 인큐베이션함으로써 항원/비드 복합체로부터 용출시켰다. 용출된 파지를 사용하여 이. 콜라이를 감염시켰고, 산출물 파지 역가는 2×10^5 내지 9×10^7 TU/ml (형질전환 단위/ml)인 것으로 결정되었다.

[0319] 제1 선별 라운드로부터 회수된 강화된 파지를 사용하여 제2 선별 라운드를 수행하였고, 이때 최종 농도 2 nM의 비오틴화 CD40에 이어서 상기 기술된 바와 같이 스트렙타비딘 비드를 사용하여 포획하였다. 산출물 역가는 3×10^4 내지 5×10^6 TU/ml 범위였다.

[0320] 2 nM 비오틴화 CD40를 사용한 후 스트렙타비딘 비드를 사용하여 포획하는 제3 선별 라운드를 수행하였다. 용

출된 파지 역가는 8×10^4 내지 4×10^6 TU/ml 범위였다.

[0321] **비아코어™ 스크리닝**

[0322] 상기 라운드 3 산출물 각각으로부터의 dAb 유전자를 풀로서 대장균 HB2151 내의 가용성 발현 벡터 pDOM13 (도만 티스) 내로 서브클로닝하였다. pDOM13 벡터는 pDOM33으로 또한 공지되어 있고, WO/2008/149143에 개시되어 있다. 이러한 벡터는 대장균에서의 유리 dAb의 발현 및 상청액으로의 분비를 허용하였다. 47개의 개별적인 콜로니들을 각각의 산출물로부터 채집하고, 코스타 96웰 셀 컬처 클러스터 (코닝 인코포레이티드, 미국)에서 250 rpm에서 진탕시키면서 37℃에서 밤새 노바젠 오버나이트 익스프레스 오토인덕션(Novagen Overnight Express Autoinduction) 배지 (머크 케미칼스(Merck Chemicals), 영국)를 함유하는 터리픽 브로스 (TB) 200 μ l에서 발현시켰다. 동일한 플레이트에서, 1개의 웰에 적합한 모 (야생형) dAb를 발현하는 이. 콜라이를 접종하였다. 배양물을 원심분리하여 세포를 펠릿화하고, 상청액을 모 dAb와 비교하여 "오프-속도" (즉, 해리 속도 상수, k_d)에서의 개선에 대해 비아코어™ 3000 기구 (GE 헬스케어) 상에서 스크리닝하였다.

[0323] 약 1600 반응 단위 (RU)의 비오틴화 인간 CD40 (BMS)을 스트렙타비딘 (SA) 비아코어™ 칩의 1개의 유동 셀 상에 고정하였다. 어떠한 리간드도 고정되지 않은 제2 유동 셀이 인라인(inline) 참조를 위한 기준 유동 셀로서의 역할을 하였다. 분석할 dAb 상청액 각각을 HBS-EP 완충제 (0.01 M HEPES pH 7.4 + 0.15 M NaCl, 3 mM EDTA 및 0.005% v/v 계면활성제 P20, GE 헬스케어)에서 1:3 희석하였다. 기구의 KINJECT 기능을 사용하여 10 μ l의 각각의 dAb 상청액을 일련의 CD40가 고정된 유동 셀 및 기준 유동 셀을 가로질러 주입하였고, 이때 기준 셀로부터의 신호를 인라인으로 차감하였다. 25℃에서 10 μ l/분의 HBS-EP 유속으로 실험을 수행하였다. 각각의 주입을 완료한 후, dAb를 120초 동안 완충제 내에서 리간드로부터 해리시키고 나서, 10 mM 글리신 pH 2.0의 5 μ l 주입으로 재생시켰다. 비아이벌류에이션(BIAevaluation) 4.1 소프트웨어 (GE 헬스케어)를 사용하여 기준 유동 셀 트레이스(trace)를 각각의 분석물 트레이스로부터 차감하였다. 동일한 소프트웨어를 사용하여, 분석물 트레이스의 해리 단계에 대한 1:1 (랭뮤어(Langmuir)) 동역학 모델의 근사 피트(fit)를 수행하였다. 이러한 모델로 각각의 클론에 대한 대략적인 해리 속도 상수 ("오프-속도" 또는 k_d)가 산출되었고, 야생형 dAb와의 상대적인 비교가 이루어졌다.

[0324] BMS3h-129 및 -197을 제외한 모든 계통에 대해 오프-속도가 개선된 클론이 확인되었다. 오프-속도가 개선된 클론을 비드- 또는 ELISA-기반 수용체-결합 검정 (RBA)으로 테스트하여, 상기 기술된 바와 같은 개선된 효능을 평가하였다. RBA로부터 수득된 효능 측정치가 "오차-경향-돌연변이 클론"으로 표지된 표에서 제공된다. 이어서, RBA에서 더 강력한 클론을 B-세포 증식 검정에서 테스트하여 강화된 생물학적 효능에 대해 평가하였고, 수득된 이러한 측정치가 표 17에서 제공된다. B-세포 증식 검정에서 효능이 개선된 도메인 항체를 다양한 기타 시험관 내 세포 검정에서 또한 테스트하였다.

[0325] **삼중자 스캐닝 다양화에 의한 친화도 성숙**

[0326] 오차-경향 성숙으로부터 단리된 5개의 효능이 개선된 dAb인 BMS3h-37-2, -38-2, -56-2, -193-25 및 -217-23을 선택하여, 삼중자 스캐닝 다양화에 의해 추가로 친화도 성숙시켰다. 오차-경향 PCR을 사용하는 대신, 일련의 중복되는 축중성 삼중자 올리고뉴클레오타이드를 사용하여 각각의 dAb의 상보성 결정 영역 (CDR)을 다양화한 것을 제외하고는 오차-경향 라이브러리에 대해 상기 기술된 바와 같이 이러한 모체들을 기초로 파지 라이브러리를 구축하였다. 친화도 성숙시킬 각각의 dAb에 대해, NNS 코돈 삼중자 (문헌 [Arkin et al. (1992) Proc. Nat'l Acad. Sci. USA 89:7811-7815] 참조)를 함유하는 올리고뉴클레오타이드를 사용하여, 중복 확장에 의한 스플라이싱 (SOE) PCR에 의해 각각의 CDR에 대해 다수의 라이브러리를 제조하였다. 소정의 CDR에 대해 올리고뉴클레오타이드에 의해 다양화된 삼중자가 코돈 2개만큼 중복되어, CDR 당 2개 내지 4개의 라이브러리가 생성되었다. BMS3h-37-2 라이브러리에서 다양화된 아미노산 잔기는 위치 30, 31, 32, 33, 35, 50, 52, 53, 55, 56, 95, 96, 97 및 98 (카바트 넘버링)에 있었다. BMS3h-38-2 라이브러리에서 다양화된 잔기는 37-2에 대한 것과 같았지만, 위치 100이 추가되었다. BMS3h-56-2 라이브러리에서 다양화된 잔기는 37-2에 대한 것과 같았지만, 위치 100 및 101이 추가되었다. BMS3h-193-25 및 -217-23 라이브러리에서 다양화된 잔기는 위치 27, 28, 30, 31, 32, 34, 49, 50, 51, 53, 89, 91, 92, 93, 94 및 96에 있었다.

[0327] 이러한 라이브러리로부터 생성된 파지를 CDR로 풀링(pooling)하고, BMS3h-37-2, -38-2, -56-2 및 -193-25에 대해, 사용된 항원 농도가 라운드 1, 2 및 3에 대해 각각 10, 1 및 0.1 nM인 것을 제외하고는 상기 기술된 바와 같이 선별을 수행하였다. BMS3h-217-23에 대해, 사용된 항원 농도는 라운드 1, 2 및 3에 대해 각각 20, 2 및 0.2 nM이었다. 시노물구스 CD40에 대해 교차-반응성인 BMS3h-193-25에 대해, 시노 CD40에 대해서도 병행하여

선별을 수행하였다. 추가적으로, 선별 라운드 2 및 3을 100배 또는 1000배 과량의 미표지 CD40의 존재 및 부재 하에 각각 수행하였다. 과지를 비오티닐화 항원과 함께 처음 1시간 동안 인큐베이션한 후에 이러한 경쟁자를 첨가하였고, 그 후 혼합물을 전과 같이 추가로 1시간 동안 인큐베이션하였다. 이러한 경쟁 단계는 오프 속도가 더 낮은 dAb의 선별을 강화하기 위한 목적으로 포함되었다. 라운드 1 산출물 역가는 1.4×10^6 내지 1.4×10^9 범 위였다. 라운드 2에서의 역가는 경쟁 부재 시에는 1.3×10^5 내지 4.0×10^8 , 경쟁 존재 시에는 8.6×10^4 내지 1.3×10^8 이었다. 라운드 3에서의 역가는 경쟁 부재 시에는 1.2×10^5 내지 1.9×10^8 , 경쟁 존재 시에는 6.0×10^5 내지 1.2×10^8 이었다.

[0328] 오차-경향 친화도 성숙에 기술된 바와 같이 이러한 선별 산출물을 서브클로닝하고 스크리닝하였다. BMS3h-193-25를 제외한 모든 계통에 대해 오프-속도가 개선된 클론이 확인되었다. 오프-속도가 개선된 클론을 ELISA 수용체-수용체-결합 검정 (RBA)에서 테스트하여, 개선된 효능에 대해 평가하였다. RBA로부터 수득된 효능 측정치가 "추가-성숙 클론"으로 표지된 표에서 제공된다. 이어서, RBA에서 더 강력한 클론을 B-세포 증식 검정에서 테스트하여 강화된 생물학적 효능에 대해 평가하였고, 수득된 이러한 측정치가 표 17에서 제공된다. B-세포 증식 검정에서 효능이 개선된 도메인 항체를 다양한 기타 시험관내 세포 검정에서 또한 테스트하였다.

[0329] 실시예 2

[0330] 수용체 결합 검정 (RBA)을 사용한 스크리닝

[0331] 여러 시험관내 수용체 결합 검정 (RBA)을 사용하여 실시예 1에서 생성된 항-인간 CD40 가변 도메인 아미노산 서열의 CD40 친화도를 결정하였다. 3가지 RBA 형식을 사용하였다: (1) 비드 RBA, (2) ELISA RBA, 및 (3) CHO 세포 RBA.

[0332] 비드 RBA:

[0333] 포스페이트 완충 염수 (PBS)로 세정된 스페로(Sphero) 스트렙타비딘 폴리스티렌 입자 (색슨 유럽(Saxon Europe), 영국)를 $0.5 \mu\text{g/ml}$ 비오티닐화 인간 IZ-CD40L (BMS)로 코팅하였다. 코팅 후, 비오티닐화 CD40L 입자를 PBS에서 세정하고, PBS 검정 완충제 내의 0.1% (w/v) 소 혈청 알부민 (BSA) (시그마-알드리치, 영국)에서 1:10으로 희석하였다. 바닥은 투명하고 벽은 흑색인 384웰 플레이트 (어플라이드 바이오시스템즈(Applied Biosystems))에서, 희석물 범위의 정제된 dAb, $0.25 \mu\text{g/ml}$ 인간 CD40 (BMS, CY24FEB06-01), 1/5000 마우스 항-인간 IgG (Fc) mAb 클론 GG-7 (시그마-알드리치, 영국), $0.25 \mu\text{g/ml}$ 염소 항-마우스 알렉사 플루오르(ALEXA Fluor) 647 (인비트로젠, 분자 프로브(Molecular probes), 영국) 및 비오티닐화 CD40L 폴리스티렌 입자를 균등하게 조합하고, 빛의 부재 하에 실온에서 6시간 동안 인큐베이션시켰다. 인큐베이션 후, AB8200 세포 검출 메커니즘 (어플라이드 바이오시스템즈)으로 상대적인 형광을 사용하여 비오티닐화 CD40L 입자에 대한 dAb 대 인간 CD40의 경쟁적 결합을 평가하였다.

[0334] ELISA RBA:

[0335] 투명한 벽의 하이 바인드(High Bind) 384웰 플레이트 (코닝, 영국)를 0.2 M 카르보네이트-바이카르보네이트 완충제, pH 9.4 내의 $1 \mu\text{g/ml}$ 뉴트라비딘 $25 \mu\text{l}$ 로 밤새 4°C에서 코팅하였다. 다음 날, 검정 플레이트를 0.1% (v/v) 트윈 PBS 완충제로 세정하고, 1시간 동안 실온에서 PBS 내의 1% (w/v) BSA로 차단하고, 다시 세정하였다. 과량의 세정 완충제를 제거한 후, $1 \mu\text{g/ml}$ 의 비오티닐화 인간 IZ-CD40L (BMS) $25 \mu\text{l}$ 를 검정 플레이트와 함께 1시간 동안 실온에서 인큐베이션하였다. 동시에, 희석물 범위의 정제된 dAb 및 $1 \mu\text{g/ml}$ 의 인간 CD40 (BMS, CY24FEB06-01)을 1:1 비로 복합체를 이루게 하였다. 검정 플레이트를 세정한 후, dAb:인간 CD40 복합체를 검정 플레이트에서 부드럽게 진탕시키면서 실온에서 2시간 동안 인큐베이션하였다. 1/5000 마우스 항-인간 IgG (Fc) mAb 클론 GG-7 (시그마-알드리치, 영국)에 이어지는 1/10,000 양고추냉이 퍼옥시다제(horse radish peroxidase) (HRP)-접합 염소 항-마우스 IgG (Fc) 2차 검출 항체 (시그마-알드리치, 영국)의 순차적인 인큐베이션으로 비오티닐화 CD40L에 대한 dAb 대 인간 CD40의 경쟁적 결합을 검출하였다. 1M HCl 용액으로의 중화 후 450 nm에서 스펙트럼맥스(SpectraMax) M5[®] 플레이트 판독기 (분자 프로브(Molecular Devices))를 사용하여 흡광도 신호를 측정하였다.

[0336] 세포 검정: CD40 CHO 세포 RBA:

[0337] 안정적으로 형질감염된 인간 CD40을 발현하는 CHO-DG44 세포 또는 천연 CHO-DG44 세포 (양쪽 모두 BMS)를 베르셀 (인비트로젠)을 사용하여 세포 배양 플라스크로부터 떼어냈다. 4만개의 세포/웰을 벽은 흑색이고 바닥은 투

명한 96웰 하이 바인드 플레이트 (코닝, 영국) 내로 0.1% (w/v) BSA PBS 검정 완충제 + 희석물 범위의 dAb, 0.25 $\mu\text{g}/\text{ml}$ 의 비오티닐화 인간 IZ-CD40L (BMS), 및 0.25 $\mu\text{g}/\text{ml}$ 의 스트렙타비딘 알렉사 플루오르 647 (인비트로젠, 몰레큘러 프로브즈, 영국) 내에 시딩(seeding)하였다. 혼합물을 빛의 부재 하에 6시간 동안 인큐베이션하였다. 인큐베이션 후, AB8200 세포 검출 메커니즘 (어플라이드 바이오시스템즈)으로 상대적인 형광을 사용하여 가용성 비오티닐화 IZ-CD40L에 대한 dAb 대 인간 CD40 CHO 세포의 경쟁적 결합을 평가하였다.

[0338] 표 5-7은 테스트된 항-인간 CD40 dAb에 대한 1차 스크리닝 시도 ("나이프 클론") 및 후속 친화도 성숙 라운드 ("오차-경향 성숙 클론" 및 "추가-성숙 클론")로부터의 결과를 각각 나타낸다.

표 5

1차 스크리닝 시도:

나이프 클론	EC ₅₀ 비드 RBA (nM)	EC ₅₀ ELISA RBA- (nM)	EC ₅₀ 세포 RBA (CHO-CD40) (nM)
BMS3h-37	100, 200		
BMS3h-38	600, 650		>10000
BMS3h-41	2000, 1600		>10000
BMS3h-43	100, 50, 50		5000
BMS3h-56	1000, 500		
BMS3h-106	300, 1000, 500, 400		>10000
BMS3h-129	5000		
BMS3h-131	500, >1000		
BMS3h-193	1000		
BMS3h-197	30		
BMS3h-198	80		600
BMS3h-202	3000, 3700		>10000
BMS3h-217	800		1400
BMS3h-231		670, 870	
BMS3h-233		2770	
BMS3h-257		3210, 1340	
BMS3h-242		390, 210	
BMS3h-262		1770, 1160	
BMS3h-263		3130	
BMS3h-271		370, 210	
BMS3h-285		168, 258	
BMS3h-287		>10000, 6758	
BMS3h-289		2390, >10000	

[0339]

표 6

오차-경향 성숙 클론:

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ 세포 RBA (CHO-CD40) (nM)
BMS3h-37-2		32
BMS3h-37-4		45
BMS3h-37-11		27
BMS3h-38-5		1000
BMS3h-38-8		2800
BMS3h-41-3		200
BMS3h-41-10		4300
BMS3h-43-3		320
BMS3h-43-5		90
BMS3h-56-1	7.1	
BMS3h-56-2	17.0	
BMS3h-56-5	4.9, 7.5, 4.7	18, 28
BMS3h-56-7	5.5	
BMS3h-56-8	6.2	
BMS3h-56-9	4.4, 5.5	
BMS3h-56-16	7.0	
BMS3h-56-17	66	
BMS3h-56-18	6.5	
BMS3h-56-19	5.5, 5.1	
BMS3h-56-20	6.8	
BMS3h-56-21	6.5, 6.2	
BMS3h-56-22	6.5	
BMS3h-56-23	24.5	
BMS3h-56-24	11.7	
BMS3h-56-25	5.5	
BMS3h-56-26	5.0	
BMS3h-56-27	16.3	
BMS3h-56-28	8.9	

[0340]

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ 세포 RBA (CHO-CD40) (nM)
BMS3h-56-29	9.7	
BMS3h-56-30	24.2	
BMS3h-56-31	61.0	
BMS3h-193-5	>300	
BMS3h-193-7	300	
BMS3h-193-10	200	
BMS3h-193-11	300	
BMS3h-193-12	200	
BMS3h-193-15		300
BMS3h-193-18	100	
BMS3h-193-19	100	
BMS3h-193-25	140	
BMS3h-193-26	100	
BMS3h-193-27	100	
BMS3h-193-29	360, 114	
BMS3h-193-30	290, 116	
BMS3h-198-1	12	70
BMS3h-198-2		115
BMS3h-198-3		330
BMS3h-198-9	20	
BMS3h-198-10	35	
BMS3h-198-11	20	
BMS3h-198-14	9	
BMS3h-198-17	20	
BMS3h-198-19	7.9	
BMS3h-198-22	10	
BMS3h-198-31	6.1	
BMS3h-198-32	24.7	
BMS3h-198-33	8.7	
BMS3h-198-34	32.6	
BMS3h-198-37	15.1	

[0341]

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ 세포 RBA (CHO-CD40) (nM)
BMS3h-198-38	7.2	
BMS3h-202-10		7200
BMS3h-202-11		8300
BMS3h-217-1	23	
BMS3h-217-2	78	
BMS3h-217-3	32	
BMS3h-217-4	partial, 15	
BMS3h-217-5	65	
BMS3h-217-6	26	
BMS3h-217-7	39	
BMS3h-217-8	6	
BMS3h-217-9	53	
BMS3h-217-14	8	
BMS3h-217-15	21	
BMS3h-217-16	9	
BMS3h-217-17	60	
BMS3h-217-23	16	

[0342]

표 7

추가-성숙 클론:

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 세포 검정 (nM)	EC ₅₀ 세포 RBA (CHO-CD40) (nM)
BMS3h-37-202	4.1, 35		
BMS3h-37-205	3.1, 4.4		
BMS3h-37-206	3.2, 8.9		
BMS3h-37-207	2.5, 6.6		
BMS3h-37-212	24		
BMS3h-37-213	16		

[0343]

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 세포 검정 (nM)	EC ₅₀ 세포 RBA (CHO-CD40) (nM)
BMS3h-38-201	3.4, 불활성		
BMS3h-38-202	4.8		
BMS3h-38-203	5.5		
BMS3h-38-204	4.8		
BMS3h-38-205	4.5, 11.1		
BMS3h-38-209	10.2		
BMS3h-38-211	2.3, 13.8		
BMS3h-38-215	2.3, 3.6		
BMS3h-38-217	1.8, 2.2		
BMS3h-38-218	3.0		
BMS3h-38-219	1.8, 7.1		
BMS3h-38-223	5.7		
BMS3h-38-224	6.3		
BMS3h-38-225	8.8		
BMS3h-38-226	18.1		
BMS3h-38-228	4		
BMS3h-38-231	4.4		
BMS3h-38-235	1.5		
BMS3h-38-237	2		
BMS3h-38-238	5.1		
BMS3h-56-201	3.7, 2.3	10.0	
BMS3h-56-202	3.4, 3.2	80.0	
BMS3h-56-203	5.2, 4.3	70.0	
BMS3h-56-204	4.5		
BMS3h-56-205	9.0		

[0344]

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 세포 검정 (nM)	EC ₅₀ 세포 RBA (CHO- CD40) (nM)
BMS3h-56-206	2.9, 2.3	5.0	
BMS3h-56-207	7.3		
BMS3h-56-215	3.2, 4.6	40.0	
BMS3h-56-217	2.1, 12.6		
BMS3h-56-220	4.2		
BMS3h-56-223	5.0		
BMS3h-56-224	2.1, 4.2		
BMS3h-56-225	2.9		
BMS3h-56-229	4.1		
BMS3h-56-232	2.8, 3.7		
BMS3h-56-239	2.7		
BMS3h-56-243	9.9		
BMS3h-56-244	6.0		
BMS3h-56-246	11.1		
BMS3h-56-248	0.7		
BMS3h-56-253	1.3		
BMS3h-56-258	5.2	23.0	15
BMS3h-56-261	5.7	42.4	17
BMS3h-56-262	4.0	135.0	42
BMS3h-56-265	18.8	289.0	88
BMS3h-56-266	3.8	31.9	27
BMS3h-56-269	3.3	34.2	24
BMS3h-56-270	11.3	93.8	91
BMS3h-193-2501	114		
BMS3h-193-2502	170		
BMS3h-193-2503	3000		

[0345]

클론	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 세포 검정 (nM)	EC ₅₀ 세포 RBA (CHO- CD40) (nM)
BMS3h-193-2504	140		
BMS3h-193-2505	500		
BMS3h-193-2506	180		
BMS3h-193-2507	160		
BMS3h-193-2510	170		
BMS3h-193-2511	270		
BMS3h-193-2512	600		
BMS3h-193-2513	130		
BMS3h-193-2514	525		
BMS3h-193-2515	100		
BMS3h-193-2516	100		

[0346]

[0347]

[0348]

[0349]

[0350]

실시예 3

CD40 결합 동역학

1차 스크리닝 시도 ("나이브 클론") 및 후속 친화도 성숙 라운드 ("오차-경향 성숙 클론")에서 확인된 항-인간 CD40 dAb에 대해 결합 동역학을 확인하였다. 사용된 방법들은 CD40에 대한 dAb의 친화도를 직접적으로 측정한다.

비아코어™ 3000 기구 (GE 헬스케어)를 사용하여 CD40에 대한 CD40-특이적 dAb의 결합 동역학을 분석하였다. 약 600 반응 단위 (RU)의 비오티닐화 인간 CD40 (BMS)을 스트렙타비딘 (SA) 비아코어™ 칩의 1개의 유동 셀 상에 고정하였다. 어떠한 리간드도 고정되지 않은 제2 유동 셀이 인라인 참조를 위한 기준 유동 셀로서의 역할을 하였다. 분석할 dAb의 적합한 일련의 배가 희석물을 HBS-EP 완충제 (0.01 M HEPES pH 7.4 + 0.15 M NaCl, 3 mM EDTA 및 0.005% v/v 계면활성제 P20, GE 헬스케어)에서 제조하였다. 180 μ l의 각각의 dAb를 기구의 KINJECT 기능을 사용하여 이중으로 주입하였다. 각각의 dAb를 일련의 CD40가 고정된 유동 셀 및 기준 유동 셀을 가로질러 주입하였고, 이때 기준 셀로부터의 신호를 인라인으로 차감하였다. 25℃ 및 30 μ l/분의 HBS-EP 유속으로 실험을 수행하였다. 각각의 주입을 완료한 후, dAb를 300초 동안 완충제 내에서 리간드로부터 해리시키고 나서, 10 mM 글리신 pH 2.0의 10 μ l 주입으로 재생시켰다. HBS-EP 완충제 블랭크(blank) (분석물을 함유하지 않음)의 기준 주입물을 동일한 조건 하에 또한 주입하여, 각각의 분석물 트래이스로부터의 차감을 위한 제2

기준물로서의 역할을 하게 하였다. 비아이밸류에이션 4.1 소프트웨어 (GE 헬스케어)를 사용하여 기준 유동 셀 트레이스 및 완충제 블랭크 트레이스 양쪽 모두를 각각의 분석물 트레이스로부터 차감하였다. 동일한 소프트웨어를 사용하여, 일련의 분석물 회석물 트레이스의 회합 및 해리 단계에 대한 1:1 (랭뮤어) 동역학 모델의 동시적인 포괄적 피트를 수행하였다. 이러한 모델로 상호작용의 회합 및 해리 속도 상수 (각각 k_a 및 k_d) 및 평형 해리 상수 (K_D)가 산출되었다: 표 8 및 9에서 이를 상술한다.

표 8

나이프 클론:

클론	비아이코어™ k_a ($M^{-1}s^{-1}$)	비아이코어™ k_d (s^{-1})	비아이코어™ K_D (M)
BMS3h-37	1.9E+04	3.6E-03	1.9E-07
BMS3h-38	2.1E+04	6.2E-03	3.0E-07
BMS3h-41	9.9E+03	8.3E-03	8.4E-07
BMS3h-43	1.4E+03	3.1E-03	2.1E-06
BMS3h-56	2.3E+04	4.0E-03	1.8E-07
BMS3h-106	1.3E+05	4.6E-02	3.5E-07
BMS3h-107	2.0E+05	1.7E-01	8.5E-07
BMS3h-129	4.7E+05	5.1E-01	1.1E-06
BMS3h-131	2.4E+04	2.2E-02	9.3E-07
BMS3h-197	8.1E+04	1.4E-02	1.8E-07
BMS3h-198	1.6E+03	3.8E-04	2.4E-07
BMS3h-202	1.7E+03	3.5E-03	2.0E-06

[0351]

표 9

오차-경향 성숙 클론:

클론	비아이코어™ k_a ($M^{-1}s^{-1}$)	비아이코어™ k_d (s^{-1})	비아이코어™ K_D (M)
BMS3h-37-2	1.0E+05	4.1E-04	4.0E-09
BMS3h-37-5	3.9E+04	2.2E-04	5.5E-09
BMS3h-37-9	1.5E+04	1.8E-04	1.2E-08
BMS3h-38-1	3.2E+04	1.1E-03	3.3E-08
BMS3h-38-2	6.1E+04	7.5E-04	1.2E-08
BMS3h-38-3	7.5E+04	4.1E-04	5.5E-09
BMS3h-41-1	5.1E+04	5.6E-04	1.1E-08
BMS3h-43-1	4.4E+03	6.3E-04	1.4E-07
BMS3h-43-3	3.1E+04	5.9E-04	1.9E-08
BMS3h-56-1	9.8E+04	5.4E-04	5.5E-09
BMS3h-56-2	1.1E+05	6.0E-04	5.3E-09
BMS3h-56-5	1.1E+05	6.3E-04	5.9E-09
BMS3h-56-7	1.3E+05	4.7E-04	3.5E-09
BMS3h-56-9	1.5E+05	3.9E-04	2.6E-09
BMS3h-131-2	7.9E+04	1.7E-03	2.1E-08
BMS3h-193-25	4.6E+05	3.7E-02	8.1E-08
BMS3h-198-1	1.5E+04	1.8E-04	1.3E-08
BMS3h-202-5	4.4E+03	1.3E-03	3.0E-07

[0352]

실시예 4

생물물리학적 특성화

1차 스크리닝 시도 ("나이프 클론") 및 후속 친화도 성숙 라운드 ("오차-경향 성숙 클론" 및 "추가-성숙 클론")에서 확인된 항-인간 CD40 dAb를 생물물리학적 파라미터의 분석에 의해 추가로 특성화하였다. dAb의 상대적인 안정성을 측정하기 위해, 이의 용점을 시차 주사 열량측정법 (DSC)으로 결정하였다. 용융 온도가 더 높은 dAb가 더 안정적이다. dAb가 용액에서 다량체성 응집물을 형성하는지를 결정하기 위해, dAb를 크기 배제 크로마토그래피/각각도 레이저 광 산란 (SEC-MALLS)으로 분석하였다. 결과가 표 10-12에서 제시된다.

[0353]

[0354]

[0355]

표 10

나이프 클론:

클론	DSC (Tm/°C)	SEC-MALS 용액 상태
BMS3h-38	59	단량체 및 이량체 (<5%)
BMS3h-41	59	단량체 및 단량체-이량체 평형 (<5%)
BMS3h-43		이량체 및 삼량체
BMS3h-56	57	단량체 및 이량체 (<10%)
BMS3h-106		단량체
BMS3h-107	63	단량체
BMS3h-129	59	단량체
BMS3h-193	56	단량체
BMS3h-197	62 & 53	단량체 및 이량체 (<5%)
BMS3h-198	61	단량체
BMS3h-202	60	단량체 및 단량체-이량체 평형 (<2%)
BMS3h-207		이량체 및 사량체
BMS3h-208		단량체 및 이량체
BMS3h-217	57	이량체
BMS3h-233		단량체
BMS3h-242		단량체 및 단량체-이량체
BMS3h-262		단량체
BMS3h-265		이량체
BMS3h-271		이량체
BMS3h-285		단량체

[0356]

표 11

오차-경향 성숙 클론:

클론	DSC Tm/°C	SEC-MALS 용액 상태
BMS3h-37-1	57.2	
BMS3h-37-2	56.2	
BMS3h-37-9	59.7	
BMS3h-37-11	60.0	

[0357]

클론	DSC Tm/°C	SEC-MALS 용액 상태
BMS3h-56-1	49.6	단량체
BMS3h-56-2	63.0	단량체 및 이량체 (<2%)
BMS3h-56-3	64.0	단량체 (>98%)
BMS3h-56-5	51.2	
BMS3h-41-1	56	단량체 (~99%)
BMS3h-41-2	53.4	
BMS3h-41-3	51.8	
BMS3h-41-9	61	단량체 및 단량체/이량체 신속한 평형 (<2%)
BMS3h-41-12	49.8	단량체/이량체
BMS3h-41-13		단량체/이량체
BMS3h-43-1	53	단량체 (~99%)
BMS3h-43-3	51.2	
BMS3h-43-5	48.2	단량체/이량체
BMS3h-43-10	51.8	
BMS3h-43-11	54.8	
BMS3h-43-12		이량체 (60%) 및 단량체 (40%)
BMS3h-56-1	59.2	단량체/이량체
BMS3h-56-2	60.1	단량체/이량체
BMS3h-56-5	57	단량체 (>95%)
BMS3h-56-6	57.5	단량체/이량체
BMS3h-56-7	61	단량체 + 단량체/이량체 신속한 평형 (<5%)
BMS3h-56-8	58	단량체 (>98%)
BMS3h-56-9	61	단량체 + 이량체 (<5%)
BMS3h-56-14	60.1	단량체
BMS3h-193-8	60	
BMS3h-193-12	52	
BMS3h-193-16	54.5 & 65.7	단량체
BMS3h-193-19	56.8	단량체
BMS3h-193-25	55.8	단량체

[0358]

클론	DSC Tm/°C	SEC-MALS 용액 상태
BMS3h-193-29	60	단량체
BMS3h-193-30	58	
BMS3h-198-1	52.5	단량체
BMS3h-198-2		단량체
BMS3h-198-3	59	
BMS3h-198-5	55.6	
BMS3h-198-19	60.7	
BMS3h-198-24	59.9	단량체
BMS3h-198-28	60.3	단량체
BMS3h-202-1	56.8	단량체
BMS3h-202-5	55.5	삼량체 (60%) 및 단량체/이량체 (40%)
BMS3h-202-10	58.3	삼량체 (60%) 및 단량체/이량체 (40%)
BMS3h-217-1		단량체/이량체
BMS3h-217-2		이량체
BMS3h-217-3		이량체
BMS3h-217-4		단량체/이량체
BMS3h-217-5		이량체
BMS3h-217-6		이량체
BMS3h-217-8		이량체
BMS3h-217-14		단량체/이량체
BMS3h-217-15		이량체
BMS3h-217-16		이량체
BMS3h-217-17		단량체/이량체
BMS3h-217-23		이량체

[0359]

표 12

추가-성숙 클론:

클론	DSC Tm/°C	SEC-MALS 용액 상태
BMS3h-37-206		단량체 (73%) 및 이량체 (20%) + HMW
BMS3h-37-212		이량체
BMS3h-38-201		단량체 (75%) 및 이량체 (15%)
BMS3h-38-228		단량체 (90%) 및 삼량체 (10%)
BMS3h-38-231		단량체 (90%) 및 이량체 (10%)
BMS3h-38-235		단량체 (90%) 및 삼량체-이량체
BMS3h-38-237		단량체 (90%) 및 사량체 (10%)
BMS3h-38-238		단량체 (95%) 및 이량체-단량체
BMS3h-56-201	57.4 + 61.8	단량체 및 이량체 (15%)
BMS3h-56-202		단량체
BMS3h-56-203		단량체 및 삼량체
BMS3h-56-206		단량체
BMS3h-56-215		단량체, 이량체 (2%) 및 삼량체 (9%)
BMS3h-56-217	52.8 + 54.6	
BMS3h-56-232	51.0 + 56.1	단량체 (95%) 및 이량체 (5%)
BMS3h-56-239	53.5	단량체
BMS3h-56-243	51.9	단량체 및 오량체
BMS3h-56-244		단량체 (90%) 및 삼량체 (10%)
BMS3h-56-248		단량체 (60%), 이량체 및 사량체
BMS3h-56-253		단량체
BMS3h-56-258	62.5 + 57.5	
BMS3h-56-261	58.6 + 61.5	
BMS3h-56-266	61.3 + 62.3	
BMS3h-56-269	64.5 + 67.2	

[0360]

[0361] 실시예 5

[0362] 경쟁 분석

[0363] 비아코어™ 3000 기구 (GE 헬스케어)를 사용하여, CD40-특이적 dAb들이 동일한 CD40 에피토프에 결합하였는지를 분석하였다. 약 600 반응 단위 (RU)의 비오티닐화 인간 CD40 (BMS)을 스트렙타비딘 (SA) 비아코어™ 칩의 1개의 유동 셀 상에 고정하였다. 어떠한 리간드도 고정되지 않은 제2 유동 셀이 인라인 참조를 위한 기준 유동 셀로서의 역할을 하였다. 각각의 분석할 dAb 또는 Fab의 적합한 희석물을 HBS-EP 완충제 (0.01 M HEPES pH 7.4 + 0.15 M NaCl, 3 mM EDTA 및 0.005% v/v 계면활성제 P20, GE 헬스케어)에서 제조하였다. 하기 기술된 바와 같이 주입되었을 때 특정 억제제에 대한 가능한 최대 결합 RU의 >80%, 전형적으로는 1 - 10 μ M을 초래한 희석물을 선택하였다. 다음으로, 상기와 동일한 dAb 또는 Fab (동일한 최종 농도)의 혼합물을 경쟁에 대해 분석할 제2 dAb 또는 Fab와 함께 제조하였다. 기구의 COINJECT 기능을 사용하여, 60 μ l의 단일-억제제 희석물을 일련

의 CD40가 고정된 유동 셀 및 기준 유동 셀을 가로질러 주입하고, 바로 이어서 60 μ l의 2-억제제 혼합물을 주입하였다. 기구의 제어 소프트웨어에 의해 기준 셀로부터의 신호의 인라인 차감을 수행하였다. 25℃ 및 30 μ l/분의 HBS-EP 유속으로 실험을 수행하였다. 각각의 공동-주입을 완료한 후, 억제제를 60초 동안 완충제 내에서 리간드로부터 해리시키고 나서, 10 mM 글리신 pH 2.0의 10 μ l 주입으로 재생시켰다. 제2 주입 (2개의 억제제의 혼합물)에 대해 수득된 최대 RU를 기록하였고, 이는 단독으로 주입되었을 때 동일한 억제제에 대해 수득된 RU의 백분율로서 표현되었다.

[0364] 제2 억제제가 단독으로 주입되었을 때 일반적으로 결합된 RU의 100% 이상을 유지하였으면, 이는 2개의 억제제가 별개의 에피토프에 결합한다는 것을 암시한다. 제2 억제제의 100% 미만의 결합이 관찰되었으면, 이는 CD40에 결합하는 것에 대한 2개의 억제제 간의 경쟁을 가리킨다. 이러한 경쟁에 대한 여러 가능한 이유가 있다: 2개의 억제제가 동일하거나 중복되는 에피토프에 결합할 수 있거나, 입체적인 결합 억제가 있을 수 있거나, 또는 제1 억제제의 결합이 제2 억제제의 결합을 방지하거나 감소시키는 항원에서의 형상 변화를 유도할 수 있다.

[0365] 각각의 계통 (BMS3h-217 제외)으로부터의 예시적인 클론을 중복 군 내의 다른 dAb와의 경쟁에 대해 테스트하였다. 표 13 및 14에 나타난 바와 같이, 테스트된 모든 dAb가 CD40에 결합하는 것에 대해 서로 경쟁하는 것으로 보인다. 이러한 데이터는 계통 BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198 및 BMS3h-202로 이루어진 군으로부터 선택된 모든 항체 폴리펩티드가 인간 CD40에 대한 이러한 계통 중 임의의 것으로부터의 dAb의 결합과 경쟁할 것임을 시사한다.

표 13

경쟁 비아코어™:

제1 주입	RU 제1 dAb 단독	제2 주입 (단일 dAb RU의 %)				
		BMS3h-56-5	BMS3h-37-11	BMS3h-131-2	BMS3h-198-1	BMS3h-202-11
BMS3h-56-5	245		-15	17	0.6	7.3
BMS3h-37-11	158	15		25	16	0.3
BMS3h-131-2	220	22	-3.7		23.2	10.3
BMS3h-198-1	176	28	6.4	41		18
BMS3h-202-11	124	50	42	57	39	

[0366]

표 14

제1 주입	RU 제1 dAb 단독	제2 주입 (단일 dAb RU의 %)			
		BMS3h-38-2	BMS3h-41-9	BMS3h-43-1	BMS3h-56-5
BMS3h-38-2	170		11	29	29
BMS3h-41-9	150	27		44	47
BMS3h-43-1	210	20	19		39
BMS3h-56-5	190	4	0	22	

[0367]

[0368] 유사하게, 표 15 및 16에 나타난 바와 같이, 다양한 dAb를 Chi220 Fab'와의 경쟁에 대해 테스트하였다. 이러한 경우에, 경쟁을 나타낸 BMS3h-217을 제외하고는 모든 dAb가 Chi220 Fab'와 경쟁하지 않았다. BMS3h-56-5 및 BMS3h-193-12 dAb는 결합된 Chi220 또는 G28-5 Fab'의 존재 하에 단일 dAb RU의 100% 이상으로 결합하였고, 이는 Fab'가 dAb와 상이한 에피토프(들)에 결합한다는 것을 시사한다. G28-5의 존재 하에 Chi220 Fab'가 결합된 RU의 감소를 나타냈다. 반대 순서의 결합에서 동일한 결과가 관찰되었다. 이는 G28-5 Fab'가 Chi220 Fab'와 동일한 에피토프에 결합한다는 것을 시사한다.

표 15

제1 주입	RU 제1 dAb/Fab 단독	제2 주입 (단일 dAb/Fab RU의 %)			
		BMS3h-56-5	Chi220 Fab	G28-5 Fab	BMS3h-193-12
BMS3h-56-5	193		98	94	64
Chi220 Fab	1089	105		11	109
G28-5 Fab	730	125	39		116
BMS3h-193-12	282	44	98	93	

[0369]

표 16

클론명	테스트된 dAb 또는 Fab의 μ M	단일 dAb RU	단일 dAb RU의 % (Chi220+dAb)
BMS3h-38-2	5	156	121
BMS3h-41-13	5	162	109
BMS3h-43-3	5	300	101
BMS3h-38-2	5	175	114
BMS3h-56-5	5	193	105
BMS3h-106	10	165	111
BMS3h-107	10	35	146
BMS3h-129	10	156	121
BMS3h-193-12	5	282	98
BMS3h-197	1	177	116
BMS3h-217	10	85	25
G28-5 Fab	1	730	11

[0370]

[0371] 실시예 6

[0372] CD40 활성화 검정

[0373] 항-인간 CD40 dAb를 CD40 활성을 길항하는 능력에 대해 기능적으로 분석하였다. 테스트된 CD40 활성화는 1차 인간 단핵구-유래 수지상 세포 (DC)의 hCD40L-구동 활성화에 의한 B 세포 증식 및 시토카인 생산이었다. 달리 언급되지 않는 한, 모든 검정을 10% 송아지 태아 혈청 (FCS)이 보충된 RPMI 배지에서 수행하였다. 다양한 검정을 사용한 결과가 표 17에서 제시된다.

[0374] 가용성 IZ-hCD40L-구동 1차 인간 B 세포 증식:

[0375] 1×10^5 개의 편도선 인간 B 세포를 96웰 둥근 바닥 플레이트에서 200 μ l/웰의 최종 부피로 다양한 적정도의 항체 폴리펩티드와 같이 0.6 μ g/ml의 IZ-hCD40L와 함께 인큐베이션하였다. 플레이트를 37°C에서 72시간 동안 인큐베이션한 후, 티미딘 (^{3} H; 0.5 μ ci/웰)을 6시간 동안 첨가하였다. 티미딘 혼입을 기초로 B 세포 증식을 정량하였다.

[0376] CHO-hCD40L-구동 1차 인간 B 세포 증식:

[0377] CHO 세포를 인간 CD40L로 형질감염시켜, 세포 표면 상에 높은 수준의 CD40L을 발현하는 안정적인 세포주를 생성시켰다. CHO-CD40L 세포에 10,000 래드를 조사한 후, 인간 B 세포와 함께 인큐베이션하였다. 1×10^5 개의 편도선 인간 B 세포를 96웰 둥근 바닥 플레이트에서 200 μ l/웰의 최종 부피로 다양한 적정도의 항체 폴리펩티드와 같이 1×10^3 개의 CHO-CD40L 세포 (1:100 비의 CHO-CD40L:인간 B 세포)와 함께 인큐베이션하였다. 플레이트를 37°C에서 72시간 동안 인큐베이션한 후, ^{3} H-티미딘 (0.5 μ ci/웰)을 6시간 동안 첨가하였다. 티미딘 혼입을 기초로 B 세포 증식을 정량하였다.

[0378] 가용성 IZ-hCD40L-구동 시노 비장 인간 B 세포 증식:

- [0379] 1×10^5 개의 시노 비장 B 세포를 96웰 둥근 바닥 플레이트에서 $200 \mu\text{l}$ /웰의 최종 부피로 다양한 적정도의 항체 폴리클로날과 같이 $0.5 \mu\text{g}/\text{ml}$ 의 IZ-hCD40L과 함께 인큐베이션하였다. 플레이트를 37°C 에서 72시간 동안 인큐베이션한 후, ^3H -티미딘 ($0.5 \mu\text{Ci}/\text{well}$)을 6시간 동안 첨가하였다. 티미딘 혼입을 기초로 B 세포 증식을 정량하였다.
- [0380] **1차 T 세포-구동 인간 B 세포 증식:**
- [0381] T 세포를 인간 말초혈 단핵 세포 (PBMC)로부터 분리하고, 양 적혈구 (SRBC) 로제팅(rosetting)을 사용하여 강화시켰다. 편도선 조직을 단일 세포 현탁액으로 균질화함으로써 인간 편도선 B 세포를 분리하였다. 피콜 (ficoll) 분리로 백혈구를 수득한 후, B 세포를 음성적으로 SRBC 로제팅을 사용하여 선별하고, 로제팅된 세포를 폐기함으로써 강화시켰다.
- [0382] 강화된 인간 T 세포를 5:1 비 (T:LCL)의 PM-LCL (EBV-형질전환 B 세포주; 10,000 래드로 조사됨)와 함께 6일 동안 37°C 에서 배양하여, 동종이형 T 세포의 집단을 생성시켰다. 제6일에, 확장된 T 세포를 분리하고, 이에 3000 래드를 조사한 후, 항-CD3 mAb (OKT3)로 코팅된 96웰 편평 바닥 플레이트에서 1:2 비의 1차 인간 편도선 B 세포 (1×10^5 개의 B 세포/웰)와 함께 배양하였다 (5×10^4 개의 T 세포/웰). 다양한 적정도의 항체 폴리클로날을 각각의 웰에 첨가하였다; 각각의 웰 내의 최종 부피는 $200 \mu\text{l}$ 였다. 테스트 플레이트를 37°C 에서 3일 동안 인큐베이션하였다. ^3H -티미딘 ($0.5 \mu\text{Ci}/\text{well}$)을 최종 18시간 동안 배양물에 첨가하는 것을 통해 인간 B 세포 증식을 결정하였다.
- [0383] **1차 인간 단핵구-유래 수지상 세포 (DC)의 CHO-hCD40L-구동 활성화:**
- [0384] SRBC 로제팅을 통해 T 세포를 고갈시킴으로써 인간 PBMC를 단핵구에 대해 강화시켰다. 단핵구가 강화된 PBMC를 $10 \text{ ng}/\text{ml}$ GM-CSF 및 $5 \text{ ng}/\text{ml}$ IL-4와 함께 6웰 플레이트에서 6일 동안 37°C 에서 배양하였다. 제2일 및 제5일에 신선한 배지 (+ GM-CSF 및 IL-4)를 배양된 플레이트에 보충하였다. 미성숙 수지상 세포 (DC)를 제6일에 세포 검정에서 사용하였다. 8×10^4 개의 미성숙 DC를 96웰 편평 바닥 플레이트에서 다양한 적정도의 항체 폴리클로날과 같이 4×10^3 개의 CHO-hCD40L 세포 (10,000 래드로 조사됨)와 함께 배양하였다. 24시간 시간 후, 상청액을 수확하고, 다양한 시토카인 (IL-12, TNF, IL-23)의 존재에 대해 테스트하였다. 시토카인 생산 수준에 의해 DC 활성화를 결정하였다.

표 17

콜론	hIZCD40L- 구동 인간 B 세포 증식 EC50 (nM)	hIZCD40L- 구동 시노 B 세포 증식 EC50 (nM)	CHO- hCD40L- 구동 인간 B 세포 증식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h-5	>7000		>7000		
3h-8	>7000		>7000		
3h-28	>7000		>7000		
3h-33	>7000		>7000		
3h-48	>7000		>7000		
3h-52	>7000		>7000		
3h-57	>7000		>7000		
3h-61	>7000		>7000		
3h-88	>7000				
3h-102	>7000				
3h-106	437.0 ± 214.0	>7000			
3h-107	>7000	>7000			
3h-112	>7000				
3h-129	2100.0 ± 1000.0				
3h-197	360.0 ± 500.0	>7000			
3h-207	>7000				
3h-208	>7000				
3h-37	3400.0 ± 2900.0	>7000			
3h-37-1	250.0 ± 100.0				
3h-37-2	5.0 ± 2.0	>7000		198 ± 35	13.0 ± 7.3
3h-37-202	0.6 ± 0.2			83 ± 18	10.0
3h-37-205	2.0 ± 1.0				6.6
3h-37-206	5.0 ± 0.8				23.0
3h-37-207	4.0 ± 2.0				15.5 ± 8.0
3h-37-212	1.0 ± 0.05				
3h-37-213	0.7 ± 0.2				
3h-37-11	8.0 ± 7.0				

[0385]

콜론	hIZCD40L- 구동 인간 B 세포 증식 EC50 (nM)	hIZCD40L- 구동 시노 B 세포 증식 EC50 (nM)	CHO- hCD40L- 구동 인간 B 세포 증식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h-38	2800.0 ± 400.0	>7000			
3h-38-1	142.0 ± 86.0				
3h-38-2	10.0 ± 6.0	>7000	723.0 ± 185.0	986 ± 383	289.0 ± 315.0
3h-38-201	>70.0		>7000		>800.0
3h-38-205	4.0 ± 2.0		1100.0 ± 141.0		29.0
3h-38-211	2.0 ± 1.0		82.0 ± 4.0	200 ± 1	18.0 ± 19.0
3h-38-215	1.0 ± 0.0		65.0 ± 1.0	163 ± 14	6.0 ± 4.0
3h-38-217	0.8 ± 0.2		34.0 ± 6.0	74 ± 22	1.7 ± 0.4
3h-38-219	2.0 ± 0.5		93.0 ± 26.0	164 ± 3	9.0 ± 5.0
3h-38-228	0.7 ± 0.05				
3h-38-231	0.66 ± 0.2				
3h-38-235	0.4 ± 0.2				
3h-38-237	0.4 ± 0.2				
3h-38-238	0.7 ± 0.03				
3h-38-3	10.0 ± 7.0				
3h-41	>7000				
3h-41-1	104.0 ± 56.0				
3h-41-2	47.0 ± 67.0				
3h-41-3	12.0 ± 7.0	>7000			
3h-41-9	148.0 ± 98.0				
3h-41-12	104.0 ± 50.0				
3h-41-13	208.0 ± 90.0				
3h-43	83.0 ± 40.0	>7000			
3h-43-1	53.0 ± 20.0				
3h-43-3	87.0 ± 19.0				
3h-43-5	180.0 ± 130.0				
3h-43-10	143.0 ± 131.0				
3h-43-11	30.0 ± 19.0				
3h-43-12	12.0 ± 6.0				
3h-56	713.0 ± 133.0	>7000			

[0386]

클론	hIZCD40L- 구동 인강 B 세포 중식 EC50 (nM)	hIZCD40L- 구동 시노 B 세포 중식 EC50 (nM)	CHO- hCD40L- 구동 인강 B 세포 중식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h-56-1	7.0 ± 5.0				
3h-56-2	3.0 ± 1.0		326.0 ± 79.0	276 ± 29	444.0, >2000.0
3h-56-201	0.12 ± 0.04		11.0 ± 6.0	7.25 ± 0.96	0.93 ± 0.7
3h-56-202	0.6 ± 0.2		39.0 ± 16.0	50 ± 9.8	2.9 ± 2.6
3h-56-203	0.45 ± 0.1		51.0 ± 29.0	52 ± 23	3.7 ± 4.0
3h-56-206	0.1 ± 0.01		6.0 ± 2.0	5.25 ± 0.5	0.7 ± 0.4
3h-56-215	0.2 ± 0.03		41.0 ± 15.0	31 ± 7	11.0 ± 12.0
3h-56-217	0.1 ± 0.04		13.0 ± 5.0	16 ± 6.7	9.4 ± 8.0
3h-56-224	0.5 ± 0.2		26.0 ± 5.0	47 ± 11	18.0 ± 22.0
3h-56-232	0.27 ± 0.1		37.0 ± 0.7	42 ± 10	7.3 ± 6.6
3h-56-239	0.11 ± 0.0		18.0 ± 4.0	13.5 ± 4.76	5.8 ± 6.5
3h-56-243	0.15 ± 0.007		13.5 ± 2.0	14.2 ± 4.6	8.8 ± 10.0
3h-56-244	0.17 ± 0.02		26.0 ± 3.0	21 ± 4.1	12.6 ± 16.0
3h-56-246	0.24 ± 0.06		34.0 ± 14.0	23.8 ± 6.2	23.2 ± 22.0
3h-56-248	0.36 ± 0.1				
3h-56-253	0.4 ± 0.2				
3h-56-258	0.079 ± 0.003		11.0 ± 3.0	8.7 ± 1.9	1.52 ± 1.6
3h-56-261	0.17 ± 0.09		25.5 ± 6.0	17 ± 5.4	3.0 ± 1.8
3h-56-262	0.31 ± 0.007				
3h-56-265	0.36 ± 0.06				
3h-56-266	0.19 ± 0.04		19.5 ± 6.0	13.8 ± 2.4	2.8 ± 2.3
3h-56-269	0.14 ± 0.02		15.0 ± 5.0	9.7 ± 1.9	1.8 ± 1.2
3h-56-270	0.31 ± 0.1				
3h-56-5	6.0 ± 4.0	>7000			
3h-56-6	4.0 ± 3.0				
3h-56-7	8.0 ± 6.0				
3h-56-8	5.0 ± 2.0				
3h-56-9	3.0 ± 0.6				
3h-56-15	2.0 ± 0.9				
3h-56-19	3.0 ± 2.0				

[0387]

클론	hIZCD40L- 구동 인강 B 세포 중식 EC50 (nM)	hIZCD40L- 구동 시노 B 세포 중식 EC50 (nM)	CHO- hCD40L- 구동 인강 B 세포 중식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h-56-21	2.0 ± 1.0				
3h-131	2700.0 ± 1000.0	>7000			
3h-131-2	55.0 ± 53.0	>7000			
3h-131-6	141.0 ± 37.0				
3h-131-14	24.0 ± 4.0				
3h-193	>7000				
3h-193-12	277.0 ± 167.0				
3h-193-16	387.0 ± 173.0				
3h-193-19	233.0 ± 110.0				
3h-193-25	303.0 ± 214.0	2200.0 ± 1200.0			
3h-193-29	1380.0 ± 721.0				
3h-198	554.0 ± 186.0	>7000			
3h-198-1	64.0 ± 47.0				
3h-198-2	207.0 ± 158.0				
3h-198-5	9.0 ± 6.0				
3h-198-19	19.0 ± 14.0				
3h-198-24	34.0 ± 37.0				
3h-198-28	20.0 ± 9.0				
3h-202	6400.0 ± 1300.0	>7000			
3h-202-1	192.0 ± 77.0	>7000			
3h-202-5	6500.0 ± 1000.0				
3h-202-10	289.0 ± 158.0				
3h-202-11	201.0 ± 103.0				
3h-217	3200.0 ± 2030.0	>7000, 5300, 1690			
3h-217-1	45.0 ± 26.0	35.0 ± 8.0			
3h-217-2	8.0 ± 4.0	7.0			335.0
3h-217-4	61.0 ± 20.0	27.0			

[0388]

클론	hIZCD40L- 구동 인간 B 세포 중식 EC50 (nM)	hIZCD40L- 구동 시노 B 세포 중식 EC50 (nM)	CHO- hCD40L- 구동 인간 B 세포 중식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h-217-5	13.0 ± 5.0	15.0			
3h-217-6	11.0 ± 3.0	10.0			
3h-217-7	220.0 ± 20.0				
3h-217-8	33.0 ± 10.0	14.0			
3h-217-9	380.0 ± 170.0				
3h-217-14	26.0 ± 10.0	8.0			
3h-217-15	47.0 ± 21.0	20.0			
3h-217-16	5.0 ± 2.0	7.0			1125.0
3h-217-17	1950.0 ± 110.0				
3h-217-23	16.0 ± 6.0	15.0			
3h-217-2305	11.0 ± 4.0				
3h-217-30	80.0 ± 9.0				>7700
3h-217-31	>700.0				
3h-231	328.0 ± 144.0	>7000			
3h-233	184.0 ± 75.0	>7000			1492.0, >2000
3h-240	>7000	>7000			
3h-242	219.0 ± 53.0	435.0 ± 62.0			2050.0
3h-257	135.0 ± 28.0	>7000			704.0 ± 445.0
3h-262	548.0 ± 121.0	>700			998.0
3h-263	>700.0	>700			
3h-264	1200.0 ± 400.0	>7000			>2000
3h-265	2400.0 ± 1000.0	>7000			>2000
3h-271	295.0 ± 92.0	446.0			>2000
3h-274	1200, >7000	>7000			
3h-275	157.0 ± 11.0	>7000			
3h-285	49.0 ± 0.7	155.0			
3h-287	287.0 ± 156.0	918.0			
3h-289	2300.0 ± 1200.0	4300.0			

[0389]

클론	hIZCD40L- 구동 인간 B 세포 중식 EC50 (nM)	hIZCD40L- 구동 시노 B 세포 중식 EC50 (nM)	CHO- hCD40L- 구동 인간 B 세포 중식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h-290	>7000	5650.0			
3h-294	>7000	>7000			
3h-295	>7000	>7000			
3h-296	306.0 ± 55.0	>7000			
3h-309	648.0 ± 268.0	838.0			
3h-312	1100.0 ± 346.0	>7000			

[0390]

[0391]

실시예 7

[0392]

CD40 및 혈청 알부민에 결합하는 이중 특이적 dAb

[0393]

CD40 및 인간 혈청 알부민 (HSA) 또는 시노물구스 혈청 알부민 (CSA)에 특이적으로 결합하는 이중 특이적 dAb를 구축하고, 세포-기반 검정에서 활성에 대해 테스트하였다. 이러한 알부민-특이적 dAb는 "AlbudAb"로 칭해진다. 이러한 실시예에서, AlbudAb 융합물은 CD40에 결합하는 BMS3h dAb 및 HSA를 인식하는 또 다른 도메인 항체인 DOM7h를 포함한다. 2개의 dAb가 인-프레임으로 아미노산 링커의 아미노 및 카르복실 말단에 융합되어 인라인 융합(inline fusion) (ILF) 폴리펩티드가 형성된다. ILF 폴리펩티드는 단일 융합 단백질로서 재조합에 의해 발현된다. AlbudAb ILF의 활성을 나타내는 RBA가 하기에 기술되고, 결과가 표 18에서 제시된다. 표 19는 테스트된 AlbudAb ILF에서 사용된 링커 서열을 요약한다. 비아코어™ 검정으로 결정된 동역학 결합 데이터가 표 20에서 제공된다.

[0394]

상청액 내의 dAb의 검출을 위한 인간 CD40 CHO 세포 ELISA:

[0395]

안정적으로 형질감염된 인간 CD40 발현 CHO-DG44 세포 또는 천연 CHO-DG44 세포 (양쪽 모두 BMS)를 0.25% 트립신 EDTA를 사용하여 세포 배양 플라스크로부터 떼어내고, 100,000개의 세포/웰을 96웰 조직 배양 처리 플레이트 (눈크) 내로 성장 배지에 시딩하였다. 37°C, 5% CO₂의 습식 대기에서 밤새 세포를 부착시켰다. 검정일에, 세포 시트를 PBS로 세정한 후, 2% 파라포름알데히드 (시그마-알드리치)로 20분 동안 고정시켰다. 고정 후, 세포 시트를 다시 PBS로 세정하였고, PBS 내의 15% 소 태아 혈청 (FBS, PAA)으로의 1시간 차단 단계가 이어졌다. 플레이트를 1번 더 세정한 후, 100 µl/웰의 dAb 상청액을 첨가하고, 2시간 동안 실온에서 인큐베이션하였다. dAb 상청액을 세포와 함께 인큐베이션한 후, 플레이트를 세정하고, dAb가 V_H 도메인인지 또는 V_L 도메인인지에

따라 양고추냉이 퍼옥시다제 (HRP)가 접합된 항-단백질 A 또는 L의 인큐베이션으로 dAb 결합을 검출하였다. 1M HCl 용액으로의 중화 후 450 nm에서 스펙트라맥스 M5[®] 플레이트 판독기 (몰레큘러 디바이시스)를 사용하여 흡광도 신호를 측정하였다.

[0396] **ICAM-1 상향조절 세포 검정:**

[0397] 안정적으로 형질감염된 인간 CD40L 발현 COS 세포를 베르센 (인비트로젠)을 사용하여 세포 배양 플라스크로부터 떼어냈다. 20,000개의 세포/웰을 벽은 흑색이고 바닥은 투명한 96웰 하이바인드 플레이트 (코닝, 영국) 내로 검정 완충제 (페놀 레드가 없는 RPMI 1640 (시그마-알드리치, 영국) + 1% 페니실린/스트렙토마이신 + 10% FBS 골드(Gold) (양쪽 모두 PAA 래버러토리즈(PAA Laboratories), 영국)) 내에 시딩하였다. 세포를 밤새 37°C, 5% CO₂의 습식 대기에서 부착시켰다. 다음날, 부착되지 않은 세포를 함유하는 소모된 검정 완충제에 100 μ l의 신선한 검정 완충제를 보충하였다. 여기에, 20,000개의 RAMOS 세포/웰을 회석물 범위의 dAb에 더하여 검정 완충제 내에 첨가하였다. 검정 플레이트를 추가로 24시간 동안 37°C, 5% CO₂의 습식 대기로 돌려보냈다. 음성 대조군 웰의 경우에는, RAMOS 세포를 첨가하지 않았다. COS 세포의 세포 표면 상의 CD40L에 대한 노출에 반응한 RAMOS 세포의 세포 표면 상의 ICAM-1 상향조절을 억제하는 dAb의 능력을 0.5 μ g/ml 마우스 항 인간 ICAM-1 항체 (R&D 시스템즈(R&D systems)) 및 0.2 μ g/ml 염소 항 마우스 알렉사 플루오르 647 (인비트로젠, 몰레큘러 프로브즈, 영국)의 첨가에 의해 평가하였다. 빛의 부재 하에서의 3시간 인큐베이션 기간 후에, AB8200 세포 검출 플랫폼 (어플라이드 바이오시스템즈)에 의해 측정되는 바와 같이 상대적인 형광을 검출하였다.

[0398] **혈청 알부민에 결합하는 것의 인라인 융합 (ILF) 동역학의 분석**

[0399] 비아코어™ 3000 기구 (GE 헬스케어)를 사용하여 인간 및 시노물구스 혈청 알부민에 대한 항-CD40-A1budAb ILF의 결합 동역학을 분석하였다. 약 400 반응 단위 (RU)의 인간 혈청 알부민 (HSA) 또는 시노물구스 혈청 알부민 (CSA)을 아민 커플링 키트(Amine Coupling Kit) (GE 헬스케어)를 사용하여 CM5 비아코어™ 칩의 유동 셀 상에 고정하였다. 어떠한 리간드도 고정되지 않은 제2 유동 셀이 인라인 참조를 위한 기준 유동 셀로서의 역할을 하였다. 각각의 분석할 dAb의 적합한 일련의 배가 회석물을 HBS-EP 완충제 (0.01 M HEPES pH 7.4 + 0.15 M NaCl, 3 mM EDTA 및 0.005% v/v 계면활성제 P20, GE 헬스케어)에서 제조하였다. 200 μ l의 각각의 ILF를 기구의 KINJECT 기능을 사용하여 이중으로 주입하였다. 일련의 혈청 알부민이 고정된 유동 셀 및 기준 유동 셀을 가로질러 주입하였고, 이때 기준 셀로부터의 신호를 인라인으로 차감하였다. 25°C 및 40 μ l/분의 HBS-EP 유속으로 실험을 수행하였다. 각각의 주입을 완료한 후, dAb를 120초 동안 완충제 내에서 리간드로부터 해리시키고 나서, 10 mM 글리신 pH 2.0의 10 μ l 주입으로 재생시켰다. HBS-EP 완충제 블랭크 (분석물을 함유하지 않음)의 기준 주입물을 동일한 조건 하에 또한 주입하여, 각각의 분석물 트레이스로부터의 차감을 위한 제2 기준물로서의 역할을 하게 하였다. 비아이벨류에이션 4.1 소프트웨어 (GE 헬스케어)를 사용하여 기준 유동 셀 트레이스 및 완충제 블랭크 트레이스 양쪽 모두를 각각의 분석물 트레이스로부터 차감하였다. 동일한 소프트웨어를 사용하여, 일련의 분석물 회석물 트레이스의 회합 및 해리 단계에 대한 1:1 (랭뮤어) 동역학 모델의 동시적인 포괄적 피트를 수행하였다. 이러한 모델로 상호작용의 회합 및 해리 속도 상수 (각각 k_a 및 k_d) 및 평형 해리 상수 (K_D)가 산출되었다. 이러한 파라미터 값들이 표 20에서 제시된다.

표 18

활성 검정

DMS 번호	N-말단 dAb	링크	C-말단 dAb	CHO-CD40 세포 RBA EC ₅₀ (nM)		ICAM-1 세포 검정 EC ₅₀ (nM)	
				0.1% BSA	50 μM HSA	10% 소 혈청	10% 인간 혈청
DMS0654	BMS3h-56-201	AST	DOM7h-11-3	15	8.6		
DMS0655	BMS3h-56-201	AST	DOM7h-11-87	6.3	2.7		
DMS0656	BMS3h-56-258	AST	DOM7h-11-3	11.8	26.8		
DMS0657	BMS3h-56-258	AST	DOM7h-11-87	6.8	16.6		
DMS0658	DOM7h-11-3	TVAAPS	BMS3h-56-201	12.2	9.1		
DMS0659	DOM7h-11-87	TVAAPS	BMS3h-56-201	7.2	3.3		
DMS0660	DOM7h-11-3	TVAAPS	BMS3h-56-258	21.8	13.1		
DMS0661	DOM7h-11-87	TVAAPS	BMS3h-56-258	4.1	5.7		
DMS0662	DOM7h-11-90	TVAAPS	BMS3h-56-201			33.5	>1000
DMS0663	DOM7h-11-86	TVAAPS	BMS3h-56-201			21.4	>1000
DMS0664	DOM7h-11-69	TVAAPS	BMS3h-56-201			16.5	>1000
DMS0677	DOM7h-11-90	TVA	BMS3h-56-258			21.7	20.35
DMS0679	DOM7h-11-90	G ₄ S	BMS3h-56-258			21.7	39.2

[0400]

DMS 번호	N-말단 dAb	링크	C-말단 dAb	CHO-CD40 세포 RBA EC ₅₀ (nM)		ICAM-1 세포 검정 EC ₅₀ (nM)	
				0.1% BSA	50 μM HSA	10% 소 혈청	10% 인간 혈청
DMS0680	DOM7h-11-90	(G ₄ S) ₃	BMS3h-56-258			39.3	74.2
DMS0681	DOM7h-11-90	(G ₄ S) ₅	BMS3h-56-258			43.6	53.3
DMS0682	BMS3h-56-258	TVA	DOM7h-11-90			10.2	94.8
DMS0683	BMS3h-56-258	ASTSGPS	DOM7h-11-90			32.4	50.9
DMS0684	BMS3h-56-258	G ₄ S	DOM7h-11-90			37.9	74.3
DMS0685	BMS3h-56-258	(G ₄ S) ₃	DOM7h-11-90			31.9	62.4
DMS0686	BMS3h-56-258	(G ₄ S) ₅	DOM7h-11-90			48.3	66.6

[0401]

표 19

대표적인 링크 서열

AST	서열 5
TVAAPS	서열 6
TVA	서열 7
GGGGS	서열 1207
(GGGGS) ₃	서열 1208
(GGGGS) ₅	서열 1209
ASTSGPS	서열 8

[0402]

표 20

비아코어™ 분석

DMS 번호	N-말단 dAb	링크 (서열 6으로 개시된 "TVAAPS"	C-말단 dAb	인간 혈청 알부민			시노 혈청 알부민		
				k _a (1/Ms) ×10 ⁻⁶	k _d (1/s) ×10 ³	K _D (nM)	k _a (1/Ms) ×10 ⁻⁶	k _d (1/s) ×10 ³	K _D (nM)
DMS0659	DOM7h-11-87	TVAAPS	BMS3h-56-201	0.85, 2.85, 2.6	1.17, 1.69, 1.2	1.37, 0.60, 0.45	0.85, 2.79, 2.9	2.37, 3.37, 2.4	2.79, 1.21, 0.83
DMS0662	DOM7h-11-90	TVAAPS	BMS3h-56-201	1.1, 1.19	1.33, 1.47	1.21, 1.23	1.01, 1.10	2.52, 2.66	2.5, 2.42
DMS0663	DOM7h-11-86	TVAAPS	BMS3h-56-201	1.25, 1.32	1.40, 1.60	1.12, 1.21	1.18, 1.18	2.81, 2.96	2.38, 2.52
DMS0664	DOM7h-11-69	TVAAPS	BMS3h-56-201	2.5, 0.93	1.42, 1.49	0.57, 1.59	2.51, 0.92	2.73, 2.72	1.09, 2.97

[0403]

[0404]

표 21은 CD40 및 HSA 또는 CSA에 특이적으로 결합할 수 있는 대표적인 AlbuAb ILF의 아미노산 서열을 열거한다. 각각의 ILF의 명칭에서 특정 링크 서열이 확인된다: "GxS"는 링크에 "x"개의 글리신 잔기에 이어지

는 세린이 있다는 것을 의미하고, "(GxS)y"는 링커에 y개의 GxS 반복 단위가 있다는 것을 의미한다. 표 22는 표 21에 열거된 ILF 서열을 코딩하는 대표적인 핵산을 개시한다. 업계에 공지된 바와 같이, 다중 코돈이 동일한 아미노산을 코딩할 수 있다. 따라서, 단백질 서열을 코딩하는 핵산 서열들은 코돈 축중성이 있는 핵산들을 포함한다.

표 21

이중 특이성 dAb 아미노산 서열

(표 21은 각각 서열 5-7, 1207-1209 및 8로 개시된 "AST", "TVAAPS", "TVA", "G4S", "(G4S)3", "(G4S)5", 및 "ASTSGPS"를 개시한다)

DMS0654 BMS3h-56-201-AST-DOM7h-11-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTIVTVSSAS
TDIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILWNSRLQSGV
PSRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKEIKR (서열
1210)

DMS0655 BMS3h-56-201-AST-DOM7h-11-87
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTIVTVSSAS
TDIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILAFSRLQSGV
PSRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHHTTFGQGTKEIKR (서열
1211)

DMS0656 BMS3h-56-258-AST-DOM7h-11-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTIVTVSSAS
TDIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILWNSRLQSGV
PSRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKEIKR (서열
1212)

DMS0657 BMS3h-56-258-AST-DOM7h-11-87
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTIVTVSSAS
TDIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILAFSRLQSGV

PSRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHHTTFGQGTKEIKR (서열
1213)

DMS0658 DOM7h-11-3-TVAAPS-BMS3h-56-201
DIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILWNSRLQSGVP
SRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTIVTVSS (서열
1214)

DMS0659 DOM7h-11-87-TVAAPS-BMS3h-56-201
DIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILAFSRLQSGVP
SRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHHTTFGQGTKEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTIVTVSS (서열
1215)

DMS0660 DOM7h-11-3-TVAAPS-BMS3h-56-258
DIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILWNSRLQSGVP
SRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTIVTVSS (서열
1216)

DMS0661 DOM7h-11-87-TVAAPS-BMS3h-56-258
DIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILAFSRLQSGVP
SRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHHTTFGQGTKEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTIVTVSS (서열
1217)

DMS0662 DOM7h-11-90-TVAAPS-BMS3h-56-201
DIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILAFSRLQSGVP
SRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTIVTVSS (서열
1218)

DMS0663 DOM7h-11-86-TVAAPS-BMS3h-56-201
DIQTQSPSSLSASVGDRTVITCRASRPISGTTLSWYQQKPKGAPKLLILAFSRLQSGVP
SRFGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTIVTVSS (서열
1219)

DMS0664 DOM7h-11-69-TVAAPS-BMS3h-56-201

[0405]

[0406]

DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISSLPEDFATYYCAQAGVHPTTFGQGTKVEIKRTVAAPSEVQL
LES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQCTRITYYADS
VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFYFHEWGQGT LVTVSS (서열
1220)

DMS0667 DOM7h-11-3-TVAAPS-BMS3h-38-240
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILWNSRLQSGVP
SRFSGSGSGTDFTLTISSLPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
LES GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTYYADS
VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSS (서열
1221)

DMS0668 BMS3h-38-240-AST-DOM7h-11-3
EVQLLES GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSSAS
TDIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILWNSRLQSGV
PSRFSGSGSGTDFTLTISSLPEDFATYYCAQAGTHPTTFGQGTKVEIKR (서열
1222)

DMS0669 DOM7h-14-10-TVAAPS-BMS3h-38-240
DIQMTQSPSSLSASVGDVRTITCRASQWIGSLSWMYQQKPGKAPKLLIMWRSSLSQSGVP
SRFSGSGSGTDFTLTISSLPEDFATYYCAQGLRHPTTFGQGTKVEIKRTVAAPSEVQL
LES GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTYYADS
VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSS (서열
1223)

DMS0670 BMS3h-38-240-AST-DOM7h-14-10
EVQLLES GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSSAS
TDIQMTQSPSSLSASVGDVRTITCRASQWIGSLSWMYQQKPGKAPKLLIMWRSSLSQSGV
PSRFSGSGSGTDFTLTISSLPEDFATYYCAQGLRHPTTFGQGTKVEIKR (서열
1224)

DMS0671 BMS3h-38-235-AST-DOM7h-11-3
EVQLLAS GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSSAS
TDIQMTQSPSSLSASVGDVRTITCRASRIGTMLSWMYQQKPGKAPKLLILWNSRLQSGV
PSRFSGSGSGTDFTLTISSLPEDFATYYCAQAGTHPTTFGQGTKVEIKR (서열
1225)

DMS0672 BMS3h-38-235-AST-DOM7h-11-90
EVQLLAS GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSSAS
TDIQMTQSPSSLSASVGDVRTITCRASRIGTMLSWMYQQKPGKAPKLLILAFSRLQSGV
PSRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (서열
1226)

DMS0674 DOM7h-11-3-TVAAPS-BMS3h-38-235
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILWNSRLQSGVP
SRFSGSGSGTDFTLTISSLPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
LAS GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTYYADS
VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSS (서열
1227)

DMS0675 DOM7h-11-90-TVAAPS-BMS3h-38-235
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
LAS GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLWVSAISRNGYSTYYADS
VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVTVSS (서열
1228)

DMS0677 DOM7h-11-90-TVA-BMS3h-56-258
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAEVQLLES
GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQCTRITYYADSVK
RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFYFHEWGQGT LVTVSS (서열
1229)

DMS0678 DOM7h-11-90-ASTSGPS-BMS3h-56-258
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRASTSGFSEVQ
LLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQCTRITYYAD
SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFYFHEWGQGT LVTVSS (서열
1230)

DMS0679 DOM7h-11-90-G4S-BMS3h-56-258
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGGSEVQLL
ES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQCTRITYYADSV
KGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFYFHEWGQGT LVTVSS (서열
1231)

DMS0680 DOM7h-11-90-(G4S)3-BMS3h-56-258
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGGSGGGGS
GGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQ
GTRTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFYFHEWGQGT LVT
VSS (서열 1232)

DMS0681 DOM7h-11-90-(G4S)5-BMS3h-56-258
DIQMTQSPSSLSASVGDVRTITCRASRPIGTMLSWMYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGGSGGGGS
GGGGSGGGGGGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGK

[0407]

[0408]

LERVSAINPQGTRTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYF
HEWGQGLVTVSS (서열 1233)

DMS0682 BMS3h-56-258-TVA-DOM7h-11-90
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERSVAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSSTV
ADIQMTQSPSSLSASVGDRTVITCRASRPITMLSWYQQKPKAPKLLILAFSRLQSGV
PSRFSGSGSDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (서열
1234)

DMS0683 BMS3h-56-258-ASTSGPS-DOM7h-11-90
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERSVAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSAS
TSGPSDIQMTQSPSSLSASVGDRTVITCRASRPITMLSWYQQKPKAPKLLILAFSRL
QSGVPSRFSGSGSDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (서열
1235)

DMS0684 BMS3h-56-258-G4S-DOM7h-11-90
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERSVAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSGG
GGSDIQMTQSPSSLSASVGDRTVITCRASRPITMLSWYQQKPKAPKLLILAFSRLQ
GVPSRFSGSGSDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (서열
1236)

DMS0685 BMS3h-56-258-(G4S)3-DOM7h-11-90
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERSVAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSGG
CGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCRASRPITMLSWYQQKPKAPK
LILAFSRLQSGVPSRFSGSGSDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVE
IKR (서열 1237)

DMS0686 BMS3h-56-258-(G4S)5-DOM7h-11-90
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERSVAINPQGTRTY
YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSGG
GGSGGGSGGGSGGGGSDIQMTQSPSSLSASVGDRTVITCRASRPITMLSWY
QQKPKAPKLLILAFSRLQSGVPSRFSGSGSDFTLTISNLQPEDFATYYCAQAGTHP
TTFGQGTKVEIKR (서열 1238)

DMS0688 DOM7h-11-90-TVAAPS-BMS3h-56-258
DIQMTQSPSSLSASVGDRTVITCRASRPITMLSWYQQKPKAPKLLILAFSRLQSGVP
SRFSGSGSDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
LESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERSVAINPQGTRTYADS
VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSS (서열
1239)

[0409]

표 22

이중 특이성 dAb를 코딩하는 폴리뉴클레오타이드

(표 22는 각각 서열 5-7, 1207-1209 및 8로 표시된 "AST", "TVAAPS", "TVA", "G4S",
"G4S)3", "G4S)5", 및 "ASTSGPS"를 제시한다)

DMS0654 BMS3h-56-201-AST-DOM7h-11-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGGGTCTC
TCCTGTGCAGCCTCCGGATTACACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGGGTACATACTAC
GCAGACTCCGTGAAGGCGCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCAAACTTCGG
TTTTACTTTACAGAGTGGGTGAGGAAACCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
ACTTGCCGGGCAAGTCTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACAGGG
AAAGCCCTAAGTCTCTGATCCTTTGGAAATCCCGTTTGCAAAAGTGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1240)

DMS0655 BMS3h-56-201-AST-DOM7h-11-87
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGGGTCTC
TCCTGTGCAGCCTCCGGATTACACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGGGTACATACTAC
GCAGACTCCGTGAAGGCGCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCAAACTTCGG
TTTTACTTTACAGAGTGGGTGAGGAAACCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
ACTTGCCGGGCAAGTCTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACAGGG
AAAGCCCTAAGTCTCTGATCCTTTGCTTTTCCCGTTTGCAAAAGTGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1241)

DMS0656 BMS3h-56-258-AST-DOM7h-11-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGGGTCTC
TCCTGTGCAGCCTCCGGATTACACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGGGTACATACTAC
GCAGACTCCGTGAAGGCGCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCAAACTTCGG
TTTTACTTTACAGAGTGGGTGAGGAAACCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
ACTTGCCGGGCAAGTCTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACAGGG
AAAGCCCTAAGTCTCTGATCCTTTGGAATTCCTGTTTGCAAAAGTGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1242)

[0410]

DMS0657 BMS3h-56-258-AST-DOM7h-11-87
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGGGTCTC
TCCTCTGCAGCCTCCGGATTCACTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGCTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAAATCCAAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTCGGTGCCAGGACACCGGGTATATTACTGTGCAAACTTCGG
TTTACTTTACAGATGGGGTCAGGGAACCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCCATC
ACTTGGCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTAACGAGAAACCCAGGG
AAAGCCCCAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCAGCT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACTGAA
GATTTTGCTACGTACTACTGTGGCAGGCTGGGACGATCATACGACGTTCCGCCAAGGG
ACCAAGGTGSAATCAACGG (서열 1243)

DMS0658 DOM7h-11-3-TVAAPS-BMS3h-56-201
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTTGGATTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGACAGGCTCCAGGGAAGGGCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGGTACATCTACGACACTCCGTGAAGGGC
CGGTTCAACATCTCCCGGACAAATCCAAAGAACCGTGTATCTGCAAAATGAACAGCTG
CGTGCCAGGACACCGGGTATATTACTGTGCGAAACTTCGGTTTACTTTACGAGGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1244)

DMS0659 DOM7h-11-87-TVAAPS-BMS3h-56-201
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGCGCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGGTACATCTACGACACTCCGTGAAGGGC
CGGTTCAACATCTCCCGGACAAATCCAAAGAACCGTGTATCTGCAAAATGAACAGCTG
CGTGCCAGGACACCGGGTATATTACTGTGCGAAACTTCGGTTTACTTTACGAGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1245)

DMS0660 DOM7h-11-3-TVAAPS-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTTGGAAATCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGCGCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGGTACATCTACGACACTCCGTGAAGGGC
CGGTTCAACATCTCCCGGACAAATCCAAAGAACCGTGTATCTGCAAAATGAACAGCTG
CGTGCCAGGACACCGGGTATATTACTGTGCGAAACTTCGGTTTACTTTACGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1246)

GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1246)

DMS0661 DOM7h-11-87-TVAAPS-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGCGCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGGTACATCTACGACACTCCGTGAAGGGC
CGGTTCAACATCTCCCGGACAAATCCAAAGAACCGTGTATCTGCAAAATGAACAGCTG
CGTGCCAGGACACCGGGTATATTACTGTGCGAAACTTCGGTTTACTTTACGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1247)

DMS0662 DOM7h-11-90-TVAAPS-BMS3h-56-201
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCCGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGCGCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGGTACATCTACGACACTCCGTGAAGGGC
CGGTTCAACATCTCCCGGACAAATCCAAAGAACCGTGTATCTGCAAAATGAACAGCTG
CGTGCCAGGACACCGGGTATATTACTGTGCGAAACTTCGGTTTACTTTACGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1248)

DMS0663 DOM7h-11-86-TVAAPS-BMS3h-56-201
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCCGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGCGCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGGTACATCTACGACACTCCGTGAAGGGC
CGGTTCAACATCTCCCGGACAAATCCAAAGAACCGTGTATCTGCAAAATGAACAGCTG
CGTGCCAGGACACCGGGTATATTACTGTGCGAAACTTCGGTTTACTTTACGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1249)

DMS0664 DOM7h-11-69-TVAAPS-BMS3h-56-201
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGGCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGGTGCATCTACGACGTTCCGCCAA
GGGACCAAGGTGAAATCAAACTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGAGGCTTGGTACAGCTTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGATTATGAGATGTGGTGGTCCGCGCAGGCTCCAGGGAAGGGTCTAGAG

[0411]

[0412]

CGGGTCTCAGCTATTAAATCCGAGGGTACGGGTACATACTACGCAGACTCCGTTGAAGGGC
CGGTTCCACCATCTCCCAGCAATTTCCAAGAACCGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGACACCGGGTATATTAATCTGTGCAAACTTCGGTTTATCTTTCAGGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1250)

DMS0667 DOM7h-11-3-TVAAPS-BMS3h-38-240
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCACTCTGTAGSAGACCGGTGTCAAC
ATCACTTGCCGGGCAAGTCTCGGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGCCCCCTAAGCTCTGATCCTTTGGAAATCCCGTTTGCAAAAGTGGGTGCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTSCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAACGTACGGTGGTGCACCATCTGAAGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGGCTCCGGA
TTCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGSGAAGGGCTCTAGAG
TGGGTCTCAGCTATTAGTAGSAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTCCACCATCTCCCAGCAATTTCCAAGAACCGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1251)

DMS0668 BMS3h-38-240-AST-DOM7h-11-3
GAGGTGCAGCTGTTGGACTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTCCCGCAGCCTCCGATTACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCT
CCAGSGAAGGGTCTAGAGTGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAAAATTCGAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCG
TTTCGTTATGACTACTGGGTGAGGGAACCTGGTCAACGCTCTGAGCGCTAGCACGCAC
ATCCAGATGACCAAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGGTGTACCATC
ACTTGCCGGGCAAGTCTGCGATTGGGACGACGTTAAGTTGGTACCAAGCAAAACAGGG
AAAGCCCCCTAAGCTCCTGATCCTTTGGAAATCCCGTTTGCAAAAGTGGGGTCCCATCAGCT
TTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1252)

DMS0669 DOM7h-14-10-TVAAPS-BMS3h-38-240
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCACTCTGTAGGAGACCGGTGTCAAC
ATCACTTGCCGGGCAAGTCAAGTGGATTGGGTCTCAGTTATCTTGGTACCAGCAGAAACCA
GGGAAGCCCCCTAAGCTCCTGATCATGTGGCGTTCCTCGTTGCAAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCT
GAGATTTTGCTACGTACTACTGTGCTCAGGGTTGAGGCATCTTACAGAGCTTGGGCCAA
GGGACCAAGTGGAAATCAAGTACGTTGGGTGCACCATCTGAGCTGAGCTGTTGGAG
TCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGSGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTCCACCATCTCCCAGCAATTTCCAAGAACCGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (서열 1253)

DMS0670 BMS3h-38-240-AST-DOM7h-14-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAAAATTCGAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCG

TTTCGTTATGACTACTGGGGTCAAGGAACCTGGTCAACGCTCTCGACGCTAGCACCCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGGTGTCAACATC
ACTTGCCGGGCAAGTCAAGTGGATTGGGTCTCAGTTATCTTGGTACCAGCAGAAACAGGG
AAAGCCCCCTAAGCTCCTGATCATGTGGCGTTCCTCGTTGCAAAAGTGGGGTCCCATCAGCT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCTCAGGGTTGAGGCACTCCTAAGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1254)

DMS0671 BMS3h-38-235-AST-DOM7h-11-3
GAGGTGCAGCTGTTGGGCTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGSGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAAAATTCGAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCG
TTTCGTTATGACTACTGGGGTCAAGGAACCTGGTCAACGCTCTCGACGCTCTCAACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGGTGTCAACATC
ACTTGCCGGGCAAGTCTGCGATTGGGACGACGTTAAGTTGGTACCAAGCAAAACAGGG
AAAGCCCCCTAAGCTCCTGATCCTTTGGAAATCCCGTTTGCAAAAGTGGGGTCCCATCAGCT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1255)

DMS0672 BMS3h-38-235-AST-DOM7h-11-90
GAGGTGCAGCTGTTGGGCTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAAAATTCGAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCG
TTTCGTTATGACTACTGGGGTCAAGGAACCTGGTCAACGCTCTCGACGCTCTCAACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGGTGTCAACATC
ACTTGCCGGGCAAGTCTGCGATTGGGACGACGTTAAGTTGGTACCAAGCAAAACAGGG
AAAGCCCCCTAAGCTCCTGATCCTTTGCTTTTCCCGTTTGCAAAAGTGGGGTCCCATCAGCT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAATCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAAGGG
ACCAAGTGGAAATCAACGG (서열 1256)

DMS0674 DOM7h-11-3-TVAAPS-BMS3h-38-235
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCACTCTGTAGGAGACCGGTGTCAAC
ATCACTTGCCGGGCAAGTCTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAGCCCCCTAAGCTCCTGATCCTTTGGAATCCCGTTTGCAAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGACGTTCCGCCAA
GGGACCAAGTGGAAATCAACGGACCGTGGCGGCCCGAGTGAAGTGCAGCTGTTGGCG
TCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGSGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGSAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTCCACCATCTCCCAGCAATTTCCAAGAACCGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGATACCGGGTATATTAATCTGTGGGAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCTGGTCAACGCTCTCCAGC (서열 1257)

DMS0675 DOM7h-11-90-TVAAPS-BMS3h-38-235
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCACTCTGTAGGAGACCGGTGTCAAC
ATCACTTGCCGGGCAAGTCTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA

[0413]

[0414]

GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGTCCCATCA
CGTTTCAGTGGCAGTGATCTCGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAAACGGACCGTGGCGGCGCCGATGAGTGCACATGTTGGCG
TCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCCTGCGAGCCTCGGA
TTCACCTTTGAGGAGGAGAGATGATTTGGTCCCGCAGGCTCCAGGGAAGGCTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTCAACATCTCCCGCGACAATTCGAAGAACACGCTGTATCTGCAAAAGAAGAGCCTG
CGTCCGAGGATACCGCGTATATTACTGTGGGAAAGAGCGTTTCGTTATGACTACTGG
GGTCAGGGAACCTGGTACCGTCTCCAGC (서열 1258)

DMS0677 DOM7h-11-90-TVA-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAAACGCGGCTAGCACCTCAGTCCATCGGAGGTGCAGCTGTG
GAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCCTGTGCGACCTCC
GGATTCACTTTCCGGATTATGAGATGTGGTGGGTCCGCGCAGGCTCCAGGGAAGGTTCTA
GAGCGGGTCTCAGCTATTAAATCCGCGAGGTTACGCTACATACTACGCAGACTCCGTGAAG
GGCGGTTTCAACATCTCCCGGACAATTCGAAGAACACGCTGTATCTGCAAAAGAAGAGC
GTGGTCCGAGGACACCGCGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAAGAG
TGGGTCAGGGAACCTGGTCAACGCTCTCCAGC (서열 1259)

DMS0678 DOM7h-11-90-ASTSGPS-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAAACGCGGCTAGCACCTCAGTCCATCGGAGGTGCAGCTGTG
GAGTCTGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCCTGTGCGACCTCC
GGATTCACTTTCCGGATTATGAGATGTGGTGGGTCCGCGCAGGCTCCAGGGAAGGTTCTA
GAGCGGGTCTCAGCTATTAAATCCGCGAGGTTACGCTACATACTACGCAGACTCCGTGAAG
GGCGGTTTCAACATCTCCCGGACAATTCGAAGAACACGCTGTATCTGCAAAAGAAGAGC
GTGGTCCGAGGACACCGCGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAAGAG
TGGGTCAGGGAACCTGGTCAACGCTCTCCAGC (서열 1260)

DMS0679 DOM7h-11-90-G4S-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAAACGGGTTGGAGTGGCTCTGAGGTGCAGCTGTTGGAGTCT
GGGGAGGCTTGGTACAGCCTCGGGGGTCCCTGCGTCTCCTGTGCGACCTCCGGATTCT
ACCTTTCCGGATTATGAGATGTGGTGGGTCCCGCAGGCTCCAGGGAAGGTTCTAGAGCGG
GTCTCAGCTATTAAATCCGCGAGGTTACGCTACATACTACGCAGACTCCGTGAAGGGCCGG
TTCACATCTCCCGGACAATTCGAAGAACACGCTGTATCTGCAAAAGAAGAGCCTGCGT
GCGGAGGACACCGCGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAAGAGTGGGGT
CAGGGAACCTGGTCAACGCTCTCCAGC (서열 1261)

[0415]

DMS0680 DOM7h-11-90-(G4S) 3-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAAACGGGTTGGAGTGGCTCTGAGGTGCGGTTAGCGGCGGA
GGCGGTTCAAGGTGCAGCTTGGAGTCTGGGGAGGCTTGGTACAGCTGGGGGGTCC
CTGCGTCTCCTGTGCGACCTCCGGATTCACTTTCCGGATTATGAGATGTGGTGGGTCT
CGCCAGGCTCCAGGGAAGGTTCTAGAGCGGGTCTCAGCTATTAAATCCGCGAGGTTACGGGT
ACATACTACGCAGACTCCGTGAAGGGCCGGTTCAACATCTCCCGGACAATTCGAAGAAC
ACGCTGTATCTGCAAAAGAAGAGCCTGCGTCCGAGGACACCGCGTATATTACTGTGCG
AAACTTCCGTTTACTTTTCAAGAGTGGGGTCCAGGGAACCTGGTCAACGCTCTCCAGC (서열
1262)

DMS0681 DOM7h-11-90-(G4S) 5-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAATCAAACGGGTTGGAGTGGCTCTGAGGTGCGGTTAGCGGCGGT
GGCGGTTCAAGTGGCGGAGGTTCTGAGGCGGTTGGATCTGAGGTGCAGCTGTTGGAGTCT
GGGGAGGCTTGGTACAGCCTCGGGGGTCCCTGCGTCTCCTGTGCGACCTCCGGATTCT
ACCTTTCCGGATTATGAGATGTGGTGGTCCGCGAGGCTCCAGGGAAGGTTCTAGAGCGG
GTCTCAGCTATTAAATCCGCGAGGTTACGCTACATACTACGCAGACTCCGTGAAGGGCCGG
TTCACATCTCCCGGACAATTCGAAGAACACGCTGTATCTGCAAAAGAAGAGCCTGCGT
GCGGAGGACACCGCGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAAGAGTGGGGT
CAGGGAACCTGCTCAACGCTCTCCAGC (서열 1263)

DMS0682 BMS3h-56-258-TVA-DOM7h-11-90
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTC
TCTGTGCGACCTCCCGATTCACTTTCCGGATTATGAGATGTTGGTGGTCCGCCAGGCT
CCAGGGAAGGCTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGTTACGCTACATACTAC
GCAGACTCCGTGAAGGSCCGGTTCAACATCTCCGCGACAATTCGAAGAACACGCTGTAT
CTGCAAATGAACAGGCTTGGTGGCGGAGACACCGGSTATATTACTGTGCGAAACTTCCG
TTTACTTTTCAAGAGTGGGTCCGCGAAGCCCTCAACGTTTCCGAGCAGGTTGGGAC
ATCCAGATGACCCAGTCTCCATCCCTGCTGCTGATCTGTAGGAGCCTCTCAGCATC
ACTTTCGCGGCAAGTCTGATCTGGGACAGTCTAAGTTGGTACCAGCAGAAACAGGG
AAGCCCTTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAA
GATTTTGTCTACTACTACTGCGCGCAGGCTGGGACGCATCTACGAGCTTCGCCCAAGGG
ACCAAGGTGGAATCAAACGG (서열 1264)

DMS0683 BMS3h-56-258-ASTSGPS-DOM7h-11-90
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTC
TCTGTGCGACCTCCCGATTCACTTTCCGGATTATGAGATGTTGGTGGTCCGCCAGGCT
CCAGGGAAGGCTCTAGAGCGGTTCTCAGCTATTAAATCCGAGGTTACGCTACATACTAC
GCAGACTCCGTGAAGGSCCGGTTCAACATCTCCGCGACAATTCGAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
TTTACTTTTCAAGAGTGGGTCCGCGAAGCCCTGGTCAACGCTCCGAGCGTAGCACTCA
GGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTCTAGGAGAC
CGTGTCAACATCACTTCCCGGGCAAGTCCGATGGGACGATGTTAAGTTGGTACCAG
CAGAAACAGGGAAGCCCTTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGG

[0416]

GTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAAT
CTGCACACCTGAAGATTTCCTACGTACTACTGCGCGCAGGCTGGGACGATCTCAGACG
TTCGGCCAAAGGACCAAGGTGGAATCAAACGG (서열 1265)

DMS0684 BMS3h-56-258-G4S-DOM7h-11-90
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCT
CCAGGGAAGGGCTTAGAGCGGCTCTCAGCTATTAAATCCGAGGGTACGGCTACATACTAC
GCAGACTCCGTTGAAGGGCGGTTACCATCTCCCGGACAAATCCAGAAACAGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAACTTCCG
TTTTACTTTACAGCTGGGTTCAGGAAACCTGGTACCGTCTCGAGCGGTGGAGCGGC
TCTGACATCCAGATCAACCACTCCATCTCCCTGCTGTCATCTGTAGGAGACCGGTCTC
ACCATCACTTGC CGGCAAGTCTCGGATTGGGACGATTTAAGTTGGTACAGCAGAAA
CCAGGGAAGCCCTTAAGCTCCTGATCCTTGTCTTTTCCCGTTTGCAAGTGGGGTCCCA
TCACGTTTCAGTGGCAGTGGATCTGGACAGATTTCACCTCACCATCAGCAATCTGCAA
CTGAAGATTTCCTACGTACTACTGCGCGCAGGCTGGGACGATCTCAGACGTTTCGGC
CAAGGACCAAGGTGGAATCAAACGG (서열 1266)

DMS0685 BMS3h-56-258-(G4S)3-DOM7h-11-90
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCT
CCAGGGAAGGGCTTAGAGCGGCTCTCAGCTATTAAATCCGAGGGTACGGCTACATACTAC
GCAGACTCCGTGAAGGGCGGTTACCATCTCCCGGACAAATCCAGAAACAGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAACTTCCG
TTTTACTTTACAGCTGGGTTCAGGGAACCTGGTACCGTCTCGAGCGGTGGAGTGGC
TCTGGAGGTGGCGGTAGCGGCGGTGGCGGTTACAGACTCCAGATGACCCAGTCTCCATCC
TCCCTGCTCGCATCTGTAGGAGACCGTGTACCATCACTTCCGCGGCAAGTCTGCGGATT
GGGACGATGTAAAGTTGGTACAGCAGAAACAGGGAAGCCCTTAAGCTCCTGATCCTT
GCTTTTCCCGTTTGCAAGTGGGGTCCCAACAGCTTCAGTGGCAGTGGATCTGGGACA
GATTTCACTCTACCATCAGCAATCTGCAACCTGAAGATTTCCTACGTACTACTGCGCG
CAGGCTGGGACGATCTCAGACGTTTCGGCCAAAGGACCAAGGTGGAATCAAACGG (서열
1267)

DMS0686 BMS3h-56-258-(G4S)5-DOM7h-11-90
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCT
CCAGGGAAGGGCTTAGAGCGGCTCTCAGCTATTAAATCCGAGGGTACGGCTACATACTAC
GCAGACTCCGTGAAGGGCGGTTACCATCTCCCGGACAAATCCAGAAACAGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACCCGCGGTATATTACTGTGCGAACTTCCG
TTTTACTTTACAGCTGGGTTCAGGGAACCTGGTACCGTCTCGAGCGGTGGAGTGGC
TCTGGAGGTGGCGGTAGCGGCGGTGGCGGTTACAGGTGGCGGAGTTCTGGAGCGGTGGA
TCTGACATCCAGATCAACCACTCCATCTCCCTGCTGTCATCTGTAGGAGACCGGTCTC
ACCATCACTTGC CGGCAAGTCTCGGATTGGGACGATTTAAGTTGGTACAGCAGAAA
CCAGGGAAGCCCTTAAGCTCCTGATCCTTGTCTTTTCCCGTTTGCAAGTGGGGTCCCA
TCACGTTTCAGTGGCAGTGGATCTGGACAGATTTCACCTCACCATCAGCAATCTGCAA
CTGAAGATTTCCTACGTACTACTGCGCGCAGGCTGGGACGATCTCAGACGTTTCGGC
CAAGGACCAAGGTGGAATCAAACGG (서열 1268)

DMS0688 DOM7h-11-90-TVAAPS-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACCGGTGTACCC
ATCACTTCCCGGCAAGTCTCGGATTGGGACGATTTAAGTTGGTACAGCAGAAACCA
GGGAAGCCCTTAAGCTCTCATCTGCTTTTCCCGTTTGCAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAATCTGCAACCT

GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGATCTCAGACGTTTCGGCCAA
GGGACCAAGGTGGAATCAAACGGACCGTAGCGCGCCGAGTGAGTGCAGCTGTGGAG
TCTGGGGGAGGCTTGGTACAGCTCGGGGTCCTTCCGCTCTCTCTGTGCAGCTCCGGA
TTCACCTTTCGGGATTATGAGATGTGGTGGGTCCCGCAGGCTCCAGGGAAGGGCTAGAG
CGGCTCTCAGCTATTAAATCCGAGGTTACCGGTACATACGACAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGGACAAATCCAGAAACAGCTGTATCTGCAAAATGAACAGCCTG
CGTCCGAGGACACCGGTTATATTACTGTGCGAACTTCCGTTTACTTTACAGAGTGG
GGTCAGGGAACCTGCTACCGTCTCCAGC (서열 1269)

실시예 8

항-시노물구스 CD40 dAb

인간 CD40에 특이적으로 결합하는 항체 폴리펩티드를 생성시키는 본원에 개시된 방법을 사용하여, 다른 종의 CD40에 특이적으로 결합하는 항체 폴리펩티드를 생성시킬 수 있다. 예를 들어, 항-시노물구스 (항-시노) CD40 항체 폴리펩티드를 본원에 개시된 방법을 사용하여 생산할 수 있다. 예를 들어, 항-인간 CD40 dAb와 동일한 초기/1차 스크리닝 및 친화도 성숙 계획을 사용하여 항-시노CD40 항체 폴리펩티드를 생성시킬 수 있다. 항-시노 CD40 dAb를 수득하는 방법이 개시되고, 항-시노CD40 dAb의 대표적인 예가 하기 표 23에서 제공된다.

ELISA RBA:

투명한 벽의 하이바인드 384웰 플레이트 (코닝, 영국)를 25 μ l의 카르보네이트 완충제 내의 1 μ g/ml 뉴트라비딘으로 밤새 4℃에서 코팅하였다. 다음날, 검정 플레이트를 0.1% 트윈 PBS 완충제로 세정하고, 1시간 동안 실온에서 PBS 내의 1% BSA로 차단하고, 다시 세정하였다. 과량의 세정 완충제를 제거한 후, 1 μ g/ml의 비오티닐화 인간 IZ-CD40L (BMS, 1.2 mg/ml 모액 농도) 25 μ l를 검정 플레이트와 함께 1시간 동안 실온에서 인큐베이션하였다. 동시에, 희석물 범위의 정제된 dAb 및 1 μ g/ml의 시노CD40 (BMS)를 1:1 비로 복합체를 이루게 하였다. 검정 플레이트를 세정한 후, dAb:시노 CD40 복합체를 검정 플레이트에서 부드럽게 진탕시키면서 실온에서 2시간 동안 인큐베이션하였다. 양고추냉이 퍼옥시다제 (HRP)-접합 항 인간 (Fc) 2차 항체 (시그마-알드리치, 영국)로 비오티닐화 CD40L에 대한 dAb 대 시노CD40의 경쟁적 결합을 검출하였다. 1M HCl로의 중화 후 450 nm에서 스펙트라맥스 M5e 플레이트 판독기 (몰레큘러 디바이시스)를 사용하여 흡광도 신호를 측정하였다.

AB8200 FMAT를 사용한 시노CD40 CHO 세포 RBA:

안정적으로 형질감염된 시노CD40-발현 CHO-DG44 세포 또는 천연 CHO-DG44 세포 (BMS)를 베르센 (인비트로젠)을 사용하여 세포 배양 플라스크로부터 떼어냈다. 40,000개의 세포/웰을 벽은 흑색이고 바닥은 투명한 96웰 하이바인드 플레이트 (코닝, 영국) 내로 0.1% BSA PBS 검정 완충제 + 희석물 범위의 dAb, 0.25 μ g/ml의 비오티닐화

인간 IZ-CD40L (BMS, 1.2 mg/ml 모액 농도), 및 0.25 µg/ml의 스트렙타비딘 알렉사 플루오르 647 (인비트로젠, 몰레큘러 프로브즈, 영국) 내에 시딩하였다. 혼합물을 빛의 부재 하에 6시간 동안 인큐베이션하였다. 인큐베이션 후, AB8200 세포 검출 플랫폼 (어플라이드 바이오시스템즈)에 의해 측정된 바와 같은 상대적인 형광을 사용하여 가용성 비오틴화 IZ-CD40L에 대한 dAb 대 시노CD40 CHO 세포의 경쟁적 결합을 평가하였다.

[0426] **CHO-hCD40L-구동 1차 인간 B 세포 증식:**

[0427] CHO 세포 (ATCC)를 인간 CD40L로 형질감염시켜, 세포 표면 상에 높은 수준의 CD40L을 발현하는 안정적인 세포주를 생성시켰다. CHO-CD40L 세포에 10,000 래드를 조사한 후, 인간 B 세포와 함께 인큐베이션하였다. 1×10^5 개의 편도선 인간 B 세포를 96웰 둥근 바닥 플레이트에서 200 µl/웰의 최종 부피로 다양한 적정도의 dAb 또는 모노클로날 항체와 같이 1×10^3 개의 CHO-CD40L 세포 (1:100 비의 CHO-CD40L:인간 B 세포)와 함께 인큐베이션하였다. 플레이트를 37°C에서 72시간 동안 인큐베이션한 후, 티미딘 (^3H ; 0.5 µci/웰)을 6시간 동안 첨가하였다. 티미딘 혼입을 기초로 B 세포 증식을 정량하였다. 달리 언급되지 않는 한, 10% 송아지 태아 혈청 (FCS)이 보충된 RPMI 배지에서 모든 검정을 수행하였다.

[0428] **가용성 IZ-hCD40L-구동 시노 비장 B 세포 증식:**

[0429] 시노몰구스 원숭이 비장으로로부터 단리된 1×10^5 개의 B 세포를 96웰 둥근 바닥 플레이트에서 200 µl/웰의 최종 부피로 다양한 적정도의 dAb 또는 mAb와 같이 0.5 µg/ml의 IZ-hCD40L과 함께 인큐베이션하였다. 플레이트를 37°C에서 72시간 동안 인큐베이션한 후, ^3H -티미딘 (µci/웰)을 6시간 동안 첨가하였다. 티미딘 혼입을 기초로 B 세포 증식을 정량하였다. 달리 언급되지 않는 한, 10% 송아지 태아 혈청 (FCS)이 보충된 RPMI 배지에서 모든 검정을 수행하였다.

표 23

클론	ELISA RBA (nM)	세포 RBA (nM)	B 세포 증식 검정 (EC50 nM)	
			인간	시노
BMS5c8				8,10,12,8,8
BMS3c-85	370		>7000, >7000	747, 2700, 7000, 7000
BMS3c-85-1	52, 8	12	2600, 1100	18, 39, 47
BMS3c-85-2	12, 4	4, 17	1800, 800	2, 5, 6, 1
BMS3c-85-3	7	23	>7000, >7000	33, 31, 21, 31
BMS3c-85-8	22	17.2	>7000, >7000	33, 33, 25
BMS3c-85-9	10		>7000, >7000	>70, >70, 104
BMS3c-85-21	11	18		24
BMS3c-85-24	8	13, 14		
BMS3c-85-25	62			
BMS3c-85-26	3		3300, 3900	>70, >70, 385
BMS3c-85-27	13	23		39
BMS3c-85-31	13	11, 9		
BMS3c-85-32	21	56		111
BMS3c-85-33	15	10, 21.3		17
BMS3c-85-34	48			
BMS3c-85-35	-	19, 1.5	>700	2
BMS3c-85-36	-	28		
BMS3c-85-37	-	71		
BMS3c-85-38	-	17		
BMS3c-85-47	-	2.9	>700	<2, 0.5
BMS3c-85-49	-	10	>700	3, 3
BMS3c-85-51	-	2.5	>700	3
BMS3c-85-52	-	8.5		
BMS3c-85-55	-	13.3, 6.7	>700	3, 3
BMS3c-85-56	-	수렴되지 않음		
BMS3c-85-57	-	13.8, 5.3	>700	2, 4
BMS3c-85-62	-	9.9, 2.7, 2.0	>700	<2, 0.63
BMS3c-85-63	-	80.9		
BMS3c-85-64	-	16.1		
BMS3c-85-65	-	13.9, 7.4	>700	3, 2

[0430]

클론	ELISA RBA (nM)	세포 RBA (nM)	B 세포 증식 검정 (EC50 nM)	
			인간	시노
BMS3c-85-67	-	1.5		0.17
BMS3c-85-69	-	1.8		0.33
BMS3c-85-72	-	2		0.16
BMS3c-85-73	-	2.3		
BMS3c-85-77	-	2.3		0.2
BMS3c-85-84	-	1.3		0.21
BMS3c-85-88	-	3		0.25
BMS3c-85-91	-	1.3		0.26

[0431]

[0432]

실시예 9

[0433]

항-인간 CD40 dAb가 시노CD40에 결합하지 않는다

[0434]

시노CD40은 인간 CD40에서와 같은 Trp109 대신에 Leu109 잔기가 있다. 마카카 과시쿨라리스 CD40의 아미노산 서열이 하기에 재현된다:

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1  MVRRLPLQCVL WGCLLTAVYP EPPTACREKQ YLINSQCCSL CQPGQKLVSD
51  CTEFTETECL PCGESEFLDT WNRSTRCHQH KYCDPNLGLR VQXKGTSETD
101  TICTCCEGLH CTSESCESCVC PHRSCLPGFG VKQIATGVSD TICEPCPVGF
151  FSNVSSAF EK CRPWTSCE TK DLVVQQAGTN KTDVVCGPQD RQRALVVIPI
201  CLGILFVILL LVLVFIKVA KKPNDKVPHP KQEPQEIINF DDLPGSNPAA
251  PVQETLHGCG PVTQEDGKES RISVQERQ (서열 2)

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[0435]

[0436]

항-인간 CD40 dAb를 시노물구스 원숭이, 레서스 마카크(rhesus macaque) 및 침팬지 혈액 내의 B 세포, 및 마모셋 혈액으로부터의 림프구에 대한 교차 반응성에 대해 테스트하였다. 하기에 상술된 절차들은 다중 실험에 걸친 CD40 dAb 검출에 사용된 방법들을 요약한다. 표 24에 제시된 결과는 항-인간 CD40 dAb가 시노CD40에 결합하지 않는다는 것을 시사한다. 이는 인간 CD40 내의 Trp109 (시노CD40에서 부재함)이 dAb와 인간 CD40 사이의 복합체 형성에 중요하다는 상기 개시된 증거 (도 1 및 2 참조)와 일관된다.

[0437]

방법:

[0438]

PEG화 항-인간 CD40 dAb (BMS3h-56-5C-40L 및 BMS3h38-2C-P40Br) 또는 비오틴-접합 dAb (BMS3h38-2-비오틴)를 인간 및 영장류 혈액 샘플과 함께 회전기 상에서 1시간 동안 37°C에서 인큐베이션하였다. 각각의 혈액 샘플로부터의 100 μ l를 12×75 mm 튜브에 분취하고, FACS 완충제 (0.5% FBS/PBS/0.1% 아지드화나트륨)로 3회 세정하였다. 튜브를 5분 동안 1500 rpm에서 원심분리하였고, 세정 사이에 상청액을 따라냈다. 세정 후, 튜브를 얼음 상에 놓고, 인간 IgG와 함께 5분 동안 인큐베이션하여, Fc 수용체를 통한 비-특이적 결합을 차단하였다.

[0439]

PEG화 dAb 검출을 위해, 항-PEG 항체 (실버 레이크 리서치(Silver Lake Research)의 클론 CH-2074, 또는 오픈 바이오시스템즈(Open Biosystems)의 클론 2-2)를 튜브에 첨가하고, 30분 동안 인큐베이션하였다. 샘플을 FACS 완충제에서 1회 세정한 후, APC-표지 CD20 항체 (BD 바이오사이언시즈(BD Biosciences)의 클론 2H7) 및 PE 표지-항-마우스 IgG (Fc γ 1 특이적; 칼바이오크(Calbiochem))와 함께 추가로 30분 동안 얼음 상에서 인큐베이션하였다.

[0440]

비오틴-접합 dAb 검출을 위해, PE-표지 스트렙타비딘 (인비트로젠) 및 APC-표지 CD20 항체 (BD 바이오사이언시즈의 2H7)를 튜브에 첨가하고, 30분 동안 실온에서 인큐베이션하였다.

[0441]

추가적으로, 인간 및 영장류 혈액 상의 CD40 수준을 측정하기 위해, 각각의 혈액 샘플 분취량을 APC-표지 CD20 항체 (BD 바이오사이언시즈의 클론 2H7) 및 영장류 종과 교차 반응하는 PE-표지 항-인간 CD40 항체 (BD 바이오사이언시즈의 클론 5C3)와 함께 30분 동안 실온에서 인큐베이션하였다.

[0442]

검출 항체 인큐베이션 후 적혈구를 용해시키고 백혈구를 고정시키기 위해, FACS 용해 용액(Lysing Solution) (BD 바이오사이언시즈)을 모든 튜브에 첨가하고, 샘플을 15분 동안 실온에서 인큐베이션하였다. 샘플을 원심분리하고, FACS 용해 용액에 재현탁시키고, 분석용으로 CD20+ B 세포 상에서 게이팅(gating)하여 BD FACSCanto™ 상에서 유동 세포측정법에 의해 분석하였다. 마모셋 샘플에 대해, CD20 항체가 반응성이 없었다; 따라서, 전 방향 및 측면 산란 성질 (크기)에 의해 확인되는 바와 같이 모든 림프구에 대해 분석을 수행하였다.

[0443]

결과:

[0444]

PEG화 및 비오틴화 항-인간 CD40 dAb의 결합을 상기 방법에 따라 인간 및 영장류 혈액 샘플에서 테스트하였다. 인간 혈액 샘플 내의 CD20+ B 세포에 대한 항-인간 CD40 dAb 결합이 검출되었다. 대조적으로,

시노몰구스, 레서스, 또는 침팬지 혈액 샘플 내의 CD20+ B 세포 또는 마모셋 혈액 샘플 내의 림프구 상에서는 PEG화 및 비오틴화 CD40 dAb의 결합이 검출되지 않았다. BMS3h-38-2C-P40Br dAb에 대한 결과가 도 3, 패널 A 및 B에서 제시된다. 유사한 결과가 다른 dAb들에 대해 획득되었다. 영장류 CD40과 교차 반응하는 항-인간 CD40 항체를 사용하여, 인간 및 영장류 종의 B 세포 상의 필적하는 수준의 CD40이 입증되었다. 이러한 데이터는 BMS3h-56 및 BMS3h-38 계통으로부터의 인간 CD40 dAb가 영장류 종의 CD40에 결합할 수 없다는 것을 가리킨다. 이러한 데이터는 도 1 및 2에 나타난 바와 같이 CD40과 항-CD40 dAb 간의 복합체를 형성하는 것에서의 Trp109 잔기의 중요성과 일관된다.

[0445] 실시예 10

[0446] CD40과 dAb BMS3h-56-5 간의 복합체의 X선 결정학

[0447] 데이터 수집 및 프로세싱:

[0448] 인간 CD40 (서열 1)/BMS3h-56-5 (서열 321) 복합체의 구조 결정 동안 2개의 상이한 결정 형태를 분석하였다. 100 K로 급속 냉각되어 100 K에서 유지되고, 리가쿠(Rigaku) AFC-9 측각기 상에 마운팅(mounting)된 CD40/BMS3h56-5 복합체의 결정으로부터 데이터를 수집하였다. X선 공급원은 마이크로맥스(MicroMax)TM 공초점 광학 및 새턴(Saturn) 92 검출기가 있는 구리 표적을 사용하는 리가쿠 FR-E였다. 극단적으로 높은 중복도로 데이터를 수집하여, 황 변칙 회절 신호를 이러한 신호를 데이터 페이징(phasing)에 사용할 것을 기대하면서 강화하였다. 데이터를 HKL2000로 프로세싱하였다 (HKL 리서치(HKL Research); 문헌 [Otwinowski et al., In Methods Enzymol. Macromolecular Crystallography part A, Carter et al., eds., vol. 276, p. 307-326, Academic Press, Inc., New York, NY (1997)]). 이러한 결정에 대한 데이터 수집 통계가 하기 및 표 24에서 요약된다:

[0449] 공간 군: I222;

[0450] 단위 셀: a = 156.6 Å; b = 158.3 Å; c = 200.7 Å;

[0451] 모자이크성(mosaicity) 0.59-0.84; 거절된 관찰: 1028; 0.06%.

표 24

s09-167	해상도 Å	측정	고유	중복도	완료%	R 값	I/ σ_1
전체	50.00-3.30	1603547	37772	42.5	99.8	0.137	33.7
제1 셀	50.00-8.94	≥38193	1971	40.1	97.1	0.049	58.7
최종 셀	3.36-3.30	≥37054	1861	43.6	99.8	0.439	12.5

[0452]

[0453] 캐네디언 라이트 소스(Canadian Light Source) 빔라인 CMCF1 (08-ID-1)에서 100 K로 급속 냉각되고 레이오닉스(Rayonix) MX-225 검출기 상에 마운팅된 결정으로부터 제2 결정 형태를 수집하였고, 파장은 0.9793 Å이었다. 이러한 데이터를 쉘락 스트럭처즈(Shamrock Structures)에 의해 수집하였고 (알. 월터(R. Walter) 및 지. 라니에리(G. Ranieri)), HKL2000로 프로세싱하였다. 이러한 결정에 대한 데이터 수집 통계가 하기 및 표 25에서 요약된다:

[0454] 공간 군: C2;

[0455] 단위 셀: a = 199.3 Å; b = 48.7 Å; c = 138.8 Å; β = 118.2° ;

[0456] 모자이크성 0.62-0.71; 거절된 관찰: 70; 0.08%.

표 25

x09-275	해상도 Å	측정	교유	중복도	완료%	R 값	I/ σ _I
전체	50.00-2.80	92545	29303	3.2	98.6	0.091	14.6
제1 셀	50.00-6.03	9265	3060	3.0	98.5	0.052	18.0
최종 셀	2.90-2.80	8857	2882	3.1	98.0	0.421	3.4

[0457]

[0458] **분자 교체 모델:**

[0459] CDR 31-35, 50-57, 및 99-111에 상응하는 순차적인 잔기가 SPLIT_PDB에 의해 제거되었고 (카바트 넘버링 31-35, 50-56, 및 95-100G에 상응함), 그 후 뮤테이트(MUTATE)를 통해 러닝(running)되었으며, 마지막으로 리넘버(RENUMBER)에 의해 재넘버링된 PDB ID 2VYR 사슬 E 잔기 1-124로부터 dAb BMS3h-56-5의 모델이 유래되었다. 뮤테이트는 동일하지 않은 잔기를 최소의 동일한 잔기, 즉 보통은 Ala 또는 Gly로 변화시키지만, 예를 들어, Tyr→Phe 및 Phe→Tyr은 Phe를 초래할 것이다. 이는 어떠한 원자도 형성하지 않지만, Thr→Val, Val→Thr, Cys→Ser, 및 Ser→Cys에 대해서는, 적합한 원자 이름을 치환할 것이나 위치를 변화시키지는 않는다. 리넘버는 CDR 및 프레임워크 잔기의 설명을 직설적이게 하는, 항체에 대한 표준 넘버링 시스템인 카바트 넘버링(문헌 [Kabat et al., Sequences of Immunological Interest, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)])으로 넘버링을 변화시켰다.

[0460] 구조 양상들을 생성시키기 위해 피닉스.앙상블러(phenix.enssembler) (유니버시티 오브 캠브리지(University of Cambridge), 영국))를 사용하여 PDB ID 1JMA (사슬 B), 1NCF (사슬 A), 1TNR (사슬 R), 2HEV (사슬 R), 2HEY (사슬 R, T), 및 2UWI (사슬 A, B)로부터 CD40 모델을 구축하였다. 이러한 분자들의 N-말단 (잔기 24-78) + 6 개의 잔기 절편 (잔기 95-100)이 Ca 원자에 대한 허용가능한 제공 평균 제공근 거리와 중첩될 수 있었고, 이를 CD40의 N-말단 영역에 대한 모델로서 사용하였다.

[0461] **분자 교체 방법:**

[0462] 페이저(PHASER) 프로그램 (문헌 [McCoy et al., J. Appl. Crystallogr. 40: 658-674 (2007)])을 분자 교체에 사용하였다. 번역 함수 Z-점수 (TFZ) 및 로그 우도 이득에서의 증가를 모니터링하여, 실제 솔루션이 발견되었는지를 결정하였다. 8 이상의 TFZ 점수는 일반적으로 솔루션을 나타낸다. 로그 우도 이득에서의 실질적인 증가 (>50)가 동반된 더 작은 TFZ 점수 또한 허용가능한 지표물이다.

[0463] **모델 설립, 밀도 변형, 및 결정학적 정련 방법:**

[0464] 분자 그래픽을 위한 모델 설립 도구는 쿠틀(COOT) 프로그램 (문헌 [Emsley et al., Acta Crystallogr Sect. D 60: 2126-2132 (2004)]; [Emsley et al., "Features and Development of Coot", Acta Crystallogr Sect. D 66: 486-501 (2010)])을 포함하였다. 비-결정학적 대칭 지도 평균화를 사용하는 밀도 변형을 공지된 밀도 변형 프로그램 및 기타 프로그램을 사용하여 수행하여, 분자들 간의 오일러 각도 및 번역을 계산하였다. 오토부스터(autoBUSTER) (글로벌페이징, 리미티드(GlobalPhasing, Ltd): 문헌 [Bricogne et al., Acta Crystallogr. Sect. D 60: 2210-2221 (2004)]; [Tronrud et al., Acta Crystallogr. Sect. A 43: 489-501 (1987)])를 사용하여 정련을 수행하였다.

[0465] **도메인 항체 넘버링 시스템:**

[0466] 도메인 항체에 대한 잔기 넘버링 시스템은 카바트의 시스템을 따른다. BMS3h-56-5에 대해 하기에서 카바트 넘버링이 직선형 순차적 넘버링과 비교된다:

-2-1							
BMS-3h-56-5 ST							
<u>CDR1</u>							
카바트		10		20		30	40
50		-		-		-	
순차적		10		20		30	40
50		-		-		-	
BMS-3h-56-5							
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSA							
<u>CDR2</u>							
카바트		60		70		80	90
	A	-		-		-	
순차적		60		70		80	90
100		-		-		-	
BMS-3h-56-5							
INPQGTRTYADSVMGRTISRDNSTLYLQMNSLRADTAVYYCAKLP							
<u>CDR3</u>							
카바트		99	101	110	116		
			-		-		
순차적			110		119		
		-		-			
BMS-3h-56-5 FTFDDWGQGLTVTVSSAAA (서열 3)							

[0467]

[0468]

카바트 넘버링에서, BMS3h-56-5는 삽입 잔기 52A, 82A, 82B, 82C가 있고, 잔기 100이 없다. 양쪽 넘버링 시스템에서, 발현 구축물의 일부인 N-말단의 Ser 및 Thr에는 음성 번호가 제공된다.

[0469]

CD40/BMS3h-56-5 복합체 구조의 결정:

[0470]

페이지는 4개의 BMS3h-56-5 dAb 분자를 I222 결정 형태에, 3개의 BMS3h-56-5 dAb 분자를 C2 결정 형태에 놓을 수 있었다. I222 결정 형태에서, TFZ 점수는 7.6 내지 41.0 범위였고, 로그 우도 이득에서의 증가는 77 내지 446 범위였다. BMS3h-56-5 dAb 분자에 대한 이러한 솔루션은 I222 결정을 통과하는 dAb 분자의 나선형 기둥을 형성하였고, 이는 대형 채널에 의해 다른 기둥들로부터 분리되었다. C2 결정에서, TFZ 점수는 7.7 내지 16.5 범위였고, 로그 우도 이득에서의 증가는 110 내지 150 범위였다. 이러한 결정 형태의 dAb의 패킹(packing)은 반복적이거나 대칭적이지 않았다.

[0471]

CD40 N-말단 도메인에 대한 앙상블 모델을 사용하여, CD40의 N-말단 도메인의 4개의 분자가 TFZ 점수가 5.7 내지 8.5 범위인 I222 결정 형태로 놓일 수 있었고, 로그 우도 이득에서의 증가는 83 내지 389 범위였다. I222 결정 형태에서의 CD40의 4개의 N-말단 도메인은 dAb 분자의 4개의 기둥 사이에 등가로 중심에 있는 클럼프(clump)를 형성하였다. 그러나, 이들은 BMS3h-56-5 dAb 분자에 닿지 않았다. C2 결정 형태에서, CD40의 N-말단 도메인의 3개의 분자가 5.8 내지 12.1 범위의 TFZ 점수로 놓일 수 있었고, 로그 우도 이득에서의 증가는 100 내지 198 범위였다. 이러한 결정 형태에서, N-말단 도메인들은 BMS3h-56-5 dAb 분자와 접촉하지 않았다.

[0472]

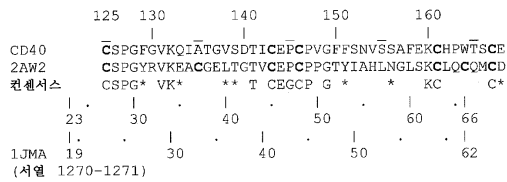
I222 결정 형태에서, CD40/Chi220 Fab 복합체로부터의 CD40의 N-말단 도메인 및 2UWI로부터의 N-말단 도메인이 CD40 N-말단 도메인 상에서 중첩되었다. N-말단과 특정 BMS3h-56-5 dAb를 회합시키는 능력은 비-결정학적 대칭(NCS) 지도 평균화를 사용하게 하였다. NCS 평균화에 대한 출발 상관 계수는 0.71-0.81의 비-대각(off-diagonal) 값을 제공하였다. 최종 비-대각 값은 0.88-0.92였다. N-말단 영역에 인접한 전자 밀도는 투명하였고, BMS3h-56-5 dAb의 CDR3에 대해 경로를 트레이싱(tracing)할 수 있었다. CD40/Chi220 Fab' 복합체로부터의 잔기 82-94 및 101-121가 2UWI 상의 상응하는 잔기에 중첩되었고, 그 후 쿼트를 사용하여 피트를 수동으로 개선시켰다. 그 후, CD40의 제2 도메인 (잔기 82-94 및 101-121)에 대한 이러한 위치를 다른 3개의 N-말단 도메인 상에 변환시켰다.

[0473]

R-프리(free)는 0.437에서 0.380으로, R-워크(work)는 0.447에서 0.381로 감소시키면서 정련 사이클을 러닝시켰고, 이때 이상치로부터의 제곱 평균 제곱근 결합 및 각도 편차가 개선되었다. 생성된 전자 밀도 지도는 잔기 109에 Trp과 일치하는 측쇄가 있었고, 이러한 밀도가 CD40의 C-말단의 70개의 잔기 내의 적어도 일부 잔기에 대해 존재하였음을 나타냈다.

[0474]

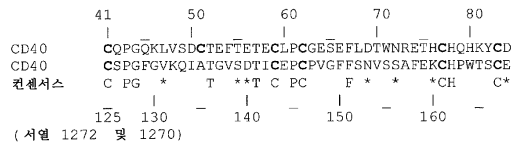
CD40의 2차 구조가 거의 없기 때문에, C-말단의 ~70개의 잔기를 전자에 피팅(fitting)하는 것은 어려운 것으로 입증되었고, 따라서 사슬 트레이싱을 안내하는 것을 돕도록 <Research Collaboratory for Structural Bioinformatics Protein Data Base>를 적절한 모델에 대해 검색하였다. 44개의 실체 중 16개 및 44개의 매치(match) 중 24개의 최상위의 2개의 히트(hit)는 2AW2 및 1JMA였고, 이들은 서열이 동일하다:



[0475]

[0476]

동일한 잔기들은 컨센서스 선 상에 적합한 단일 문자 코드로 표시되고, 유사한 잔기들은 컨센서스 선 상에 별표로 표시된다. 이는 CD40의 N-말단 도메인의 잔기 41-84에 대한 것과 동일한 잔기 신장물이었다:



[0477]

[0478]

동일한 잔기들은 컨센서스 선 상에 적합한 단일 문자 코드로 표시되고, 유사한 잔기들은 컨센서스 선 상에 별표로 표시된다.

[0479]

디설피드 결합의 매칭:

[0480]

CD40의 잔기 41-84 및 125-168에서의 디설피드 결합의 비교

잔기 41-84	잔기 125-168
C41-C59	C125-C143
[C38]-C51	
C62-C77	C146-C161
C83[-C103]	C167[-C186]

[0481]

[0482]

각괄호 내의 잔기는 서열 반복물 내의 잔기 범위에서 벗어난다.

[0483]

1JMA/2AW2 모델을 안내물로 하여, 쿼트 프로그램을 사용하여 CD40 사슬 중 하나를 피팅하였다. 그 후, 이러한 피팅 모델을 다른 3개의 CD40 사슬 중 하나에 중첩시켰다. 그러나, 이러한 새로운 잔기 신장물의 위치가 다른 2개의 CD40 사슬에서 상이하게 배향되는 것으로 나타났고, 이들은 이번에는 피팅되지 않았다. R-프리는 0.393에서 0.366으로, R-워크는 0.400에서 0.349로 감소시키면서 정련 사이클을 러닝시켰고, 이때 이상치로부터의 제곱 평균 제곱근 결합 및 각도 편차가 개선되었다.

[0484]

I222 결정 형태의 분자들 중 하나로부터의 BMS3h-56-5 dAb를 C2 결정 형태의 3개의 dAb 각각에 중첩시켰다. 이러한 변환 매트릭스를 사용하여 I222 결정 형태의 제2 및 C-말단 도메인을 배향시켰다. 이러한 모델을 쿼트 프로그램을 사용하여 재설정하였다. R-프리를 0.361에서 0.334로, R-워크를 0.375에서 0.306으로 감소시키면서 정련 사이클을 러닝시켰고, 이때 이상치로부터의 제곱 평균 제곱근 결합 및 각도 편차가 개선되었다. 생성된 전자 밀도 지도는 다수의 더 많은 CD40 잔기를 배치하는 것에 대한 지침을 제공하였다. R-프리를 0.302에서 0.287로, R-워크를 0.299에서 0.270으로 감소시키면서 또 다른 정련 사이클을 러닝시켰고, 이때 이상치로부터의 제곱 평균 제곱근 결합 및 각도 편차가 개선되었다.

[0485]

그 후, 통상적인 모델 설립 및 정련을 사용하여 구조 결정을 완료하였다. 수회의 더 많은 최적화 라운드로 최종 정련에 이르렀고, 이때 통계는 하기와 같았다: R-프리 0.260, R-워크 0.228, 제곱 평균 제곱근 결합 0.010 Å, 제곱 평균 제곱근 각도 1.4°. 실제 공간 상관 계수는 주쇄 원자의 경우는 0.92, 측쇄 원자의 경우는 0.80이다. 최종 모델에는 13개의 물 분자가 있었다.

[0486]

C2 결정 형태로부터의 C-말단 도메인의 모델을 안내물로 사용하여, I222 결정 형태의 CD40 모델을 추가로 정련하였다. 쿼트 프로그램을 사용하는 수회의 더 많은 모델 설립 사이클 및 오토부스터 프로그램으로의 정련으로 하기의 통계에 이르렀다: R-프리 0.323, R-워크 0.292, 제곱 평균 제곱근 결합 0.011 Å, 제곱 평균 제곱근 각도 1.5°. 실제 공간 상관 계수는 주쇄 원자의 경우는 0.91, 측쇄 원자의 경우는 0.80이다. 이러한 모델은 물 분자를 함유하지 않았다.

[0487]

CD40/BMS3h-56-5 복합체의 전반적인 구조:

[0488]

1개의 BMS3h-56-5 dAb가 1개의 CD40 분자에 결합한다. 도 1에 나타난 바와 같이, BMS3h-56-5는 N-말단 영역에서 결합하는 항체 Chi220의 것과 별개인 에피토프에 결합한다. 에피토프 잔기를 제외하고는 CD40 잔기 (서열 1)가 녹색으로 제시된다. Chi220에 대한 CD40 에피토프 잔기는 청색으로 제시되고, BMS3h-56-5 dAb 에피토프

잔기는 청록색으로 제시된다. Chi220 Fab 및 BMS3h-56-5 β -가닥은 적색으로 제시되고, CDR 잔기는 마젠타색으로 제시되며, 다른 루프들은 오렌지색으로 제시된다. 황색의 황 원자로 디설피드 결합이 CD40, Chi220, 및 BMS3h-56-5 분자에 대해 제시된다.

[0489] I222 결정 형태는 4개의 결정학적으로 독립적인 CD40/BMS3h-56-5 복합체를 함유하고, C2 결정 형태는 3개의 결정학적으로 독립적인 CD40/BMS3h-56-5 복합체를 함유한다. CD40 분자는 특정량의 유연성이 있고, 도메인들은 7개의 독특한 복합체 버전에서 상이하게 배열되지만, 상호작용의 전반적인 성질이 모든 사례에서 유지된다.

[0490] **BMS3h-56-5 dAb 에피토프 잔기:**

[0491] BMS3h-56-5에 대한 최소 CD40 에피토프는 BMS3h-56-5 원자와 반 테르 발스 또는 수소-결합 접촉 상태인 1개 이상의 원자를 함유하는 CD40 잔기들로 정의된다. 모든 복합체 내의 최소 에피토프는 서열 1을 참조로 하기의 CD40 잔기를 함유한다: Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, 및 His162. 일부 복합체에서 하기의 추가적인 잔기들이 반 테르 발스 또는 수소-결합 접촉 상태이다: Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, Lys160.

[0492] 최대 CD40 에피토프는 1.7 Å 프로브 구체에 의해 매립되는 원자들을 함유하는 잔기들로 정의된다. 이러한 잔기들은 모든 복합체에서 상기의 잔기 모두 + Val 154를 포함한다. 일부 복합체에서는, 추가적인 매립 잔기는 Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, 및 Pro163이다.

[0493] 접촉 잔기들이 있는 BMS3h-56-5의 표면의 도해가 도 2에서 제시된다. 접촉성 BMS3h-56-5 잔기가 제시된다. 매립 잔기가 또한 제시된다. CD40이 카툰으로서 제시되고, 이때 주황색은 비-반복적 2차 구조를 나타내고, 마젠타색은 에피토프 잔기를 나타낸다. CD40 잔기 Trp109, Ala115, Leu121, Ser126, 및 His162가 또한 막대로서 제시되고 (청록색 탄소 원자), 이들은 인간과 시노몰구스 원숭이 (마카카 파시쿨라리스) 사이에 상이한 7개의 잔기 중 5개이다. Ala115 및 Ser126은 BMS3h-56-5 결합 부위로부터 CD40의 반대쪽에 있다. Trp109 및 Leu121은 CDR3과 FR-2 (BMS-3h-56-5 잔기 Leu45 및 Arg47) 사이에 놓인 BMS-h-56-5의 틈새에서 결합한다. CD40의 His162는 BMS3h-56-5 dAb의 CDR-2의 Arg56과 상호작용한다. Trp109의 돌연변이는 BMS3h-56-5 활성을 상당히 감소시키거나 또는 제거한다.

[0494] 결정학적으로 독립적인 복합체에 따라, 더 미세한 수준에서 46-67개의 접촉 원자로 표현되는 16-21개의 접촉 잔기로 660-740 Å²의 CD40 표면적이 매립된다. BMS3h-56-5에 대해, 더 미세한 수준에서 48-62개의 접촉 원자로 표현되는 14-17개의 접촉 잔기로 660-780 Å²의 표면적이 매립된다. 결정학적으로 독립적인 복합체에 따라, 이러한 접촉으로 3-7개의 수소 결합 및 111-142개의 반 테르 발스 상호작용이 산출된다.

[0495] **실시예 11**

[0496] **CD40 상의 dAb 결합 에피토프의 확인**

[0497] CD40 상의 dAb 결합 에피토프를 확인하기 위해, 잔기 76, 109, 또는 121에서의 특정 아미노산 잔기 치환을 함유하는 7개의 CD40-Fc 융합 단백질에 대해 dAb 결합을 테스트하였다. 이러한 CD40-Fc 융합 단백질에는 야생형 인간 CD40 (wt-hCD40), 야생형 시노몰구스 원숭이 CD40 (wt-cCD40), 및 특정 아미노산 잔기가 시노몰구스 원숭이 CD40 (M1, M2, M4, M5) 또는 침팬지 CD40 (M3)의 서열로부터의 상응하는 잔기로 돌연변이된 5개의 돌연변이체 인간 CD40 단백질 (M1-M5)가 포함된다. 이러한 아미노산 치환이 표 26에서 열거된다.

[0498] 야생형 인간 CD40 세포의 도메인 (1-193)의 서열은 REFSEQ:접속 NM_001250.3으로부터의 것이다. 표 26에 제시된 위치에서의 야생형 서열의 부위-지정 돌연변이유발을 사용하여 시노몰구스 및 돌연변이체 구축물을 생성시켰다. 세포외 도메인을 인간 IgG1 Fc와 융합된 트롬빈-절단성 링커 DPGGGGGRLVPRGFGTGDP (서열 1273)와 융합시켰다. TIG-pYD7-GATE 듀로처(Durocher) 발현 벡터로 형질감염된 HEK-293-6E 세포에서 단백질을 발현시켰다. 5일 후 상청액을 수확하였다. 각각의 CD40 단백질을 단백질 A 패스트 플로우(fast flow) 크로마토그래피를 사용하여 컨디셔닝 배지로부터 정제하였다. 칼럼을 PBS (20 mM 인산나트륨, 0.15 M NaCl, pH 7.2)로 세정한 후, 80 mM 아세트산나트륨, pH 3을 사용하여 1/5 부피의 1 M 트리스-HCl, pH 8 내로 용출시켰다. 용출액을 PBS 내의 슈퍼덱스(Superdex)-200 칼럼 상에 러닝시켰다.

표 26

명칭	단속명	잔기 76	잔기 109	잔기 121
야생형 인간 CD40 Fc 융합물	wt-hCD40	H	W	L
인간 CD40 (H76R) Fc 융합물	hCD40-M1	R	W	L
인간 CD40 (W109L) Fc 융합물	hCD40-M2	H	L	L
인간 CD40 (W109R) Fc 융합물 (침팬지 CD40)	hCD40-M3	H	R	L
인간 CD40 (W109L, L121P) Fc 융합물	hCD40-M4	H	L	P
인간 CD40 (H76R, W109L, L121P) Fc 융합물	hCD40-M5	R	L	P
야생형 시노물구스 원숭이 CD40 Fc 융합물	wt-시노- CD40	R	L	P

[0499]

[0500]

3h217, 3h37, 3h38, 및 3h56 계통으로부터의 대표적인 dAb를 표 26에 열거된 CD40-Fc 융합 단백질에 결합하는 것에 대해 검정하였다. 바이오래드(BioRad) 프로테온(ProteOn) XPR36 SPR 기구 상에서 검정을 수행하였다. 에탄올아민 차단과 함께, 표준 에틸(디메틸아미노프로필) 카르보디이미드 (EDC) / N-히드록시숙신이미드 (NHS) 화학을 사용하여, 10 mM 아세트산나트륨 pH 4.5 내의 8 $\mu\text{g}/\text{ml}$ 항-인간 IgG(Fc) 항체 (비야코어/GE 헬스케어)를 바이오래드 GLC 센서 칩 상에 고정시킴으로써 SPR 표면을 제조하였다. 고정 및 동역학 결합 분석용 러닝 완충제는 10 mM 인산나트륨, 130 mM 염화나트륨, 0.05% 트윈 20, pH 7.1이었다. 20 $\mu\text{g}/\text{ml}$ 농도의 CD40-Fc 융합 단백질이 Fc 꼬리를 통해 이러한 표면 상에 수직 배향으로 포착되었고, CD40-Fc 단백질이 없는 기준물 표면은 기준물 차감용으로 사용되었다. 포착된 CD40-Fc 표면에 대해 수평 배향으로 30 μl /분의 유속으로 240초 회합 시간 및 420초 해리 시간을 사용하여 25°C에서 405, 135, 45, 15, 및 5 nM dAb 분석물을 유동시킴으로써 동역학 실험을 수행하였다. 3 M MgCl_2 의 30초 펄스 후에 60 μl /분으로 완충제를 러닝시킴으로서 수평 및 수직 배향 양쪽 모두로 표면을 재생시켰다. 센소그램 데이터를 이중으로 대조(referencing)한 후, 바이오래드의 프로테온 매니저(ProteOn Manager) V.2.1.0.38 소프트웨어를 사용하여 1:1 랭뮤어 모델에 피팅하여, 회합 속도 상수 (k_a), 해리 속도 상수 (k_d), 및 평형 해리 상수 (K_D)를 결정하였다.

[0501]

3h-37, 3h-38 및 3h-56 계통의 모든 dAb가 인간 CD40 잔기 W109 및 L121을 함유하는 CD40-Fc 융합 단백질에 높은 친화도 ($K_D < 10^{-8}$ M)로 결합하는 것으로 확인되었지만, 시노물구스 원숭이 CD40 (L109, P121) 또는 침팬지 CD40 (R109)로부터의 상응하는 잔기가 있는 CD40-Fc 융합 단백질에 대해서는 결합이 유의하게 감소되거나 검출 불가능하였다. 이는 3h37-, 3h38- 및 3h56-계통 각각으로부터의 dAb가 인간 CD40의 잔기 109 및 121을 포함하는 에피토프에 특이적으로 결합한다는 것을 가리킨다. 대조적으로, 3h-217 계통의 테스트된 구성원 모두는 테스트된 CD40-Fc 융합 단백질 모두에 유사한 친화도로 결합하였고, 이는 3h-217 계통의 구성원이 잔기 76, 109, 또는 121을 포함하지 않는 CD40 상의 부위에 결합한다는 것을 가리킨다. 따라서, 3h-217 계통은 3h-37, 3h-38- 및 3h-56 계통과 상이한 에피토프에 결합한다. 표 27은 프로테온 XPR36 기구 상에서 SPR을 사용하여 CD40-Fc 융합 단백질에 대한 dAb 결합에 대해 결정된 K_D 값을 요약한다. 표 27의 "X"는 이러한 조건 하에 결합에 대한 증거가 확인되지 않았음을 의미한다.

표 27

	wt-hCD40	hCD40-M1 (H76R)	hCD40-M2 (W109L)	hCD40-M3 (W109R)	hCD40-M4 (W109L, L121P)	hCD40-M5 (H76R, W109L, L121P)	서노 CD40
3h-217-5	0.47, 0.48	0.94	0.99	0.72	0.93	1.0	0.9
3h-217-16	0.22, 0.26	0.35	0.41	0.27	0.35	0.5	0.4
3h-217-23	0.78, 1.5	1.6	2.0	1.2	1.6	2.2	1.9
3h-37-2	2.0, 2.0	2.6	>1000	X	X	X	X
3h-37-11	1.9, 2.3	2.4	>1000	X	X	X	X
3h-38-2	5.1, 8.0	7.2	X	X	X	X	X
3h-38-211	3.3, 6.1	4.0	>1000	X	X	X	X
3h-38-215	2.1, 6.0	3.0	>1000	X	X	X	X
3h-38-217	2.3, 2.4	3.4	>1000	X	X	X	X
3h-56-1	3.0, 5.4	4.2	29	>1000	X	X	X
3h-56-2	3.8, 3.2	6.1	44	>1000	X	X	X
3h-56-5	5.3, 4.7	7.2	65	>1000	X	X	X
3h-56-202	2.3, 1.3	3.3	160	X	X	X	X
3h-56-206	0.60, 1.4	1.0	55	X	X	X	X
3h-56-217	1.0, 1.9	1.4	2.5	23	X	X	X

[0502]

[0503]

표 28은 프로테온 XPR36 기구 상에서 SPR을 사용하여 CD40-Fc 융합 단백질에 대한 dAb 결합에 대해 결정된 회합 속도 상수 (k_a), 해리 속도 상수 (k_d), 및 평형 해리 상수 (K_D)를 나타낸다. 표 28의 "X"는 이러한 조건 하에 결합에 대한 증거가 확인되지 않았음을 의미한다.

표 28

리간드	dAb	k_a (1/Ms)	k_d (1/s)	K_D (nM)
wt-hCD40	3h-217-5	2.71×10^6	1.27×10^{-3}	0.47
wt-hCD40 (반복)	3h-217-5	2.03×10^6	9.81×10^{-4}	0.48
hCD40 M1 (H76R)	3h-217-5	3.17×10^6	2.99×10^{-3}	0.94
hCD40 M2 (W109L)	3h-217-5	2.55×10^6	2.51×10^{-3}	0.99
hCD40 M3 (W109R)	3h-217-5	2.73×10^6	1.96×10^{-3}	0.72
hCD40 M4 (W109L, L121P)	3h-217-5	2.78×10^6	2.59×10^{-3}	0.93
hCD40-M5 (H76R, W109L, L121P)	3h-217-5	2.44×10^6	2.42×10^{-3}	0.99
wt-cCD40	3h-217-5	2.46×10^6	2.12×10^{-3}	0.86
wt-hCD40	3h-217-16	4.47×10^6	9.91×10^{-4}	0.22
wt-hCD40 (반복)	3h-217-16	3.30×10^6	8.47×10^{-4}	0.26
hCD40 M1 (H76R)	3h-217-16	4.83×10^6	1.68×10^{-3}	0.35
hCD40 M2 (W109L)	3h-217-16	4.06×10^6	1.67×10^{-3}	0.41
hCD40 M3 (W109R)	3h-217-16	3.78×10^6	1.04×10^{-3}	0.27
hCD40 M4 (W109L, L121P)	3h-217-16	4.39×10^6	1.52×10^{-3}	0.35
hCD40-M5 (H76R, W109L, L121P)	3h-217-16	3.65×10^6	1.70×10^{-3}	0.47
wt-cCD40	3h-217-16	3.44×10^6	1.47×10^{-3}	0.43
wt-hCD40	3h-217-23	1.64×10^6	1.27×10^{-3}	0.78
wt-hCD40 (반복)	3h-217-23	1.07×10^6	1.63×10^{-3}	1.52
hCD40 M1 (H76R)	3h-217-23	1.64×10^6	2.62×10^{-3}	1.59
hCD40 M2 (W109L)	3h-217-23	1.49×10^6	2.91×10^{-3}	1.95
hCD40 M3 (W109R)	3h-217-23	1.53×10^6	1.86×10^{-3}	1.22
hCD40 M4 (W109L, L121P)	3h-217-23	1.67×10^6	2.68×10^{-3}	1.61
hCD40-M5 (H76R, W109L, L121P)	3h-217-23	1.30×10^6	2.87×10^{-3}	2.21
wt-cCD40	3h-217-23	1.24×10^6	2.35×10^{-3}	1.90

[0504]

wt-hCD40	3h-37-2	2.12x10 ⁵	4.17x10 ⁻⁴	1.96
wt-hCD40 (반복)	3h-37-2	2.13x10 ⁵	4.26x10 ⁻⁴	2.00
hCD40 M1 (H76R)	3h-37-2	2.17x10 ⁵	5.62x10 ⁻⁴	2.58
hCD40 M2 (W109L)	3h-37-2			>1000
hCD40 M3 (W109R)	3h-37-2			X
hCD40 M4 (W109L, L121P)	3h-37-2			X
hCD40-M5 (H76R, W109L, L121P)	3h-37-2			X
wt-cCD40	3h-37-2			X
wt-hCD40	3h-37-11	2.91x10 ⁵	5.60x10 ⁻⁴	1.92
wt-hCD40 (반복)	3h-37-11	2.81x10 ⁵	6.40x10 ⁻⁴	2.28
hCD40 M1 (H76R)	3h-37-11	3.00x10 ⁵	7.17x10 ⁻⁴	2.39
hCD40 M2 (W109L)	3h-37-11			>1000
hCD40 M3 (W109R)	3h-37-11			X
hCD40 M4 (W109L, L121P)	3h-37-11			X
hCD40-M5 (H76R, W109L, L121P)	3h-37-11			X
wt-cCD40	3h-37-11			X
wt-hCD40	3h-38-2	1.20x10 ⁵	6.08x10 ⁻⁴	5.07
wt-hCD40 (반복)	3h-38-2	1.42x10 ⁵	1.14x10 ⁻³	8.04
hCD40 M1 (H76R)	3h-38-2	1.40x10 ⁵	1.00x10 ⁻³	7.15
hCD40 M2 (W109L)	3h-38-2			X
hCD40 M3 (W109R)	3h-38-2			X
hCD40 M4 (W109L, L121P)	3h-38-2			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-2			X
wt-cCD40	3h-38-2			X
wt-hCD40	3h-38-211	1.11x10 ⁵	3.62x10 ⁻⁴	3.26
wt-hCD40 (반복)	3h-38-211	1.20x10 ⁵	7.28x10 ⁻⁴	6.08
hCD40 M1 (H76R)	3h-38-211	1.28x10 ⁵	5.10x10 ⁻⁴	3.98

[0505]

hCD40 M2 (W109L)	3h-38-211			>1000
hCD40 M3 (W109R)	3h-38-211			X
hCD40 M4 (W109L, L121P)	3h-38-211			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-211			X
wt-cCD40	3h-38-211			X
wt-hCD40	3h-38-215	1.37x10 ⁵	2.88x10 ⁻⁴	2.10
wt-hCD40 (반복)	3h-38-215	1.36x10 ⁵	8.20x10 ⁻⁴	6.02
hCD40 M1 (H76R)	3h-38-215	1.75x10 ⁵	5.30x10 ⁻⁴	3.03
hCD40 M2 (W109L)	3h-38-215			>1000
hCD40 M3 (W109R)	3h-38-215			X
hCD40 M4 (W109L, L121P)	3h-38-215			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-215			X
wt-cCD40	3h-38-215			X
wt-hCD40	3h-38-217	1.27x10 ⁵	2.96x10 ⁻⁴	2.34
wt-hCD40 (반복)	3h-38-217	1.44x10 ⁵	3.40x10 ⁻⁴	2.37
hCD40 M1 (H76R)	3h-38-217	1.41x10 ⁵	4.81x10 ⁻⁴	3.41
hCD40 M2 (W109L)	3h-38-217			>1000
hCD40 M3 (W109R)	3h-38-217			X
hCD40 M4 (W109L, L121P)	3h-38-217			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-217			X
wt-cCD40	3h-38-217			X
wt-hCD40	3h-56-1	2.52x10 ⁵	7.50x10 ⁻⁴	2.97
wt-hCD40 (반복)	3h-56-1	1.93x10 ⁵	1.03x10 ⁻³	5.35
hCD40 M1 (H76R)	3h-56-1	2.31x10 ⁵	9.67x10 ⁻⁴	4.18
hCD40 M2 (W109L)	3h-56-1	1.92x10 ⁵	5.57x10 ⁻³	29.10
hCD40 M3 (W109R)	3h-56-1			>1000
hCD40 M4 (W109L, L121P)	3h-56-1			X

[0506]

hCD40-M5 (H76R, W109L, L121P)	3h-56-1			X
wt-cCD40	3h-56-1			X
wt-hCD40	3h-56-2	2.46x10 ⁵	9.27x10 ⁻⁴	3.77
wt-hCD40 (반복)	3h-56-2	1.97x10 ⁵	6.24x10 ⁻⁴	3.17
hCD40 M1 (H76R)	3h-56-2	2.20x10 ⁵	1.33x10 ⁻³	6.05
hCD40 M2 (W109L)	3h-56-2	1.89x10 ⁵	8.30x10 ⁻³	43.90
hCD40 M3 (W109R)	3h-56-2			>1000
hCD40 M4 (W109L, L121P)	3h-56-2			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-2			X
wt-cCD40	3h-56-2			X
wt-hCD40	3h-56-5	1.78x10 ⁵	9.38x10 ⁻⁴	5.26
wt-hCD40 (반복)	3h-56-5	1.53x10 ⁵	7.19x10 ⁻⁴	4.69
hCD40 M1 (H76R)	3h-56-5	1.69x10 ⁵	1.21x10 ⁻³	7.18
hCD40 M2 (W109L)	3h-56-5	1.38x10 ⁵	8.89x10 ⁻³	64.60
hCD40 M3 (W109R)	3h-56-5			>1000
hCD40 M4 (W109L, L121P)	3h-56-5			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-5			X
wt-cCD40	3h-56-5			X
wt-hCD40	3h-56-202	1.82E+05	4.15x10 ⁻⁴	2.27
wt-hCD40 (반복)	3h-56-202	1.77E+05	2.21x10 ⁻⁴	1.25
hCD40 M1 (H76R)	3h-56-202	1.76E+05	5.79x10 ⁻⁴	3.29
hCD40 M2 (W109L)	3h-56-202	1.35E+05	2.00x10 ⁻²	155.00
hCD40 M3 (W109R)	3h-56-202			X
hCD40 M4 (W109L, L121P)	3h-56-202			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-202			X
wt-cCD40	3h-56-202			X
wt-hCD40	3h-56-206	6.48E+05	3.89x10 ⁻⁴	0.60

[0507]

wt-hCD40 (반복)	3h-56-206	3.27E+05	4.72x10 ⁻⁴	1.44
hCD40 M1 (H76R)	3h-56-206	5.65E+05	5.45x10 ⁻⁴	0.96
hCD40 M2 (W109L)	3h-56-206	3.38E+05	2.00x10 ⁻²	54.70
hCD40 M3 (W109R)	3h-56-206			X
hCD40 M4 (W109L, L121P)	3h-56-206			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-206			X
wt-cCD40	3h-56-206			X
wt-hCD40	3h-56-217	4.71E+05	4.70x10 ⁻⁴	1.00
wt-hCD40 (반복)	3h-56-217	2.91E+05	5.46x10 ⁻⁴	1.87
hCD40 M1 (H76R)	3h-56-217	4.45E+05	6.35x10 ⁻⁴	1.43
hCD40 M2 (W109L)	3h-56-217	4.25E+05	1.05x10 ⁻³	2.48
hCD40 M3 (W109R)	3h-56-217	2.91E+05	6.70x10 ⁻³	23.00
hCD40 M4 (W109L, L121P)	3h-56-217			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-217			X
wt-cCD40	3h-56-217			X

[0508]

[0509] 실시예 12

[0510] Fc 융합 폴리펩티드의 구축

[0511] 본원에 개시된 바와 같이, dAb를 포함하는 항체 폴리펩티드를 다양한 형상으로 구축할 수 있다. 이러한 실시예에서, 다양한 dAb를 Fc 도메인에 융합시켜 항-인간 CD40 가변 도메인 구축물 예컨대 3h37-202, 3h37-235, 3h37-258, 및 3h37-202의 Fc 융합 폴리펩티드를 생성시켰다.

[0512] 한 대표적인 예에서, dAb BMS3h-56-269 (서열 417)를 변형된 IgG1 (IgG1*) Fc 도메인 (서열 1284)에 융합시켰다. 이러한 dAb-IgG1* Fc 도메인 융합 폴리펩티드에서, dAb BMS3h-56-269의 C-말단이 서열 Ala-Ser-Thr의 3-펩티드 링커에 융합되었고, 차례로 링커가 IgG1* Fc 도메인 (서열 1284)과 융합되었다. IgG1* Fc 도메인은 서열 1284에서의 위치 넘버링을 참조로 변형 C5S를 함유하였다. IgG1 Fc 도메인의 C5는 보통 IgG 분자의 경쇄 내의 Cys 잔기와 디설피드 결합을 형성한다. IgG1* Fc 도메인은 IgG1 힌지 영역에서의 사슬간 디설피드 결합을 제거하도록 C11S 및 C14S 돌연변이를 또한 함유하였다. 마지막으로, IgG1* Fc 도메인은 Fc 도메인 이펙터 기능을 낮추도록 P23S 돌연변이를 함유하였다. dAb-IgG1* Fc 융합 폴리펩티드의 서열은 하기와 같고, 이때 Ala-

Ser-Thr 링커는 볼드체이고, Fc 도메인에 대한 변형은 이탤릭 볼드체이다:

```

1  EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYEMWWVRQA PGKGLERVSA
51  INPQGTITYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP
101 FRFSDRGGGT LVTVSSASTE PKSSDKHTS PPSPAPELLG GSSVFLFPFK
151 PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY
201 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
251 QVYTLPPSRD ELTKNQVSLT CLVKGYFSPD IAVEWESNGQ PENNYKTTTP
301 VLDSGGSEFFL YSKLTVDKSR WQGNVFSCS VMHEALHNHY TQKSLSLSPG
351 K (서열 1286)

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[0513]

[0514]

서열 1286에 도해된 dAb-IgG1* Fc 융합 폴리펩티드는 분자량 계산값이 39,127 Da인 단량체이다. 이는 분자량 계산값이 78,254 Da인 이량체를 형성할 수 있다.

[0515]

대안적으로, dAb BMS3h-56-269 (서열 417)를 인간 IgG₄ Fc 도메인 (서열 1285)과 융합시켰다. dAb BMS3h-56-269의 C-말단을 IgG₄ Fc 도메인 (서열 1285)과 융합된 Ala-Ser-Thr 링커에 다시 융합시켰다. IgG₄ Fc 도메인은 서열 1285에서의 위치 넘버링을 참조로 변형 S10P를 함유하였다. BMS3h-56-269-IgG₄ Fc 융합 폴리펩티드의 서열은 하기와 같고, 이때 Ala-Ser-Thr 링커는 볼드체이고, S10P 변형은 이탤릭 볼드체이다:

```

1  EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYEMWWVRQA PGKGLERVSA
51  INPQGTITYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP
101 FRFSDRGGGT LVTVSSASTE SKYGPCCPPC PAPEFLGGPS VFLEPPKPKD
151 TIMISRTPEV TCVVVDVSQD DEVDQFNWVY DGVGVHNAKT KPREEQFNST
201 YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPVY
251 TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVL
301 SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGK
(서열 1287)

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[0516]

[0517]

서열 1287에 도해된 BMS3h-56-269-IgG₄ Fc 융합 폴리펩티드는 분자량 계산값이 38,867 Da인 단량체이다. 이는 분자량 계산값이 77,734 Da인 이량체를 형성할 수 있다.

[0518]

BMS3h-56-269 (서열 417), BMS3h-56-269-IgG1* Fc 융합 폴리펩티드 (서열 1286), 및 BMS3h-56-269-IgG₄ Fc 융합 폴리펩티드 (서열 1287)의 서열이 하기에 정렬되고, 이때 Fc 도메인의 시작이 화살표로 표시된다:

```

BMS3h56-269 (서열 417) (1)
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSA
BMS3h56-269-CTL2 (서열 1286) (1)
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSA
BMS3h56-269-Ig4 (서열 1287) (1)
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSA

BMS3h56-269 (서열 417) (34)
INPQGTITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLP
BMS3h56-269-CTL2 (서열 1286) (51)
INPQGTITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLP
BMS3h56-269-Ig4 (서열 1287) (51)
INPQGTITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLP

BMS3h56-269 (서열 417) (84)
FRFSDRGGGTLTVVSS-----
BMS3h56-269-CTL2 (서열 1286) (101)
FRFSDRGGGTLTVVSSASTEPKSSDKHTSSPAPELLGGSSVFLFPFK
BMS3h56-269-Ig4 (서열 1287) (101)
FRFSDRGGGTLTVVSSASTESYG---PPCPAPELLGGSSVFLFPFK
↑
Fc 시작

BMS3h56-269 (서열 417) (117)
-----
BMS3h56-269-CTL2 (서열 1286) (151)
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
BMS3h56-269-Ig4 (서열 1287) (148)
PKDTLMISRTPEVTCVVVDVSHEDPEVFNWYVDGVEVHNAKTKPREEQF
BMS3h56-269 (서열 417) (117)
-----
BMS3h56-269-CTL2 (서열 1286) (201)
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
BMS3h56-269-Ig4 (서열 1287) (198)
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLESSIEKTISKAKGQPREP
BMS3h56-269 (서열 417) (117) -----
BMS3h56-269-CTL2 (서열 1286) (251)
QVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTP
BMS3h56-269-Ig4 (서열 1287) (248)
QVYTLPPSQEEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTP
BMS3h56-269 (서열 417) (117)
-----
BMS3h56-269-CTL2 (서열 1286) (301)
VLDSGGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG
BMS3h56-269-Ig4 (서열 1287) (298)
VLDSGGSEFFLYSRLLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPG

BMS3h56-269 (서열 417) (117) -
BMS3h56-269-CTL2 (서열 1286) (351) K
BMS3h56-269-Ig4 (서열 1287) (348) K

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[0519]

[0520] 실시예 11에 개시된 세포 배양 방법을 사용하여 이러한 Fc 융합 폴리펩티드들을 발현시켰다. 칼럼을 PBS (20 mM 인산나트륨, 0.15 M NaCl, pH 7.2)로 세정한 후, 80 mM 아세트산나트륨, pH 3을 사용하여 1/5 부피의 1 M 트리스-HCl, pH 8 내로 용출시켰다. 용출액을 PBS 내의 수퍼텍스-200 칼럼 상에 러닝시켰다.

[0521] 실시예 13

[0522] CD40 Fc 융합 폴리펩티드 활성 검정

[0523] 항-인간 CD40 Fc 융합 폴리펩티드를 CD40 활성을 길항하는 능력에 대해 기능적으로 검정하였다. 테스트된 CD40 활성은 1차 인간 단핵구-유래 수지상 세포 (DC)의 hCD40L-구동 활성화에 의한 B 세포 증식 및 시토카인 생산이었다. 실시예 6에 개시된 검정을 사용하여 B 세포 증식 및 시토카인 생산을 측정하였다. 달리 언급되지 않는 한, 모든 검정을 10% 송아지 태아 혈청 (FCS)이 보충된 RPMI 배지에서 수행하였다. dAb-Fc 도메인 융합 폴리펩티드들이 CD40-의존적 활성화의 강력한 억제 (즉, 길항작용)를 나타냈다. 인간CD40-특이적 dAb-Fc 도메인 융합 폴리펩티드 중 어느 것에서도 작동성 성질이 나타나지 않았다. 다양한 검정을 사용한 결과가 표 29에서 제시된다. 3h56-269-IgG4를 고정된 인간-CD40에 결합하는 것에 대해 실시예 11에 개시된 검정을 사용하여 검정하였다. 3h56-269-IgG4에 대해, 고정된 인간-CD40에 결합하는 것이 25°C에서는 30 pM, 37°C에서는 40 pM에서 측정되었기 때문에, 겔보기 결합력이 Kd 값에 영향을 미쳤다.

표 29

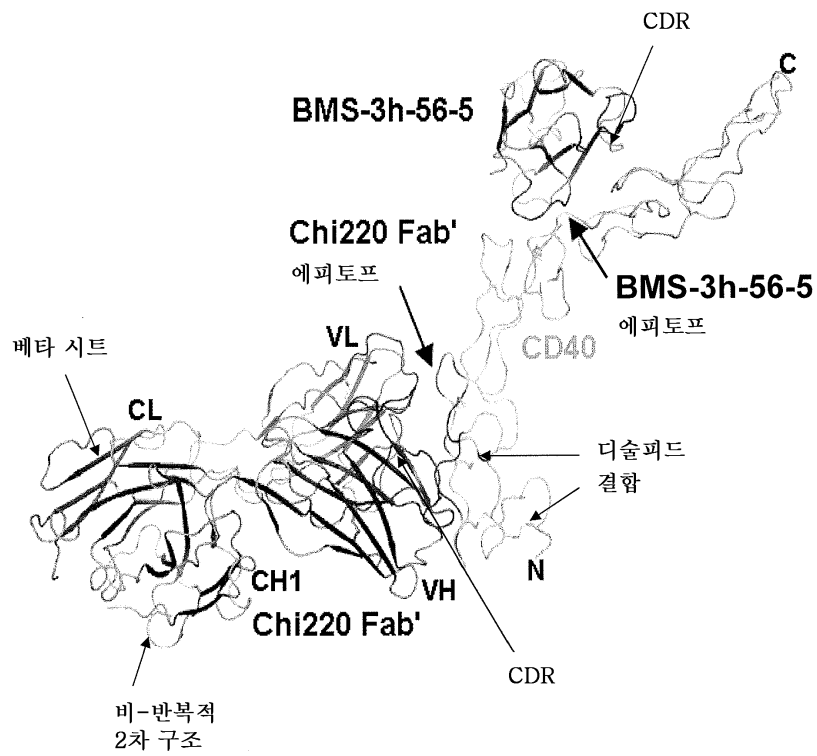
dAb-Fc	hZCD40L-구동 인간 B 세포 증식 EC50 (nM)	CHO- hCD40L- 구동 인간 B 세포 증식 EC50 (nM)	T-B 세포 MLR EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 TNF EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-6 EC50 (nM)	CHO- hCD40L- 구동 DC 활성화 IL-12 EC50 (nM)
3h37-202-IgG4	0.16 ± 0.08	5.0, 3.0	5.0, 6.0			0.53 ± 0.1
3h37-202-IgG1*	0.27, 0.22	3.0, 7.0				0.74 ± 0.2
3h38-235-IgG4	0.20, 0.15	6.0, 10.0	16.7 ± 5.7			0.67 ± 0.3
3h38-235-IgG1*	0.25 ± 0.1	4.0 ± 1.0				0.88 ± 0.3
3h56-258-IgG4	0.16 ± 0.05	1.0 ± 0.8	2.4 ± 0.99	0.22 ± 0.08	0.11 ± 0.05	0.3 ± 0.2
3h56-258-IgG1*	0.063 ± 0.03	0.6 ± 0.4	2.0 ± 0.63			0.31 ± 0.1
3h56-269-IgG4	0.028 ± 0.01	0.27 ± 0.08	0.52 ± 0.07	0.16 ± 0.03	0.09 ± 0.02	0.092 ± 0.03
3h56-269-IgG1*	0.025 ± 0.01	0.25 ± 0.04	0.53 ± 0.1	0.27 ± 0.06	0.15 ± 0.05	0.14 ± 0.06

[0524]

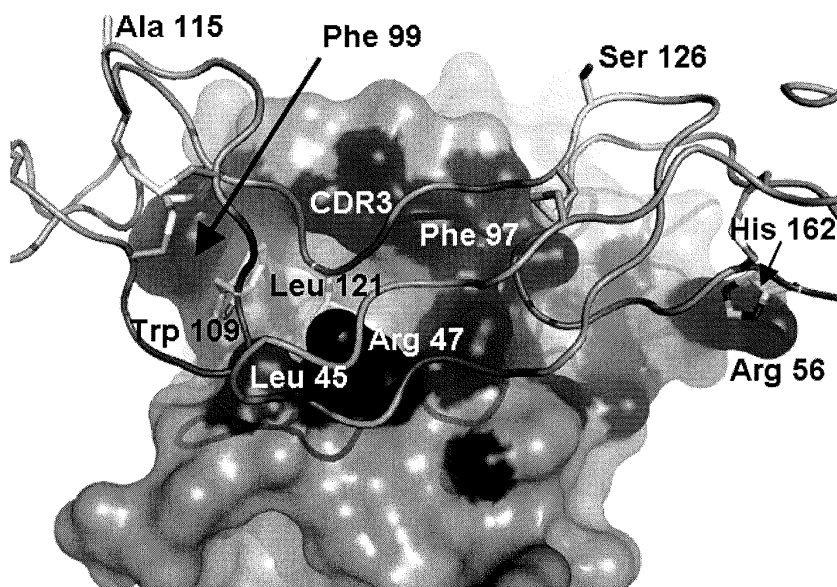
[0525] 본 발명의 실시양태들이 상기 실시예를 참조로 상세하게 기술되었지만, 다양한 변형이 이러한 실시양태들의 취지를 벗어나지 않으면서 이루어질 수 있고, 당업자에게 쉽게 알려질 것임이 이해된다.

도면

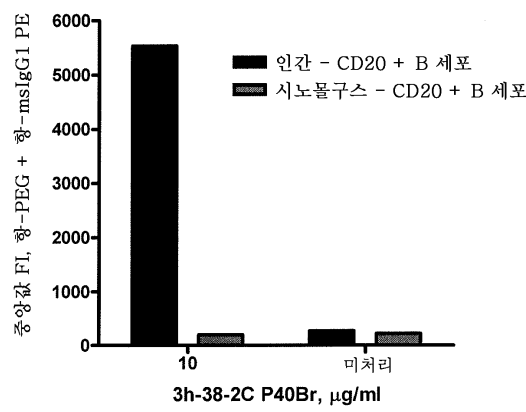
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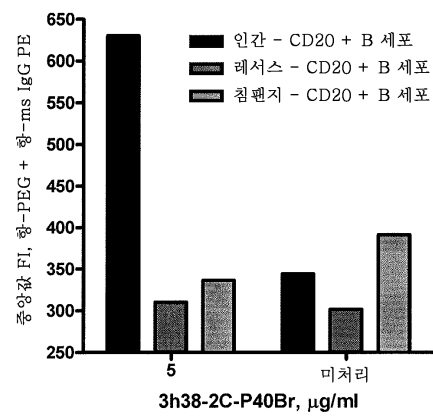
도면2



도면3



도 3A



도 3B

도면4

서열 번호

사원 9
사원 10
사원 353
사원 355
사원 410
사원 413
사원 418
사원 324
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사원 421
사원 325
사원 341
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사원 345
사원 332

CDR1

CDR2

CDR3

[illegible]

도면5

BMS3h-37-207	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	CDR1	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	CDR2	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	60
BMS3h-37-213	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	60
BMS3h-37-212	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	60
BMS3h-37-205	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	60
BMS3h-37-206	EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY		EVQLLESGGGGLVQPGGSLRLSCAAGFTFEWYEMQWVRAPGKGLEWVSAISGDGRITYY	60
	*****		*****		*****	
	CDR2		CDR3			
BMS3h-37-207	ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS	116 (44 226)
BMS3h-37-213	ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS	116 (44 232)
BMS3h-37-212	ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS	116 (44 231)
BMS3h-37-205	ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS	116 (44 224)
BMS3h-37-206	ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS		ADSVKGRFTISRDNKNTLYIQMSIARAEDTAVYYCAKEIAFEDYWGRTLVTVSS	116 (44 225)
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도면6

BMS3h-38-217	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	CDR1	CDR2
BMS3h-38-238	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60		
BMS3h-38-228	BMS3h-38-235	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	
BMS3h-38-231	BMS3h-38-237	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	
BMS3h-38-218	BMS3h-38-215	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	
BMS3h-38-215	BMS3h-38-223	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	
BMS3h-38-224	BMS3h-38-225	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	
BMS3h-38-219	BMS3h-38-219	EVQLIASGGGLVDPGGSLRLSCAASGFTPEEEMIMWRQAPKGLEWVSAISRGSITYY 60	
	*****	*****	*****
	CDR2	CDR3	
BMS3h-38-217	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 264)		
BMS3h-38-238	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 285)		
BMS3h-38-228	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 275)		
BMS3h-38-235	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 282)		
BMS3h-38-231	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 278)		
BMS3h-38-237	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 265)		
BMS3h-38-218	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 262)		
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BMS3h-38-225	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 266)		
BMS3h-38-219	ADSVKGRFTISRDNASKNTLIYIQNNSLRAEDTAVYYCGKEPERFYDWGGTLVTVSS 116 (4월 266)		

도면7

BMS3h-198-22	EVOLLESGGGIIVOPGGSLRLCSAAGFTPAEYEWTRQAPGKGLERVAISISGGSGTXY	CDR1	CDR2
BMS3h-198-21	EVOLLESGGGIIVOPGGSLRLCSAAGFTPAEYEWTRQAPGKGLERVAISISGGSGTXY		
BMS3h-198-19	EVOLLESGGGIIVOPGGSLRLCSAAGFTPAEYEWTRQAPGKGLERVAISISGGSGTXY		
BMS3h-198-13	EVOLLESGGGIIVOPGGSLRLCSAAGFTPAEYEWTRQAPGKGLERVAISISGGSGTXY		
BMS3h-198-8	EVOLLESGGGIIVOPGGSLRLCSAAGFTPAEYEWTRQAPGKGLERVAISISGGSGTXY		
BMS3h-198-14	EVOLLESGGGIIVOPGGSLRLCSAAGFTPAEYEWTRQAPGKGLERVAISISGGSGTXY		

	CDR2		CDR3
BMS3h-198-22	ASVYGRFTISDDSKNTLYIQMMSLRADPAVYCAKEPEYSDYMGOGTLTVSS		116 (4# 523)
BMS3h-198-21	ASVYGRFTISDDSKNTLYIQMMSLRADPAVYCAKEPEYSDYMGOGTLTVSS		116 (4# 532)
BMS3h-198-19	ASVYGRFTISDDSKNTLYIQMMSLRADPAVYCAKEPEYSDYMGOGTLTVSS		116 (4# 524)
BMS3h-198-13	ASVYGRFTISDDSKNTLYIQMMSLRADPAVYCAKEPEYSDYMGOGTLTVSS		116 (4# 520)
BMS3h-198-8	ASVYGRFTISDDSKNTLYIQMMSLRADPAVYCAKEPEYSDYMGOGTLTVSS		116 (4# 539)
BMS3h-198-14	ASVYGRFTISDDSKNTLYIQMMSLRADPAVYCAKEPEYSDYMGOGTLTVSS		116 (4# 515)

서 열 목 록

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<110>	Domantis Limited
	Bristol-Myers Squibb Company
<120>	Antibody Polypeptides That Antagonize CD40
<130>	200896-0004-00-WO (481834)
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<141>	2012-04-20
<150>	61/477904
<151>	2011-05-18
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1 5 10 15

Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
20 25 30

Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
35 40 45

Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
50 55 60

Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
65 70 75 80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
85 90 95

Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
100 105 110

Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
115 120 125

Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
145 150 155 160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
180 185 190

Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
195 200 205

Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
210 215 220

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

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

Val Gln Glu Arg Gln

275

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<212> PRT

<213> Macaca fascicularis

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 20 25 30
 Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
 35 40 45

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

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

Cys Arg Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Gln
180 185 190

Arg Ala Leu Val Val Ile Pro Ile Cys Leu Gly Ile Leu Phe Val Ile
195 200 205

Leu Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Asn
210 215 220

Asp Lys Val Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro
225 230 235 240

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

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

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

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<222> (1)..(25)

<223> This sequence may encompass 1 to 5 "Gly Gly Gly Gly Ser"
 repeating units

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1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser

20 25

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1 5

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1 5

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

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

 100 105 110
 Thr Val Ser Ser
 115
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 1 5 10 15
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 20 25 30

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

 Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

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Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

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<213> Artificial Sequence

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 13

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

115

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 15

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 15

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Thr Val Ser Ser
115

<210> 16

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 16

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

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

Ala Lys Pro Gly Pro Gln Phe Gly Gln Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 17

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 17

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr

20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 18

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 18

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

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

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

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

50 55 60

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

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Gly Trp Pro Gly

85 90 95

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

100 105

<210> 19

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 19

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105
 <210> 20
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 20
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 21
 <211> 120
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 21
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 22

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 22

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

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

100 105

<210> 23

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 23

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asn Arg Ile Pro Asp Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 24

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 24

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

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

<210> 25

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 25

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

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

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

<210> 26

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 26

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 27

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 27

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu His

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Gly Pro Asp Gly Phe His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 28

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 28

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Tyr

20 25 30

His Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

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

100 105 110

Thr Leu Val Thr Val Ser Ser

<210> 29

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 29

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45

Ser Arg Ile Ser Pro Gly Gly Asp Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Arg Val Pro Asp Leu Leu Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 30

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 30

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Ser Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Arg Val Pro Asp Leu Leu Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 31

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 31

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Asp

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Ala Val Asp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Lys Val Pro Ser Leu His Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 32

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 32

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Thr Met

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 33

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 33

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Asp

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asn Ala Gly Gly Val His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 34

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 34

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Asp

20 25 30

Ser Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Ser Ser Asp Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 35

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 35

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Glu
20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asp Ser Val Gly Glu Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 36
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 36

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

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

Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 37
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 37

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln His

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Glu Val Pro Arg Leu His Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 38

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 38

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln Glu

20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
 Ala Lys Gly Ile Thr Pro Asn Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 39
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 39

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 40
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 40

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Gln Gly Val Val Pro Tyr Leu Ala Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 41

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ala Asp

20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

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

<210> 42

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 42

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

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

Thr Leu Val Thr Val Ser Ser
 115

<210> 43

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Trp Glu

20 25 30

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

35 40 45

Ser Arg Ile Asn Ser Ser Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Met Val Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 44

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 44

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Glu

20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

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

 Ala Lys Gly Ile Thr Pro Asn Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 45
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 45
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Asn His

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

 85 90 95
 Ala Lys Gly Ile Val Pro Asp Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 46

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 46

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Ile Ile Pro Ala Met Gln Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 47

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 47

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45
Ser Arg Ile Asp Pro Tyr Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Gly Ile Met Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110
Thr Leu Val Thr Val Ser Ser

115

<210> 48

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 48

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 49

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 49

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr

20 25 30

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

35 40 45

Ser Gly Ile Val Pro Ser Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Arg Ile Pro Asp Leu His Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 50

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 50

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30
Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 51

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 51

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

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

Ala Lys Gly Ala Pro Lys Phe Met Thr Thr Tyr Thr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 52

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 52

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Ser Tyr

20 25 30

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly His Ser Trp Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 53

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 53

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45

Ser Arg Ile Asn Pro Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 54

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 54

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Arg

20 25 30

Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Glu Gly Ala Gln Gly Val Leu Leu Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 55

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 55

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr

20 25 30

Arg Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Val Thr Val Ser Ser

115

<210> 56

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 56

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Tyr

20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Val Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 57

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

Description of Artificial Sequence: Synthetic polypeptide

<400> 57

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Thr Val Ser Ser

115

<210> 58

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 58

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Glu

20

25

30

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

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Thr Val Ser Ser

115

<210> 59

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 59

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Tyr

20 25 30

Asp Met Val Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Gln Ser Ala Ser Arg Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 60

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 60

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr

	20	25	30
Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Ser Ile Ser Thr Leu Gly Thr Lys Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Gln Ser Ser Thr His Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
100	105	110	
Val Thr Val Ser Ser			
115			
<210> 61			
<211> 117			
<212> PRT			
<213> Artificial Sequence			
<220><223> Description of Artificial Sequence: Synthetic polypeptide			
<400> 61			
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Arg Tyr			
20	25	30	
Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Ser Ile Ser Ser Ser Gly Trp Thr Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

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

100 105 110

Val Thr Val Ser Ser

115

<210> 62

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 62

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Ala Tyr

20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Leu Gly Gln Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 63

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 63

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp His

20 25 30

Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 64

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 64

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ser Gln

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Gly Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

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

<210> 65

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223>

Description of Artificial Sequence: Synthetic polypeptide

<400> 65

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

50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Ala Val Pro Lys Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115

<210

> 66

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 66

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Asp Pro Gln Gly Gly Met Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ala Arg Ile Pro Asn Leu Glu Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 67

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 67

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asn Pro Thr Gly Ser Tyr Thr Tyr Tyr Ala Asp Ser Val

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

 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 68
 <211> 121
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 68
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Ser
 20 25 30

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

 Ala Lys Ala Gly His Pro Gln Gln Thr Glu Ala Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120
 <210> 69

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69

Glu Met Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Thr Tyr

20 25 30

Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Tyr Gln Thr His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 70

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 70

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Asp Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Tyr Pro Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 71

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 71

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

115

<210> 72

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 72

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Lys Tyr

20 25 30

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

35 40 45

Ser Thr Ile Asp Tyr Trp Gly Gln His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 73

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 73

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Tyr Val Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Lys Ala Leu Arg Gly Glu Ala Phe Thr Glu Arg Phe Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 74

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 74

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

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

100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 75

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 75

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Thr Thr

20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Gly Ser Ala Gly Ala Trp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ile Gly Gly His Pro Gln Gly Gln Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 76

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 76

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Arg Glu
 20 25 30

Trp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gln Pro Met Gly Gln Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Ser Arg Asn Lys Gly Phe Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 77

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 77

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ser Glu
 20 25 30

Tyr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gln Arg Tyr Gly Ser Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys His Glu Ser Asn Trp Glu Thr Phe Asp Tyr Trp Gly Gln Gly

100

105

110

Thr Leu Val Thr Val Ser Ser

115

<210> 78

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 78

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

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

35

40

45

Ser Ala Ile Thr Pro Asn Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 79

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 79

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 80

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 80

1	5	10	15
Glu	Val	Gln	Leu
Leu	Glu	Ser	Gly
Gly	Gly	Leu	Val
Gln	Pro	Gly	Gly
20	25	30	
Ser	Leu	Arg	Leu
Ser	Cys	Ala	Ala
Ser	Gly	Phe	Thr
Phe	Ser	Thr	Tyr
35	40	45	
Asp	Met	Ile	Trp
Val	Arg	Gln	Ala
Pro	Gly	Lys	Gly
Leu	Glu	Trp	Val
100	105	110	
Ser	Ala	Ile	Ser
Pro	Asn	Gly	Thr
Gly	Ile	Tyr	Tyr
Ala	Asp	Ser	Val

[illegible]

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 81

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asn Tyr
20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Ala Pro His Gly Arg Leu Thr Tyr Tyr Ala Asp Ser Val

50					55					60									
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr				
65					70					75					80				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys				
					85					90					95				
Ala	Lys	Gly	Gln	Ile	Pro	Met	Leu	Asp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly				
					100					105					110				
Thr	Leu	Val	Thr	Val	Ser	Ser													
115																			

<210> 82

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 82

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr

20 25 30

Met Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser His Phe Gly Asp Ile Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asn Asp Met Val Met Lys Asn Gly Gly Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 83

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 83

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asp Ser Arg Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Leu Val Pro His Leu Arg Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 84

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 84

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Gln Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asp Ala Met Gly Asp Ala Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Val Thr Val Ser Ser

115

<210> 85

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 85

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Gln Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asp Ala Met Gly Asp Ala Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Val Thr Val Ser Ser

115

<210> 86

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 86

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asn Asp

20 25 30

Arg Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Thr Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gln Thr Gly Thr Asn Arg Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 87

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gln Pro

20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Asp Ala Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 88

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 88

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Gln Val Pro Glu Leu Leu Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 89

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 89

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Ser

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 90

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 90

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Ser

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

Thr Leu Val Thr Val Ser Ser
115

<210> 91

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 91

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 92

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 92

Glu Met Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 93

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 93

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Glu

20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Ile Gly Gly Gly His Glu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Gly Thr Ile Pro Leu Leu Glu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 94

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 94

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Glu
20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val
35 40 45

Ser Arg Ile Thr Glu Arg Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Thr Leu Val Thr Val Ser Ser

115

<210> 95

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 95

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Glu

20 25 30
Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Arg Ile Ile Gly Gly Gly His Glu Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly

100 105 110
Thr Leu Val Thr Val Ser Ser

115

<210> 96

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 96

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Glu Thr

20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Asn Arg Leu Gly Gln Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

<210> 97

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 97

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

Thr Leu Val Thr Val Ser Ser

115

<210> 98

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 98

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 99

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 99

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Asp
20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Ile Thr Pro Asn Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 100

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 100

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Glu

20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 101

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 101

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Ser

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ala Ala Pro Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Arg Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 102

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 102

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Asp
20 25 30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Arg Ile Asp Gly Thr Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Gln Val Pro Glu Leu Leu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 103

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 103

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Ser
20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ala Ala Pro Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 104

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 104

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe Asp Leu Ala

20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ala Glu Gly Val Ile Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 105

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 105

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

His Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Ser Pro Asp Gly Thr Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ala Glu Gly Val Ile Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 106

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 106

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Asp

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

 Thr Leu Val Thr Val Ser Ser
 115
 <210> 107
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 107
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe Asp Leu Ala
 20 25 30
 Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

Thr Leu Val Thr Val Ser Ser

115

<210> 108

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 108

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Ser

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 109

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 109

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu His Ala

20 25 30

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

35 40 45

Ser Arg Ile Asp Asn Ser Gly Gln Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 110

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 110

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Ala

20 25 30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115
<210> 111
<211> 119
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide
<400> 111

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 112
<211> 121
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 112

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Val Ala
20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys His Ala Ser Thr Glu Gly Pro Thr Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 113

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 113

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Tyr
20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Trp Ile Ser Ala His Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Thr Val Ser Ser

115

<210> 114

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 114

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Gly

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Met Val Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 115

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 115

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 116

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 116

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Ser

20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val

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

 85 90 95
 Ala Lys Ser Pro Ser Ser Arg Leu Lys Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 117
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 117
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 118

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 118

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Ala Tyr

20 25 30
Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Trp Ile Ala Ser Gly Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Arg Thr Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 119

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 119

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Ser Tyr

20 25 30
Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Gly Ile Thr Ser Asn Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

<210> 120

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 120

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

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

115

120

<210> 121

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 121

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Glu Ser

20 25 30

Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Arg His Pro Gly Glu Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 122

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 122

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Met Tyr

20 25 30
Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Ser Ile Ala Pro Pro Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 123

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 123

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Asn

20 25 30

Pro Met Ser Trp Val Arg His Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Pro Ala Asn Gly Arg Pro Thr Ser Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Tyr Ser Gln Gln Pro Gly Arg Arg Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 124

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 124

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Tyr

20 25 30

His Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 125

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 125

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gln Tyr

20 25 30

His Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 126

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 126

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Arg Glu His Ala Gly Gln Pro Pro Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 127

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 127

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gly Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Lys Leu Thr Leu Ala Ser Asn Tyr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 128

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 128

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Asp Tyr

20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 129

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 129

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro His Tyr

20 25 30

Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 130

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 130

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

35 40 45
Ser Arg Ile Gly Asp Glu Gly Gln Glu Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
100 105 110
Thr Leu Val Thr Val Ser Ser
115

<210> 131

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 131

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser

20 25 30

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

35 40 45

Ser Ala Ile Gly Ser Asp Gly Pro Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 132

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 132

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Pro Gly

20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Asp Gly Ser Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 133

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 133

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Ser
20 25 30

Met Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Gly Tyr Pro Gly Ala Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Gly Ser Arg Asp Asp Asn Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 134

<211> 124

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 134

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln His

20 25 30
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Ser Ile Ser Val Pro Gly Pro Lys Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Ser Leu Arg Asp Leu Arg Pro Gly Asp Ser Lys Ser Phe Asp

100 105 110
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 135

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 135

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Ala

20 25 30

Ala Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Asn Asp Met Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

<210> 136

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 136

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

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

Leu Val Thr Val Ser Ser

115

<210> 137

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 137

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Tyr

20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Glu Gly Val Val Pro Asp Leu Asn Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 138

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 138

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Lys Tyr
20 25 30

Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Gly Ser Tyr Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 139

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 139

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr

20 25 30

Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ala His Arg Gly Asp Ile Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 140

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 140

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln Phe

20 25 30

Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Pro Ala Gly Thr Gly Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 141

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 141

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Asp Thr
20 25 30

Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Tyr Gly Arg Asp Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

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

Leu Val Thr Val Ser Ser
115

<210> 142

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 142

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Tyr
20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Ala Pro Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Gln Gln Met Ser Ser Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 143

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 143

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Gln

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Lys Ser Leu Ala Arg Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 144

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 144

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Ser

20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Pro Ala Gln Val Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210

> 145

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 145

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gln Tyr

20 25 30

Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Gln Arg Arg Ser Leu Thr Arg Val His Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 146

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 146

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

His Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Thr Val Ser Trp Asn Gly Arg Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 147

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 147

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Trp Tyr

20 25 30

Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Ala Pro Ser Gly Ile Ile Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Leu Arg Gly Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 148

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 148

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr

20 25 30

Glu Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ser Ala Gly Thr Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 149

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 149

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ile Ile Asp Pro Gly Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Ser Asn Ser Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115
<210> 150
<211> 121
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide
<400> 150

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 151
<211> 119
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 151

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Arg Pro Tyr Ala Ser Lys Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 152

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 152

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Pro Tyr

20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser His Gln Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

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

115

<210> 153

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 153

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

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

Leu Val Thr Val Ser Ser
 115

<210> 154

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 154

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Val Lys Lys His Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 155

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 155

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala His Tyr

20 25 30

Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

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

 Ala Lys Ala Gly Gln Phe Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115
 <210> 156
 <211> 118
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 156
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Pro Tyr

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

 85 90 95
 Ala Glu Asp Ser Leu Lys Ala Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115
 <210> 157

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 157

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Leu Tyr

20 25 30

Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Lys Arg Lys Lys Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 158

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 158

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Arg Tyr

20 25 30

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

35 40 45
 Ser Ser Ile Thr Pro Tyr Gly Ala His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Tyr Gly Lys Trp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115
 <210> 159
 <211> 117
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 159
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr
 20 25 30
 Ala Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Thr Ile Asp Arg Leu Gly Leu His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

115

<210> 160

<211> 117

<212> PRT

<213> Artificial Sequence

<

220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 160

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr

20 25 30

Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ala Gly Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210

> 161

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 161

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ile Tyr

20 25 30
Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Leu Val Thr Val Ser Ser
115

<210> 162

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 162

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

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

Ala Lys Tyr Pro Pro Ala Gly Arg Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 163

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 163

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

Asp Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Pro Pro Gln Val Asn Thr Glu Phe Asp Tyr Arg Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 164

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 164

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser His Ile Ser Pro Asn Gly Tyr Ala Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ser Trp Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 165

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 165

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Thr

20 25 30

Pro Met Glu Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Trp Asn Ser Thr Thr Gly Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 166

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 166

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Val

20 25 30

Asp Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Glu Ala Pro His Arg Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 167

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 167

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Lys

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 168

<211> 114

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 168

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Asn Pro Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

100 105 110

Ser Ser

<210> 169

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 169

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro His

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Gly Ile Gly Pro Asp Gly Thr Thr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Arg Ser Tyr Ser Trp Asp Arg Gly Trp Thr Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 170

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 170

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Ala Ser

20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ala Asp Tyr Thr Tyr His Ser Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 171

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 171

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala His Tyr

	20	25	30
Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Thr Ile Thr Lys Thr Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Lys Ala Gly Gln Phe Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu			
100	105	110	
Val Thr Val Ser Ser			
115			
<210> 172			
<211> 118			
<212> PRT			
<213> Artificial Sequence			
<220><223> Description of Artificial Sequence: Synthetic polypeptide			
<400> 172			
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr			
20	25	30	
His Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Val Ile Gly Pro Arg Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

Ala Lys Ser Pro Ser Arg His Arg Phe Asp Tyr Trp Gly Gln Gly Thr

100

105

110

Leu Val Thr Val Ser Ser

115

<210> 173

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 173

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr

20

25

30

Ala Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Ser Gly Pro Phe Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100

105

110

Val Thr Val Ser Ser

115

<210> 174

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 174

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 175

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 175

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

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Ser Leu Tyr Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 176

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 176

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Pro Thr Tyr

20 25 30

Lys Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Phe Ile Asp Tyr Trp Gly Trp Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ser Pro Tyr Ser Trp Thr His Asp Ser Pro His Phe Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 177

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 177

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Pro Tyr

20 25 30

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

35 40 45

Ser Cys Ile Ser Asp Ala Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Arg Met Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 178

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 178

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asn Tyr

20 25 30

Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

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

 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120
 <210> 179
 <211> 118
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 179
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Tyr
 20 25 30

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

 Ala Lys Pro Leu Asn Trp Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115
 <210> 180

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 180

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ala Tyr

20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Arg Ile Asp Gly Tyr Gly Arg His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Ile Ile Pro Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu

100 105 110

Val Thr Val Ser Ser

115

<210> 181

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 181

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Val

20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Arg Val Pro Asp Leu Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 182

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 182

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

115

<210> 183

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 183

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Arg Tyr

20 25 30

Gln Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Val Ile Asn Val Trp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Met Ser Gly Lys Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 184

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 184

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr

20 25 30
 Ser Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Thr Ile Ile Pro Ala Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Pro Ser Ile Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser
 115
 <210
 > 185
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 185
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Tyr
 20 25 30
 Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Trp Ile Ser Pro Asn Gly Tyr Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Gly Gly Val Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 186

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 186

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Trp Tyr

20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 187

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 187

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asn Tyr
20 25 30

Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Asp Asp Leu Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Trp Arg Leu Lys Asn Ser Gln Pro Thr Asp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 188

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 188

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gln Ala

20 25 30
His Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Phe Ile Asn Pro Ser Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Pro Ser Leu Ser Pro Ser Ser Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 189

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 189

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Thr Gly

20 25 30

Gln Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 190

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 190

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Tyr

20 25 30
Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Ser Ile His Lys Asp Gly Arg Ile Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Gln Gly Thr Pro Val Asp Gly Phe Asp Tyr Trp Gly Gln Gly

100 105 110
Thr Leu Val Thr Val Ser Ser

115

<210> 191

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 191

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asp Glu

20 25 30
Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Thr Ile Glu Thr Gly Gly Thr Val Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Met Asp Gly Ser Gly Thr Trp Gln Thr Phe Asp Tyr Trp Gly

100

105

110

Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 192

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 192

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ser Leu

20

25

30

Gly Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Tyr Leu Ala Asp Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 193

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 193

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Ser

20 25 30

Tyr Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Gly Ile Asp His Ile Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Asp Gly Arg Gly Gly Ser Met Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 194

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 194

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Gly

20 25 30

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

Ala Lys Thr Gly Gly Arg Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 195

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 195

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Gly

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

Thr Leu Val Thr Val Ser Ser

115

<210> 196

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 196

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Thr Ser

20 25 30

Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Asp Arg Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gln Ala Leu Leu Thr Asp Ala Lys Arg Phe Asp Tyr Trp Gly

100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 197

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 197

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

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

<210> 198

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 198

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

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

Ala Lys Asp Ser Met Arg His Gln Pro Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 199

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 199

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Thr

20 25 30

Tyr Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Gly Ala Ser Gly Ala Asp Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Phe Thr His Leu Asn Gly Arg Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 200

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 200

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

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

Thr Leu Val Thr Val Ser Ser
 115

<210> 201

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 201

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Pro Ser Lys Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 202

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 202

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Thr Gly

20 25 30

Gln Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Ala Val Arg Asn Phe Ala Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 203

<211> 124

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 203

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly His

20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 204

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 204

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ser Asp Gly Thr His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Gln Glu Leu Gly Gly Ser Trp Gln Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 205

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 205

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Arg

20 25 30

Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Gly Ile Gly Ala Ser Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Gly Thr Gly Pro Thr Asp Leu Trp Asp Phe Asp Tyr Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 206

<211> 119

<212

> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 206

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Glu

20 25 30

Lys Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Val Ser Gly Leu His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Glu Ala Gly Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 207

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 207

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln Glu

20 25 30

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

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

100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

<210> 208

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 208

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

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

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

115

<210> 209

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 209

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 210

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

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

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

Thr Val Ser Ser

115

<210> 211

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 211

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

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

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 212

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 212

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 213

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 213

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 214

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 214

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

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

85 90 95
 Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

 Thr Val Thr Ser
 115
 <210> 215
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 215
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30
 Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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

 100 105 110
 Thr Val Ser Ser
 115
 <210> 216
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 216

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Ile

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 217

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 217

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65						70						75						80
Leu	Leu	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys			
					85						90						95	
Ala	Lys	Glu	Leu	Gly	Tyr	Phe	Asp	Tyr	Trp	Gly	Arg	Gly	Thr	Leu	Val			
					100						105						110	
Thr	Val	Ser	Ser															
					115													
<210>	218																	
<211>	116																	
<212>	PRT																	
<213>	Artificial Sequence																	
<220><223>	Description of Artificial Sequence: Synthetic polypeptide																	
<400>	218																	
Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly			
1					5					10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Glu	Trp	Tyr			
					20						25						30	
Glu	Met	Gln	Trp	Val	Arg	Lys	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val			
					35						40						45	
Ser	Ala	Ile	Ser	Gly	Asp	Gly	Tyr	Arg	Thr	Tyr	Tyr	Ala	Asp	Ser	Val			
					50						55						60	
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr			
65					70					75					80			
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys			
					85						90						95	
Ala	Lys	Glu	Leu	Gly	Tyr	Phe	Asp	Tyr	Arg	Gly	Arg	Gly	Thr	Leu	Val			
					100						105						110	
Thr	Val	Ser	Ser															
					115													
<210>	219																	
<211>	116																	
<212>	PRT																	

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 219

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15
Ser Met Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr			

20	25	30
Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val		

35	40	45
Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val		

50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		

65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			

85	90	95
Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Arg Gly Arg Gly Thr Leu Val		

100	105	110
Thr Val Ser Ser		

115

<210> 220

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 220

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr			

20	25	30
Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val		

35	40	45
Ser Met Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val		

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

115

<210> 221

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 221

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

50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
	85	90	95
Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val			
	100	105	110
Thr Val Ser Ser			
115			

<210> 222

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 222

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Leu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 223

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 223

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Gly Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 224

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 224

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Glu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 225

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 225

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Gly Leu Glu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 226

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 226

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Ala Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 227

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 227

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Leu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 228

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 228

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Glu Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 229

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 229

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Leu Gln Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 230

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 230

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

Thr Val Ser Ser
115

<210> 231

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 231

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

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

Thr Val Ser Ser
115

<210> 232

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 232

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 233

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 233

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

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

Thr Val Ser Ser

115

<210> 234

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 234

Glu Val Arg Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Thr Val Ser Ser

115

<210> 235

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 235

Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ser Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 236

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 236

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

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

<210> 237

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 237

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

Thr Val Ser Ser

115

<210> 238

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 238

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 239

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 239

Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

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

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 240

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 240

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 241

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 241

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 242

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 242

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile His Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Thr Val Ser Ser
115

<210> 243

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 243

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 244

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 244

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

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 245

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 245

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Arg Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 246

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 246

Glu Val Arg Leu Leu Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 247

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 247

Glu Val Gln Gln Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 248

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 248

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 249

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 249

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 250

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 250

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
 Gly Lys Glu Pro Phe Phe Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 251
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 251

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 252
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400>

> 252

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Ala Ala
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 253

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 253

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Pro Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

115
 <210> 254

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 254

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

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

Thr Val Ser Ser
 115

<210> 255

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 255

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Arg Trp Gly His Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 256

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 256

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

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

 Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 257
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 257
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

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

 85 90 95
 Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 258

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 258

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 259

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 259

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45
Ser Ala Ile Ser Val Ser Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 260

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 260

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Arg Trp Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 261

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 261

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 262

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 262

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Thr Val Ser Ser
115

<210> 263

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 263

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

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

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 264

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 264

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 265

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 265

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Arg His Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 266

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 266

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 267

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 267

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 268

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 268

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly His Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 269

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 269

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Arg Trp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 270

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 270

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20

25

30

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

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Thr Val Ser Ser

115

<210> 271

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 271

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Pro Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 272

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 272

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

	20	25	30
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Ala Ile Ser Gly Ser Gly Gly Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val			
100	105	110	
Thr Val Ser Ser			
115			
<210> 273			
<211> 116			
<212> PRT			
<213> Artificial Sequence			
<220><223> Description of Artificial Sequence: Synthetic polypeptide			
<400> 273			
Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu			
20	25	30	
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
35	40	45	
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

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

100

105

110

Thr Val Ser Ser

115

<210> 274

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 274

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20

25

30

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

35

40

45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Gly Lys Glu Pro Met Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 275

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 275

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Arg Asn Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 276

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 276

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

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

<210> 277

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 277

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

50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 278

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 278

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 279

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 279

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

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

 100 105 110
 Thr Val Ser Ser
 115
 <210> 280
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 280
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

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

 Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 281

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 281

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 282

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 282

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 283

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 283

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

115

<210> 284

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 284

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

Ser Ala Ile Ser Arg Gly Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 285

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 285

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30
 Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Arg Ser Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val

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

115

<210> 286

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 286

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

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

100 105 110

Thr Val Ser Ser

115

<210> 287

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 287

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 288

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 288

Glu Val Gln Leu Leu Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu His
 20 25 30

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

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

<210> 289

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 289

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 290

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 290

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30

Glu Met Ile Trp Val Arg Lys Ala Pro Gly Lys Gly Met Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 291

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 291

Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 292

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 292

Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Ser Leu Glu Trp Val

35 40 45
Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Tyr Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser

115

<210> 293

<211> 116

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle \langle 223$

> Description of Artificial Sequence: Synthetic polypeptide

<400> 293

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

50						55						60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
65						70						75					
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
					85						90						
Ala	Lys	Glu	Pro	Leu	Arg	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val		
					100						105						
Thr	Val	Ser	Ser														
115																	

<210> 294

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 294

Glu Val Gln Leu Leu Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 295

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 295

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Ser

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 296

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 296

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30

Glu Met Ile Trp Val Arg Lys Ala Pro Gly Lys Gly Met Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 297

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 297

Glu Val Gln Leu Leu Glu Ser Gly Val Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30

Glu Met Ile Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 298

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 298

Glu Val Gln Leu Leu Glu Ser Arg Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu His

20 25 30

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

35 40 45

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

50 55 60

Lys Gly Arg Phe Ser Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 299

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 299

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 300

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 300

Glu Val Gln Leu Leu Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Tyr

20

25

30

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

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Thr Val Ser Ser

115

<210> 301

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 301

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 302

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 302

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20 25 30

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

35 40 45

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

50 55 60

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

Ser Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 303

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 303

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

35 40 45
Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Pro Ile Thr Tyr Ala Thr Arg Tyr Ala Arg Phe Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 304

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 304

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Gly Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 305

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 305

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20 25 30

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

35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Asn
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asn
115 120

<210> 306

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 306

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Leu Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Ser Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 307

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 307

Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
Ser	Cys	Thr	Ala
Ser	Gly	Phe	Ser
Phe	Asn	Met	Tyr

20	25	30
Glu	Met	Ser
Trp	Val	Arg
Gln	Ala	Pro
Gly	Lys	Gly
Leu	Glu	Trp
Val		

35	40	45
Ser	Gly	Ile
Ser	Arg	Arg
Gly	Tyr	Thr
Thr	Tyr	Tyr
Ala	Asp	Ser
Val		

50	55	60
Lys	Gly	Arg
Phe	Thr	Ile
Ser	Arg	Asp
Asn	Ser	Lys
Asn	Thr	Leu
Tyr		

65	70	75	80
Leu	Gln	Met	Asn
Ser	Leu	Arg	Ala
Glu	Asp	Thr	Ala
Val	Tyr	Tyr	Cys

85	90	95
Ala	Lys	Glu
Pro	Ile	Thr
Tyr	Asp	Met
Arg	Tyr	Ala
Arg	Phe	Asp
Tyr		

100	105	110
Trp	Gly	Arg
Gly	Thr	Leu
Val	Thr	Val
Ser	Ser	

115	120

<210> 308

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 308

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15
Ser	Leu	Arg	Leu
Ser	Cys	Thr	Ala
Ser	Gly	Phe	Ala
Phe	Asn	Met	Tyr

20	25	30

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

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

<210> 309

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 309

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

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

100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 310

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 310

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Ser Gly Leu Gly Thr Met Val Thr Val Ser Ser

115 120

<210> 311

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 311

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
 20 25 30

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

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

<210> 312

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 312

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 313

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 313

Glu Val Gln Leu Phe Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20

25

30

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

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 314

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 314

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 315

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 315

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Gly

115

120

<210> 316

<211> 123

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 316

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr

20

25

30

Glu Met Ser Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 317

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 317

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 318

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 318

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

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

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 319

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 319

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

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

85 90 95
 Thr Lys Leu Pro Phe Ile Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser

115

<210> 320

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 320

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 321

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 321

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

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

<210> 322

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 322

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

Ala Lys Leu Pro Phe Ile Phe Asp Asn Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 323

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 323

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ser Val Tyr His Cys

85 90 95

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

100 105 110

Thr Val Ser Ser
115

<210> 324

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 324

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

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

Thr Val Ser Ser
 115

<210> 325

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 325

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 326

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 326

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Val Leu Glu Arg Val

35

40

45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 327

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 327

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 328

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 328

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Leu Lys Leu Pro Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 329

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 329

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr His Cys

85 90 95
Thr Lys Leu Pro Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 330

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 330

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Met Val Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 331

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 331

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 332

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 332

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 333

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 333

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 334

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 334

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

	20	25	30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Val Leu Glu Arg Val			
35	40	45	
Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val			
100	105	110	
Thr Val Ser Ser			
115			
<210> 335			
<211> 116			
<212> PRT			
<213> Artificial Sequence			
<220><223> Description of Artificial Sequence: Synthetic polypeptide			
<400> 335			
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr			
20	25	30	
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val			
35	40	45	
Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys			
85	90	95	

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 336

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 336

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35

40

45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Thr Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 337

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 337

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Leu Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 338

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 338

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

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

<210> 339

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 339

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

50 55 60
 Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Pro Tyr Ser Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 340

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 340

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 341

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 341

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

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

 100 105 110
 Thr Val Ser Ser
 115
 <210> 342
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 342
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

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

 Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 343

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 343

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 344

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 344

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115

<210> 345

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 345

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

115

<210> 346

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 346

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 347

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 347

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

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

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

115

<210> 348

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 348

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

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

100 105 110

Thr Val Ser Ser

115

<210> 349

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 349

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 350

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 350

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

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

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

<210> 351

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 351

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Phe Phe Glu Glu Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 352

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 352

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35

40

45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Thr Tyr Phe Lys Asp Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 353

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 353

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 354

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 354

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

[illegible]

115

<210> 355

<211> 116

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle \langle 223$

> Description of Artificial Sequence: Synthetic polypeptide

<400> 355

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

50					55					60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
65					70					75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					85					90					95	
Ala	Lys	Leu	Pro	Phe	Pro	Phe	Ser	Glu	Trp	Gly	Gln	Gly	Thr	Leu	Val	
100					105					110						
Thr	Val	Ser	Ser													
115																

<210> 356

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 356

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe Ser Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 357

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 357

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 358

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 358

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 359

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 359

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 360

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 360

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 361

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 361

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser His Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 362

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 362

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35

40

45

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

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Arg Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 363

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 363

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 364

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 364

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

Thr Val Ser Ser
115

<210> 365

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 365

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

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

Thr Val Ser Ser
115

<210> 366

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 366

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 367

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 367

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Asp Ser Gly Phe Thr Phe Pro Pro Val

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 368

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 368

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Tyr Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 369

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 369

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Asn Pro Trp Gly Asn His Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 370

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 370

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro His Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 371

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 371

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Pro Gly Met Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 372

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 372

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 373

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 373

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 374

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 374

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 375

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 375

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 376

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 376

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Ser Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 377

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 377

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Tyr Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 378

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 378

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 379

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 379

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 380

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

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

Thr Val Ser Ser

115

<210> 381

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 381

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15

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

20	25	30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

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

Thr Val Ser Ser

115

<210> 382

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 382

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 383

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 383

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 384

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 384

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser
115
<210> 385
<211> 116
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide
<400> 385

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 386
<211> 116
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide
<400>

> 386

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 387

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 387

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

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

115
 <210> 388

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 388

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

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

Thr Val Ser Ser
 115

<210> 389

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 389

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 390

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 390

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

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

 Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 391
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 391
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

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

 85 90 95
 Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 392

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 392

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 393

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 393

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Asn Pro Tyr Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 394

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 394

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 395

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 395

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 396

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 396

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Thr Val Ser Ser
115

<210> 397

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 397

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

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

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 398

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 398

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 399

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 399

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 400

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 400

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

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

50 55 60

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

[illegible]

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

[illegible]

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 402

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Trp Phe Thr Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 403

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 403

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 404

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 404

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Leu Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 405

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 405

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Thr Arg Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 406

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 406

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

	20	25	30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val			
35	40	45	
Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val			
100	105	110	
Thr Val Ser Ser			
115			
<210> 407			
<211> 116			
<212> PRT			
<213> Artificial Sequence			
<220><223> Description of Artificial Sequence: Synthetic polypeptide			
<400> 407			
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly			
1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr			
20	25	30	
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val			
35	40	45	
Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val			
50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr			
65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 408

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 408

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35

40

45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

100

105

110

Thr Val Ser Ser

115

<210> 409

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 409

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 410

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 410

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

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

Thr Val Ser Ser

115

<210> 411

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 411

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Gln Leu Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 412

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 412

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95

Ala Lys Leu Pro Phe Gly Phe Ser Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 413

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 413

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

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

 100 105 110
 Thr Val Ser Ser
 115
 <210> 414
 <211> 116
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 414
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

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

 Ala Lys Leu Pro Phe Phe Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115
 <210> 415

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 415

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro His Tyr Phe Lys Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 416

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 416

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Leu Pro Phe Tyr Phe Glu Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

<210> 417

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 417

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

115

<210> 418

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 418

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 419

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 419

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

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

115

<210> 420

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 420

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

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

100 105 110

Thr Val Ser Ser

115

<210> 421

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 421

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 422

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 422

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Asn

115

<210> 423

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 423

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 424

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 424

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

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

20

25

30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35

40

45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val

50

55

60

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

65

70

75

80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100

105

110

Thr Val Ser Ser

115

<210> 425

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 425

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

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

<210> 426

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 426

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

[illegible]

115

<210> 427

<211> 116

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle \langle 223$

> Description of Artificial Sequence: Synthetic polypeptide

<400> 427

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

50					55					60									
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr				
65					70					75					80				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	His	Cys				
					85					90					95				
Ala	Lys	Leu	Pro	Met	Phe	Phe	Glu	Asp	Trp	Gly	Gln	Gly	Thr	Leu	Val				
100					105					110									
Thr	Val	Ser	Asn																
115																			

<210> 428

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 428

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 429

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 429

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 430

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 430

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

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

100 105 110

Thr Val Ser Ser

115

<210> 431

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 431

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 432

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 432

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Asn

115

<210> 433

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 433

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 434

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 434

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 435

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 435

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Phe Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 436

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 436

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95
Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 437

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 437

Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30
His Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
Ser Met Ile Asp Ala Asp Gly Leu Gly Thr Tyr Tyr Ala Asp Pro Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Lys Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Pro Gly Pro Gln Phe Gly Gln Phe Asp Tyr Leu Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 438

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 438

Glu Val Gln Leu Phe Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

20 25 30

His Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Met Ile Asp Ala Asp Gly Leu Gly Lys Tyr Tyr Ala Asp Pro Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Val Lys Pro Gly Pro Gln Phe Gly Gln Tyr Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 439

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 439

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Gly Tyr

20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Tyr Pro Asn Arg Phe Ala Leu Asn Ser Phe Asp Tyr Arg Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 440

<211> 121

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 440

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Tyr Thr Tyr Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Thr Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Lys Tyr Pro Asn Arg Phe Ala Arg Asn Asn Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 441

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 441

Asp Ile Leu Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Asn	Ser	Ser
Ile	Leu	Trp	Ala
20	25	30	
Leu	Ala	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Glu	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Glu	Ser	Ser	Ser
Gly	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Leu	Gln	Pro

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
Val	Gln	Asn	Ala
Val	Trp	Pro	Gly
85	90	95	
Thr	Phe	Ser	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 442

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 442

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Asp	Ser	Ser
Ile	Leu	Trp	Ala
20	25	30	
Leu	Ala	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 443

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 443

Asp Ile Gln Met Thr Val Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Ser Ser Ile Leu Trp Ala

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 444

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 444

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Asn	Ser	Ser
Ile	Leu	Trp	Ala
20	25	30	
Leu	Ala	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Glu	Ser	Ser	Ser
Gly	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Leu	Gln	Pro

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
Val	Gln	Asn	Ala
Val	Trp	Pro	Gly
85	90	95	
Thr	Phe	Asp	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 445

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 445

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Asn	Ser	Ser
Ile	Leu	Trp	Ala
20	25	30	
Leu	Ala	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Glu	Ser	Ser	Thr
Gly	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Leu	Gln	Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 446

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 446

Asp Ile Gln Met Thr Val Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 447

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 447

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Ser Ser Ile Leu Trp Ala
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Asp Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 448

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 448

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
 35 40 45
 Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 449

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 449

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg

100 105

<210> 450

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 450

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
 Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 451

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 451

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Glu Ser Ser Ser Gly Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 452

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 452

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr	Ile Thr Cys Arg	Ala Asn Ser Ser	Ile Leu Trp Ala
20	25	30	
Leu Ala Trp Tyr	Gln Gln Lys Pro	Gly Lys Ala Pro	Lys Leu Leu Ile
35	40	45	
Glu Ser Ser Ser	Gly Leu Gln Ser	Gly Val Pro Ser	Arg Phe Ser Gly
50	55	60	
Ser Gly Ser Gly	Thr Asp Phe Thr	Leu Thr Ile Ser	Ser Leu Gln Pro

65	70	75	80
Glu Asp Phe Ala	Thr Tyr Tyr Cys	Val Gln Asn Ala	Val Trp Pro Gly
85	90	95	
Thr Phe Gly Gln	Gly Thr Lys Val	Glu Ile Lys Arg	
100	105		

<210> 453

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 453

Asp Ile Leu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr	Ile Thr Cys Arg	Ala Asn Ser Ser	Ile Leu Trp Ala
20	25	30	
Leu Ala Trp Tyr	Gln Gln Lys Pro	Gly Lys Ala Pro	Lys Leu Leu Ile
35	40	45	
Glu Ser Ser Ser	Gly Leu Gln Ser	Gly Val Pro Ser	Arg Phe Ser Gly
50	55	60	

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 454

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 454

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Thr Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly

85 90 95

Thr Phe Asp Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 455

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 455

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Pro Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Ala Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 456

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 456

Asp Ile Gln Met Ala Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu

85 90 95
 Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105
 <210> 457
 <211> 108
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 457

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Asn Val Glu Ile Lys Arg
 100 105

<210> 458
 <211> 108
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 458

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Ala Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 459

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 459

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 460

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 460

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Glu Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65 70 75 80
Glu Asp Ser Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu

85 90 95
Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 461

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 461

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
85 90 95

Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 462

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 462

Asp Ile Gln Ile Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Asp Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 463

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 463

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg			
20	25	30	
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile			
35	40	45	
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly			
50	55	60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro			

65	70	75	80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu			
85	90	95	
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Trp			
100	105		

<210> 464

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 464

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg			
20	25	30	
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile			
35	40	45	
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly			
50	55	60	
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro			

65	70	75	80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 465

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 465

Asp Ile Gln Met Ser Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu

85 90 95

Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 466

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 466

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Asp Pro Lys Leu Leu Ile
35 40 45
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 467

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 467

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 468

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 468

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Phe Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Thr
Ile	Glu	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Ser
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
His	Gln	Tyr	Glu
Ser	Pro	Pro	Leu
85	90	95	
Thr	Phe	Gly	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 469

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 469

Asp Ile Gln Met Thr Gln Tyr Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Ser
Ile	Glu	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Glu	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 470

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 470

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Pro Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 471

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 471

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Ala
Ile	Glu	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Ser
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
His	Gln	Tyr	Ala
Ser	Pro	Pro	Leu
85	90	95	
Thr	Leu	Gly	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 472

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 472

Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Ala
Ile	Glu	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Ser
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 473

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 473

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Gly Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 474

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 474

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 475

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 475

Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Lys Ile Lys Arg

100 105

<210> 476

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 476

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 477

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 477

His Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 478

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 478

Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Leu Thr Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 479

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 479

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Thr
Ile	Glu	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Ser
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
His	Gln	Tyr	Glu
Ser	Pro	Pro	Leu
85	90	95	
Thr	Phe	Gly	Gln
Gly	Thr	Lys	Val
Val	Ile	Lys	Arg
100	105		

<210> 480

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 480

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Thr
Ile	Glu	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Thr
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 481

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 481

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 482

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 482

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr	Ile Thr Cys Arg Ala Ser	Gln Thr Ile Gly Arg Arg	
20	25	30	
Leu Asn Trp Tyr	Gln Gln Lys Pro Gly Lys Ala Pro	Lys Leu Leu Ile	
35	40	45	
Tyr Leu Ala Ser	Arg Leu Gln Ser Gly Val Pro Ser	Arg Phe Ser Gly	
50	55	60	
Ser Gly Ser Gly	Thr Asp Phe Thr Leu Thr Ile Ser	Ser Leu Gln Pro	

65	70	75	80
Glu Asp Phe Ala	Thr Tyr Tyr Cys His Gln Tyr	Glu Ser Pro Pro Leu	
85	90	95	
Thr Phe Gly Gln	Gly Thr Lys Val Glu Ile Lys Arg		
100	105		

<210> 483

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 483

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp Arg Val Thr	Ile Thr Cys Arg Ala Ser	Gln Ser Ile Glu Arg Arg	
20	25	30	
Leu Asn Trp Tyr	Gln Gln Lys Pro Gly Lys Ala Pro	Lys Leu Leu Ile	
35	40	45	
Tyr Leu Ala Ser	Arg Leu Gln Ser Gly Val Pro Ser	Arg Phe Ser Gly	
50	55	60	
Ser Gly Ser Gly	Thr Asp Phe Thr Leu Thr Ile Ser	Ser Leu Gln Pro	

65	70	75	80
Glu Asp Phe Ala	Thr Tyr Tyr Cys His Gln Tyr	Glu Ser Pro Pro Leu	

85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Ile Arg
 100 105
 <210> 484
 <211> 108
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 484

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 485
 <211> 108
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 485

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Glu Arg Arg

20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 486

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 486

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Phe Glu His Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 487

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 487

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Phe Pro Ile Asp Arg Arg

20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile

35 40 45
Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu

85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 488

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 488

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Thr Ile Gly Arg Arg

20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile

35 40 45
Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 489

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 489

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Gln Ile Gly Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 490

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 490

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Glu	Arg
Ile	Gly	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Thr
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Leu	Gln	Pro

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
His	Gln	Tyr	Glu
Ser	Pro	Pro	Leu
85	90	95	
Thr	Phe	Gly	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 491

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 491

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Gln
Ile	Gly	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Thr
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Leu	Gln	Pro

65	70	75	80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 492

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 492

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Ala Arg Arg

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile

35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 493

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 493

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile Gly Arg Arg
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 494

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 494

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Asp Arg Arg
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45
Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 495

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 495

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Ser
Ile	Gly	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Thr
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
His	Gln	Tyr	Glu
Ser	Pro	Pro	Leu
85	90	95	
Thr	Phe	Gly	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 496

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 496

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Gln	Asn
Ile	Gly	Thr	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 497

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 497

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Val Ile Gly Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 498

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 498

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Glu	Ala
Ile	Gly	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Thr
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65	70	75	80
Glu	Asp	Phe	Ala
Thr	Tyr	Tyr	Cys
His	Gln	Tyr	Glu
Ser	Pro	Pro	Leu
85	90	95	
Thr	Phe	Gly	Gln
Gly	Thr	Lys	Val
Glu	Ile	Lys	Arg
100	105		

<210> 499

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 499

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1	5	10	15
Asp	Arg	Val	Thr
Ile	Thr	Cys	Arg
Ala	Ser	Thr	Ser
Ile	Ala	Arg	Arg
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Arg	Leu	Leu	Ile
35	40	45	
Tyr	Leu	Ala	Thr
Arg	Leu	Gln	Ser
Gly	Val	Pro	Ser
Arg	Phe	Ser	Gly
50	55	60	
Ser	Gly	Ser	Gly
Thr	Asp	Phe	Thr
Leu	Thr	Ile	Ser
Ser	Ser	Leu	Gln
Pro			

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 500

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 500

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Leu Asn Ile Gly Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 501

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 501

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Leu Ser Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 502

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 502

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Ile Ala Gly Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 503

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 503

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Ile

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 504

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 504

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Ser Thr Phe Ala Gly Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Ser Val Ser Ser

115

<210> 505

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 505

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

 Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95
Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 506
<211> 116
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide
<400> 506

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95
Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser
115

<210> 507
<211> 116
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 507

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Val Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 508

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 508

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Ile Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Pro Val

100 105 110

Thr Val Ser Ser

115

<210> 509

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 509

Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Arg Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 510

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 510

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Glu Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 511

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 511

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Ile Ala Gly Tyr

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

[illegible]

115

<210> 512

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 512

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ala	Gly	Tyr
			20					25					30		
Glu	Met	Trp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Arg	Val
		35					40						45		
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val

50					55					60									
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Thr	Leu	Tyr				
65					70					75					80				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys				
85					90					95									
Ala	Arg	Asp	Pro	Tyr	Ser	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val				
100					105					110									
Ser	Val	Ser	Ser																
115																			

<210> 513

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 513

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 514

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 514

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 515

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 515

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Thr Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Arg Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 516

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 516

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr

20 25 30

Glu Val Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 517

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 517

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Ile

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Lys Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 518

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 518

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 519

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 519

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ala Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 520

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223>

> Description of Artificial Sequence: Synthetic polypeptide

<400> 520

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 521

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 521

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Pro Gly Phe Thr Leu Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 522

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 522

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr
20 25 30
Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Thr Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 523

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 523

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly His Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 524

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 524

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys

85 90 95
Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 525

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 525

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 526

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 526

Glu Ala Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr

20 25 30
Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser

115

<210> 527

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400>

> 527

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp His Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 528

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 528

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 529

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 529

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 530

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 530

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp His Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 531

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 531

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp His Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 532

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 532

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 533

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 533

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 534

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 534

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 535

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400

> 535

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 536

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223

> Description of Artificial Sequence: Synthetic polypeptide

<400> 536

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys

85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 537

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 537

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

	35	40	45	
Ser	Ala	Ile	Ser	Gly
		Ser	Gly	Gly
		Ser	Thr	Tyr
		Tyr	Tyr	Ala
		Asp	Ser	Val
50		55		60
Lys	Gly	Arg	Phe	Thr
	Ile	Ser	Arg	Asp
	Asp	Ser	Lys	Asn
	Thr	Leu	Tyr	
65		70		75
				80
Leu	Gln	Met	Asn	Ser
	Leu	Arg	Ala	Glu
	Asp	Thr	Ala	Val
	Tyr	Tyr	Cys	
	85		90	
				95
Ala	Lys	Asp	Pro	Tyr
	Ser	Phe	Asp	Asn
	Trp	Gly	Gln	Gly
	Thr	Leu	Val	
	100		105	
				110

Thr Val Ser Ser

115

<210> 538

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 538

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5	10	15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20	25	30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

	35	40	45	
Ser	Ala	Ile	Ser	Gly
		Ser	Gly	Gly
		Ser	Thr	Tyr
		Tyr	Tyr	Ala
		Asp	Ser	Val
50		55		60
Lys	Gly	Arg	Phe	Thr
	Ile	Ser	Arg	Asp
	Asp	Ser	Lys	Asn
	Thr	Leu	Tyr	
65		70		75
				80
Leu	Gln	Met	Asn	Ser
	Leu	Arg	Ala	Glu
	Asp	Thr	Ala	Val
	Tyr	Tyr	Cys	
	85		90	
				95
Ala	Lys	Asp	Pro	Tyr
	Ser	Phe	Asp	Tyr
	Arg	Gly	Gln	Gly
	Thr	Leu	Val	
	100		105	
				110

Thr Val Ser Ser

115

<210> 539

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 539

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr

20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 540

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 540

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Leu Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 541

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 541

Glu Val Gln Leu Leu Val Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120
<210> 542
<211> 120
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide
<400> 542

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30
Glu Met Val Trp Val Arg Lys Ala Pro Gly Met Gly Leu Glu Trp Val
35 40 45
Ser Ser Ile Ser Ala Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
100 105 110
Gly Ala Leu Val Thr Val Thr Ser
115 120

<210> 543
<211> 120
<212> PRT
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 543

Glu Val Gln Leu Leu Val Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly His
100 105 110

Gly Ala Leu Val Thr Val Ser Ser
115 120

<210> 544

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 544

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 545

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 545

Glu Ala Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30
 Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Arg
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 546

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 546

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Pro

100 105 110

Gly Ala Leu Val Thr Val Ser Ser

115 120

<210> 547

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 547

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Leu Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120
 <210> 548
 <211> 120
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 548
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

 20 25 30
 Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

 85 90 95
 Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Pro
 100 105 110
 Gly Ala Leu Val Thr Val Ser Ser
 115 120
 <210> 549

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 549

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Glu Pro Val Tyr Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 550

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 550

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala

20 25 30

Glu Met Leu Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45
 Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 551

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 551

Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30
 Leu Thr Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 552

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 552

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Arg Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu His Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 553

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 553

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Thr Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Ile Arg

100 105

<210> 554

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 554

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 555

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 555

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Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly
1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Thr Leu
           20           25           30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
           35           40           45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
           50           55           60

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
           85           90           95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
           100          105

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<210> 556

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 556

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
           20           25           30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Thr Lys Leu Leu Ile
           35           40           45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
           50           55           60

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 557

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 557

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 558

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 558

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
20 25 30
Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 559

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 559

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
20 25 30
Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Thr Tyr Gly Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 560

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 560

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 561

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 561

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Thr Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 562

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 562

Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
20 25 30

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 563

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 563

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Asn Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 564

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 564

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Thr Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 565

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 565

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Tyr Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Val Ser His Phe Ile Gly Thr Leu
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gln
 100 105

<210> 566

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 566

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Arg Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 567

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 567

Asp Ile Gln Ile Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 568

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 568

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 569

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 569

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
 Thr Tyr Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg
 100 105

<210> 570

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 570

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 571

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 571

Asp Ile Gln Met Thr Gln Ala Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg

100 105

<210> 572

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 572

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 573

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 573

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 574

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 574

Asp Ile Leu Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 575

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 575

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30
 Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Tyr Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100

105

<210> 576

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 576

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20

25

30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg

100

105

<210> 577

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 577

Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20

25

30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 578

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 578

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Phe Ile Gly Thr Leu
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 579

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 579

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 580

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 580

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 581

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 581

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Glu Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 582

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 582

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10          15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
          20          25          30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60

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Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75          80
Glu Asp Leu Ala Thr Tyr Tyr Cys Gly Gln Glu Val Leu Trp Pro Ala
          85          90          95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
          100         105

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<210> 583

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 583

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1           5           10          15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Phe Ile Gly Thr Leu
          20          25          30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60

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Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75          80

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Glu Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 584

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 584

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Phe Gly Thr Glu Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg

100 105

<210> 585

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 585

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
20 25 30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Thr Lys Leu Leu Ile
35 40 45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 586

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 586

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Ser Leu
20 25 30
Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95
Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 587

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 587

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Gln Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 588

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 588

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Gln Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Arg Arg
100 105

<210> 589

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 589

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Tyr Ile Ala Ser Leu
20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Ala Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 590

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 590

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Trp Ala Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 591

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 591

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Trp Thr Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 592

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 592

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Trp Ser Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 593

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 593

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Trp Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 594

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 594

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Trp Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 595

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 595

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Trp Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 596

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 596

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Trp Ile Ala Gln Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 597

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 597

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30

Leu Arg Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 598

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 598

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Arg Ile Ala Gln Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 599

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 599

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Tyr Ile Ala Ser Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 600

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 600

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Arg Phe Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 601

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 601

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Lys Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 602

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 602

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Trp Gly Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100

105

<210> 603

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 603

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Trp Gly Pro

20

25

30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65

70

75

80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85

90

95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100

105

<210> 604

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 604

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Trp Ile Ala Thr Leu

20

25

30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 605

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 605

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Trp Gly Pro
20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 606

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 606

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Asn Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 607

<211> 108

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 607

Gly Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu

20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Thr Tyr Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala

85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

100 105

<210> 608

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400

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tcctgtgcag cctccggatt caccttccgg gattatgaga tgttgtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgagc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc aggagtgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 609

<211> 348

<212> DNA

<213

> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 609

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttccgg gattatgaga tgttgtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgagc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 610

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 610

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt      300
```

```
gggtattttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 611

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 611

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg      300
tttcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 612

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 612

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact gagtatgaga tgatttgggt ccgccaggct      120
```

ccaggaagg gtctggagtg ggtctcatct atttcgggta atgggtctaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 613

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 613

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaagagccg 300

attacgtatg ctatgaggta tgccggtttt gactactggg gtcaggaacc cctggtcacc 360

gtctcgagc 369

<210> 614

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 614

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc agggtagcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttcgc 300

tttatttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 615

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 615

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg acttatcata tgcagtgggt ccgccaggct	120
ccaggaagg gtctggagtg ggtctcaatg attgatgcgg atggtcttgg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt	300
ccgcagtttg gtcagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 616

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 616

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cttccggatt caccttttcg gggtatgata tgcagtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaacg attagtgcgt cgggtgtttt tacatactac	180
gcagactccg tgaagggccg gttcaccacc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcct	300

aatcgttttg cgcttaataa ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 617

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 617

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaaatag ttctattttg tgggcgttag cttggtacca gcagaaacca	120

gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgttcag aatgcgggtt ggcttggtac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 618

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 618

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgttcacc 60

atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 619

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 619

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtgttggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 620

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 620

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttccg actgctgaga tgggtgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcatct atttcgcta gtggtgttc tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300
gtgagttatg tggcgacgtt tgactactgg ggtcaggga ccctggtcac cgtctcgagc	360

<210> 621

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 621

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagt gtcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggaccaagg tggaatcaa acgg	324

<210> 622

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 622

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttccg aagaatgaga tgacgtgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcagcg attgagtcgg atggtcaggc tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gaaaaatcgg	300

attcctgatac ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 623

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 623

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat gctggggcta tgacgtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcatct attgataagg agggctctgc tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtagg 300

attcctgggc tggtttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 624

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 624

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gatgcggcga tgacttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcagcg attcagccta tgggtgatgg tacatactac 180

gcagactccg tgaaggccg gttcaccgtc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt 300

attcctactc ttcagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 625

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 625

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gattcgcta tgacttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attacttga atggttatga gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggcgct 300

attcctactc ttcatTTtga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 626

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 626

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat gagcatgata tgagtgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcacgt attggtccgg atggttttca tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggcgct 300

attcctactc ttcatTTtga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 627

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 627

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gattatcata tgtcttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaagg attactctc ttggtacgct tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggcgct 300

attccttgcg ttacgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 628

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 628

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt acgaatgcga tgagtgggt cgcgcaggct      120
ccaggaagg gtctggagtg ggtctcaagg atttcgccgg gtggtgatta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtgt attactgtgc gaaagggcgt      300
gttccggatc tgctttttga ctactgggggt caggaaccc tggtcaccgt ctcgagc      357
```

<210> 629

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 629

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttccg tctgaggaga tgtcttgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcaagg atttcgctg atggtgctaa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagggcgt      300
gttccggatc tgctttttga ctactgggggt caggaaccc tggtcaccgt ctcgagc      357
```

<210> 630

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 630

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gaggatgata tgacttgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcacgt attgcggttg atggtgatcg gacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtaag 300

gttccgtctc ttcattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 631

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 631

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggatc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg acgatggata tgtcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacgt attacgggtg atggtatgaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccggggac accgcggtat attactgtgc gaaaggggtg 300

actccggatt tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 632

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 632

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag cgtgatgata tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcacgt attaattctg ggggtgtgca tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggggtg 300

actccggatt tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 633

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 633

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat gatgattcta tgacgtgggt cgcgcaggt 120

ccaggaagg gtctagagtg ggtctcacgg atttcgagtg atggtgcgag tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300

actccggatt tgacttttga ctactggggg caggaaccc tggtcaccgt ctcgagc 357

<210> 634

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 634

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gaggaggata tgacgtgggt cgcgcaggt 120

ccaggaagg gtctagagtg ggtctcacgt attgatagtg ttggtgaggg gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300

actccggatt tgacttttga ctactggggg caggaaccc tggtcaccgt ctcgagc 357

<210> 635

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 635

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct gattcggcga tgagtgggt cgcgcaggt 120

ccaggaagg gtctagagtg ggtctcacgg attgataatc ctggtcagca tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtact 300

gttcctacgc tggagtttga ctactggggg caggaaccc tggtcaccgt ctcgagc 357

<210> 636

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 636

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg cagcatagta tgacttgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcacgt attgatggtg ggggttataa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggag      300
```

```
gttcctcgtc ttcatTTTga ctactgggggt cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 637

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 637

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt caggagccta tgacttgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcacgg attgcgtata atggtgggtga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt      300
actctaatt tgacttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 638

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 638

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag aattatccga tgtcttgggt ccgccaggct      120
```

ccaggaagg gtctagagt ggtctcacgt attaagtcta cgggttctat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtt 300

attcctcatt tgatgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 639

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 639

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgt gattatgata tgagtgggt cgcagggt 120

ccaggaagg gtctagagt ggtctcacgt attactggta ctggtaatag tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaggggtg 300

gtgccgtatc ttgcttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 640

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 640

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gctgatgcga tgactgggt cgcagggt 120

ccaggaagg gtctagagt ggtctcaagg attaagtgg atggtgatcg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300

gttcctacgc tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 641

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 641

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat cgggcggata tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaagg atttcggggg agggttaagt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg	300
gttcctaatt tggtttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 642

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 642

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcat tgggagccga tgtcttgggt ccgccaggct	120
ccggggaagg gtctagagt ggtctcacgt attaatctt ctggttgga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg	300
gttcctaatt tggtttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 643

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 643

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct gatgagccga tgacttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcacgt attcctcctg aggtgtctcc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt	300

actcctaatt tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 644

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 644

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcat aatcatgata tgtcttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcacgt attagtcggg gtggtcttca gacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggatt 300

gtgccggatc tgcattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 645

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 645

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat gagtatccta tgtcgtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcacgt attaatgggg atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggatt 300

attccggcta tgcagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 646

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 646

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gatgtgccta tgtcgtgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaagg attgacctt atggttctaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtatt 300

atgcctagtc ttacttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 647

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 647

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg gattatgata tgtcttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcacgt atttcggcgc ttggtgctac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcag 300

cttccggcgt tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 648

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 648

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaag cgttattata tgacttgggt ccgccaggct 120

ccaggaagg atctagagt ggtctcaggc attgttcctt ctggtaatag gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg 300

attccggatc tgcattttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 649

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 649

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct gattatgata tgacttgggt cgcgcaggt	120
ccagggaagg gtctagagtg ggtctcaagg atttctccga cgggtgggca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtgtt	300
attccgtatt tgcctttttc tccgtttgac tactggggtc agggaaacct ggtcacgtc	360

tcgagc	366

<210> 650

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 650

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttct aagtattgga tgggttgggc ccgccaggt	120
ccagggaagg gtctagagtg ggtctcatcg attgattcgc atggtgctgg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgctcaggac accgcggtat attactgtgc gaaagtgct	300
cctaagttta tgactacgta tacgtttgac tactggggtc agggaaacct ggtcacgtc	360
tcgagc	366

<210> 651

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 651

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60

tcctgtgcag cctccggatt cacctttttg tcttatccga tgcattgggt cgcagggt 120

ccagggaagg gtctagagt ggtctcatcg attgattcga ggggttcggt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaaggtcat 300

agttggacgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 652

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 652

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg aatagtaata tgacttgggt cgcagggt 120

ccagggaagg gtctagagt ggtctcacgt attaatccgg atggtgggtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc ggaagggcgt 300

attcctactc ttcatTTTga ctactgggggt cagggaacce tggtcaccgt ctcgagc 357

<210> 653

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 653

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg ccgaggagga tgggttgggt cgcagggt 120

ccagggaagg gtctagagt ggtctcatcg attgatgata ttggtcgtag gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc ggaagggcgc 300

cagggtgtgt tgttgtttga ctactgggggt cagggaacce tggtcaccgt ctcgagc 357

<210> 654

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 654

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gattatagga tggtttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg atttctactt ctggtgagct gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc ggaaacggcg      300
ggtcagtttt ttgactactg gggtcaggga accctgggtca ccgtctcgag c              351
```

<210> 655

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 655

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttccg gattatgaga tggtttgggt ccgccaggct      120
ccaggaagg gtctggagtg ggtctcagcg atttcgctg agggtcgggc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acaacctcgc tgccgaggat accgcggtat attactgtgc gaaagagcct      300
```

```
gttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc              348
```

<210> 656

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 656

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttcg acttatgaga tgctttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcttctt ctggttaatta tacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300

ctgatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 657

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 657

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat actgaggaga tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagcg attagtccta atggtgcttt tacattctac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagcct 300

attctgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 658

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 658

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt cattatgata tggtttgggt ccgccaggct 120

ccagggaggg gtctagagtg ggtctcaact attaatggtg ctggctctgaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaagtgt 300

agtcgtat ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 659

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 659

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagg agttatgaga tggcgtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcatct attagtactc tgggtacgaa gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaatcttct 300

actcatatct ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 660

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 660

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatt aggtatgaga tggcttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaagt atttcgtcgt ctggttggac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaagtgat 300

gctcatatct ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 661

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 661

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttat gcttatgaga tggcttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcatct atttcggatg atggtacgcg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatctg 300

gggcagggtt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 662

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 662

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gatcatggga tgacgtgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcaggg attggtccgt ctggtgaggc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt      300
```

```
attcctaate ttgtgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 663

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 663

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tctcaggata tgtcttgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcagggt attagtccga atggttggga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatagg      300
tctgattttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 664

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 664

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg gattatgata tgtggtgggt ccgccaggct      120
```

ccaggaagg gtctagagt ggtctcaagg attcgtcatc cgggtggtgt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgtt 300

cctaagggtt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 665

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 665

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gtttattgga tgacttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcatct attgatccgc aggggtgggat gacatactac 180

gcagactccg tgaagggccg gttcaccatc tctcgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagcgcgt 300

attcctaatt tggagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 666

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 666

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggagtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt gcttatgata tgacgtgggt ccgccaggct 120

ccaggaagg gtcttgagt ggtctcacgt attaatccga cgggttctta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagctaag 300

attccgaatt tggtttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 667

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 667

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgcg gatagtgaga tgatgtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagggt attgcgcata atggtgggca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggt      300
caccctcagc agactgagge ttttgactac tggggtcagg gaaccctggt caccgtctcg      360
agc
```

<210> 668

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 668

```
gagatgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct acttatgata tgtattgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaaag atttctccga atggttggag tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcag      300
acgcattttg actactgggg tcaggaacc ctggtcaccg tctcgagc                      348
```

<210> 669

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 669

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt gtttatgata tgaggtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaacg atttcttctt cgggtacgta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcct 300
aagaattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348
<210> 670
<211> 351
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 670
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttct catgaggata tgacttgggt cgcgcaggct 120
ccaggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtact 300
aggagtaagt ttgactactg gggtcaggga accctggtea cgtctcgag c 351
<210> 671
<211> 360
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 671
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag aagtatatta tgggttgggc cgcgcaggct 120
ccaggaagg gtctagagtg ggtctcaacg attgattatt ggggtcagca tacatactac 180
gcagactccg tgaagggccg gttcactatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtagt 300
catcttattc ctctgcagtt tgactactgg ggtcaggga ccctggtcac cgtctcgagc 360
<210> 672
<211> 369
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 672

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct gattatgcga tgggtgggt ccgccaggct 120

ccaggaagg gtctggagt ggtctcaacg atttcgtatg tgggttatta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaggct 300

ctgcgggggg aggcgtttac ggagcgtttt gactactggg gtcaggaac cctggtcacc 360

gtctcgagc 369

<210> 673

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 673

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttgg cgtatatga tgcatgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaacg attgaggtta atggtaatag gacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatgggtt 300

ggttcgaaga cgtcgtcgga taagagtttt gactactggg gtcaggaac cctggtcacc 360

gtctcgagc 369

<210> 674

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 674

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttgg acgacggaga tggttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaagt attggtagt ctggtgcttg gacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaattggt 300

gggcacccctc agggtcagtt tgactactgg ggtcaggga cccctggtcac cgtctcgagc 360

<210> 675

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 675

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60

tcctgtgcag cctccggatt cacctttcct agggagtga ttgcttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attcagccta tgggtcagac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatattct 300

cgggaataagg ggttttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 676

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 676

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttacg agtgagtata tggggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatct attcagaggt atggtagtagac gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacatgag 300

tctaattggg agacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 677

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 677

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg gtgtatagta tgcagtgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcagc attactccta atgtactcg gacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactctt	300
ggtcggggtt cttatcctgg tgttgatttt gactactggg gtcaggaac cctggtcacc	360
gtctcgagc	369

<210> 678

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 678

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg agttatgcta tgactgggt cgcaggct	120
ccaggaagg gtctgagtg ggtctcacgt attacggcg atgtactgt tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttct	300
attccgatgc ttacgtttga ctactgggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 679

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 679

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg acttatgata tgatttgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcagct atttctccta atgtactgg tatatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatcag	300

agtgttcatc atgtgtttt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc	360

<210> 680

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 680

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag aattatgaga tgacgtgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcacgt attgcgccgc atggtcggct tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtcag	300
attccgatgc ttgattttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 681

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 681

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg cattatatga tgatgtgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaacg atttctcatt ttggtgatat tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatgat	300
atggtgatga agaattggggg gtttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 682

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 682

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag aggtatgata tgagtgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcacgt attgattcgc ggggttggtc tacatactac	180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggttg 300
gtgccgcacg tgaggtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 683

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 683

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgcg aatgcgcaga tgacttgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcaagg attgatgcta tgggtgatgc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttaag 300
gttccgagta ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 684

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 684

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgcg aatgcgcaga tgacttgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcaagg attgatgcta tgggtgatgc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtgtt 300
attccggcgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 685

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 685

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcag aatgatcgga tgcattgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatcg atttctgcta ctggttggtga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagacg	300

ggtacgaatc gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 686

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 686

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat cagccttata tgtcgtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatct attgatgctt cgggtgggtac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagatcgt	300
attcctaate ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 687

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 687

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatgagaata tgacttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcacgt attgatggtg ggggttataa tacatactac	180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcag	300
gttcctgagc tgctgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 688

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 688

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgtt tcgtcgaata tgacttgggt cgcgcaggct      120

ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactat      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcgg      300
attctactgt tgggtgttga ctactggggg caggaaccc tggtcaccgt ctcgagc          357
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<210> 689

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 689

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttgtt tcgtcgaata tgacttgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactat      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt      300
attcctaate ttgtgttga ctactggggg caggaaccc tggtcaccgt ctcgagc          357
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<210> 690

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 690

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttct gatgattcga tgagtgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcacgt attaatgatg ctggtagtgc tacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300
attcctcttc tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 691

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 691

gagatgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt tcggatacta tgagtgggt cgcgcaggct 120
ccagggaagg gtctagagtg ggtctcacgt attgatggga ctggtgggtga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccggggac accgcggtat attactgtgc gaaagggtctt 300
attcctgac ttcagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 692

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 692

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat gaggaggaga tgacgtgggt cgcgcaggct 120
ccagggaagg gtctagagtg ggtctcacgt attattggtg gtggtcatga gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300

attcctcttc tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 693

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 693

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aatgagaata tgacttgggt ccgccaggct	120
ccaggaagg atctagagtg ggtctcacgg attactgaga ggggtgatgt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact	300
gttcctacgc tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 694

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 694

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat gaggaggaga tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcacgt attattggtg gtggtcatga gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact	300
gttcctacgc tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 695

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 695

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcat gagacggaga tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcagct attaatcggc tgggtcagga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg	300
attcctgggc tggtttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 696

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 696

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct gatgattcga tgagttgggt cgcgcaggct 120

ccaggaagg gtctagagtg ggtctcacgt attaatgatg ctggtagtgc tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300

gttctactgc tggagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 697

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 697

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatgagaata tgacttgggt ccgcaggct 120

ccaggaagg atctagagtg ggtctcacgg attactgaga ggggtgatgt gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcgg 300

attcctactg tgggtgttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 698

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 698

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct gatgattcga tgagttgggt cgcgcaggct 120

ccaggaagg gtctagagtg ggtctcacgt attaatgatg ctggtagtgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtt 300
actcctaatt tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 699

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 699

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgct gatgagccga tgacttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcacgt attcctcctg aggggtgtcc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtt 300

attcctgac ttcagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 700

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 700

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcag gatagtata tgacttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagct attgctgcgc ctggtggttag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt 300

attcctaate ttaggtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 701

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 701

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt tcggatacta tgagtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcacgt attgatggga ctggtggtga tacatactac	180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggcag	300
gttcctgagc tgctgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 702

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 702

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcag gatagtata tgacgtgggt ccgccaggct	120

ccaggaagg gtctagagtg ggtctcagct attgtgcgc ctggtggtag tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcgt	300
attcctaate ttgtgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 703

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 703

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag ccgccggatt cacctttgat ctggcggaga tgacttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcacgt attgatgagg atggtgcttc tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc ggaaggtgtt	300
attccgtctc tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 704

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 704

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt caccittact gataagcata tgagttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcacgg atttcgctg atggtacgta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc ggaagggtgt      300
attccgtctc tgacttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 705

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 705

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt caccittgct gaggatgata tgacttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcacgt attgcggttg atggtgatcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg taccgaggac accgcggtat attactgtgc gaaagggaag      300
acgccgcac cttgtgttga ctactggggg cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 706

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 706

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag ccgccggatt caccittgat ctggcggaga tgacttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcacgt attgatgagg atggtgcttc tacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcag 300

gttccctgctt tggtttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357
<210> 707
<211> 357
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 707

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag gattcgatga tgcgtgggt ccgccaggcg 120
ccaggaagg gtctagagt ggtctcacgg attgatcctg ggggtgtca gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300
actccggatt tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357
<210> 708
<211> 357
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 708

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag catgcggata tgagtgggt ccgccaggct 120
tcaggaagg gtctagagt ggtctcacgt attgataata gtgtcagtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300
actccggatt tgacgtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357
<210> 709
<211> 357
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 709

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt gaggcggaga tgaattgggt ccgccaggct	120

ccaggaagg gtctagagtg ggtctcacgt attacgacgg atggtgattc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt	300
attcctactc ttcatTTtga ctactggggT cagggaaccc tggTcacCGt cTcgagc	357

<210> 710

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 710

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctcaggatt cacctttgat gatagtata tgacttgggt ccgccaggct	120
ccaggaaga gtctagagtg ggtctcatat attcggggtg atgatgatga gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatcgg	300
attcctgacT ttgtgtttga ctactggggT cagggaaccc tggTcacCGt cTcgagc	357

<210> 711

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 711

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaat gtggcgata tgcagtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatgct	300
tctacggagg ggccgactgc ttttgactac tggggtcagg gaaccctggt caccgtctcg	360

agc 363

<210> 712

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 712

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg ccgtatgata tggggtgggt cgcgcaggct	120
ccagggaagg gtctggagtg ggtctcatgg atttctgctc atggttcgtt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggcct	300

tataagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 713

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 713

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg agtgggtcta tgagttgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcacgg attggtagta atggtgcgga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg	300
gttcctaatt tggtttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 714

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 714

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60

tcctgtgcag cctccggatt cacctttaat cgttttgata tgacgtgggt cgcaggct 120
ccagggaagg gtctagagt ggtctcagct attagtggta gtggtgtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt 300
attcctaate ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 715
<211> 357
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 715

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggg gagagtgata tgaagtgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcaagt attagtccga atggttggga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctcct 300
tcttctcgtc ttaagtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 716
<211> 357
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 716

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat agtagtgaga tgagtgggt cgcaggct 120
ccagggaagg gtctagagt ggtctcatcg attgagaatc aggggtggtc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcgt 300
attcctaate ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 717
<211> 348
<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 717

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacccttgat gcgtatccta tgtattgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatgg attgcttcgg gtggtggtgc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtacg      300
aagaattttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 718

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 718

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacccttatg agttattcta tggtctgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggg attacttcta atggtaatcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatcgact      300
ggggctaata gtaggaattt tgactactgg ggtcaggga ccctggtcac cgtctcgagc      360
```

<210> 719

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 719

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacccttgag gggtatctga tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attgcgcta atggtatgca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagccg 300

aggggatattt gggatgggga ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 720

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 720

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcat gagtctacga tgacgtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaact attcggcatc cgggtgagtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccggggac accgcggtat attactgtgc gaaagggtt 300

attcctgatac ttcatgttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 721

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 721

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg atgtatagta tgagttgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcatcg attgcgccgc cgggtggttag gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacagtcg 300

ctgacggggg atagtaggtc ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 722

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 722

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg cagaatccga tgcgtgggt ccgccacgct	120
ccaggaagg gtctagagt ggtctcaacg attcctgcga atggtcgtcc tacatcctac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatagt	300
cagcagccgg gtcgtcggtt tgactactgg ggtcaggga ccctggtcac cgtctcgagc	360

<210> 723

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 723

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct aattatcata tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcatcg attcctgata gtggttaagca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctacaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg	300
attcgtctc ttctttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 724

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 724

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgcg cagtatcata tgcgttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaacg attaataata ttggtagtaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtggg	300

gggcggggga gtttttcttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 725

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 725

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttct tcgtatgata tgaagtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaacg attagtgcgt ctggtgtgtt tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgggag 300

catgctgggc agccgccttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 726

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 726

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat gggtatgcta tgagttgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaact attaattgcta atggttaagta tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagttg 300

actcttgctt ctaattattt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 727

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 727

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttatg gattatgata tgaagtgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcaagt attactgcgc ttgtaagaa gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagt 300

gttaagtatc ctcttaatct ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 728

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 728

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg cattatacga tggcgtgggt cgcaggct 120

ccagggaagg gtctggagtg ggtctcatct attcagtcgc ctggttggcg gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatggg 300

gatggtcttc ctttgacttt tgactactgg ggtcaggga ccctggtcac cgtctcgagc 360

<210> 729

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 729

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttagt ggtacgccga tgtcttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcacgt attggggatg agggtcagga gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300

actccggatt tgacttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 730

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 730

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt agtagttcga tgtcttgggt cgcgcaggct      120
ccaggaagg gtctagagt ggtctcagc attgggtctg atgggtccag tacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt      300
```

```
attcctactc ttcatTTtga ctactgggggt cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 731

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 731

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaat cctggtgaga tgacgtgggt cgcgcaggct      120
ccaggaagg gtctagagt ggtctcaagt attgatgggt ctggttcttc gacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgatgac accgcggtat attactgtgc gaaagggcgt      300
attcctactc ttcatTTtga ctactgggggt cagggaaccc tggtcaccgt ctcgagc      357
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<210> 732

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 732

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcct gagtctatga tgggtgggt cgcgcaggct      120
ccaggaagg gtctagagt ggtctcatcg attgggtatc ctggtgtctac tacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtggt 300
agtcgggatg ataattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 733

<211> 372

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 733

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgcctc 60
tcctgtgcag cctccggatt cacctttggt cagcatagta tgcattgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaagt attagtgttc cgggtccgaa gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtctt 300
agggatttgc gtccgggtga tagtaagagt ttgactact ggggtcaggg aaccctggtc 360
accgtctcga gc 372

<210> 734

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 734

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggt tctgctgcta tggattgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatct attaatgata tgggttctaa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagggt 300
ggtcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 735

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 735

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggt tatgatagga tggcttgggt cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcatcg attgatggtc ctggtggggc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggagg	300
agggttctcg attttgacta ctggggtcag ggaaccctgg tcaccgtctc gagg	354

<210> 736

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 736

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggt gattatgaga tgacttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaagg attgatccgt ttggttctga gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggtgtg	300

gttctgtatt tgaattttga ctactggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 737

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 737

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat aagtatgtta tgggttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaact attggtagtt atggtggggc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaggctt	300
actcttagtg cgactaagtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc	360

<210> 738

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 738

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag gattatgtga tgggttgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaact attgcgcac ggggtgatat tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtagg	300
cgtcttagtg attatcggtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc	360

<210> 739

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 739

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg cagtttgata tgtattgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcagcg attagtccgg ctggtactgg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg	300
gatcgggtcta gtctttttga ctacaggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 740

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 740

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttaag gatacgggta tgacgtgggt ccgccaggct	120

ccagggaagg gtctagagtg ggtctcaagt atttctagtt atggctgtga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaattgaat 300
gcggcgctgg gttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 741

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 741

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttgt ccgtatccga tgagtgggt cgcgcaggct 120
ccagggaagg gtctagagtg ggtctcaggt attaatgcgc cgggtacgag gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaacagatg 300
tctagtgggg tttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 742

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 742

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttcg aatcaggata tgacttgggt cgcgcaggct 120
ccagggaagg gtctagagtg ggtctcaagt attgatagtt ctggtcagct tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttaag 300
tctcttgcgc ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 743

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 743

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgctcag cctccggatt cacctttcct gagtctgata tgaagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaccggct      300
```

```
caggttctgt ttgactactg gggtcaggga accctggtca ccgtctcgag c                  351
```

<210> 744

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 744

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtcagc cctccggatt cacctttgag cagtatgtga tgggttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaacg attggtacgt cgggtaagta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaacgtagg      300
```

```
tctctgactc ggggttcattt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc      360
```

<210> 745

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 745

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtcagc cctccggatt cacctttggt gtggagcata tgagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagcg attacgggtg atggtgatcg tacatactac      180
```

```
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacggtt      300
```

```
tcgtggaatg gtcgttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc        357
```

<210> 746

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 746

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgcg tggataata tgggttgggt cgcgcaggct      120

ccaggaagg gtctggagtg ggtctcaagg attgctccgt ctggtattat tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagggttg      300
cgtggtaagt ttgactactg gggtcaggga accctggtca ccgtctcgag c              351
```

<210> 747

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 747

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt caccttttcg aattatgaga tgaggtgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcttcgg ctggtactga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacagtcg      300
cttaattttg actactgggg tcaggaacc ctggtcaccg tctcgagc              348
```

<210> 748

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 748

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgtag cctccggatt cacctttgat gaggagccga tgacttgggt cgcgcaggct      120
```

ccagggaagg gtctagagtg ggtctcaatt attgatccgg gtggtggggc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctaata 300
agtatgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 749

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 749

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttct gcgtatccta tgcatagggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatct attgcttctt cgggtattac gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttact 300
cggctgcatt ttctgcgca gtttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 750

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 750

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgct gattatgcga tgggttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaagg atttctctg agggttctag gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaattgcgg 300
ccgtatgcgt cgaagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 751

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 751

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccitttagg ccgtatgata tgggttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaacg atttctcatc agggtaatcg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgtct	300
catcattttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 752

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 752

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccitttct gcgtataata tgtgttgggc ccgccaggct	120
ccaggaagg gtttagagtg ggtctcatgg attaattcga ctggttctcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatttg	300
catcggggga ggtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc	354

<210> 753

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 753

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccittgat aggtatcgga tgggttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaacg attaatcggc tgggtcagag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgaag	300

aagcataagt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 754

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 754

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg cattataata tgccgtgggt cgcgcaggct 120

ccagggaagg gtctagagtg ggtctcaacg attacgaaga ctgggttttcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg 300

cagtttgatt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 755

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 755

gaggtgcagc tgttggagtc tgggggaggc ttagtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttat cttatagta tgcatgggt cgcgcaggct 120

ccagggaagg gtctggagtg ggtctcaact attgatggta gtggtatgtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagattct 300

ctgaaggctt cttttgacta ctgggggtcag ggaacctgg tcaccgtctc gaggc 354

<210> 756

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 756

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg ctttatggga tgtggtgggt cgccaggct 120
ccagggaagg gtctagagt ggtctcatat attgggcctt atggtcatac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaaaagcgg 300

aagaagaagt ttgactactg gggtcaggga accctggta ccgtctcgag c 351

<210> 757

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 757

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcct aggtatcgga tgagttgggt cgccaggct 120
ccagggaagg gtctagagt ggtctcaagt attactcgt atggtgctca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaatatggt 300

aagtggatt ttgactactg gggtcaggga accctggta ccgtctcgag c 351

<210> 758

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 758

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat gattatcgga tgagttgggt cgccaggct 120
ccagggaagg gtctagagt ggtctcaacg attgatcgtc tgggtcttca tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaaagtggg 300

ccttttacgt ttgactactg gggtcaggga accctggta ccgtctcgag c 351

<210> 759

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 759

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag cggataata tgcgttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaacg attgatcggc tgggtcttgc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt 300
tcgtgtctt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 760

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 760

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt atttatgata tgaagtgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcaacg atttcgtcgt cgggtactca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcct 300
cagccttacc cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 761

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 761

gaggtgcagc tattggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttgg gtgtatgata tgcgttgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcaacg atttctcgca ctggtgtgca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatccg 300

cctgctggtc ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 762

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 762

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg acttatgata tgatttgggt cgcgcaggct	120
ccaggaagg gtctagagtg ggtctcagct atttctccta atggtactgg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctccg	300
caggtgaata ctgagtttga ctaccggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 763

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 763

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag aaggaggata tggggtgggt cgcgcaggct	120
ccaggaagg gtctagagtg ggtctcacat atttcgccga atggttatgc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtgg	300

tctagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 764

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 764

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60

tcctgtgcag cctccggatt cacctttagt gctactccga tggagtgggc cgccaggct 120
ccaggaagg gtctagagt ggtctcaact atttctgaga gtggttatag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggaat 300
tcgactactg gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 765

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 765

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttaat acggtggata tggagtgggt cgccaggct 120
ccaggaagg gtctagagt ggtctcaagt attagtccga atggttggga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagctccg 300
catcgggcgt ttgactactg gggtcaggga accctggtea ccgtctcgag c 351

<210> 766

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 766

gaggtgcagc tgttggagtc tggggggggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag gataaggaga tgagtgggt cgccaggct 120

ccaggaagg gtctagagt ggtctcacgg attgatgctt tgggtgattc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggatg 300
gttcctcgtc tgaagtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc 357

<210> 767

<211> 342

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 767

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tctgtgcag cctccggatt cacctttagt gatcattcga tgatgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagat attgagccgc atggtgttca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaatcctact      300
tttgactact ggggtcaggg aaccttggtc accgtctcga gc                          342
```

<210> 768

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 768

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tctgtgcag cctccggatt caccttttcg ccgcatacta tgcatgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attggtccgg atggtactac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgttcg      300
tatagttggg atcgtgggtg gacgtttgac tactggggtc agggaaacct ggtcacctgc      360
tcgagc                                          366
```

<210> 769

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 769

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tctgtgcag cctccggatt caccttttat gcttcggata tgaagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgat 300

tatacttatac attcttttga ctactggggt caggggaccc tggtcaccgt ctcgagc 357

<210> 770

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 770

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgcg cattataata tgcggtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attacgaaga ctggttttcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg 300

cagtttgatt ttgactactg gggtcaggga accctgtca ccgtctcgag c 351

<210> 771

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 771

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg cattatcata tgggttgggc ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagtt attgggccga ggggtatttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgctt 300

tcgcgtcata ggtttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 772

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 772

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat gattatgcga tgaagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcaacg attgacgctc tgggtcttca tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtggg 300
 ccttttacgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 773
 <211> 369
 <212> DNA
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polynucleotide
 <400> 773

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggt aattatagta tgaagtgggc ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaact attactcctg atggttggta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgggg 300
 gatgtgtttt ggggggtggt tgggtgggtt gactactggg gtcagggaac cctggtcacc 360
 gtctcgagc 369

<210> 774
 <211> 348
 <212> DNA
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polynucleotide
 <400> 774

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg gattatggta tgaagtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagct attactcta atggtgattt tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctttg 300
 tataagtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 775

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 775

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag gctccggatt cacctttcct acttataaga tggggtgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcattt attgattatt ggggttggcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtccg      300
```

```
tattcttggg ctcatgatag tcctcathtt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
```

<210> 776

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 776

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagg ccttatacga tgtgttgggc ccgccaggct      120
ccaggaagg gtctagagt ggtctcatgt attagtgatg ctggttcttt tacatactac      180
```

```
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaggatg      300
tcttcttttg actactgggg tcaggaacc ctggtcaccg tctcgagc                      348
```

<210> 777

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 777

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
```

tcctgtgcag cctccggatt cacctttcag aattatcaga tggcttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcaact attagtggga ctgtaagaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactcct 300

cagaattatt ttagtgtcg tgggtttgac tactggggtc agggaaccct ggtcaccgtc 360

tcgagc 366

<210> 778

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 778

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gcgtatacta tggggtgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcaaag atttcgacgt ctggtgggca gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctttg 300

aattggtggg cgtttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 779

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 779

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat gcgtatccta tgacttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcacgg attgatggtt atggtcggca tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtat 300

attcctaatt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 780

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 780

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggg gcggttgata tgacgtgggt cgcgcaggct      120
ccaggaagg gtctagagt ggtctcagc atttcgccta gtggttctgc tacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggcgt      300

gtgccggtc ttggttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc      357
```

<210> 781

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 781

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgat agttatgcga tggggtgggc cgcgcaggct      120
ccaggaagg gtctagagt ggtctcagc attggggcta agggtttgc tacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcggct      300
aggggtaagt ttgactactg gggtcaggga accctggtca ccgtctcgag c      351
```

<210> 782

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 782

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact cggtatcaga tgggttgggt cgcgcaggct      120
ccaggaagg gtctagagt ggtctcagtt attaattgtt ggggttcgag tacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaatgtct 300
 gggaagtttg cctactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 783

<211> 351

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 783

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctt 60
 tcctgtgcag cctccggatt cacctttggg aattatagta tgatgtgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaacg attattcctg ctggtacgac tacatactac 180
 gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgtcg 300
 attagttgt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 784

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 784

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gcgtatgata tggggtgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatgg atttctccga atggttatga tacatactac 180
 gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggggt 300
 gtgaagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 785

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 785

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt tggatatgaga tggcttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaacg attcaggctg atggtgagca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagcttcg	300
tatgctcttg tgiatcctcc tgaggagttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 786

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 786

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttacg aattatagga tgtcttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attgatgac tgggtgtgtc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggagg	300
cttaagaata gtcagccgac ggattttgac tactggggtc agggaaacct ggtcaccgtc	360
tcgagc	366

<210> 787

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 787

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat caggctcata tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcattt attaatcctt cgggttatta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccttcg	300

cttagtcctgt cttcttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 788

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 788

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag actggtcaga tgggttgggc ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaaat attgatgggt ctggtacgta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtacg 300

cagaattatc ggtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 789

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 789

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggt gcttatccga tgtattgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcatct attcataagg atggtaggat tacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagggt 300

acgccggttg atgggtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 790

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 790

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcct gatgagggtg tgacgtgggt cgcaggct 120
ccaggaagg gtctagagt ggtctcaacg attgagactg gtggtacgtg gacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaatggat 300
gggtctggta catggcagac gtttgactac tgggtcagg gaaccctgtt caccgtctcg 360
agc 363

<210> 791

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 791

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat agtctgggta tgggttgggc cgcaggct 120
ccaggaagg gtctagagt ggtctcatat attcgggctg aggtgtctta tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatctt 300

gcggattctg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 792

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 792

gaggtgcagc tgttgaatc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttagt gactcgtata tggagtgggt cgcaggct 120
ccaggaagg gtctagagt ggtctcagg attgatcata ttggtgtgg gacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatgat 300
ggtcgtgggt ggtctatgtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc 360

<210> 793

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 793

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttct ggtgggtata tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagt attggggcta gtggtgcgta tacatactac      180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgggg      300
ggtaggttag actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 794

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 794

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgat gaggggcata tggggtgggt ccgccaggct      120

ccaggaagg atctagagtg ggtctcatat attgggagtc tgggtttgca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgggag      300
tttagtaatg gggggtttga ctactggggt caggaaccc tggtcaccgt ctcgagc      357
```

<210> 795

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 795

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttaag actagtccta tgtattgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatcg attgatcgga ctggtgggca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacaggct 300
ctgcttactg atgcgaagcg ttttgactac tggggtcagg gaaccctggt caccgtctcg 360
agc 363

<210> 796

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 796

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat ggtcgggata tggtttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagct attagtccga gtggtctgga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacgtcct 300
cagatgctgg ttactaattt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 797

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 797

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggt aatgatccga tgagttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcaggg attggtcggg aggggtgattc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagattct 300

atgcggcatc agccgtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc 357

<210> 798

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 798

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgat gagacttata tgaagtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcagcg attggggcgt cgggtgctga tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttacg	300
catctgaatg gtcggtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 799

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 799

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg gggtggccta tggggtgggt ccgccaggct	120
ccaggaagg gtctagagt ggtctcaggt attgatattg atggtgctcc gacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggag	300
gcgggttctt ggtcttttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 800

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 800

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt gatcaggcga tgtggtgggc ccgccaggct	120
ccaggaagg gtctagagt ggtctcattt attcagggtg atggtggttt tacatactac	180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctagt	300
aagccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 801

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 801

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag actggtcaga tgggttgggc cgcgcaggct	120
ccagggaagg gtctagagtg ggtctcaaatt attgatgggt ctggtacgta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggtg	300
cggaaattttg cttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc	354

<210> 802

<211> 372

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 802

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt gggcatgata tgtcttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtctc atggtacgca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtt	300
aggggttggg ttggtcatga tacgcagcct ttgactact ggggtcaggg aaccctggtc	360
accgtctcga gc	372

<210> 803

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 803

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag agtaaggata tgctttgggt ccgccaggct	120

ccaggaagg gtctagagt ggtctcatct atttcgtcgg atggtactca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaagagctg 300

ggtgggtctt ggcagtttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 804

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 804

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgcg gatcgtgata tggtttgggt cgcaggct 120
ccaggaagg gtctagagt ggtctcaggc attggggcgt cgggtacgac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaaggtggg 300
acgggtccta ctgatttgtg ggattttgac tactggggtc agggaaacct ggtcaccgac 360
tcgagc 366

<210> 805

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 805

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat gatgagaaga tgctttgggt cgcaggct 120

ccaggaagg gtctagagt ggtctcaagt attagtgtga gtggtctgca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggag 300
gcgggttctt ggtcttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 806

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 806

gaggtgcagc tgttggagtc cgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg caggagagga tgatttgggt ccgccaggct 120

cctgggaagg gtctagagtg ggtctcagat atttcggctt cgggtgggac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggag 300

gcgggttctt ggtcttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 807

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 807

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc tctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccaggct 120

ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccatgaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttg actacagggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 808

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 808

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 809

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 809

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttg actaccgggt tcagggaacc ctggtcaccg tctcgagc 348

<210> 810

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 810

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgcaaggct 120
ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 811

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 811

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt cgcagggt 120
ccaggaagg gtctagagt gatctcagc atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actacagggt tcaggaacc ctggtcaccg tctcgagc 348

<210> 812
<211> 348
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 812

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt cgcagggt 120

ccaggaagg gtctagagt ggtctcagc atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccgagaa cacgtgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 813
<211> 348
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 813

gaggtgcagc tgttggagac tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt cgcagggt 120
ccaggaagg gtctagagt ggtctcagc atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240
ctgcaaatgg acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actactgggg tcggggaacc ctggtcaccg tcacgagc 348

<210> 814
<211> 348
<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 814

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt      300
gggtattttc actactgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 815

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 815

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgtag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccaggct      120
ccaggaatg gtctagagtg gatctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt      300
gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 816

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 816

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctctggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct      120
ccaggaagg gtctagagtg ggtctcagcg atatctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

ctgctaata ga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttc actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 817

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 817

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgcaaggct 120

ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttt actacagggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 818

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 818

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc catgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300

gggtattttt actacagggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 819

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 819

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccgggct 120

ccaggaagg gattagagt ggtctcaatg atttccgggg atggttatcg tacatactac 180
 gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 820
 <211> 348
 <212> DNA
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polynucleotide
 <400> 820

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagt ggtctcagcg atttctggtg acggttggcg cacatactac 180
 gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 821
 <211> 348
 <212> DNA
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 821

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg tggatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagt ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctg 300
 ctctactttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 822
 <211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 822

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct      120
ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagctg      300
gggttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 823

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 823

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct      120
ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagttg      300
```

```
gagtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 824

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 824

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct      120
ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
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gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggttg 300

gagtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 825

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 825

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctg 300

gccttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 826

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 826

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctc 300

ttgtactttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 827

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 827

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagttg 300

gagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 828

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 828

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagctg 300

cagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 829

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 829

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaagagctg 300

ctcttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 830

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 830

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacggc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct      120
ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagttg      300
```

```
gagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 831

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 831

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct      120
ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagttg      300
ctcttctttg actaccgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 832

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 832

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt catctttgag tggatatgaga tgcagtgggt ccgccgggct      120
```

ccaggaagg gactagagt ggtctcagc atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaacttg 300

gagtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 833

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 833

gaggtgcggc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag tggatatgaga tgcagtgggt ccgccgggct 120

ccaggaagg gactagagt ggtctcagc atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagttg 300

cagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 834

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 834

gaggtgcagc tgttggggtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagc attagtggta gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgttc gaaagagccg 300

tttcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 835

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 835

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct	120
ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 836

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 836

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccaggaagg gtctagagtg gatctcagct attagtggaa gtggtggttag cacatactac	180
gcagactccg tgaagggccg gtttaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 837

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 837

gaggtgcagc tgttggatcc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttggg aaggaggaga tgatttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcatct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300

tttcgttttg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 838

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 838

gaggtgcagc tgttggggc tgggggaggc ttggtacagc ctggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttttg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 839

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 839

gaggtgcagc tgttggagcc tgggggaggc ttggtacagc ctggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgctaataga acagcctgcg tgccgaggat accgcggtat attactgttc gaaagagccg 300

tttcgttttg actactgggg tcaggggagcc ctggtcaccg tctcgagc 348

<210> 840

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 840

gaggtgcagc tgttggatcc tgggggaggc ttggtacagc ctggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg aaggaggaga tgatttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcatct attagtggta gtggtgtag cacatactac 180

gcagactccg ttaagggccg gttcaccatc tccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300

ttacgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 841

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 841

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatctgggt cgcaggct 120

cctgggaagg gtctagagt gatctcagct attagtggta gtggtgtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc caccgcgaca attctaagaa cactctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgttc gaaagagccg 300

tttcgttttg actacagggg tctgggaacc ttggtcaccg tctcgagc 348

<210> 842

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 842

gaggtgcagc tgttggatcc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg aaggaggaga tgatttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcatct attagtggta gtggtgtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaggaa cacgtgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300

ttacgttttg actactgggg tcaggggacc ctggtcaccg tctcgagc 348

<210> 843

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 843

```
gaggtgcagc tgttggattc tgggggaggc ttgtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg gatctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtgt attactgtgc gaaagagccg      300
tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 844

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 844

```
gaggtgcagc tgttggatcc tgggggaggc ttgtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg gatctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaataa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gagagagccg      300
tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 845

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 845

```
gaggtgcggc tgttggagtc tggggaaggc ttgtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 846

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 846

gaggtgcagc agttggagtc tgggggaggc ctggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 847

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 847

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct 120

ccaggaagg gtctagagt ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

ttctactacg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 848

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 848

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct 120

ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

ttctacttcg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 849

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 849

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gagaaggaga tgatttgggt ccgtcaggct 120

ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

ttcttctacg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 850

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 850

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttccc caggaggaga tgatttgggt ccgtcaggct 120

ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 851

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 851

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttttc gccgccgaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
```

```
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 852

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 852

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagttagc ccggtacgag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
```

```
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 853

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 853

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
```

ccaggaagg gtctagagt ggtctcagct attagtcgga tgggtttcag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 854

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 854

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtcggt ggggtcacag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 855

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 855

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtcgcc tcggttggag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 856

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 856

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtcgct ggggtgccag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 857

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 857

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtaggc aggggtgggag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 858

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 858

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtgtgt ccggttggag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg	300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 859

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 859

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcagct attagtcggt ggggttggag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 860

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 860

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcagct attagtcgga acggtctgag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 861

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 861

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcaggct 120

ccaggaagg gtctagagt ggtctcagct attagtgggc tgggttgag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 862

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 862

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcaggct 120

ccaggaagg gtctagagt ggtctcagct attagtgcgt tgggttgag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 863

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 863

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcaggct 120

ccaggaagg gtctagagt ggtctcagct attagtgcga ggggttacag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgtgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 864

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 864

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtaggc acggttgag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 865

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 865

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaagc attagcagga gtggtggttag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 866

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 866

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtcgga tcggtaacag cacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 867

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 867

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtgggc acggttggag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 868

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 868

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct atttcgaggt ggggtggttag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 869

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 869

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg	300
ttcattgtatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 870

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 870

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg	300
ttcccgtacg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 871

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 871

gaggtgcagc tgttggcgtc tgggggaggc ttggtgcagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtgg cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 872

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 872

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
```

```
ttgtactatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 873

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 873

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccc      300
atgtactatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 874

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 874

```
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
```

ccaggaagg gtctagagt ggtctcagct attagtagga acggtttcag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 875

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 875

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtcgca cgggtgggag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 876

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 876

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtcggg aggggtgggag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 877

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 877

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccgggtt cccctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtcggc aggggttgag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 878

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 878

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtaggg gcggtgggag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 879

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 879

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtcgca cgggttacag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 880

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 880

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcagct attagtagga acggtaggag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 881

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 881

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 882

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 882

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcagct attagtagga agggtagcag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 883

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 883

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcagct attagtcggg gcggttggag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 884

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 884

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcaggct 120

ccagggaagg gtctagagt ggtctcagct attagtcgct cgggttacag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 885

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 885

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gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtagga acggtatgag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 886

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 886

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 887

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 887

```
gaggtgcagc tgttggagtc tggggaaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact gagcatgaga tgatttgggt ccgccaggct      120
ccagggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tcccaggac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg actactgggg ccagggaacc ctggtcaccg tctcgagc 348

<210> 888

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 888

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatc cacctttact gagtatgaga tgatttgggt ccgccaggct 120

ccagggaagg gtctggagtg gatctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggac accgcggtat atttctgtgc gaaagagccg 300

cttaggtttg actacagggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 889

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 889

gaggtgcagc tgttgagcc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gagtatgaga tgatttgggt ccgcaaggct 120

ccagggaagg gtatggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240

ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg gctactgggg tcagggtacc ctggtcaccg tctcgagc 348

<210> 890

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 890

gaggtgcagc tgttggattc tgggggaggc ttggtacagc ctggggggtc actgcgtctc 60

tcctgtgcag cctccggatt cacctttact gattatgaga tgatttgggt ccgccaggct 120

ccaggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctacaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 891

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 891

gaggtgcagc tgttggggtc agggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gattatgaga tgatttgggt ccgccaggct 120

ccaggaaga gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300

cttaggtatg acgactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 892

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 892

gaggtgcagc cgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgttcag cctccggatt cacctttaat gattatgaga tgatttgggt ccgccaggct 120

ccaggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 893

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 893

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gaggtgcagc tgttggagtc tggggaaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gattatgaga tgatttgggt ccgccaggct      120
ccagggaag gctcggagtg ggtctcatct atttcgggta atggtgctaa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg      300
```

```
cttaggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 894

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 894

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gaggtgcagc tgttggaccc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact gattctgaga tgatttgggt ccgccaggct      120
ccagggaagg gctcggagtg ggtctcatct atttcgggaa atggtgctaa tacatactac      180
gcggactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg      300
```

```
cttaggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 895

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 895

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gaggtgcagc tgttggagcc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttact gattatgaga tgatttgggt ccgcaaggct      120
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ccaggaagg gtaggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tcccaggagac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 896

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 896

gaggtgcagc tgttggagtc tgggtaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gtagtgaga tgatttgggt ccgcaaggcc 120

ccaggaagg gtaggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tcccaggagac accgcggtat attactgtgc gaaagaaccg 300

cttaggtttg acaactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 897

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 897

gaggtgcagt tgttggagtc tcggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttact gagcatgaga tgatttgggt ccgccaggct 120

ccaggaagg gtaggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180

gcagactccg tgaaggccg gttctccgtc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tcccaggagac accgcggtat attactgtgc gaaagagccg 300

cttaggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 898

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 898

gaggtgcagc cgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgctg cctccggatt cacctttact gaggatgaga tgatttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300
cttaggtttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 899

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 899

gaggtgcagc tgttggagtc tgccggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct gaggatgaga tgatttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatca atttcgggta atggtgctaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300
cttaggtttg actactgggg tcagggagcc ctggtcaccg tctcgagc	348

<210> 900

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 900

gaggtgcagc tgttggagcc tgggggaggc ttggtacagc ctggggggtc gctgcgtctc	60
tcctgtgcag cctccggatt cacctttact gaggatgaga tgatttgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300

cttaggtttg acaactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 901

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 901

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc tctgcgtctc 60

tcctgtacag cctccgatt cacctttaat atgtatgaga tgcgtgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaggt attagtagac gtggttttac tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggat accgcgtat attactgtgc gaaagagccg 300

attacgtatg attgaggta tgcgcgtttt gactactcgg gtcaggaac cctggtcacc 360

gtctcgagc 369

<210> 902

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 902

gaggagcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtacag cctccgatt cacctttaat atgtatgaga tgcgtgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcaggt attagtagac gtggttttac tacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaggat accgcgtat attactgtgc gaaagagccg 300

attacgtatg ctacgaggta tgcgcgtttt gactactggg gtcaggaac cctggtcacc 360

gtctcgagc 369

<210> 903

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 903

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attagtaggc gtgggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca atttcaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg	300
attacgtatg atatgaggtg tgccggtttt gactacgggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 904

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 904

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attagtaggc gtgggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg	300
attacgtatg atatgaggtg tgccggtttt gacaactggg gtcagggaac cctggtcacc	360
gtctcgaac	369

<210> 905

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 905

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtacag cctccggatt cacctttaat acgtatgaga tgtcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attggttaggc gtgggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg	300

attacgtatg atttgaggta tgcgcgtttt gactactcgg gtcaggggaac cctggtcacc 360
gtctcgagc 369

<210> 906
<211> 369
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 906

gaggtgcagc tgatggagtc agggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtacag cctccggatt ctctttaat atgtatgaga tgcgtgggt ccgccaggct 120
ccagggaag gtctagagt ggtctcaggt attagtaggc gtggttatac tacatactac 180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcgggggaac cctggtcacc 360
gtctcgagc 369

<210> 907
<211> 369
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 907

gaggtgcagc tggtggagtc tggggaggc ttggtgcagc ctggggggtc cctgcgtctc 60
tcctgtacag cctccggatt cgcctttaat atgtatgaga tgcgtgggt ccgccaggct 120
ccagggaagg gactagagt ggtctcaggt attagtaggc atggttttac tacgtactac 180
gcagactccg tgaaggccg gttcaccgtc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atatgcggta tgcgcgttct gactactggg gtcaggggaac cctggtcacc 360

gtctcgagc 369

<210> 908
<211> 369
<212> DNA
<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 908

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atttctgtgc gaaagagccg	300
attacgtatg atatgaggta tgccggttct gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 909

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 909

gaggtgcagc tgttggagtc tggggggggc ttggttcagc ctggggggtc cctgcgtctc	60
tcctgtacag cctccgggtt cacctttaat atgtatgaga tgcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg	300
attacgtatt ctatgaggta tgccggtttt gactactcgg gtctgggaac catggtcacc	360
gtctcgagc	369

<210> 910

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 910

gaggtgcagc tgctggagtc tgggggaggc ttggtacagc ctggggggtc ccttcgtctc	60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgcgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
 attacgtatg atatgaggta tgcgcgtttt gactacagtg gtcaggaac cctggtcacc 360
 gtctcgagc 369

<210> 911

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 911

gaggtgcagc tgttgagtc tggaggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtacag cctccggatt cacctttaat atgtatgaga tgtctgaggc ccgcaaggct 120
 ccagggaagg gtctagagt ggtctcaggt attagtaggc atggttttac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300

attacgtatg atatgaggta tgcgcgtttt gactactggg gtcaggaac cctggtcacc 360
 gtctcgagc 369

<210> 912

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 912

gaggtgcagc tgttcgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtacag cctccggatt cacctttaat atgtatgaga tgtctgaggc ccgccaggct 120
 ccagggaagg gtctagagt ggtctcaggt attagtaggc gtggttttac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaagagccg 300
 attacgtatg atatgaggta tgcgcgtttt gactactggg gtcggggaac cctggtcacc 360
 gtctcgagc 369

<210> 913

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 913

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggagc cctgcgtctc      60
tcctgtacag cctccggttt cacctttaat atgtatgaga tgcgtgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcagg attagtaggc gtggttttac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaagagccg      300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcggggaac cctggtcacc      360
gtctcgagc                                     369
```

<210> 914

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 914

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gaggtgcagc tgttggagtc tgggggaggc tcggtacagc ctgggggggc cctgcgtctc      60
tcctgtacag cctccggatt ctcctttaat atgtatgaga tgcgtgggt ccgccaggct      120
ccaggaagg gtctagagt ggtctcagg attagtaggc gtggttttac tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaagagccg      300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcagggaac cctggtcacc      360
gtctcgggc                                     369
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<210> 915

<211> 369

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 915

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gaggtgcagc tgttggagtc tgggggaggc ttggtacaac ctgggggggc cctgcgtctc      60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgcgtgggt ccgcaaggct      120
ccaggaagg gtctagagt ggtctcagg attagtaggc gtggttttac tacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300

attacgtatg atatgaggta tgcgcgtttt gactactggg gtcagggaac cctggtcacc 360

gtctcgagc 369

<210> 916

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 916

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 917

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 917

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 918

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 918

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtac gaaacttccg	300
tttatTTTTT aatactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 919

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 919

gaggtgcagc tgttggagtc cgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttatgtttg acgaccgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 920

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 920

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300

tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 921

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 921

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt ctcttttcgg gattatgaga tgtggtggta ccgccaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatattac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttatttttg acaaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 922

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 922

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat acctcggtat atcactgtgc gaaacctccg 300

tttatttttg gcgactgggg tccgggaacc ctggtcaccg tctcgagc 348

<210> 923

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 923

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc ccggcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccggggaagg gtctagagcg ggtctcagct attaatccgc agggtagcg tacatactac 180

gcagactccg tgaagggccg gttcacgac tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 924

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 924

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcg tacatactac 180

gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300

tttatgtttg acgaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 925

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 925

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggaagg ttctagagcg ggtctcagct attaatccgc agggtagcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300

tttatgtttg acgaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 926

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 926

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc agccgaggat actgcggtat attactgtgc gaaacttccg      300
tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 927

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 927

```
gaggtgcagc tgttggagtc tgggggaggc ttgatacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgttt gaaacttccg      300
```

```
tttattttcg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 928

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 928

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaacccgc aggttacgcg tacatactat      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgatgat accgcggtat atcactgtac gaaacttccg 300

tttatttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 929

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 929

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggatgg ttctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctatat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttttttttg actccagggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 930

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 930

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccgggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180

gcagactctg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 931

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 931

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac	180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 932

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 932

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt ctcctttcgg gattatgaga tgtggtggta ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatattac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 933

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 933

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg ttctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat	240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 934

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 934

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg      300
```

```
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 935

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 935

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtac gaaacttccg      300
```

```
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 936

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 936

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
```

ccaggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgttt gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 937

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 937

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta 60

tcctgtgcag cctccgatt caccttcgg gattatgaga tgtgtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaacccgc agggtaacgc tacatactat 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgatgat accgcggtat atcactgtac gaaacttccg 300

tttatttttg aatactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 938

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 938

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccgatt caccttcgg gattatgaga tgtgtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180

gcagactccg tgatggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaacct 300

tatagttttg actcctgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 939

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 939

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaagaacct	300
tatagttagt actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 940

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 940

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccgggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 941

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 941

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccgggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg	300

tttatgtttg acgaccgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 942

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 942

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180

gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300

tttatgtttg acgactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 943

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 943

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgagt tgtggtgggt cgcgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180

gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 944

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 944

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgagt tgtggtgggt cgcaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300

tttatgtttg acgaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 945

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 945

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 946

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 946

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300

tttatgtttg acgaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 947

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 947

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagct attaatccgc aggttacgcg tacatactac      180
gcagactccg tgatgggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 948

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 948

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtcta      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagct attaatccgc aggttacgcg tacatactac      180
gcagactccg tgatgggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccaggat actgcggtat attactgtgc gaaacttccg      300
tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 949

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 949

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

acctactttt ccgaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 950

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 950

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

tttttcttg aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 951

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 951

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

acgtacttta aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 952

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 952

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttt ccgagtgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 953

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 953

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat atcactgtgc gaaacttccg 300

atgttctttg aggactgggg tcagggaacc ctggtcaccg tctcgaac 348

<210> 954

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 954

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacttccg 300

tttccgtttt cggagtgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 955

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 955

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatgg acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
```

```
ttttactttt ccgagtgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 956

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 956

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt acggtaacct cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
```

```
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 957

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 957

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
```

ccaggaagg gtctagagcg ggtctcagct attaatccgc ccggtacatt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 958

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 958

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtggctt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 959

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 959

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccga tgggtgggtt cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 960

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 960

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgca cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 961

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 961

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ccggtgggct gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 962

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 962

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc acggttcgtt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300

tttacttttg acgactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 963

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 963

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgg ccggtcgggtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 964

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 964

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtagctt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 965

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 965

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccc gactacgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 966

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 966

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag actccggatt cacctttccg cccgtggaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 967

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 967

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt acggtgggct gacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 968

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 968

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtaacca cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 969

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 969

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc acggtggcta cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 970

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 970

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaggg gtctagagcg ggtctcagct attaatccgc ccggtatgct cacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 971

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 971

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtcagtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 972

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 972

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtggcta cacatactac 180

gcagactccg tgaagggccg attcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 973

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 973

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgt cgggtgggct gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 974

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 974

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgt cgggtggggt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 975

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 975

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgt cgggtacgct cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 976

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 976

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt acggttcgtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
```

```
tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 977

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 977

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtlggcta cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
```

```
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 978

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 978

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
```

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggggtgggct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 979

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 979

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttccca cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 980

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 980

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtacctt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 981

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 981

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccga acggtcggct gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg cggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 982

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 982

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtcagct gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 983

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 983

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc acggtggcct cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300

tttacttttg acgactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 984

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 984

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctggagcg ggtctcagct attaatccgg cgggtatgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 985

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 985

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgc acggtacatt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 986

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 986

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgtt gacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 987

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 987

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt acggtggcct gacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 988

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 988

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattacgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgg ccggtttctt gacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 989

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 989

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacggc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctggagcg ggtctcagct attaatccgt acggtggcct gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 990

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 990

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc      348
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<210> 991

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 991

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac      180
```

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 992

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 992

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt acggtgggct gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatgg acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 993

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 993

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtacgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 994

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 994

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtggcta cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcggggaacc ctggtcaccg tctcgagc	348

<210> 995

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 995

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgt acggtaacct gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 996

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 996

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc acggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 997

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 997

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgg ccggtttcta cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
```

```
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 998

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 998

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgg cgggtlggcct cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
```

```
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc      348
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<210> 999

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 999

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cgcctttcgg gattatgaga tgtggtgggt ccgccaggct      120
```

ccaggaagg gtctagagcg ggtctcagct attaatccgc acggttcct cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1000

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1000

gaggtgcagc tgttgagtc tgggggagcg ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgt gattatgaga tgtgtgggt cgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgg ccggtgggta cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300

tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1001

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1001

gaggtgcagc tgttgagtc tgggggagcg ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgtgggt cgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgac tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttggttta cggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1002

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1002

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
ttcatgtttt ccgaccgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 1003

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1003

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
tttttgtttc aggagtgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 1004

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1004

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300

acgcggtttg aggactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1005

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1005

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc acgagtgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1006

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1006

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1007

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1007

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

acgttcttta aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1008

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1008

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacagc tacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttttcttte aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1009

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1009

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

cagttgtttc acgaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1010

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1010

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccaggac accgcggtat attactgtgc gaaacttccg      300
cacgtctttg aggactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 1011

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1011

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccaggat accgcggtat atcactgtgc gaaacttccg      300
```

```
tttgggtttt ccgagtgggg tcaggaacc ctggtcaccg tctcgagc      348
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<210> 1012

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1012

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
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gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

cagttgtttc aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1013

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1013

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttctttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1014

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1014

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

cactacttta aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1015

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1015

gaggtgcagc tgttggagtc tgggggaggc ttggtacagt ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg	300
ttttactttg aggagtgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 1016

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1016

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttaggtttt ccgaccgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 1017

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1017

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaacttccg	300
acgctgtttc aggactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 1018

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1018

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
```

```
ttttactttt ccgagtgggg tcagggaacc ctggtcaccg tctcgaac      348
```

<210> 1019

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1019

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
ttttggtttc aggagtgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 1020

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1020

```
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
```

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1021

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1021

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300

atgttctttg aggactgggg tcaggaacc ctggtcaccg tctcgaac 348

<210> 1022

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1022

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgttgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1023

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1023

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgtt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttctttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1024

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1024

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgtt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttctttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1025

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1025

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300

ttttactttc aggagtgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1026

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1026

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300

atgttctttg aggactgggg tcaggggaacc ctggtcaccg tctcgaac 348

<210> 1027

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1027

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc acgagtgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1028

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1028

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

tttttctttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1029

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1029

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttttctttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1030

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1030

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1031

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1031

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg      300
atgttctttg aggactgggg tcagggaacc ctggtcaccg tctcgaac      348
```

<210> 1032

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1032

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
```

```
ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 1033

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1033

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

ttttctttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1034

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1034

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

ttttctttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1035

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1035

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat atcactgtgc gaaacttccg 300

atgttctttg aggactgggg tcaggaacc ctggtcaccg tctccagc 348

<210> 1036

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1036

gaggtgcagc tgttggagac tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg acttatcata tgcagtgggt cgcgggggt 120

ccagggaagg gcctggagtg ggtctcaatg attgatgcgg atggctcttg gacatactac 180

gcagaccccc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccaaggac accgcggtat attactgtgc gagaccgggt 300

ccgcagtttg gtcagtttga ctacttgggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 1037

<211> 357

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1037

gaggtgcagc tgtttgagtc tgggggaggc ttggtacaga ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccttttcg acttatcata tgcagtgggt cgcgggggt 120

ccagggaagg gtcctggagtg ggtctcaatg attgatgcgg atggctcttg gaaatactac 180

gcagaccccc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attacttgtt gaaaccgggt 300

ccgcagtttg gtcagtatga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 1038

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1038

gaggtgcagc tgttggagtc agggggaggc ttggtacagc ctggggggtc cctgcggctc 60

tcctgttcag cttccggatt caccttttcg gggtatgata tgcagtgggt cgcgggggt 120

ccagggaagg gtctagagtg ggtctcaacg attagtgcgt cgggtgttta tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatactct 300

aatcgttttg cgcttaatag ttttgactac aggggtcggg gaaccctggt caccgtctcg 360

agc 363

<210> 1039

<211> 363

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1039

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cttccggatt caccttttcg gggtatgata tgcagtgggt ccgccaggct 120

ccaggaggagg gtctagagtg ggtctcaacg attagtgcgt cgggtgttta tacatactac 180

acagactccg tgaagggccg gttcaccacc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtac gaaatatcca 300

aatcgttttg cgcgtaataa ttttgactac tggggtcagg gaaccctggt caccgtctcg 360

agc 363

<210> 1040

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1040

gacatcctga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaaatag ttctattttg tgggcgttag cttggtacca gcagaaacca 120

ggggaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagt gtagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctgtgtac gttcagccaa 300

gggaccaagg tggaatatcaa acgg 324

<210> 1041

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1041

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcagacag ttctatTTTg tgggcgttag cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgagagt tcatccggtt tgcaaagtgg ggtcccatca 180

cgTTTcagtG gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagatTTTg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgGCCaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1042

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1042

gacatccaga tgaccgtGtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcagatag ttctatTTTg tgggcgttag cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagcgg ggtcccatca 180

cgTTTcagtG gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagatTTTg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgGCCaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1043

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1043

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaaataG ttctatTTTg tgggcgttag cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca 180

cgTTTcagtG gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagatTTTg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgacca 300

gggaccaagg tggaaatcaa acgg 324

<210> 1044

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1044

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaaatag ttctattttg tgggcgttag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tctaccggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgccaa      300
```

```
gggaccaagg tggaaatcaa acgg                                             324
```

<210> 1045

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1045

```
gacatccaga tgaccgtgtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaaatag ttctattttg tgggcgttag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tctccggat tgcaaagcgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgccaa      300
gggaccaagg tggaaatcaa acgg                                             324
```

<210> 1046

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1046

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcagatag ttctattttg tgggcgttag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tctccggtt tgcaaagtgg ggtcccatca      180
```

cgtttcagtgc gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcgaccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1047

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1047

gacatccaga tgaccagtc tccatcctca ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaaatag ttctattttg tgggcgttag cttggtacca gcagaaacca 120

gggaaagccc ctgagctcct gatcgagagt tcttcggtc tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcgcccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1048

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1048

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcgaatag ttctatattg tgggcgttgg cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgagagt tcttcggtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcgcccaa 300
gggaccaagg tggaaaacaa acgg 324

<210> 1049

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1049

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaaataag ttctattctg tgggcgttag cttggtacca gcagaaacct	120
gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaaccc	240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1050

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1050

gacatccaga tgaccagtc tccatcctcc ctgtctgctt ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaaataag ttctattttg tgggcgttag cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg gatcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1051

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1051

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttgaga ccgtgtcacc	60
atcacttgcc gggcaaataag ttctattttg tgggcgttag cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagcgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1052

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1052

```
gacatcctgt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc      60
atcacttgcc gggcaaata tagttatcttg tgggcgttag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240

gaagatcttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgccaa      300
gggaccaagg tggaataca acgg                                     324
```

<210> 1053

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1053

```
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc      60
atcacttgcc gggcaaata tagttatcttg tgggcgttag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca      180

cgtttcagtg gaagtggaa tgggacagat ttcactctca ccatcagcgg tctgcaacct      240
gaagatcttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcgacaa      300
gggaccaagg tggaataca acgg                                     324
```

<210> 1054

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1054

```
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc      60
atcccttgcc gggcaaata tagttatcttg tgggcgttag cttggtacca gcagaaacca      120

gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca      180
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cgtttcagtgcagtcgcatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtag gttcggccaa 300
gggaccaagg tggagatcaa acgg 324

<210> 1055

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1055

gacatccaga tggcccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattgag cgtcggttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtgcagtcgcatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttaggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1056

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1056

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagtgtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcggttaa attggtatca gcagaaacca 120
ggggaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtgcagtcgcatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgccatcag tatgcgagtc cacctttgac gttcggccaa 300
gggaccaatg tggaaatcaa acgg 324

<210> 1057

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1057

gacatccaga tgaccagtc tccatcctcc ctatctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagt gtagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctgcgtacta ctgtcatcag tacgagagtc cacctttgac gtttgccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1058

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1058

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagt gtagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcgccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1059

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1059

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga acgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagt gtagtgatc tgggacagat ttactctca ccatcagcaa tctgcaacct	240
gaagattctg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttaggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1060

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1060

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gggcaagcca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaggccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttaggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1061

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1061

gacatccaga taaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagacc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc ctcctttgac gttcgccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1062

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1062

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
ggggaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180

cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa atgg 324

<210> 1063

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1063

gacatccagt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagaa ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1064

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1064

gacatccaga tgtcccagtc tccatccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgat gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1065

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1065

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
attacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagacc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagt ggcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacca	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300

gggaccaaag tggaaatcaa acgg	324

<210> 1066

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1066

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ccgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa actggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagt ggcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300

gggaccaaag tggaaatcaa acgg	324

<210> 1067

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1067

gacatccaga tgaccagtc tccatcctcc ctgtttgcat ctgtaggga ccgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180

cgtttcagt ggcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300

gggaccaaag tggaaatcaa acgg	324

<210> 1068

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1068

gacatccaga tgacccagta tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtcgattgag cgtcgtttaa attggtatca gcagaaacca	120
ggggaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggactaaag tggaaatcaa acgg	324

<210> 1069

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1069

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtgc gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcgcgtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatccg tatgagagtc cacctttgac gttcggccaa	300
gggaccaaaag tggaaatcaa acgg	324

<210> 1070

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1070

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ggcgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatct	180

cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcagcca 240
gaagattttg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gtcgggcca 300
gggaccaaag tggaaatcaa acgg 324

<210> 1071

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1071

aacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ggcgattgag cgtcggttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttctcggt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcgggcca 300
gggaccaaag tggaaatcaa acgg 324

<210> 1072

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1072

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gacgattggg cgtcggttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttccggtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggtcagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcgggcca 300

gggaccaaag tggaaatcaa acgg 324

<210> 1073

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1073

gacatccaga tgaccagtc tccatcctcc ctttctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gagcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagaa ttactctca ccatcagcag tctgcaacct	240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1074

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1074

gacatccaga tgaccagac tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
ggggaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ccacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tgaaaatcaa acgg	324

<210> 1075

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1075

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaaccc	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1076

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1076

cacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgccatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1077

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1077

gacgtccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120

ggggaagccc ctaagctcct gatctatctt acttcccgtt tgcaaagcgg ggtcccatca 180

cgtttcagtg gtagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgccatcag tatgcgagtc cacctttgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1078

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1078

gacatccaga tgaccagtc gccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcaccag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggtaatcaa acgg 324

<210> 1079

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1079

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacct 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtgc gcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1080

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1080

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gccgattgag cgtcgtttta attggtatca gcagaagcca 120
gggaaagccc ctaagctcct gatctatctt gcttccggtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacatacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1081

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1081

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtca gacgattggg cgtcggttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1082

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1082

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtca gtcgattgag cgccgttaa attggtatca gcagaaacca	120

gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc ctcctttgac gttcggccaa	300
gggaccaaag tggaaatcat acgg	324

<210> 1083

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1083

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60

atcacttgcc gggcaagtca gacgattgag cgtcggttaa attggtatca gcagaaacct	120
gggaaagccc ctaagctcct gatctatctt gctaccggt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1084

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1084

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtcgattgag cgccgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc ctcctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1085

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1085

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacct	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag ttcgagcacc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1086

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1086

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagttt cccattgac cgtcgtttaa attggtatca gcagaaacct	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180

cgcttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324
<210> 1087	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	
<400> 1087	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagttc caccattggc cgtcgtttta attggtatca gcagaaacct	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324
<210> 1088	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	
<400> 1088	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagttacc	60
atcacttgcc gggcaagttc ccagattggg cgtcgtttta attggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324
<210> 1089	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	

<400> 1089

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtga gcggattggg cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagt ggcagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1090

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1090

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtga gcgattggc cgccgtttaa attggtatca gcagaaacct	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagt ggcagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1091

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1091

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtga gccgattgcc cgccgtttaa attggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagt ggcagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1092

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1092

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtgg gaacattggc cgtcgtttaa attggtacca gcagaaacca	120
gggaaagccc ctaggtcctt gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa gcgg	324

<210> 1093

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1093

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtgc gaacattgac cgtcgtttaa attggtacca gcagaaacca	120
gggaaagccc ctaggtcctt gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300

gggaccaaag tggaaatcaa acgg	324

<210> 1094

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1094

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagtca gagcattggg cgtcgtttaa attggtacca gcagaaacct	120
gggaaagccc ctaggtcctt gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180

cgcttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1095

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1095

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtca gaacattggg acgcgtttaa attggtacca gcagaaacca 120

gggaaagccc ctaggtcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180

cgcttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1096

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1096

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtga ggtcattggg cgtcgtttaa attggtacca gcagaaacca 120

gggaaagccc ctaggtcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180

cgcttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1097

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1097

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtga ggcgattggc cgtcggttaa attggtatca gcagaaacca 120

gggaaagccc ctaggtcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180

cgcttcagt ggcagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1098

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1098

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtac cagcattgcg cgtcggttaa attggtatca gcagaaacct 120

gggaaagccc ctaggtcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180

cgcttcagt ggcagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1099

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1099

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtgt gaacattggg cgtcggttaa attggtacca gcagaaacca 120

gggaaagccc ctaggtcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180

cgcttcagt ggcagtgatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1100

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1100

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc      60
atcacttgcc gggcaagtc gacgattgag cgtcgtttaa attggtacca gcagaaacca      120
gggaaagccc ctaggctcct gatctatctt tcgtcgaagt tgcaaagtgg ggtcccatca      180
cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa      300
```

```
gggaccaaag tggaaatcaa acgg                                           324
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<210> 1101

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1101

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gaggtgcagc tgttgagtc tgggggaggc ttggttcagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatc caccattgct gggtatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg tgtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccagagcg attccaagaa cacgctgtat      240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct      300
tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 1102

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1102

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gaggtgcagc cgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt ccgccaggct      120
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ccaggaagg gtctagagcg gatctcagct attagcggta gtggtgtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1103

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1103

gaggtgcagc tgttgagtc tgggggaggc tcggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag ccaccggatc cacctttgct gggtatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtgtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gagagatcct 300

tacagttatg actactgggg tcaggaacc ctggtctccg tctcgagc 348

<210> 1104

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1104

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggact cacctttgct gggtatgaga tgtggtgggt ccgccaggca 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtgtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcagtat atcactgtgc gagagatcct 300

tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1105

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1105

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactctg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaagaacct	300
tatagtatat actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1106

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1106

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatc cacctttgct gggtatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tcccaggat accgcggtat attactgtgt gaaagatcct	300
tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1107

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1107

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatc caccattgcc gggtatgaga tgtggtgggt ccgccaggct	120
ccgggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct	300

tatagttttg actactgggg tcagggaacc cgggtcaccg tctcgagc 348

<210> 1108

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1108

gaggtgcagc tgatggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatc cacctttgct gggtatgaga tgtggtggta cggccaggct 120

ccagggaagg gtctagagcg ggtctcagct attagtggaa gtggtagaag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg actactgggg tcagggaacc ctgggtcaccg tctcgagc 348

<210> 1109

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1109

gaggtgcagc tgctggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cggccaggct 120

ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacgtactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcagtat attactgtgc gaaagaacct 300

tatagttttg actactgggg tcagggaacc ctgggtcaccg tctcgagc 348

<210> 1110

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1110

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatc caccattgct gggtatgaga tgtggtgggt cgcaggct 120

ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcca 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1111

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1111

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcaggct 120

ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaaggcccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagaccct 300

tatagttttg actactgggg tcagggaacc ctggtctccg tctcgagc 348

<210> 1112

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1112

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt caccattgct gggtatgaga tgtggtgggt cgcaggct 120

ccagggaagg gtctagagcg ggtctccgct attagtggta gtggtggttag cacatactac 180

gcggactccg tgaaggcccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tttcgagc 348

<210> 1113

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1113

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgtgggt cgcgcaggct      120
ccagggaagg gtctagagcg tgtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc acccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat acccggtat attactgtgc gaaagagcct      300
tatagttttg actactggcg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 1114

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1114

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgtgggt cgcgcaggct      120
ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg ataccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat acccggtat attactgtgc gaaagatcct      300
tatagttttg actactggcg tcagggaacc ctggtcaccg tctcgagc      348
```

<210> 1115

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1115

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatc cacctttgct gggtatgagg tgtgtgggt cgcgcaggct      120
ccagggaagg gtctggagcg ggtctcagct attagtggta gtggtggtag cacatactac      180
```

gcagactccg tgaaggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1116

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1116

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatc cacctttgct gggtatgaga tgtgtgggt ccgccaggct 120

ccaggaagg gtctagagcg gatctcagct attagtggta gtgtggttag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1117

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1117

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtgtggttag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1118

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1118

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggact cacctttgct gggtatgaga tgtggtgggt cgcggggct 120

ccagggaagg gtctagagcg ggtcgcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1119

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1119

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgagt tgtggtgggt cgcggggct 120

ccagggaagg gtctagagcg ggtctcagct attagtggaa gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300

tatagttttg actaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1120

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1120

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag ccccgagatt caccttagct gggtatgaga tgtggtgggt cgcggggct 120

ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1121

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1121

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggact cacctttgct gggtatgaga tgttggtgggt ccgtcgggct      120
ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac      180
gcagactccg tgaagggccg gttcaccacc tcccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct      300
```

```
tatagttttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
```

<210> 1122

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1122

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ccggggggtc cctgcgtctc      60
tcctgtgccg cctccggatt cacctttgct gggtatgaga tgttggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attagtggta gcggtggttag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct      300
tatagttagt actactgggg tcatggaacc ctggttactg tctcgagc      348
```

<210> 1123

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1123

```
gaggtgcagc cggttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgttggtgggt ccgccaggct      120
```

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtaa cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgggggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcagggtacc ctggtcaccg tctcgagc 348

<210> 1124

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1124

gagggtcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcgggtat attactgtgc gaaagaacct 300

tatagttttg actcctgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1125

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1125

gaggcgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt aaccttcgct gggtatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg cgtctcagct attagtggta gtggcggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcgggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1126

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1126

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatc cacctttgct gggtatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttctccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct	300
tatagttttg accactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1127

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1127

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatc cacctttgct gggtatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct	300
tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1128

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1128

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct	300

tatagttttg acaactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1129

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1129

gaggtgcagc tgttggagtc tgggggaggc ttggtagagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300

tatagttttg accaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1130

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1130

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggata cacctttgct gggtatgaga tgtggtgggt cgcgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300

tatagttttg accaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1131

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1131

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaagaacct 300

tatagttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1132

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1132

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg acaactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1133

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1133

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcaggct 120

ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180

gcagactctg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300

tatagttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1134

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1134

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgtgggt cgcgcaggct      120
cccgggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgc gaaagatcct      300
tatagttttg acaactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 1135

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1135

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgtgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactctg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctcgc tgccgaggat accgcggtat atcactgtgc gaaagaacct      300
tatagttatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
```

<210> 1136

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1136

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtgtggtt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
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gcagactccg tgaaggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg acaactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1137

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1137

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgagt tgttggtgggt ccgccaggcc 120

ccagggaagg gtctagagcg ggtctcagct attagtggaa gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300

tatagttttg actaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1138

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1138

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgct gggtatgagt tgttggtgggt ccgccaggcc 120

ccagggaagg gtctagagcg ggtctcagct attagtggaa gtggtggtag cacatactac 180

gcagactccg tgaaggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300

tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1139

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1139

gaggtgcagc tgttggagtc tggggggggc ttggtacagc ctgggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg actgctgaga tgctgtgggt ccgcaagget 120

ccagggaagg gtctagagtg ggtctcatct atttcggcta gtggtgggtc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagccg 300

gtgagttatg tggcgacgtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc 360

<210> 1140

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1140

gaggtgcagc tgttgggtgc tggggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttccg actgctgaga tgttgtgggt ccgccaggct 120

ccagggaagg gtccagagtg ggtctcatca atttcggcta gtggtgggtc tacatactat 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagccg 300

gtgagttatg tggcgacgtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc 360

<210> 1141

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1141

gaggtgcagc tgttggagtc tggggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60

tcgtgtgcag cctccggatt cacctttccg actgccgaga ttggtgtgggt ccgcaagget 120

ccagggatgg gtctagagtg ggtctcatct atttcggcta gtggtgggtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240

ctgcaaatga acagcctcgc tgccgaggac accgcggtat attactgtgc gaaagagccg 300

gtgagttatg tggcgacgtt tgactactgg ggtcagggag ccctgggtcac cgtcacgagc 360

<210> 1142

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1142

```
gaggtgcagc tgttgggtgc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttccg actgctgaga tgggtgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac      180
gcagactccg tgaagggccg gttctccatc tccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg      300
```

```
gtgagttatg tggcgacgtt tgactactgg ggtcatggag ccctgggtcac cgtctcgagc      360
```

<210> 1143

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1143

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat      240
```

```
ctgcaaatga acagcctgcg agccgaggac accgcggtat attactgtgc gaaagagccg      300
```

```
gtgagttatg tggcaacgtt tgactactgg ggtcaggga ccctgggtcac cgtctcgagc      360
```

<210> 1144

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1144

```
gaggcgcagc tgttggagtc tgggggtggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttccg actgctgaga tgggtgtgggt ccgccaggct      120
```

ccaggaagg gtctagagtg gatctcatct atttcggcta gtggtggttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaattga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300

gtgagttatg tggcgacgtt tgactactgg ggtcggggaa ccctggtcac cgtctcgagc 360

<210> 1145

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1145

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagag cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300

gtgagttatg tggcgacgtt tgactactgg ggtccaggag ccctggtcac cgtctcgagc 360

<210> 1146

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1146

gaggtgcagc tgttggagtc cgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt ccgcaaggct 120

ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc caaagagccg 300

gtgagttatg tggcgacgtt tgactactgg ggtcaggga ccctggtcac cgtctcgagc 360

<210> 1147

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1147

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg      300
gtgagttatg tggcgacgtt tgactactgg ggtccaggag ccctggtcac cgtctcgagc      360
```

<210> 1148

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1148

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacatttccg actgctgaga tgctgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ttgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg      300
gtgtattatg tggcgacgtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc      360
```

<210> 1149

<211> 360

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1149

```
gaggtgcagc tgttggagtc cgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacatttccg actgctgaga tgctgtgggt ccgcaaggct      120
ccaggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagagccg      300
```


gtgagttatg tggcgacgtt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 1150

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1150

aacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt actctgttaa cttggtacca gcataaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1151

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1151

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca 120

cggaaagccc ctaaactcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcatcct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcgggtcaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1152

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1152

gacatccaga tgaccagtc tccgtcctcc ctgactgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct ggtcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagt ggcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctcctac gttcggccaa	300
gggaccaagg tggaaaacat acgg	324
<210> 1153	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	
<400> 1153	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtcacc	60
atcacttgcc gggcaagtc ttttattgct actctgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gacacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagt ggcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324
<210> 1154	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	
<400> 1154	
gacatccaga tgaccagtc tccatccttc ctgtctgcat ctgtaggaga cctgtcacc	60
atcacttgcc gggcaagtc ttttattgct actctgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gacacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagt ggcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324
<210> 1155	
<211> 324	

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1155

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggc actctgttat cttggtacca gcagaaacca      120
gggaaagcca ctaagctcct gatcacttat ggttccttgc tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagactttg ctacgtacta ctgtggtcag ggggtgctgt ggccccgcac gttcggccag      300
gggaccaagg tggaaatcaa acgt                                           324
```

<210> 1156

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1156

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggc tctctgttat cttggtacca gcataaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgc tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggccctgcac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                           324
```

<210> 1157

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1157

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggc actctgttat cttggtacca gcataaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgc tgcaaagtgg ggtcccatca      180
```

cgtttcagtgc gcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1158

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1158

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttatttgt actctgttat cttggtacca gcataaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccatgt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1159

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1159

gacatccaga tgactcagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

atcacttgcc gggcaagtc ttttatttgt actctgttat cctggtacca gcataaacca 120

gggaaagccc ctaagctcct gatcacctat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggtatc tgggacagaa ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggagtgtgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1160

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1160

gacatccaga tgaccagtc tccatcctcc ctgactgcat ctgtaggaga cctgtgcacc 60

atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcataaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt ggcagtgatc tgggacagaa ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1161

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1161

aacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60

atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcataaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt ggcagtgatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1162

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1162

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc 60

atcaattgcc gggcaagtc ttttattggt actctgttat cttggtacca gcataaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt ggcagtgatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1163

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1163

```
gacatccagt tgaccagtc accatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca      120
gggaaagcca ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggccctcgac gttcggccaa      300
```

```
gggaccaagg tggaaatcaa acgg      324
```

<210> 1164

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1164

```
gacatccaga tgacacagtc tccatcctcc ctgtatgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggtaagtc ttttattggt actctgttat cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca gcatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcccccgcac gttcggacaa      300
gggaccaagg tggaaatcaa acag      324
```

<210> 1165

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1165

```
gacattcaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca      120
```

aggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1166

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1166

gacatccaga ttatccagtc tccatcctcc ctttctgcat ctgtaggaga cegtgtcacc 60

atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1167

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1167

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cegtgtcacc 60

atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gctgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1168

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1168

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gctgaaacca	120
gggaaagccc caaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggaccaagg tagaaaacaa acgg	324

<210> 1169

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1169

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcttaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaacgtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1170

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1170

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gctgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcagagtgg ggtcccatca	180
cgtttcagtg gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300

gggaccaagg ttgaaaacaa acgg 324

<210> 1171

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1171

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt tctctgttat cttggtacca gcagaaacca 120

gggaaagccc caagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcgtctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1172

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1172

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1173

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1173

gacatcctga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1174

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1174

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtcacc 60

atcacttgcc gggcaagtc ttttattggt actctggtat cttggtacca gcagaaaccg 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gtacggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1175

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1175

gacatccaga tgaccagtc tccatcctct ctgtctgcat ctgtaggaga cctgtcacc 60

atcacttgcc gggcaagtc ttttattggt actctggtat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac tttcggccaa 300

gggaccaagg tggaaaacaa acgg 324

<210> 1176

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1176

```
gacatcaaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc      60
atcacttgcc gggcgagtc ttttattggt actctggtat cttggtacca gcagaaacca      120
gggaaagccc caaagctcct gatcacttat ggttccatgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggccctgcgac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                           324
```

<210> 1177

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1177

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc      60
atcacttgcc aggcaagtc ttttattggt actctggtat cctggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcccgcgac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                           324
```

<210> 1178

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1178

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc      60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttcctggt tgcaaagtgg ggtcccatca      180
```

cgtttcagtgcgcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1179

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1179

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttgaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttatttgt actctgttat cttggtacca gctgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtgcgcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1180

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1180

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttatttgt actctgttat cttggtacca gcagaaaccg 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtgcgcagtggtatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag gaggtgctgt ggcctgcgac gttcggccaa 300

gggactaagg tggaaatcaa acgg 324

<210> 1181

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1181

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtctcc 60

atcacttgcc gagcaagtc ttttattggt actctgttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt gcaagtggatt tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagatcttg ctacgtacta ctgtggtcag gaggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1182

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1182

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgttcacc 60

atcacttgcc aggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt gcaagtggatt tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag gaggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1183

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1183

gacatccaga tgaccagtc tccatcctcc ctgtctgcat cagtaggaga cctgttcacc 60

atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacct 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt gcaagtggatt tgggacagaa ttcactctca ccatcggcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1184

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1184

```
gacatccaga tgaccagtc accatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggt actctgttat cttggtacca gcagaaacca      120
gggaaagcca ctaagtcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa      300
```

```
gggaccaagg tggaaatcaa acgg                                           324
```

<210> 1185

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1185

```
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc cttcattgcc agtctgttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagtcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                           324
```

<210> 1186

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1186

```
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc tttcattgcc cagctgttat cttggtacca ggtgaaacca      120
```

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1187

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1187

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ttcatctgcc cagctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcag acgg 324

<210> 1188

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1188

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ttacattgcc tcctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcagagtgg ggcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1189

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1189

gacatccaga tgaccacagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttgg gcctcctact tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324

<210> 1190

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1190

gacatccaga tgaccacagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttgg acgtcctact tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324

<210> 1191

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1191

gacatccaga tgaccacagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttgg tcgtcctact tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300

gggacaacgg tggaaatcaa acgg 324

<210> 1192

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1192

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattgg agtctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttgg gggctctggt tgcaaagtgg ggtcccatca 180

cgtttcagt gcatggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1193

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1193

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattgg agtctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttgg ggcctctggt tgcaaagtgg ggtcccatca 180

cgtttcagt gcatggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1194

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1194

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttgg agtccttggg tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324
<210> 1195	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	
<400> 1195	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgttcacc	60
atcacttgcc gggcaagtc ttggattgcc cagctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324
<210> 1196	
<211> 324	
<212> DNA	
<213> Artificial Sequence	
<220><223> Description of Artificial Sequence: Synthetic polynucleotide	
<400> 1196	
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgttcacc	60
atcacttgcc gggcaagtc ttttattggt tcgctcttac gctggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324
<210> 1197	
<211> 324	

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1197

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc      60
atcacttgcc gggcaagtca tcggattgcc cagctgttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                           324
```

<210> 1198

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1198

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc      60
atcacttgcc gggcaagtca ttacattgcc tcctgttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                           324
```

<210> 1199

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1199

```
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc      60
atcacttgcc gggcaagtca ttttatttgt agtctgttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagctcct gatccggttc ggctccttgt tgcaaagtgg ggtcccatca      180
```

cgtttcagtgcgcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1200

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1200

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttac aagtcctact tgcaaagtgg ggtcccatca 180

cgtttcagtgcgcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1201

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1201

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttattggt agtctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttgg ggctcctact tgcaaagtgg ggtcccatca 180

cgtttcagtgcgcagtggtac tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1202

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1202

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttatttgg gggcccttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt ggcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattctg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1203

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1203

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttggattgcc accctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt ggcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1204

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1204

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtc ttttatttgg gggcccttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagt ggcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1205

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1205

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggc agcctcttaa actggtacca ggtgaaacca      120
gggaaagccc ctaagtcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa      300
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gggacaacgg tggaaatcaa acgg      324
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<210> 1206

<211> 324

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1206

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ggcatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtc ttttattggc agtctgttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagtcct gatcacttac ggttcctggc tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa      300
gggacaacgg tggaaatcaa acgg      324
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<210> 1207

<211> 5

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic peptide

<400> 1207

Gly Gly Gly Gly Ser

1 5

<210> 1208

<211> 15

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic peptide

<400> 1208

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10 15

<210> 1209

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic peptide

<400> 1209

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser

20 25

<210> 1210

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140
 Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160
 Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
 165 170 175
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205
 Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg

225

<210> 1211

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1211

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45
Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95
Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val

100 105 110
Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser

115 120 125
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

130 135 140
Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly

145 150 155 160
Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly

165 170 175
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

180 185 190
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala

195 200 205
Gln Ala Gly Thr His His Thr Thr Phe Gly Gln Gly Thr Lys Val Glu

210 215 220
Ile Lys Arg

225

<210> 1212

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1212

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125
 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

 Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160
 Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
 165 170 175
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

 Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220
 Ile Lys Arg
 225
 <210> 1213
 <211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1213

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser

115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

130 135 140

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly

145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly

165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala

195 200 205

Gln Ala Gly Thr His His Thr Thr Phe Gly Gln Gly Thr Lys Val Glu

210 215 220

Ile Lys Arg

225

<210> 1214

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1214

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro

115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg

130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp

165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

180 185 190
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205
 Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
 210 215 220

 Leu Val Thr Val Ser Ser
 225 230
 <210> 1215
 <211> 230
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 1215
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

 35 40 45
 Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His His Thr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

 100 105 110
 Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140
 Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

145 150 155 160
Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp

 165 170 175
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

 180 185 190
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

 195 200 205
Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr

 210 215 220

Leu Val Thr Val Ser Ser

225 230

<210> 1216

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1216

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140
 Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160
 Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205
 Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr
 210 215 220
 Leu Val Thr Val Ser Ser
 225 230

<210> 1217

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1217

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His His Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110
Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro

115 120 125
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
130 135 140
Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
145 150 155 160
Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
165 170 175
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

180 185 190
Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
195 200 205
Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr
210 215 220
Leu Val Thr Val Ser Ser

225 230

<210> 1218

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1218

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
20 25 30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
210 215 220

Leu Val Thr Val Ser Ser
225 230

<210> 1219

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1219

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

 65 70 75 80
 Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg

 130 135 140
 Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160
 Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

 195 200 205
 Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
 210 215 220
 Leu Val Thr Val Ser Ser
 225 230
 <210> 1220
 <211> 230
 <212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1220

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Val His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro

115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg

130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp

165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr

210 215 220

Leu Val Thr Val Ser Ser

225 230

<210> 1221

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1221

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro

115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu

130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp

165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

195 200 205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr

210 215 220

Leu Val Thr Val Ser Ser

225 230

<210> 1222

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1222

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu

20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser

115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

130 135 140

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly

145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly

165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala

195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu

210 215 220

Ile Lys Arg

225

<210> 1223

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1223

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu
 130 135 140
 Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160
 Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp

165 170 175
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205
 Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr
 210 215 220
 Leu Val Thr Val Ser Ser
 225 230

<210> 1224

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1224

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30
 Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
115 120 125
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
130 135 140
Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly
145 150 155 160
Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser Leu Gln Ser Gly
165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
180 185 190
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
195 200 205
Gln Gly Leu Arg His Pro Lys Thr Phe Gly Gln Gly Thr Lys Val Glu
210 215 220

Ile Lys Arg

225

<210> 1225

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1225

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30
Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
130 135 140

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
210 215 220

Ile Lys Arg

225

<210> 1226

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1226

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30
 Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125
 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

 130 135 140
 Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160
 Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly
 165 170 175
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190
 Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala

 195 200 205
 Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220
 Ile Lys Arg
 225
 <210> 1227
 <211> 230
 <212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1227

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro

115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu

130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp

165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

195 200 205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr

210 215 220

Leu Val Thr Val Ser Ser

225 230

<210> 1228

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1228

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala

100 105 110

Pro Ser Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro

115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu

130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu

145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp

165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr

180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

195

200

205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr

210

215

220

Leu Val Thr Val Ser Ser

225

230

<210> 1229

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1229

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met

20

25

30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Glu

100

105

110

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser

115

120

125

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr Glu

130

135

140

Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val Ser

145 150 155 160

Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys

165 170 175

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

180 185 190

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

195 200 205

Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val Thr

210 215 220

Val Ser Ser

225

<210> 1230

<211> 231

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1230

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Ser

100 105 110

Gly Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 115 120 125
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 130 135 140
 Arg Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 145 150 155 160
 Glu Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala

165 170 175
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 180 185 190
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 195 200 205
 Tyr Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly
 210 215 220
 Thr Leu Val Thr Val Ser Ser
 225 230

<210> 1231

<211> 229

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1231

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
100 105 110

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
115 120 125
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp
130 135 140
Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg
145 150 155 160
Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser
165 170 175

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
180 185 190
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
195 200 205
Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu
210 215 220

Val Thr Val Ser Ser

225

<210> 1232

<211> 239

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1232

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
20 25 30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

65

70

75

80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly

100

105

110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu

115

120

125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser

130

135

140

Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr Glu Met Trp Trp Val

145

150

155

160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val Ser Ala Ile Asn Pro

165

170

175

Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr

180

185

190

Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser

195

200

205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Leu Pro Phe

210

215

220

Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

225

230

235

<210> 1233

<211> 249

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1233

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly

 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 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 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 130 135 140
 Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 145 150 155 160
 Thr Phe Arg Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys
 165 170 175
 Gly Leu Glu Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr

 180 185 190
 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 195 200 205
 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 210 215 220
 Ala Val Tyr Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly
 225 230 235 240
 Gln Gly Thr Leu Val Thr Val Ser Ser
 245

<210> 1234

<211> 227

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1234

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser Thr Val Ala Asp Ile Gln Met Thr Gln Ser Pro Ser

115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala

130 135 140

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly

145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly

165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

180 185 190

Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala

195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu

210 215 220

Ile Lys Arg

225

<210> 1235

<211> 231

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1235

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser Ala Ser Thr Ser Gly Pro Ser Asp Ile Gln Met Thr

115 120 125

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

130 135 140

Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln

145 150 155 160

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg

165 170 175

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
180 185 190

Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr
195 200 205

Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly
210 215 220

Thr Lys Val Glu Ile Lys Arg
225 230

<210> 1236

<211> 229

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1236

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
115 120 125

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

130 135 140
 Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys
 145 150 155 160
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln
 165 170 175
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 180 185 190
 Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr

 195 200 205
 Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys
 210 215 220
 Val Glu Ile Lys Arg
 225
 <210> 1237
 <211> 239
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polypeptide
 <400> 1237
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val

100 105 110
 Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 130 135 140

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile
 145 150 155 160
 Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 165 170 175
 Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg
 180 185 190
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn
 195 200 205

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr
 210 215 220
 His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 225 230 235

<210> 1238

<211> 249

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1238

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30
 Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45
 Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65						70						75						80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys			
					85						90						95	
Ala	Lys	Leu	Pro	Phe	Tyr	Phe	His	Glu	Trp	Gly	Gln	Gly	Thr	Leu	Val			
					100						105						110	
Thr	Val	Ser	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	Asp	Ile	Gln			
			130				135				140							

Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val
145					150					155					160
Thr	Ile	Thr	Cys	Arg	Ala	Ser	Arg	Pro	Ile	Gly	Thr	Met	Leu	Ser	Trp
				165					170						175
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Leu	Ala	Phe
			180						185					190	
Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser
		195					200					205			

Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe
210 215 220
Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly
225 230 235 240
Gln Gly Thr Lys Val Glu Ile Lys Arg
245

<210> 1239

<211> 230

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1239

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro

 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg

 130 135 140
 Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160
 Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

 195 200 205
 Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr
 210 215 220
 Leu Val Thr Val Ser Ser
 225 230
 <210> 1240
 <211> 681
 <212> DNA
 <213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1240

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcaccgac	360
atccagatga cccagtctcc atcctccctg tctgcactcg taggagaccg tgtcaccatc	420
acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg	480
aaagccccta agctcctgat cctttggaat tccgtttgc aaagtggggt cccatcacgt	540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa	600
gattttgcta cgtactactg tgccgaggct gggacgcac ctacgacgtt cggccaaggg	660
accaaggtgg aaatcaaacg g	681

<210> 1241

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1241

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaaggcccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcaccgac	360
atccagatga cccagtctcc atcctccctg tctgcactcg taggagaccg tgtcaccatc	420
acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg	480
aaagccccta agctcctgat ccttgctttt tccgtttgc aaagtggggt cccatcacgt	540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa	600
gattttgcta cgtactactg tgccgaggct gggacgcac atacgacgtt cggccaaggg	660

accaaggtgg aaatcaaacg g 681

<210> 1242

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1242

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagcgc tagcaccgac 360

atccagatga cccagtctcc atctccctg tctgcatctg taggagaccg tgtcaccatc 420

acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg 480

aaagccccta agctcctgat cctttggaat tccggtttgc aaagtgggt cccatcacgt 540

ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa 600

gattttgcta cgtactactg tgccgaggct gggacgcac ctacgacgtt cggccaaggg 660

accaaggtgg aaatcaaacg g 681

<210> 1243

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1243

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagcgc tagcaccgac 360

atccagatga cccagtctcc atctccctg tctgcatctg taggagaccg tgtcaccatc 420

acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg 480
aaagccccta agtcctgat ccttgctttt tcccgtttgc aaagtggggt cccatcacgt 540

ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa 600
gattttgcta cgtactactg tgcgcaggct gggacgcatc atacgacgtt cggccaaggg 660
accaaggtgg aaatcaaacg g 681

<210> 1244
<211> 690
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 1244

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc 60
atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcctttgg aattcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcacat ctgaggtgca gctgttggag 360
tctgggggag gcttggtaca gcctgggggg tccctgcgtc tctcctgtgc agcctccgga 420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctctagag 480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgca caattccaag aacacgtgt atctgcaaat gaacagcctg 600
cgtgccgagg acaccgcgtg atattactgt gcgaaacttc cgttttactt tcaggagtgg 660
ggtcaggga cctggtcac cgtctccagc 690

<210> 1245
<211> 690
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 1245

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc 60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgct ttttccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggtac tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcatacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag 360
 tctgggggag gcttggtaca gcctgggggg tcctgcgtc tctcctgtgc agcctccgga 420
 ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctctagag 480
 cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgca caattccaag aacacgtgt atctgcaaat gaacagcctg 600
 cgtgccgagg acaccgcgtt atattactgt gcgaaacttc cgttttactt tcaggagtgg 660
 ggtcaggga cctggtcac cgtctccagc 690

<210> 1246

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1246

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc 60
 atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcctttgg aattccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggtac tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag 360
 tctgggggag gcttggtaca gcctgggggg tcctgcgtc tctcctgtgc agcctccgga 420
 ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctctagag 480
 cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgca caattccaag aacacgtgt atctgcaaat gaacagcctg 600
 cgtgccgagg acaccgcgtt atattactgt gcgaaacttc cgttttactt tcaggagtgg 660
 ggtcaggga cctggtcac cgtctccagc 690

<210> 1247

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1247

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttccggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcatacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttggag	360
tctgggggag gcttggatca gcctgggggg tccctgcgtc tctcctgtgc agcctccgga	420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggcttagag	480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc	540
cggttcacca tctcccgca caattccaag aacacgtgt atctgcaaat gaacagcctg	600
cgtgccgagg acaccgcgt atattactgt gcgaaacttc cgttttactt tcacgagtgg	660
ggtcaggga cctggtcac cgtctccagc	690

<210> 1248

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1248

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttccggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct	240
gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttggag	360
tccgggggag gcttggatca gcctgggggg tccctgcgtc tctcctgtgc agcctccgga	420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggcttagag	480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc	540
cggttcacca tctcccgca caattccaag aacacgtgt atctgcaaat gaacagcctg	600
cgtgccgagg acaccgcgt atattactgt gcgaaacttc cgttttactt tcaggagtgg	660

ggtcagggaa ccctggtcac cgtctccagc 690

<210> 1249

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1249

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgct ttttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagatgttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acgtacggtg gctgcacat ctgaggtgca gctgttgag 360

tctgggggag gcttggtaca gcctgggggg tcctgcgctc tctcctgtgc agcctccgga 420

ttcacctttc gggattatga gatgtgggtg gtccgccagg ctccaggga ggtctagag 480

cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgga caattccaag aacacgtgt atctgcaaat gaacagcctg 600

cgtgccgagg acaccggtg atattactgt gcgaaacttc cgtttactt tcaggagtgg 660

ggtcagggaa ccctggtcac cgtctccagc 690

<210> 1250

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1250

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgct ttttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgcgcag gctggggtgc atcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acgtacggtg gctgcacat ctgaggtgca gctgttgag 360

tctgggggag gcttggtaca gcctgggggg tcctgcgctc tctcctgtgc agcctccgga 420

ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctctagag 480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgcga caattccaag aacacgtgt atctgcaaat gaacagcctg 600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcaggagtgg 660
ggtcaggga ccctgggtcac cgtctccagc 690

<210> 1251
<211> 690
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 1251

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcctttgg aattcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gctgcacat ctgaggtgca gctgttggag 360
tctgggggag gcttggtaca gcctgggggg tccttgcgtc tctcctgcgc agcctccgga 420
ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga gggctctagag 480
tgggtctcag ctattagtag gaacggttac agcacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgcga caattccaag aacacgtgt atctgcaaat gaacagcctg 600
cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgta tgactactgg 660
ggtcaggga ccctgggtcac cgtctccagc 690

<210> 1252
<211> 681
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 1252

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120

ccaggaagg gtctagagt ggtctcagct attagtagga acggttacag cacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc tagcaccgac 360
atccagatga cccagtctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc 420
acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg 480
aaagccccta agtcctgat cctttggaat tccggtttgc aaagtggggt cccatcacgt 540

ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa 600
gattttgcta cgtactactg tgcgcaggct gggacgcata ctacacgtt cggccaaggg 660
accaaggtgg aaatcaaacg g 681

<210> 1253

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1253

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcatgtgg cgttctcgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgtcag ggtttgaggc atcctaagac gttcggccaa 300
gggaccaagg tggaatcaa acgtacggtg gctgcacat ctgaggtgca gctgttgag 360
tctgggggag gcttggtaca gcctgggggg tcctgcgtc tctctgcgc agcctccgga 420
ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga ggtctagag 480
tgggtctcag ctattagtag gaacggttac agcacatact acgcagactc cgtgaagggc 540

cggttcacca tctccgcga caattccaag aacacgtgt atctgcaaat gaacagcctg 600
cgtgccgagg ataccggt atattactgt gggaaagagc cgttcgtta tgactactgg 660
ggtcaggga cctggtcac cgtctccagc 690

<210> 1254

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1254

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc tagcaccgac	360
atccagatga cccagctccc atcctccctg tctgcactcg taggagaccg tgtcaccatc	420
acttgccggg caagtcagtg gattgggtct cagttatctt ggtaccagca gaaaccaggg	480
aaagccccta agctcctgat catgtggcgt tcctcgttgc aaagtggggg cccatcacgt	540
ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa	600
gattttgcta cgtactactg tgctcagggt ttgaggcatc ctaagacgtt cggccaaggg	660
accaaggtgg aaatcaaacg g	681

<210> 1255

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1255

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc ttcaaccgac	360
atccagatga cccagctccc atcctccctg tctgcactcg taggagaccg tgtcaccatc	420
acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg	480
aaagccccta agctcctgat cctttggaat tcccgtttgc aaagtggggg cccatcacgt	540
ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa	600
gattttgcta cgtactactg tgctcagggt gggacgcac ctaagacgtt cggccaaggg	660

accaaggtgg aaatcaaacg g 681

<210> 1256

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1256

gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggcc 120

ccaggggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tccgcgcaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctcgc tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc ttcaaccgac 360

atccagatga cccagtctcc atcttccttg tctgcatctg taggagaccg tgtcaccatc 420

acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg 480

aaagccccta agctcctgat ctttgccttt tcccgtttgc aaagtggggg cccatcacgt 540

ttcagtggca gtggatctgg gacagatttc actctacca tcagcaatct gcaacctgaa 600

gattttgcta cgtactactg cgcgaggct gggacgcac ctacgacgtt cggccaaggg 660

accaaggtgg aaatcaaacg g 681

<210> 1257

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1257

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttttg aattcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acggaccgtg gcggcgccga gtgaggtgca gctgttggcg 360

tctgggggag gcttgggtaca gcctgggggg tcctgcgtc tctcctgcgc agcctccgga 420

ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga gggcttagag 480
 tgggtctcag ctattagtag gaacgggttac agcacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgcga caattccaag aacacgtgt atctgcaaat gaacagcctg 600
 cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgta tgactactgg 660
 ggtcaggga ccctgggtcac cgtctccagc 690

<210> 1258
 <211> 690
 <212> DNA
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polynucleotide
 <400> 1258

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc 60
 atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgc ttttccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaatcaa acggaccgtg gcggcgccga gtgaggtgca actgttggcg 360
 tctgggggag gcttggtaca gcctgggggg tccttgcgtc tctctgcgc agcctccgga 420
 ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga gggcttagag 480
 tgggtctcag ctattagtag gaacgggttac agcacatact acgcagactc cgtgaagggc 540

cggttcacca tctcccgcga caattccaag aacacgtgt atctgcaaat gaacagcctg 600
 cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgta tgactactgg 660
 ggtcaggga ccctgggtcac cgtctccagc 690

<210> 1259
 <211> 681
 <212> DNA
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic polynucleotide
 <400> 1259

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cgtgtcacc 60
 atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca 180
 cgtttcagt ggcagtgatc tgggacagat ttactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgtacgggt gcggaggtgc agctgttga gttcggggga 360
 ggcttggtac agcctggggg gtccctgcgt ctctctgtg cagcctccgg attcaccttt 420
 cgggattatg agatgtggtg ggtccgccag gtcacaggga aggtctaga gcgggtctca 480
 gctattaatc cgcagggtac gcgtacatac tacgcagact ccgtgaaggg ccggttcacc 540

atctcccgcg acaattccaa gaacacgtg tatctgcaa tgaacagcct gcgtgccgag 600
 gacaccgagg tatattactg tgcgaaactt ccgttttact ttacagagtg gggtcaggga 660
 accctgggtc ccgtctccag c 681

<210> 1260

<211> 693

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1260

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca 180
 cgtttcagt ggcagtgatc tgggacagat ttactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgggctagc acctcaggtc catcgaggt gcagctgttg 360
 gagtctgggg gaggtttgtt acagcctggg gggtccctgc gtctctctg tgcagcctcc 420
 ggattcacct ttcgggatta tgagatgtgg tgggtccgcc aggtccagg gaagggtcta 480
 gagcgggtct cagctattaa tccgcagggt acgcgtacat actacgcaga ctccgtgaag 540

ggccggttca ccatctcccg cgacaattcc aagaacacgc tgtatctgca aatgaacagc 600
 ctgcgtgcc aggacaccgc ggtatattac tgtcgaaac ttccgtttta ctttcacgag 660
 tggggtcagg gaacctggt caccgtctcc agc 693

<210> 1261

<211> 687

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1261

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggtac tgggacagat ttcactctca ccatcagcaa tctgcaacct	240
gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgggggtgga ggtggctctg aggtgcagct gttggagtct	360
gggggaggct tggtagacc tgggggggtcc ctgcgtctct cctgtgcagc ctccggattc	420
acctttcggg attatgagat gtggtgggtc cgccaggctc cagggaaggg tctagagcgg	480
gtctcagcta ttaatccgca gggtacgcgt acatactacg cagactccgt gaagggccgg	540
ttcaccatct cccgcgacaa ttccaagaac acgctgtatc tgcaaatgaa cagcctgcgt	600
gccgaggaca ccgcggtata ttactgtgcg aaacttccgt tttactttca cgagtggggt	660
cagggaaccc tggtcaccgt ctccagc	687

<210> 1262

<211> 717

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1262

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cctgtgcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggtac tgggacagat ttcactctca ccatcagcaa tctgcaacct	240
gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgggggtgga ggtggctctg gagtggcgg tagcggcgg	360
ggcggttcag aggtgcagct gttggagtct gggggaggct tggtagacc tgggggggtcc	420
ctgcgtctct cctgtgcagc ctccggattc acctttcggg attatgagat gtggtgggtc	480
cgccaggctc cagggaaggg tctagagcgg gtctcagcta ttaatccgca gggtacgcgt	540
acatactacg cagactccgt gaagggccgg ttcacatct cccgcgacaa ttccaagaac	600
acgctgtatc tgcaaatgaa cagcctgcgt gccgaggaca ccgcggtata ttactgtgcg	660

aaacttccgt tttactttca cgagtggggt caggggaaccc tggtcaccgt ctccagc 717

<210> 1263

<211> 747

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1263

gacatccaga tgaccacgtc tccatcctcc ctgtctgcat ctgtaggaga cctgttcacc 60

atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatccttgct ttttccggtt tgcaaagtgg ggtcccatca 180

cgtttcagt gtcagtggatc tgggacagat ttactctca ccatcagca tctgcaacct 240

gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300

gggaccaagg tggaaatcaa acgggggtgga ggtggctctg gaggtggcgg tagcggcggg 360

ggcgggttcag gtggcggagg ttctggaggc ggtggatctg aggtgcagct gttggagtct 420

gggggaggct tggtagagcc tgggggggtcc ctgcgtctct cctgtgcagc ctccggattc 480

acctttcggg attatgagat gtggtgggtc cgccaggctc caggggaaggg tctagagcgg 540

gtctcagcta ttaatccgca gggtacgct acatactacg cagactccgt gaagggccgg 600

ttccacctt cccgcgacaa ttccaagaac acgctgtatc tgcaaatgaa cagcctgcgt 660

gccgaggaca ccgcggtata ttactgtgcg aaacttccgt tttactttca cgagtggggt 720

caggggaaccc tggtcaccgt ctccagc 747

<210> 1264

<211> 681

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1264

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtgtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc acgagtgggg tcaggggaacc ctggtcaccg tttcgagcac ggtggcggac 360

atccagatga cccagtctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc 420
acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg 480

aaagccccta agctcctgat ccttgctttt tcccgtttgc aaagtggggt cccatcacgt 540
ttcagtggca gtggatctgg gacagatttc actctcacca tcagcaatct gcaacctgaa 600
gattttgcta cgtactactg cgcgaggct gggacgcac ctagacgtt cggccaaggg 660
accaaggtagg aaatcaaagc g 681

<210> 1265
<211> 693
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 1265

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cggccaggt 120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgtgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttcg 300
ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagcgc tagcacctca 360
ggtcctcagg acatccagat gaccagctct ccactctccc tgtctgcac tgtaggagac 420
cgtgtcacca tcaattgccg ggcaagtcgt ccgattggga cgatgttaag ttggtaccag 480

cagaaaccag ggaaagcccc taagtcctg atccttgcct tttcccgttt gcaaagtggg 540
gtcccatcac gtttcagtgg cagtggatct gggacagatt tcaactctac catcagcaat 600
ctgcaacctg aagattttgc tacgtactac tgcgcgcagg ctgggacgca tcctacgacg 660
ttcggccaag ggaccaaggt ggaaatcaaa cgg 693

<210> 1266
<211> 687
<212> DNA
<213> Artificial Sequence
<220><223> Description of Artificial Sequence: Synthetic polynucleotide
<400> 1266

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagcgg tggaggcggc 360
tctgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agaccgtgtc 420
accatcactt gccgggcaag tcgtccgatt gggacgatgt taagttggta ccagcagaaa 480

ccagggaag cccctaagct cctgatactt gctttttccc gtttgcaaag tggggtccca 540
tcacgtttca gtggcagtgg atctgggaca gatttcactc tcaccatcag caatctgcaa 600
cctgaagatt ttgctacgta ctactgcgcg caggctggga cgcatcctac gacgttcggc 660
caagggacca aggtggaaat caaacgg 687

<210> 1267

<211> 717

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1267

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtaacgc tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagcgg tggaggtggc 360
tctggaggtg gcggtagcgg cggtggcggc tcagacatcc agatgaccca gtctccatcc 420
tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcgtccgatt 480

gggacgatgt taagttggta ccagcagaaa ccagggaag cccctaagct cctgatactt 540
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gatttcactc tcaccatcag caatctgcaa cctgaagatt ttgctacgta ctactgcgcg 660
caggctggga cgcatcctac gacgttcggc caagggacca aggtggaaat caaacgg 717

<210> 1268

<211> 747

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1268

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgttgtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgagc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgagc tgccgaggac accgcggtat attactgtgc gaaacttcg      300
ttttactttc acgagtgggg tcagggaacc ctggtcaccg tctcgagcgg tggaggtggc      360
tctggagggtg gcggtagcgg cggtggcggc tcagggtggc gaggttctgg aggcggtgga      420
tctgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agaccgtgtc      480

accatcactt gccgggcaag tcgtccgatt gggacgatgt taagtggta ccagcagaaa      540
ccagggaag cccctaagct cctgacctt gctttttccc gtttgcaaag tgggggtccca      600
tcacgtttca gtggcagtgg atctgggaca gatttcactc tcaccatcag caatctgcaa      660
cctgaagatt ttgtacgta ctactgcgag caggctggga cgcacacctac gacgttcggc      720
caagggacca aggtggaaat caaacgg      747
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<210> 1269

<211> 690

<212> DNA

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 1269

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gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttgtacca gcagaaacca      120
gggaaagccc ctaagctcct gatccttgc ttttccggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcaa tctgcaacct      240
gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa      300
gggaccaagg tggaaatcaa acggaccgta gcggcgccga gtgaggtgca gctgttgag      360
tctgggggag gcttggtaga gcctgggggg tcctgcgtc tctcctgtgc agcctccgga      420

ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga ggggtctagag      480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc      540
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cggttcacca tctccgcga caattccaag aacacgctgt atctgcaaat gaacagcctg 600
 cgtgccgagg acaccgcggg atattactgt gcgaaacttc cgttttactt tcacgagtgg 660
 ggtcagggaa ccctgggtcac cgtctccagc 690

<210> 1270

<211> 44

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1270

Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp

1 5 10 15

Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser

20 25 30

Ala Phe Glu Lys Cys His Pro Trp Thr Ser Cys Glu

35 40

<210> 1271

<211> 44

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1271

Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly

1 5 10 15

Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn

20 25 30

Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp

35 40

<210> 1272

<211> 44

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1272

Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu

1 5 10 15

Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn

20 25 30

Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp

35 40

<210> 1273

<211> 19

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic peptide

<400> 1273

Asp Pro Gly Gly Gly Gly Gly Arg Leu Val Pro Arg Gly Phe Gly Thr

1 5 10 15

Gly Asp Pro

<210> 1274

<211> 5

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic peptide

<220><221> MOD_RES

<222> (1)..(1)

<223> Asp or Gly

<220><221> MOD_RES

<222> (4)..(4)

<223> Met or Leu

<400> 1274

Xaa Tyr Glu Xaa Trp

1 5

<210> 1275

<211> 17

<212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic peptide
 <220><221> MOD_RES
 <222> (5)..(5)
 <223> Gln, Tyr, Pro, Trp or Ala
 <220><221> MOD_RES
 <222> (7)..(7)
 <223> Thr, Ser, Asn, Gly, Met or Gln
 <220><221> MOD_RES
 <222> (8)..(8)
 <223> Arg, Leu, Tyr, His or Phe
 <220><221> MOD_RES
 <222> (16)..(16)
 <223> Lys or Met
 <400> 1275

Ala Ile Asn Pro Xaa Gly Xaa Xaa Thr Tyr Tyr Ala Asp Ser Val Xaa

1 5 10 15

Gly

<210> 1276
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220><223> Description of Artificial Sequence: Synthetic peptide
 <220><221> MOD_RES
 <222> (1)..(1)
 <223> Leu or Pro
 <220><221> MOD_RES
 <222> (3)..(3)
 <223> Phe, Gln, Thr or Met
 <220><221> MOD_RES
 <222> (4)..(4)
 <223> Tyr, Pro, Leu, Thr, Ile, Phe or Met

<220><221> MOD_RES

<222> (6)..(6)

<223> Gln, His, Asp, Ser, Lys, Glu or Gly

<220><221> MOD_RES

<222> (7)..(7)

<223> Glu, Asp or Tyr

<400> 1276

Xaa Pro Xaa Xaa Phe Xaa Xaa

1 5

<210> 1277

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<220><221> MOD_RES

<222> (18)..(18)

<223> Leu or Arg

<220><221> MOD_RES

<222> (30)..(30)

<223> Arg or Ala

<400> 1277

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Xaa Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa

20 25 30

<210> 1278

<211> 14

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic peptide

<220><221> MOD_RES

<222> (4)..(4)

<223> Gln or Arg

<220><221> MOD_RES

<222> (8)..(8)

<223> Lys or Arg

<220><221> MOD_RES

<222> (9)..(9)

<223> Gly or Val

<400> 1278

Trp Val Arg Xaa Ala Pro Gly Xaa Xaa Leu Glu Arg Val Ser

1 5 10

<210> 1279

<211> 32

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<220><221> MOD_RES

<222> (12)..(12)

<223> Thr or Met

<220><221> MOD_RES

<222> (23)..(23)

<223> Glu or Asp

<220><221> MOD_RES

<222> (26)..(26)

<223> Ala or Ser

<220><221> MOD_RES

<222> (29)..(29)

<223> Tyr or His

<220><221> MOD_RES

<222> (31)..(31)

<223> Ala or Thr

<400> 1279

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Xaa Leu Tyr Leu Gln

1 5 10 15

Met Asn Ser Leu Arg Ala Xaa Asp Thr Xaa Val Tyr Xaa Cys Xaa Lys

	20	25	30
<210>	1280		
<211>	11		
<212>	PRT		
<213>	Artificial Sequence		
<220><223>	Description of Artificial Sequence: Synthetic peptide		
<220><221>	MOD_RES		
<222>	(1)..(1)		
<223>	Trp or Arg		
<220><221>	MOD_RES		
<222>	(3)..(3)		
<223>	Gln or Pro		
<220><221>	MOD_RES		
<222>	(11)..(11)		
<223>	Ser or Asn		
<400>	1280		
	Xaa Gly Xaa Gly Thr Leu Val Thr Val Ser Xaa		
	1 5 10		
<210>	1281		
<211>	116		
<212>	PRT		
<213>	Artificial Sequence		
<220><223>	Description of Artificial Sequence: Synthetic polypeptide		
<220><221>	MOD_RES		
<222>	(13)..(13)		
<223>	Gln or Arg		
<220><221>	MOD_RES		
<222>	(99)..(99)		
<223>	Glu or Gly		
<220><221>	MOD_RES		
<222>	(101)..(101)		
<223>	Ala, Leu or Glu		
<220><221>	MOD_RES		
<222>	(102)..(102)		

<223> Phe or Tyr

<220><221

> MOD_RES

<222> (106)..(106)

<223> Trp or Arg

<400> 1281

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Xaa Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr

20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Xaa Leu Xaa Xaa Phe Asp Tyr Xaa Gly Arg Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 1282

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<220><221> MOD_RES

<222> (28)..(28)

<223> Thr or Pro

<220><221> MOD_RES

<222> (50)..(50)

<223> Ala or Ser

<220><221> MOD_RES

<222> (53)..(53)

<223> Arg or Gly

<220><221> MOD_RES

<222> (54)..(54)

<223> Arg, Ser, Asn, Gln, Gly, His or Leu

<220><221> MOD_RES

<222> (56)..(56)

<223> Tyr, Phe, Trp or Gly

<220><221> MOD_RES

<222> (57)..(57)

<223> Ser or Gly

<220><221> MOD_RES

<222> (102)..(102)

<223> Arg, Met or Pro

<400> 1282

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Xaa Phe Glu Glu Glu

20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Ser Xaa Ile Ser Xaa Xaa Gly Xaa Xaa Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Gly Lys Glu Pro Phe Xaa Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 1283

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<220><221> MOD_RES

<222> (36)..(36)

<223> Met or Leu

<220><221> MOD_RES

<222> (39)..(39)

<223> Val or Phe

<220><221> MOD_RES

<222> (76)..(76)

<223> Asp or Asn

<220><221> MOD_RES

<222> (77)..(77)

<223> Ser or Thr

<220><221> MOD_RES

<222> (97)..(97)

<223> Tyr or His

<220><221> MOD_RES

<222> (100)..(100)

<223> Lys or Arg

<220><221> MOD_RES

<222> (101)..(101)

<223> Asp or Glu

<220><221> MOD_RES

<222> (105)..(105)

<223> Tyr or Phe

<220><221> MOD_RES

<222> (108)..(108)

<223> Trp or Arg

<220><221> MOD_RES

<222> (109)..(109)

<223> Gly or Arg

<220><221> MOD_RES

<222> (110)..(110)

<223> Gln or His

<400> 1283

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Thr

20 25 30

Arg Tyr Glu Xaa Trp Trp Xaa Arg Gln Ala Pro Gly Lys Gly Leu Glu

35 40 45

Arg Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp

50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Xaa Xaa Lys Asn Thr

65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

85 90 95

Xaa Cys Ala Xaa Xaa Pro Tyr Ser Xaa Asp Tyr Xaa Xaa Xaa Gly Thr

100 105 110

Leu Val Thr Val Ser Ser

115

<210> 1284

<211> 232

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1284

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala

1 5 10 15

Pro Glu Leu Leu Gly Gly Ser 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> 1285

<211> 229

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1285

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe

1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val

50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser

65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser

100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln

130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu

180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser

195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

210 215 220

Leu Ser Leu Gly Lys

225

<210> 1286

<211> 351

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1286

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Lys Leu Pro Phe Arg Phe Ser Asp Arg Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp Lys Thr His

115 120 125

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val

130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr

145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu

165 170 175

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

180 185 190

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

210 215 220
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile

225 230 235 240
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro

245 250 255
Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu

260 265 270
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn

275 280 285
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser

290 295 300
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg

305 310 315 320
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu

325 330 335
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

340 345 350

<210> 1287

<211> 348

<212> PRT

<213> Artificial Sequence

<220><223> Description of Artificial Sequence: Synthetic polypeptide

<400> 1287

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr

20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val

35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val

50

55

60

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr				
65					70					75					80				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys				
85					90					95									
Ala	Lys	Leu	Pro	Phe	Arg	Phe	Ser	Asp	Arg	Gly	Gln	Gly	Thr	Leu	Val				
100					105					110									
Thr	Val	Ser	Ser	Ala	Ser	Thr	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro				
115					120					125									
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe				
130					135					140									
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val				
145					150					155					160				
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe				
165					170					175									
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro				
180					185					190									
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr				
195					200					205									
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val				
210					215					220									
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala				
225					230					235					240				
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln				
245					250					255									
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly				
260					265					270									
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro				
275					280					285									
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser				
290					295					300									
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln				

305		310		315		320									
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
				325						330					335
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
				340										345	