



등록특허 10-2785809



(19) 대한민국특허청(KR)

(12) 등록특허공보(B1)

(45) 공고일자 2025년03월26일

(11) 등록번호 10-2785809

(24) 등록일자 2025년03월19일

(51) 국제특허분류(Int. Cl.)
C07K 16/28 (2006.01) A61K 39/00 (2006.01)
A61P 35/00 (2006.01)

(52) CPC특허분류
C07K 16/2818 (2013.01)
A61P 35/00 (2018.01)

(21) 출원번호 10-2020-7009543

(22) 출원일자(국제) 2018년11월01일

심사청구일자 2021년08월06일

(85) 번역문제출일자 2020년04월01일

(65) 공개번호 10-2020-0091382

(43) 공개일자 2020년07월30일

(86) 국제출원번호 PCT/US2018/058810

(87) 국제공개번호 WO 2019/090002

국제공개일자 2019년05월09일

(30) 우선권주장

62/580,845 2017년11월02일 미국(US)

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WO2014209804 A1*

*는 심사관에 의하여 인용된 문헌

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전체 청구항 수 : 총 29 항

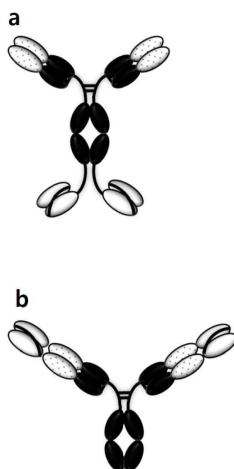
심사관 : 김종호

(54) 발명의 명칭 이중특이성 항체 및 이의 제조 및 사용 방법

(57) 요약

본 개시 내용은 적어도 2개의 인간 CTLA4, PD-1 또는 PD-L1에 대한 결합 특이성을 갖는 이중특이성 항체를 제공한다. 한 실시양태에서, 이중특이성 항체는 중쇄 및 경쇄를 갖는 IgG 도메인, 및 중쇄의 C-말단 또는 경쇄의 N-말단에 연결되어있는 2개의 scFv 성분을 포함하고, 여기서 IgG 도메인은 제1 항원에 대한 결합 특이성을 갖고, 여기서 scFv 성분은 제2 항원에 대한 결합 특이성을 가지며, 여기서 제1 항원 및 제2 항원은 상이하고 CTLA4, α-PD-1 및 α-PD-L1으로부터 독립적으로 선택된다.

대표도 - 도1



(52) CPC특허분류

C07K 16/2827 (2013.01)
A61K 2039/505 (2013.01)
C07K 2317/31 (2013.01)
C07K 2317/622 (2013.01)
C07K 2317/64 (2013.01)
C07K 2317/92 (2013.01)

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명세서

청구범위

청구항 1

중쇄 및 경쇄를 포함하는 IgG 도메인; 및 중쇄의 C 말단 또는 경쇄의 N 말단에 연결된 2개의 scFv 성분을 포함하는 이중특이성 항체(bispecific antibody)로서, 여기서 IgG 도메인이 제1 항원에 대한 제1 결합 특이성을 갖고, scFv 성분이 제2 항원에 대한 제2 결합 특이성을 가지며, 상기 제1 항원이 α -CTLA4를 포함하고, 제2 항원이 α -PD-1 또는 α -PD-L1을 포함하며,

상기 IgG 도메인이 서열번호 141 내지 143의 중쇄 가변 영역의 CDR 1 내지 3, 및 서열번호 144 내지 146의 경쇄 가변 영역의 CDR 1 내지 3을 포함하고;

상기 scFv 성분이 서열번호 153 내지 155의 중쇄 가변 영역의 CDR 1 내지 3, 및 서열번호 156 내지 158의 경쇄 가변 영역의 CDR 1 내지 3; 또는 서열번호 159 내지 161의 중쇄 가변 영역의 CDR 1 내지 3, 및 서열번호 162 내지 164의 경쇄 가변 영역의 CDR 1 내지 3을 포함하는, 이중특이성 항체.

청구항 2

제1항에 있어서,

IgG 도메인이 서열번호 94를 포함하는 가변 경쇄, 및 서열번호 92를 포함하는 가변 중쇄를 포함하고;

scFv 성분이 서열번호 98을 포함하는 가변 경쇄, 및 서열번호 96을 포함하는 가변 중쇄; 또는 서열번호 122을 포함하는 가변 경쇄, 및 서열번호 120을 포함하는 가변 중쇄를 포함하는, 이중특이성 항체.

청구항 3

제1항에 있어서, 2개의 scFv 성분이 중쇄의 C 말단에 연결된, 이중특이성 항체.

청구항 4

제1항에 있어서, 2개의 scFv 성분이 경쇄의 N 말단에 연결된, 이중특이성 항체.

청구항 5

제1항에 있어서, 이중특이성 항체가 단리된 단일클론(monoclonal) 항체인, 이중특이성 항체.

청구항 6

제1항에 있어서, α -CTLA4에 대한 제1 결합 특이성, 및 α -PD-1 또는 α -PD-L1에 대한 제2 결합 특이성을 가지며, 상기 제1 및 제2 결합 특이성 모두 70nM 이하의 Kd를 갖는, 이중특이성 항체.

청구항 7

제1항에 있어서, α -CTLA4에 대한 제1 결합 특이성, 및 α -PD-1에 대한 제2 결합 특이성을 가지며, 상기 제1 및 제2 결합 특이성 모두 70nM 이하의 Kd를 갖는, 이중특이성 항체.

청구항 8

제1항에 있어서, α -CTLA4에 대한 제1 결합 특이성, 및 α -PD-L1에 대한 제2 결합 특이성을 가지며, 상기 제1 및 제2 결합 특이성 모두 70nM 이하의 Kd를 갖는, 이중특이성 항체.

청구항 9

제1항에 있어서, 인간 프레임워크(framework) 영역을 포함하는, 이중특이성 항체.

청구항 10

제1항에 있어서, 항체가 인간화 항체, 키메라 항체(chimeric antibody), 또는 재조합 항체인, 이중특이성 항체.

청구항 11

제1항에 있어서, IgG 도메인이 IgG1 불변 영역을 포함하고, 상기 IgG1 불변 영역이 서열번호 136와 적어도 98% 유사성(similarity)을 갖는 아미노산 서열을 포함하는, 이중특이성 항체.

청구항 12

제1항 내지 제11항 중 어느 한 항의 이중특이성 항체를 암호화하는, 단리된 핵산.

청구항 13

제12항의 단리된 핵산을 포함하는, 발현 벡터.

청구항 14

제13항에 있어서, 벡터는 세포 내에서 발현가능한 것인, 발현 벡터.

청구항 15

제12항의 핵산 또는 상기 핵산을 포함하는 발현 벡터를 포함하는 단리된 숙주 세포.

청구항 16

제15항에 있어서, 숙주 세포가 원핵 세포 또는 진핵 세포인, 숙주 세포.

청구항 17

제15항의 숙주 세포를 배양하여 이중특이성 항체를 생산하는 단계를 포함하는, 이중특이성 항체를 생산하는 방법.

청구항 18

제1항 내지 제11항 중 어느 한 항의 이중특이성 항체 및 세포독성제(cytotoxic agent)를 포함하는 면역접합체(immunoconjugate).

청구항 19

제18항에 있어서, 세포독성제가 화학치료제, 성장 억제제, 독소, 또는 방사성 동위원소인, 면역접합체.

청구항 20

제1항 내지 제11항 중 어느 한 항의 이중특이성 항체 및 약학적으로 허용되는 담체를 포함하는, 암을 가진 대상체를 치료하기 위한 약학 조성물.

청구항 21

제20항에 있어서, 방사성동위원소, 방사성핵종, 독소, 치료제, 화학치료제, 또는 이의 조합을 추가로 포함하는, 약학 조성물.

청구항 22

제18항의 면역접합체 및 약학적으로 허용되는 담체를 포함하는, 암을 가진 대상체를 치료하기 위한 약학 조성물.

청구항 23

유효량의 제1항 내지 제11항 중 어느 한 항의 이중특이성 항체를 포함하는, 암을 가진 대상체를 치료하기 위한 약학 조성물.

청구항 24

제23항에 있어서, 암이 PD-L1을 발현하는 세포를 포함하는, 약학 조성물.

청구항 25

제23항에 있어서, 암이 유방암, 결장직암, 췌장암, 두경부암, 흑색종, 난소암, 전립선암, 비소세포폐암, 소세포폐암, 신경교종, 식도암, 비인두암, 신장암, 위암, 간암, 방광암, 자궁경부암, 뇌암, 림프종, 백혈병, 또는 골수종을 포함하는, 약학 조성물.

청구항 26

제23항에 있어서, 치료가 유효량의 치료제의 공동 투여를 포함하는, 약학 조성물.

청구항 27

제26항에 있어서, 치료제가 항체, 화학요법제, 효소, 또는 이의 조합을 포함하는, 약학 조성물.

청구항 28

제26항에 있어서, 치료제가 카페시타빈(capecitabine), 시스플라틴(cisplatin), 트라스투주맙(trastuzumab), 플베스트란트(fulvestrant), 타목시펜(tamoxifen), 레트로졸(letrozole), 엑세메스탄(exemestane), 아나스트로졸(anastrozole), 아미노글루테티미드(aminoglutethimide), 테스톨락톤(testolactone), 보로졸(vorozole), 포르메스탄(formestane), 파드로졸(fadrozole), 레트로졸(letrozole), 에를로티닙(erlotinib), 라파티닙(lafatinib), 다사티닙(dasatinib), 게피티닙(gefitinib), 이마티닙(imatinib), 파조피닙(pazopinib), 라파티닙(lapatinib), 수니티닙(sunitinib), 닐로티닙(nilotinib), 소라페닙(sorafenib), 남-팔리탁셀(nab-palitaxel), 또는 이의 조합을 포함하는, 약학 조성물.

청구항 29

제23항에 있어서, 대상체가 인간인, 약학 조성물.

청구항 30

삭제

청구항 31

삭제

청구항 32

삭제

청구항 33

삭제

청구항 34

삭제

청구항 35

삭제

청구항 36

삭제

청구항 37

삭제

청구항 38

삭제

청구항 39

삭제

청구항 40

삭제

청구항 41

삭제

발명의 설명

기술 분야

[0001] 관련 출원에 대한 상호 참조

[0002] 본 출원은 2017년 11월 2일에 출원된, "이중특이성 항체 및 이의 제조 및 사용 방법"이라는 명칭의 미국 가특허 출원 제62580845호에 대한 이익을 주장하며, 이는 그 전문이 본원에 참조로 명확히 포함된다.

[0003] 기술분야

[0004] 본 개시내용은 일반적으로 생물학적 치료제의 기술 분야에 관한 것이며, 보다 특히 이중특이성 항체(bispecific antibody)를 제조하고 사용하는 방법에 관한 것이다. 모든 참고문헌은 그 전문이 본원에 포함된다.

배경 기술

[0005] 암 세포는 면역감시(immunosurveillance)를 피하기 위한 다양한 전략을 개발한다. 특정 종양 항원의 부재 및 주 조직적합성 복합체(major histocompatibility complex; MHC) 분자의 발현 손실은 T 림프구에 의한 암 세포의 인식을 방해한다. 면역억제 종양 미세환경 또한 면역계에 의한 종양 세포의 감소된 인식에 기여한다. 종양 미세 환경은 조절 T 세포, 골수 유래 억제 세포, 종양 관련 대식세포, 억제 B 세포, TGF-베타 또는 IL-10과 같은 종양 또는 기질 세포에 의해 생산되는 면역억제 사이토카인, 및 T 세포 기능을 조절하는 면역 체크포인트(checkpoint) 분자로 구성되어있는 면역억제 세포 집단에 의해 나타난다(문헌[Marshall HT et al., Front Oncol 2018, 8:315]).

[0006] 환자 자신의 면역계를 관여(engaging)시키는 것이 정상 조직을 손상시키지 않으면서, 종양 성장 제어 및 종양 세포의 특이적인 제거에 효과적이라는 것이 밝혀졌다. 면역요법(immunotherapy)이 암 치료에 대해 추가적인 관점을 제공했다(문헌[Khalil DN et al., Adv Cancer Res 2015, 128:1-68]).

[0007] 면역계의 다수의 조절인자(modulator)를 조합하는 것은 면역-종양학(immuno-oncology) 분야의 빠르게 발전하는 새로운 영역이다. 다수의 경로를 통해 종양 세포에 대한 면역 반응을 조절할 수 있는 새로운 치료제는 환자 반응을 증가시키고 일부 경우에는 독성을 감소시킴으로써 암 환자에게 매우 유익할 수 있다.

[0008] 면역계를 표적화하는 하나 이상의 단일클론 항체와의 조합 요법은 암의 치료에 있어서 단일 제제에 의한 치료보다 더 효력이 있다는 것이 밝혀졌다(문헌[Hellman MD et al., Adv Immunol 2016, 130: 251-77]). 증가된 효능 및 반응률 이외에, 조합 요법은 종종 단일 제제 치료보다 더 큰 독성을 가진다. 면역계를 조절하는 이중특이성 제제는 환자에게 덜 독성일 수 있고/있거나 더욱 강력할 수 있고, 동일한 특이성을 갖는 단일클론 항체의 조합으로 구성된 치료에 비해 추가적인 작용 기전을 갖는다.

발명의 내용

[0009] 요약

[0010] 본 개시내용은 이중특이성 항체, 특히, IgG 성분을 포함하여 BiTE 분자의 빠른 클리어런스(clearance)를 극복하고, 환자의 면역 세포의 생체외 확장을 필요로하지 않는 오프-더-셀프(off-the-shelf) 요법으로서 CAR-T 세포

요법보다 이점을 갖는, 이중특이성 항체에 관한 것이다. 이중특이성 항체의 다른 이점은 2개의 체크포인트 수용체의 동시 관여에 의해 억제 종양 미세환경을 극복하는 향상된 능력이다.

- [0011] 본 개시내용의 이중특이성 항체는 다른 제제, 예를 들어 T-세포 관여항체(T-cell engager)와 조합할 수 있고, 그의 활성을 추가로 향상시킬 수 있다.
- [0012] 본 개시내용은 면역 및 종양 세포 상에 발현된 2개의 구별된 표적에 결합하는 이중특이성 항체에 관한 것이다. 두 표적 모두 체크포인트 항원일 수 있다. 한 실시양태에서, 두 표적 모두 면역 세포 상의 체크포인트 항원일 수 있다. 한 실시양태에서, 두 표적 모두 종양 세포 상의 체크포인트 항원일 수 있다. 한 실시양태에서, 하나의 표적은 면역 세포 상의 체크포인트 항원이고 다른 표적은 종양 세포 상의 체크포인트 항원이다. 한 실시양태에서, 체크포인트 항원은 PD-1, PD-L1 및 CTLA4로부터 선택될 수 있다. 한 실시양태에서, 표적은 PD-1, PD-L1 및 CTLA4의 임의의 조합을 포함할 수 있다.
- [0013] 본 개시내용은 이중특이성 제제의 조성물, 및 암 및 자가면역 결핍증의 치료를 위한 이의 치료적 용도를 추가로 제공한다.
- [0014] 한 실시양태에서, 본 출원은 IgG 중쇄 및 경쇄, 및 중쇄의 C 말단 또는 경쇄의 N 말단에 연결되어있는 2개의 scFv 성분을 포함하는 이중특이성 항체로서, 여기서 IgG는 제1 항원에 결합 특이성을 갖고, 여기서 scFv 성분은 제2 항원에 결합 특이성을 가지며, 여기서 제1 항원 및 제2 항원은 상이하고 α -CTLA4, α -PD-1, 및 α -PD-L1으로부터 독립적으로 선택되는, 이중특이성 항체를 개시한다.
- [0015] 한 실시양태에서, 이중특이성 항체는 중쇄의 C 말단에 연결되어있는 2개의 scFv 성분을 갖는다. 한 실시양태에서, 제1 항원은 α -CTLA4를 포함하고 제2 항원은 α -PD-1 또는 α -PD-L1을 포함한다. 다른 실시양태에서, 제1 항원은 α -PD-1 또는 α -PD-L1을 포함하고 제2 항원은 α -CTLA4를 포함한다.
- [0016] 한 실시양태에서, 이중특이성 항체는 경쇄의 N 말단에 연결되어있는 2개의 scFv 성분을 갖는다. 한 실시양태에서, 제1 항원은 α -PD-1 또는 α -PD-L1을 포함하고 제2 항원은 α -CTLA4를 포함한다. 다른 실시양태에서, 제1 항원은 α -CTLA4를 포함하고 제2 항원은 α -PD-1 또는 α -PD-L1을 포함한다.
- [0017] 한 실시양태에서, 이중특이성 항체는 단리된 단일클론 항체이다.
- [0018] 한 실시양태에서, 이중특이성 항체는 본원에 개시된 바와 같은 서열을 갖는 항원 펩타이드 서열을 포함한다. 한 실시양태에서, 이중특이성 항체는 개시된 아미노산 서열과 적어도 70%, 80%, 90%, 95%, 98%, 또는 99% 유사성(similarity)을 갖는 항원 펩타이드 서열을 가질 수 있다.
- [0019] 한 실시양태에서, 이중특이성 항체는 본원에 개시된 바와 같은 서열을 갖는 항원-결합 단편을 포함한다. 한 실시양태에서, 이중특이성 항체는 개시된 항체 서열과 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 지닌 서열을 갖는 항원-결합 단편을 가질 수 있다.
- [0020] 한 실시양태에서, 이중특이성 항체는 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, 또는 5nM 이하의 Kd로 α -CTLA4, α -PD-1 또는 α -PD-L1에 대한 결합 친화성을 가질 수 있다.
- [0021] 한 실시양태에서, 이중특이성 항체는 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, 또는 5nM 이하의 Kd로 α -CTLA4 및 α -PD-1에 대한 결합 친화성을 가질 수 있다.
- [0022] 한 실시양태에서, 이중특이성 항체는 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, 또는 5nM 이하의 Kd로 α -CTLA4 및 α -PD-L1에 대한 결합 친화성을 가질 수 있다.
- [0023] 한 실시양태에서, 이중특이성 항체는 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, 또는 5nM 이하의 Kd로 α -CTLA4, α -PD-1, 또는 α -PD-L1 중 2개에 대한 결합 친화성을 가질 수 있다.
- [0024] 한 실시양태에서, 이중특이성 항체는 α -CTLA4, α -PD-1, 또는 α -PD-L1에 대한 고 친화성 결합, PD-1에 대한 PD-L1의 결합 억제, T 세포 활성화 향상, 항체 반응을 자극하는 능력 및/또는 면역억제 세포, 예를 들어 T 조절 세포의 억제 기능을 역전시키는 능력으로부터 선택된 하나 이상의 기능적 특성(functional property)을 나타낼 수 있다.
- [0025] 한 실시양태에서, T-세포 활성화를 향상시키는 것은 T-세포 증식, IFN- γ 및/또는 IL-2 분비, 또는 이의 조합을 포함한다.
- [0026] 한 실시양태에서, 이중특이성 항체는 인간 프레임워크(architecture) 영역을 포함한다.

- [0027] 한 실시양태에서, 이중특이성 항체는 인간화 항체, 키메라 항체(chimeric antibody), 또는 재조합 항체일 수 있다.
- [0028] 한 실시양태에서, 이중특이성 항체는 IgG1 불변 영역(constant region)을 포함하여 이중특이성 분자의 순환 반감기를 연장시킨다. 한 실시양태에서, 이중특이성 항체의 IgG1 불변 영역은 서열번호 136과 적어도 98% 유사성을 갖는 아미노산 서열을 포함한다.
- [0029] 한 실시양태에서, 본 출원은 기재된 또는 본원에 개시된 바와 같은 기재된 특성을 갖는 클론들로 구성된 군으로부터 선택된 단리된 이중특이성 항체를 개시한다.
- [0030] 한 실시양태에서, 본 출원은 본원에 개시된 바와 같은 서열로부터 선택된 아미노산 서열을 포함하는, 이중특이성 항체를 위한 IgG1 중쇄를 개시한다. 한 실시양태에서, IgG1 중쇄는 서열번호 02, 06, 08, 10, 12, 14, 16, 18, 20, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 72, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 또는 132와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 가질 수 있다.
- [0031] 한 실시양태에서, 본 출원은 이중특이성 항체를 위한 카파 경쇄를 개시한다. 한 실시양태에서, 카파 경쇄는 서열번호 04, 28, 32, 36, 40, 44, 48, 52, 56, 60, 및 64와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 가질 수 있다.
- [0032] 한 실시양태에서, 본 출원은 본원에 개시된 바와 같은 아미노산 서열을 포함하는, 이중특이성 항체를 위한 가변 경쇄를 개시한다. 한 실시양태에서, 가변 경쇄는 서열번호 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 또는 134와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 가질 수 있다.
- [0033] 한 실시양태에서, 본 출원은 본원에 개시된 바와 같은 아미노산 서열을 포함하는, 이중특이성 항체를 위한 가변 중쇄를 개시한다. 한 실시양태에서, 가변 중쇄는 서열번호 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 또는 132와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 가질 수 있다.
- [0034] 한 실시양태에서, 본 출원은 본원에 개시된 IgG1 중쇄, 본원에 개시된 카파 경쇄, 본원에 개시된 가변 경쇄, 또는 본원에 개시된 가변 중쇄를 포함하는, 이중특이성 항체를 암호화하는 단리된 핵산을 개시한다. 한 실시양태에서, 본 출원은 서열번호 02, 06, 08, 10, 12, 14, 16, 18, 20, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 72, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 또는 132와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 갖는 IgG1 중쇄, 서열번호 04, 28, 32, 36, 40, 44, 48, 52, 56, 60, 및 64와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 갖는 카파 경쇄, 서열번호 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 또는 134와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 갖는 가변 경쇄, 또는 서열번호 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, 또는 132와 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 아미노산 서열을 갖는 가변 중쇄를 포함하는, 이중특이성 항체를 암호화하는 단리된 핵산을 개시한다.
- [0035] 한 실시양태에서, 본 출원은 본원에 개시된 단리된 핵산을 포함하는 발현 벡터를 개시한다. 한 실시양태에서, 발현 벡터는 본원에 개시된 핵산 서열과 적어도 70%, 80%, 90%, 98%, 또는 99% 유사성을 갖는 서열을 갖는 단리된 핵산을 포함한다.
- [0036] 한 실시양태에서, 발현 벡터는 세포 내에서 발현가능하다.
- [0037] 한 실시양태에서, 본 출원은 본원에 개시된 핵산을 포함하는 숙주 세포를 개시한다.
- [0038] 한 실시양태에서, 본 출원은 발현 벡터를 포함하는 숙주 세포를 개시한다.
- [0039] 한 실시양태에서, 본 출원은 숙주 세포를 개시하고, 여기서 숙주 세포는 원핵 세포 또는 진핵 세포이다.
- [0040] 일부 실시양태에서, 본 출원은 항체가 생산되도록 이의 제공된 숙주 세포를 배양하는 단계를 포함하는 항체를 생산하는 방법을 개시한다.
- [0041] 일부 실시양태에서, 본 출원은 이중특이성 항체 및 세포독성제(cytotoxic agent)를 포함하는 면역접합체(immunconjugate)를 개시한다. 일부 실시양태에서, 세포 독성제는 화학치료제, 성장 억제제, 독소, 또는 방사성 동위원소이다.
- [0042] 한 실시양태에서, 본 출원은 이중특이성 항체 및 약학적으로 허용되는 담체를 포함하는 약학 조성물을 개시한다. 한 실시양태에서, 본 출원은 면역접합체 및 약학적으로 허용되는 담체를 포함하는, 약학 조성물을 개

시한다. 한 실시양태에서, 약학 조성물은 방사성동위원소, 방사성핵종, 독소, 치료제, 화학치료제 또는 이의 조합을 추가로 포함한다.

[0043] 한 실시양태에서, 본 출원은 본원에 개시된 이중특이성 항체의 유효량을 대상체에게 투여하는 단계를 포함하는, 암을 가진 대상체를 치료하는 방법을 개시한다. 한 실시양태에서, 암은 유방암, 결장직암, 췌장암, 두경부암, 흑색종, 난소암, 전립선암, 비소세포폐암, 소세포폐암, 신경교종, 식도암, 비인두암, 신장암, 위암, 간암, 방광암, 자궁경부암, 뇌암, 림프종, 백혈병, 골수종을 포함한다.

[0044] 한 실시양태에서, 본 출원은 암을 가진 대상체를 치료하는 방법을 개시하며, 여기서 암은 PD-L1을 발현하는 세포를 포함한다.

[0045] 한 실시양태에서, 본 출원은 치료제의 유효량을 공동 투여하는 단계를 추가로 포함하는, 암을 가진 대상체를 치료하는 방법을 개시한다. 일부 실시양태에서, 치료제는 항체, 화학요법제, 효소, 또는 이의 조합을 포함한다.

[0046] 일부 실시양태에서, 치료제는 카페시타빈(capecitabine), 시스플라틴(cisplatin), 트라스투주맙(trastuzumab), 플베스트란트(fulvestrant), 타목시펜(tamoxifen), 레트로졸(letrozole), 엑세메스탄(exemestane), 아나스트로졸(anastrozole), 아미노글루테티미드(aminoglutethimide), 테스톨락톤(testolactone), 보로졸(vorozole), 포르메스탄(formestane), 파드로졸(fadrozole), 레트로졸(letrozole), 에를로티닙(erlotinib), 라파티닙(lapatinib), 다사티닙(dasatinib), 게피티닙(gefitinib), 이마티닙(imatinib), 파조피닙(pazopinib), 라파티닙(lapatinib), 수니티닙(sunitinib), 닐로티닙(nilotinib), 소라페닙(sorafenib), 남-팔리탁셀(nab-palitaxel), 이의 유도체 또는 조합을 포함한다.

[0047] 한 실시양태에서, 본 출원은 암을 가진 대상체를 치료하는 방법을 개시하며, 여기서 대상체는 인간이다.

[0048] 한 실시양태에서, 본 출원은 본원에 개시된 이중특이성 항체의 유효 농도를 포함하는 용액을 개시하며, 여기서 용액은 대상체 내의 혈장이다.

[0049] 본 출원의 또 다른 실시양태는 본 출원을 수행하기 위해 위해 고려되는 최상의 모드를 예시하는 방식으로 본 출원의 실시양태를 기재한, 하기의 상세한 설명으로부터 당해 분야의 숙련자에게 용이하게 명백해질 것이다. 알 수 있는 바와 같이, 본 출원은 다른 및 상이한 실시양태가 가능하며 이의 몇몇 세부 사항들이 모두 본 출원의 사상 및 범위를 벗어나지 않고, 다양하고 명백한 측면에서 수정될 수 있다. 따라서, 도면 및 상세한 설명은 제한적인 것이 아니라 사실상 예시적인 것으로 간주되어야 한다.

도면의 간단한 설명

[0050] 본 개시내용의 상기 및 다른 특징들은 첨부 도면과 관련하여, 하기의 설명 및 첨부된 청구범위로부터 보다 완전히 명백해질 수 있다. 이들 도면이 본 개시내용에 따라 배열된 몇몇 실시양태만을 묘사하므로, 그의 범위를 제한하는 것으로 고려되지 않아야 한다는 것을 이해하고, 본 개시내용은 하기의 첨부 도면을 사용하여 추가의 특이성 및 세부 사항과 함께 기재될 수 있다:

도 1은 CTLA4, PD-1 및 PD-L1 항원을 표적화하는 예시적인 이중특이성 항체의 다이어그램을 나타낸다;

도 2는 CHO 세포주의 표면 상에 발현된 PD-1 항원에 대한 예시적인 항-PD-1 항체의 결합을 나타낸다;

도 3은 CTLA4와 CD80 사이의 상호작용을 차단하는 대표적인 이중특이성 항체의 능력을 평가하는 생화학적 분석으로부터의 결과를 묘사한다.

도 4는 슈퍼 항원 SEB에 의한 PBMC의 자극을 나타내고; 도 4a는 PD224D1 x CT4 IgG1 널(null) 및 PL230C6 x CT4 IgG1 널에 의한 치료를 나타내고; 도 4b는 CT4 x PD224D1 IgG1 널, CT4 x PL221G5 IgG1 및 CT4 x PL221G5 IgG1 널에 의한 치료를 나타낸다;

도 5는 PD-1/PDL-1 경로에 대한 신호전달 분석으로부터의 결과를 나타낸다;

도 6은 수지상 세포 혼합된 림프구 반응(Dendritic Cell Mixed Lymphocytes Reaction) 연구로부터의 결과를 나타낸다;

도 7은 조절 T 세포 억제 분석으로부터의 결과를 나타내고; 도 7a는 CD8+ T 세포의 증식을 나타내고; 도 7b는 IFN γ 생산을 나타낸다;

도 8은 예시적인 이중특이성 항체에 의한 치료에 대한 반응으로 CD8 T 세포 탈과립화(degranulation)를 나타낸

다;

도 9는 MiXeno HCC287 마우스 종양 모델로부터의 결과를 나타낸다;

도 10은 Flu-특이적 CD8 T 세포의 증식에 대한 예시적인 이중특이성 항체의 효과를 나타낸다;

도 11은 CEFT 펩타이드 풀(pool)에 대한 PBMC 기억 반응으로부터의 결과를 나타낸다; 및

도 12는 예시적인 이중특이성 항체에 의한 방향전환된 T 세포 세포독성(Redirected T Cell Cytotoxicity)의 향상을 나타낸다.

발명을 실시하기 위한 구체적인 내용

- [0051] 본 출원의 실시양태에 대한 하기의 상세한 설명에서, 첨부 도면에 참조(reference)가 있고, 여기서 유사한 참조는 유사한 요소를 나타내며, 여기서 본 출원이 실시될 수 있는 구체적인 실시양태를 예시로서 나타낸다. 이들 실시양태는 당해 분야의 숙련가가 본 출원을 실시 할 수 있도록 충분히 상세하게 기재된다. 다른 예에서, 공지된 회로, 구조, 및 기술은 본 설명의 이해를 모호하게 하지 않기 위해 상세하게 나타내지 않았다. 따라서, 하기의 상세한 설명은 제한적인 의미로 받아들여지지 않아야하고, 본 출원의 범위는 첨부된 청구범위에 의해서만 한정된다.
- [0052] 본 개시내용은 인간 CTLA4, PD-1 또는 PD-L1에 특이적으로 결합하는 이중특이성 항체에 관한 것이다. 일부 실시양태에서, 이중특이성 항체는 CTLA4에 결합하는 제1 아암(arm) 및 PD-1 또는 PD-L1에 결합하는 제2 아암을 포함한다. 일부 실시양태에서, 이중특이성 항체는 PD-1 또는 PD-L1에 결합하는 제1 아암 및 CTLA4에 결합하는 제2 아암을 포함한다. 아암을 포함하는 도메인의 예는 Fab 및 scFv 도메인을 포함하나, 이에 제한되지는 않는다. 각 아암은 2개의 항원-결합 도메인을 함유하고 Fc 도메인을 통해 다른 아암에 연결된다. Fc 도메인은 인간 IgG1, IgG2, IgG3, IgG4 또는 조각된 동형(isotype)의 것일 수 있다.
- [0053] 본 출원의 이중특이성 항체(도 1)는 인간 CTLA4, 인간 PD-1 및 인간 PD-L1을 표적화한다. 이러한 표적화된 이중특이성 항체 각각은 항-CTLA4 (서열번호 91, 93) 및 항-인간 PD-1 (서열번호 95, 97, 131, 133) 또는 PD-L1 결합 도메인(서열번호 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129)을 지닌다. 결합 도메인 중 어느 하나는 C-말단에 배치하기 위해 scFv(VH-VL 배향)로, 또는 N-말단에 배치하기 위해 scFv(VL-VH 배향)로 전환되었다(각각 도 1a 및 도 1b).
- [0054] 일부 실시양태에서, 본원에 기재된 scFv 분자는 V-영역 배향(LH 또는 HL)에 상관 없이, VH 및 VL을 작동적으로 연결하는 20-아미노산 가요성 gly-gly-gly-gly-ser (G4S) X4 링커를 함유한다. 이중특이성 항체의 나머지 위치는 인간 IgG1 Fc 또는 IgG1 널 Fc 중쇄, VH-CH1-힌지(Hinge)-CH2-CH3, 및 이의 상응하는 카파 경쇄, VL-CL로 구성될 수 있다. scFv 도메인은 10-아미노산 (G4S) x 2 링커를 통해 IgG1 중쇄의 N-말단 또는 C-말단에 유전적으로 연결되어 있어서, 연속적인 ~ 100kDa의 중쇄 단량체 펩타이드를 생성한다. 적합한 경쇄와 공동 형질감염된 경우, 최종 대칭적 이중특이성 분자는 인간 IgG1 Fc (단백질 A)를 통해 정제되어 기능 활성을 평가하기 위해 분석될 수 있다.
- [0055] 중쇄 및 경쇄 유전자 "카세트(cassette)"는 V-영역이 제한 효소 부위를 사용하여 클로닝(cloning)될 수 있도록 이전에 작제되었다(도 1a 예: 중쇄의 경우 HindIII/NotI 및 경쇄의 경우 HindIII/BsiWI). 한 실시양태에서, "제한-없는(restriction-free) 클로닝" NEBuilder (NEB, 미국 매사추세츠주 Ipswich, MA) 소재)가 사용되었다.
- [0056] 이중특이성 항체는 무손상 분자의 설계, 각각의 도메인에 대한 뉴클레오타이드 서열의 합성 및 클로닝, 포유동물 세포에서의 발현 및 최종 산물의 정제를 수반하는 공정을 통해 생산된다. 뉴클레오타이드 서열은 Geneious 10.2.3 소프트웨어 패키지(Biomatters, 뉴질랜드 오클랜드(Auckland, NZ) 소재)를 사용하여 조립되었고 유전자 합성을 위해 그들의 성분 도메인으로 해체되었다(Genewiz, 미국 뉴저지주 사우쓰 플레인스필드(South Plainsfield, NJ) 소재). 하나의 예에서(도 1a), CT4 x PD224D1 IgG1 널 이중특이성 항체 (서열번호 2)의 중쇄는 인간 IgG1 널 Fc 도메인에 융합된 항-CTLA4 VH 도메인으로 구성되어있고(힌지, CH1, 및 CH2), 항-PD-1 scFV 도메인에 융합된 10-아미노산 (G4S) x 2 링커(클론 PD224D1)가 뒤따른다. NEBuilder 웹-기반 도구를 사용하여, 각각의 도메인이 이의 인접 도메인(flanking domain)을 20-30개의 뉴클레오타이드에 의해 겹치도록(overlap) 5' 및 3' 뉴클레오타이드를 각각의 도메인에 첨부하였고, 이는 부위-특이적인 재조합을 지시하므로, 단일 유전자 조립(assembly) 단계에서 각각의 도메인을 유전적으로 융합시킨다.

[0057] CT4 x PD224D1 IgG1 널의 경쇄는 인간 C 카파 도메인에 융합된 항-CTLA4 VL 도메인으로 구성되어 있다. 합성된 유전자 단편은 제한 효소 HindIII 및 BsiWI에 의해 분해된 후, 인간 C 카파 도메인과 함께 프레임-내 결합되었다. 두 작제물 모두에 대해, 소량의 분취물을 이. 콜라이 DH10b (Invitrogen, 미국 캘리포니아주 칼스배드 (Carlsbad, CA) 소재)로 형질전환시키고 TB + 카르베니실린(carbenicillin) 100 μ g/ml 플레이트(Teknova, 미국 캘리포니아주 홀리스터(Hollister, CA) 소재)에 플레이팅하고 37 $^{\circ}$ C에서 밤새 배양(incubating)하였다. 생성된 콜로니를 선택하고 2ml의 밤샘 배양물을 TB + 카르베니실린에 접종하였다. 밤샘 배양물로부터 DNA를 제조하고 (Thermo-Fisher, 미국 캘리포니아주 칼스배드 소재) 후속적으로 각각의 도메인에 인접한 서열분석 프라이머 (Sigma, 미국 미주리주 세인트루이스(St. Louis, MO) 소재)를 사용하여 서열분석하였다(Genewiz, 미국 뉴저지주 사우쓰 플레인스필드 소재). 모든 DNA 서열은 Geneious에서 조립하고 분석하였다.

[0058] 실시예

[0059] 실시예 1: PD-L1 항원에 대한 항-PD-L1 항체의 결합

[0060] PD-L1 재조합 단백질에 대한 항-PD-L1 항체의 결합 친화성 및 동역학을 ForteBio Octet RED96 기기 상에서 표면 플라즈몬 공명(Surface Plasmon Resonance)을 통해 평가하였다. 항원을 센서 칩 표면에 고정화하고 시험된 항체를 고정화된 항원 위에 흘렸다. 모든 분자는 예를 들어 표 1에 나타낸 바와 같이 항원에 대한 강한 결합을 나타냈다.

표 1

PD-L1 항원에 대한 항-PD-L1 항체의 결합

샘플 ID	mAb			scFv-Fc			Fc-scFv		
	KD (M)	kon(1/Ms)	kdis(1/s)	KD (M)	kon(1/Ms)	kdis(1/s)	KD (M)	kon(1/Ms)	kdis(1/s)
PL004B9	1.37E-09	5.08E+05	6.95E-04	1.42E-09	3.87E+05	5.50E-04	1.54E-09	3.07E+05	4.71E-04
PL221G5	4.83E-10	5.72E+05	2.76E-04	5.97E-10	5.08E+05	3.03E-04	4.12E-10	4.14E+05	1.71E-04
PL230C6	7.69E-10	6.09E+05	4.68E-04	9.17E-10	5.03E+05	4.61E-04	8.68E-10	4.18E+05	3.62E-04
PL231H2	7.81E-10	5.01E+05	3.91E-04	9.99E-10	4.20E+05	4.19E-04	4.62E-10	8.40E+05	3.89E-04

[0061]

[0062] 실시예 2: PD-1 항원에 대한 항-PD-1 항체의 결합

[0063] CHO 세포주의 표면에 발현되는 PD-1 항원에 대한 이중특이성 항체 및 이의 성분의 결합을 FACS 방법을 사용하여 평가하였다. 이중특이성 항체를 PD-1 항원을 발현하는 CHO 세포주와 배양시킨 후 Alexa Fluor 647 형광색소 (fluorochrome)에 직접 결합된 2차 항-인간 항체로 검출하였다. 시험 항체의 세포 결합을 유동 세포분석기 BD LSRFortessa 상에서 분석하였다. 시험된 모든 항체가 한 자릿수의 나노몰 범위의 KD로 항원에 결합하였다(도 2).

[0064] 실시예 3: CTLA4와 CD80 사이의 상호작용의 차단

[0065] CTLA4와 이의 리간드 CD80 사이의 상호작용을 차단하는 이중특이성 항체의 능력을 생화학적 상호작용 분석 (Cisbio)에서 시험하였다. 요약하면, 이중특이성 항체를 CTLA4 및 CD80 단백질과 함께 배양하였다. CTLA4 및 CD80 단백질을 인식하고 HTRF 공여체/수여체 형광 쌍으로 표지한 검출 항체를 이후에 혼합물에 첨가하였다. CTLA4와 CD80 사이의 상호작용을 FRET 효율을 통해 평가하였다. 시험된 모든 이중특이성 항체가 CTLA4와 CD80 사이의 상호작용을 차단할 수 있었다(도 3).

[0066] 실시예 4: 슈퍼항원 SEB에 의한 PBMC의 자극

[0067] 슈퍼 항원 SEB에 의한 자극 후에 인간 말초 혈액 단핵 세포(PBMC)로부터 사이토카인 방출을 향상시키는 이중특이성 항체의 능력을 평가하였다. 도 4a 및 도 4b에서 나타낸 바와 같이, 모든 이중특이성 분자는 SEB에 의한 자극 시에 PBMC에 의한 IL-2의 생산을 유의적으로 향상시킬 수 있었다.

[0068] 실시예 5: PD-1/PD-L1 경로 신호전달

[0069] PD-1/PD-L1 경로를 차단하는 능력에 대해 이중특이성 항체를 시험하였다. 요약하면, 시험 분자를 PD-1 수용체 및 루시페라아제(luciferase) NFAT 리포터를 발현하는 Jurkat 리포터 세포주 및 CHO-PD-L1 세포주 (Promega)와 함께 배양하였다. PD-1/PD-L1 경로를 통한 신호전달을 차단하는 시험 항체의 능력을 NFAT 신호전달에서의 증가를 통해 평가하였다. 결과적으로 NFAT 신호전달을 루시페라아제 리포터 유전자의 활성을 통해 모니터링하였다.

분석을 플레이트 판독기(plate reader)(Clariostar, BMG) 상에서 판독하였다. 시험된 모든 이중특이성 항체 및 단일클론 항체 대조군은 PD-1/PD-L1 신호전달을 차단할 수 있었다(도 5).

실시예 6: 수지상 세포 혼합된 백혈구 반응

수지상 세포 혼합된 백혈구 반응(MLR)을 향상시키는 능력에 대해 이중특이성 항체를 시험하였다. 시험 분자를 하나의 공여체로부터의 수지상 세포 및 다른 공여체로부터 단리된 T 세포와 함께 6일 동안 함께 배양하였다. 수지상 세포를 GM-CSF 및 IL-4의 존재 하에서 단핵구로부터 시험관내 분화시켰다. StemCell 단리 키트로 단핵구 및 T 세포 집단을 PBMC로부터 단리시켰다. MLR을 향상시키는 시험 분자의 능력을 분비된 IFN γ 를 통해 평가하였다. 도 6에 나타난 바와 같이, 시험된 모든 이중특이성 항체는 IFN γ 의 생산을 증대시킬 수 있었다.

실시예 7: 조절 T 세포에 의한 CD8 T 세포의 억제

효과기(effector) CD8 T 세포 증식 및 사이토카인 생산에 대한 조절 T 세포의 억제 효과를 차단하는 능력에 대해 이중특이성 항체를 시험하였다. CD8 T 세포를 StemCell 단리 키트로 단리하고 셀트레이스(CellTrace) 염료(썬피셔)로 표지하였다. 수지상 세포를 상기 MLR 연구에서 기재한 바와 같이 제조하였다. 조절 T 세포를 StemCell 단리 키트에 의해 PBMC로부터 단리하고 시험관 내 확장시켰다. 이중특이성 항체를 효과기 CD8 T 세포, 수지상 세포 및 조절 T 세포와 함께 4일 동안 배양하였다. 조절 T 세포의 존재 하에서 효과기 CD8 T 세포 기능을 구출하는 이중특이성 항체의 능력을 효과기 CD8 T 세포의 증식(도 7a) 및 분비된 IFN γ (도 7b)를 통해 평가하였다.

실시예 8: CD8 T 세포 탈과립화(degranulation)

세포독성 CD8 T 세포에 영향을 끼치는 이중특이성 분자의 능력을 본 연구에서 평가하였다. 요약하면, CD8 T 세포를 StemCell 단리 키트로 정제하고 이중특이성 시험 분자의 존재 하에 CEFT 펩타이드 풀(pool)(JPT Peptide Technologies)로 자극시켰다. 배지를 IL-7 및 IL-21로 보충하였다. 11일째에 CD8 T 세포를 브레펠딘(Brefeldin) 및 모넨신(Monensin) 및 형광색소로 직접 표지된 항-CD107a 항체의 존재 하에 펩타이드로 재자극시켰다. 24시간 후 CD8 T 세포를 형광색소에 직접 접합된 항-IFN γ 항체로 염색하고 유동 세포분석기 BD LSRFortessa 상에서 평가하였다. 도 8에 나타난 바와 같이, 시험된 모든 이중특이성 항체는 세포독성 IFN γ 양성 T 세포의 수를 증가시킬 수 있었다.

실시예 9: 믹세노(MiXeno) 마우스 종양 모델

인간화 마우스 모델을 사용하여 생체내 종양 성장을 억제하는 이 부류의 이중특이성 항체의 능력을 평가하였다. 요약하면, NOG 마우스를 인간 PBMC (마우스 당 5×10^6 개 세포)로 재구성하였다. 3일째에 동물에게 인간 폐암 세포주 HCC827 (0.5E6 세포/동물)를 피하 접종하고 이중특이성 항체 및 대조군 항체로 격주 치료를 시작하였다. 종양 용적을 2-3일 마다 측정하였다. 동물 중량을 모니터링하였다. 시험된 이중특이성 항체는 대조군 항체보다 종양 성장을 더 우수하게 억제할 수 있었다(도 9).

실시예 10: Flu-특이적 T 세포의 증식

항원 특이적 CD8 T 세포의 증식을 증대시키는 이중특이성 항체의 능력을 본 연구에서 평가하였다. CD8 T 세포를 StemCell 단리 키트로 PBMC로부터 정제하고, 인플루엔자 특이적 펩타이드(JPT Peptide Technologies)로 펄스(pulse)시키고 이중특이성 항체의 존재 하에서 14일 동안 배양하였다. 배지를 IL-7 및 IL-21로 보충하였다. 15일째에 세포를 펩타이드 특이적 MHC 텍스트라머(dextramer)(Immudex)로 염색시키고 유동 세포분석기 BD LSRFortessa 상에서 평가하였다. 시험된 모든 이중특이성 항체는 항원 특이적 CD8 T 세포의 수를 증가시킬 수 있었다(도 10).

실시예 11: CEFT 펩타이드 풀에 대한 PBMC 기억 반응

T 세포 기억 반응을 증대시키는 이중특이성 항체의 능력을 평가하였다. 요약하면, PBMC를 CMV, EBV, 인플루엔자 및 테타너스(Tetanus)(JPT Peptide Technologies)에 특이적인 펩타이드의 존재 하에 4-5일 동안 배양하였다. 분비된 IFN γ 의 양을 정량화하였다. 도 11에 나타난 바와 같이, 이중특이성 CT4 x PD224D1는 대조군 치료에 비해 IFN γ 의 생산을 수배 향상시킬 수 있었다.

실시예 12: 방향전환된 T 세포 세포독성의 향상

종양 세포주 표적에 대한 방향전환된 T 세포 세포독성(Redirected T cell Cytotoxicity; RTCC)을 향상시키는 능력에 대해 이중특이성 항체를 평가하였다. 종양 세포주는 렌티바이러스 형질도입(Sartorius)을 통해 전달된

핵-국재화된 적색 형광 단백질(nucleus-localized Red Fluorescent Protein ;RFP)을 안정적으로 발현하였다. 종양 세포를 PBMC 및 주어진 종양 세포주에 대해 특이적인 T 세포 관여항체 분자와 함께 공동 배양하였다. 이중 특이성 항체를 공동 배양물에 첨가하였다. 종양 세포의 분해를 RFP 표지된 종양 세포 핵을 계수함으로써 평가하였다. 이미지(image)를 살아있는 세포 이미저(imager) 인큐사이트(Incucyte)(사르토리우스) 상에서 획득하였다. 항체의 활성을 96 시간의 배양 후 평가하였다. 4개의 PBMC 공여체를 본 연구에서 시험하였다. 시험된 모든 이중 특이성 항체는 적어도 하나의 시험된 PBMC 공여체 내에서 RTCC 활성을 향상시킬 수 있었다(도 12).

[0084]

본 개시내용은 특정 실시양태 또는 실시예를 참조하여 기재되었지만, 실시양태가 예시적이라는 것과 개시 범위가 이에 제한되지 않는다는 것이 이해될 수 있다. 본 개시 내용의 대안적인 실시양태는 본 개시 내용이 속하는 당해 분야의 숙련가에게 명백해질 수 있다. 이러한 대안적인 실시양태는 본 개시내용의 범위 내에 포함되는 것으로 고려된다. 따라서, 본 개시 내용의 범위는 첨부된 청구범위에 의해서 한정되고 상기 설명에 의해 뒷받침된다. 본 개시내용에 인용되거나 언급된 모든 참고문헌은 그 전문이 본원에 참고로 포함된다.

서열목록

서열번호	설명
1	CT4 x PD224D1 뉴클레오타이드
2	CT4 x PD224D1 아미노산
3	CT4 경쇄 뉴클레오타이드
4	CT4 경쇄 아미노산
5	CT4 x PL230C6 뉴클레오타이드
6	CT4 x PL230C6 아미노산
7	CT4 x PL221G5 뉴클레오타이드
8	CT4 x PL221G5 아미노산
9	CT4 x PL231H2 뉴클레오타이드
10	CT4 x PL231H2 아미노산
11	CT4 x PL004B5 뉴클레오타이드
12	CT4 x PL004B5 아미노산
13	CT4 x PL004B9 뉴클레오타이드
14	CT4 x PL004B9 아미노산
15	CT4 x PD206F12 뉴클레오타이드
16	CT4 x PD206F12 아미노산
17	CT4 x PD215A1 뉴클레오타이드
18	CT4 x PD215A1 아미노산
19	CT4 x PD220F6 뉴클레오타이드
20	CT4 x PD220F6 아미노산
21	CT4 x PD225G11 뉴클레오타이드
22	CT4 x PD225G11 아미노산
23	Gly 4 Ser x 4 뉴클레오타이드
24	Gly 4 Ser x 4 아미노산
25	PL230C6 x CT4 뉴클레오타이드
26	PL230C6 x CT4 아미노산
27	PL230C6 경쇄 뉴클레오타이드
28	PL230C6 경쇄 아미노산
29	PD224D1 x CT4 뉴클레오타이드
30	PD224D1 x CT4 아미노산

[0085]

31	PD224D1 경쇄 뉴클레오타이드
32	PD224D1 경쇄 아미노산
33	PL221G5 x CT4
34	PL221G5 x CT4
35	PL221G5 경쇄
36	PL221G5 경쇄
37	PL231H2 x CT4 뉴클레오타이드
38	PL231H2 x CT4 아미노산
39	PL231H2 경쇄 뉴클레오타이드
40	PL231H2 경쇄 아미노산
41	PL004B5 x CT4 뉴클레오타이드
42	PL004B5 x CT4 아미노산
43	PL004B5 경쇄 뉴클레오타이드
44	PL004B5 경쇄 아미노산
45	PL004B9 x CT4 뉴클레오타이드
46	PL004B9 x CT4 아미노산
47	PL004B9 경쇄 뉴클레오타이드
48	PL004B9 경쇄 아미노산
49	PD206F12 x CT4 뉴클레오타이드
50	PD206F12 x CT4 아미노산
51	PD206F12 경쇄 뉴클레오타이드
52	PD206F12 경쇄 아미노산
53	PD215A1 x CT4 뉴클레오타이드
54	PD215A1 x CT4 아미노산
55	PD215A1 경쇄 뉴클레오타이드
56	PD215A1 경쇄 아미노산
57	PD220F6 x CT4 뉴클레오타이드
58	PD220F6 x CT4 아미노산
59	PD220F6 경쇄 뉴클레오타이드
60	PD220F6 경쇄 아미노산

[0086]

61	PD225G11 x CT4 뉴클레오타이드
62	PD225G11 x CT4 아미노산
63	PD225G11 경쇄 뉴클레오타이드
64	PD225G11 경쇄 아미노산
65	CT4 신호 펩타이드 뉴클레오타이드
66	CT4 신호 펩타이드 아미노산
67	중쇄신호 펩타이드 뉴클레오타이드
68	중쇄신호 펩타이드 아미노산
69	경쇄 신호 펩타이드 뉴클레오타이드
70	경쇄 신호 펩타이드 아미노산
71	CT4 scFv 뉴클레오타이드
72	CT4 scFv 아미노산
73	PD224D1 scFv 뉴클레오타이드
74	PD224D1 scFv 아미노산
75	PD206F12 scFv 뉴클레오타이드
76	PD206F12 scFv 아미노산
77	PD215A1 scFv 뉴클레오타이드
78	PD215A1 scFv 아미노산
79	PD225G11 scFv 뉴클레오타이드
80	PD225G11 scFv 아미노산
81	PL230C6 scFv 뉴클레오타이드
82	PL230C6 scFv 아미노산
83	PL231H2 scFv 뉴클레오타이드
84	PL231H2 scFv 아미노산
85	PL221G5 scFv 뉴클레오타이드
86	PL221G5 scFv 아미노산
87	PL004B5 scFv 뉴클레오타이드
88	PL004B5 scFv 아미노산
89	PL004B9 scFv 뉴클레오타이드
90	PL004B9 scFv 아미노산

[0087]

91	CT4 VH 뉴클레오타이드
92	CT4 VH 아미노산
93	CT4 VL 뉴클레오타이드
94	CT4 VL 아미노산
95	PD224D1 VH 뉴클레오타이드
96	PD224D1 VH 아미노산
97	PD224D1 VL 뉴클레오타이드
98	PD224D1 VL 아미노산
99	PD206F12 VH 뉴클레오타이드
100	PD206F12 VH 아미노산
101	PD206F12 VL 뉴클레오타이드
102	PD206F12 VL 아미노산
103	PD215A1 VH 뉴클레오타이드
104	PD215A1 VH 아미노산
105	PD215A1 VL 뉴클레오타이드
106	PD215A1 VL 아미노산
107	PD225G11 VH 뉴클레오타이드
108	PD225G11 VH 아미노산
109	PD225G11 VL 뉴클레오타이드
110	PD225G11 VL 아미노산
111	PL230C6 VH 뉴클레오타이드
112	PL230C6 VH 아미노산
113	PL230C6 VL 뉴클레오타이드
114	PL230C6 VL 아미노산
115	PL231H2 VH 뉴클레오타이드
116	PL231H2 VH 아미노산
117	PL231H2 VL 뉴클레오타이드
118	PL231H2 VL 아미노산
119	PL221G5 VH 뉴클레오타이드
120	PL221G5 VH 아미노산

[0088]

121	PL221G5 VL 뉴클레오타이드
122	PL221G5 VL 아미노산
123	PL004B5 VH 뉴클레오타이드
124	PL004B5 VH 아미노산
125	PL004B5 VL 뉴클레오타이드
126	PL004B5 VL 아미노산
127	PL004B9 VH 뉴클레오타이드
128	PL004B9 VH 아미노산
129	PL004B9 VL 뉴클레오타이드
130	PL004B9 VL 아미노산
131	PD220F6 VH 뉴클레오타이드
132	PD220F6 VH 아미노산
133	PD220F6 VL 뉴클레오타이드
134	PD220F6 VL 아미노산
135	인간 IgG1 불변 도메인 뉴클레오타이드
136	인간 IgG1 불변 도메인 아미노산
137	인간 IgG1 불변 도메인 널 뉴클레오타이드
138	인간 IgG1 불변 도메인 널 아미노산
139	PD220F6 scFv 뉴클레오타이드
140	PD220F6 scFv 아미노산

[0089]

[0090]

서열번호 01: CT4 x PD224D1 뉴클레오타이드 서열 (nt)

[0091]

CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCAAGAGCACC
TCTGGGGGCACAGCGGCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGGCTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTGTGACAAAACCTACACATGCCACCGTGGCCAGCACCTGAAGCCGCGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTT
GAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTACCGTCTCTGCACAGGACTGGTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAAGCTTCTAT
CCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCTGTACAGCCTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTACATCGGCTACATTGGTGAT
ACTACTGGCATAGCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGC
GGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCCTTGTGATGACCGAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAAC
ATCACTTGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGAAAGTTCTAAGCTCCTGATCTATCAGGCTCCACTCTG
GCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATATGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTATTACTGT
CAAGGCGGTTATTATAGTGTGCCCTTAATACTTTCCGGCGAGGGACCAAGGTGGAGATCAAA

[0092]

서열번호 02: CT4 x PD224D1 아미노산 서열 (aa)

[0093]

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN

HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPPKPDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLY
SKLTVDKSRWQQGNVSCFSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTASGFSLSYAMS¹WVRQAPGKGLLEYIGYIGD
TTG²IAYASWANGRFTISKDNTKNTVDLQMNSLRAEDTAVYYCARGWSYLD³IWQGT⁴LVTVSSGGGSGGGGSGGGGSGGGGSALVMTQSPSSLSASVGRVIT
ITCQASQNIYSNLAWYQQKPKGVKLLIYQASTLASGVPSRFSGSGYGTDFLT⁵ITSSLPEDVATYYCQGGYSAALNTFGGGGKVEIK

[0094] 서열번호 03: CT4 카파 경쇄 nt

[0095] GAAATGTGTGTGACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTA
GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTAGCAGGGCCACTGGCATCCCAGACAGGTTAGTGGCAGTGGGTCT
GGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTACCGTGGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAA

[0096] CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTGTGTGCGCTGCTGAATAACTTCTATCCC
AGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
AACAGGGGAGAGTGT

[0097] 서열번호 04: CT4 카파 경쇄 aa

[0098] EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGA⁶FSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWF⁷FGQG
TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSS
PVTKSFNRGEC

[0099] 서열번호 05: CT4 x PL230C6 nt

[0100] CAGGTGCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACCGCTGTATCTGCAATGAACAGCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGACC
TCTGGGGGCACAGCGCCTGGGTGCTGGTCAAGGACTACTTCCCGAACCAGGTGACGGTGTCTGTGAACTCAGGCGCCTGACCAGCGGCTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTC
GAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTC
CTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACCTCTCCAAAGCC
AAAGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCATCCCGGATGAGGTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAAGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCCGAGAACAACTACAAGACCACGCTCCCGTGTGAGTCCGACGGCTCCTTCTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCCAGTCCGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTC
TCCTGTACCGCTCTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGAATCATTACTTATAGT
GGTAGTAGATACTACGGAATGGGCGAAAGCCGATTACCATCTCCAAAGACAATAACGAACACCGTGTATCTGCAATGAACAGCTGAGAGCTGAG
GACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTCCCCTTGTGGGGCCAGGGAACCTGGTCACCGTCTCTCCCGTGGAGGCGGTTCAGGC
GGAGGTGAAGTGGTGGTGGCGCTCTGGAGGCGGCGATCTGCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAAC
ATCAAGTGTGAGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGATCCATTCTGCATCTCTCTG
GCATCTGGGGTCCCATCAAGGTTACGCGGAGTGGATCTGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGT
CAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0101] 서열번호 06: CT4 x PL230C6 aa

[0102] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGN⁸NKY⁹ADSVKGRFTISRDN¹⁰SKNTLYLQMN¹¹SLRAEDTAIYYCARTGWL¹²
GPF¹³DYWGQGT¹⁴LVTVSSASTKGPSVFPLAPSSKSTSGGTAA¹⁵LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV¹⁶TPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPPKPDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLY
SKLTVDKSRWQQGNVSCFSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVESGGGLVQPGGSLRLSCTASGID¹⁷LN¹⁸TYD¹⁹MI²⁰WVRQAPGKGLEWVGII²¹ITYS
GSRY²²YANWAKGRFTISKDNTKNTVYLQMN²³SLRAEDTAVYYCARDYMSG²⁴SHLWQGT²⁵LVTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGRVIT

IKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYGKNNVDNAFGGGTKVEIK

[0103] 서열번호 07: CT4 x PL221G5 널2 Fc nt

[0104] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCT
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCAGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGGCTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGGCCAGCACCTGAAGCCGCGGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACCTCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCTCCCGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGTGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGA
CTCTCTGTGCAGCCTCTGGATTCTCTTCAGTAGCGGTACGACATGTGCTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCT
GCTGGTAGTGTGGTATCACTTACGACGCGAACTGGGCGAAAGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
CTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGCGTTTTCTGTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCTGGTACCGTCTCG
AGCGGTGGAGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCA
TCTGTAGGAGACAGAGTACCATCACTTGCAGGCCAGTCAGAGCATTAGTTCCTAACTAACTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTG
ATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCTGCAGCCTGAT
GATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0105] 서열번호 08: CT4 x PL221G5 널 Fc aa

[0106] QVQLVESGGGVVQPRSLRLSCAASGFTFSYTMHWVRQAPGKLEWVTFISYDGNKKYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLLQVPGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIACTIA
AGSAGITYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSAFSFDYAMDWLGQGLTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSTLSA
SVGDRVTITCQASQSISSHLNWIYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDDEFATYYCQQGYSGWNVNDFGGGKVEIK

[0107] 서열번호 09: CT4 x PL231H2 nt

[0108] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCT
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCAGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGGCTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGGCCAGCACCTGAAGCCGCGGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACCTCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCTCCCGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGTGCAGTGGTGGAGTCTGGGGGAGGCTGGTCCAGCCTGGGGGCTCCCTGAGA
CTCTCTGTACAACCTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTAT
GTTGGTAACATACTACGCGAGCTGGGCGAAAGCCGATTACCCCTCTCCAAAGACAATACCTCGACCAGGTGGATCTGCAATGAACAGCCTGAGAGCT

GAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGTTCCCACTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCT
GGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTCGCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTC
ACCATCAATTGTGACGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGATCTTTCTGCATCCACT
CTGGCATCTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTAT
TGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0109] 서열번호 10: CT4 x PL231H2 aa

[0110] QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLY
SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLPGGGGSGGGGSGVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIISY
VGNTYYASWAKGRFTLSKNDTSTTVDLQMNSLRAEDTAVYYCARDIFISGSHLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGD
RTINQASESISFLSWYQQKPKGAPKLLIFSASTLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQOQYSKSNVDNAFGGGTKVEIK

[0111] 서열번호 11: CT4 x PL004B5 nt

[0112] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACC
TCTGGGGGCACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCT
GAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAGGTGCAATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACGCTC
CTACCGTCTGCAACAGGACTGGTGAATGGCAAGGAGTACAAGTGCAGGCTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGCGAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCTTCTTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGTCCGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCTGTGACGCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTGATACT
AATGTTTATATACTACGGAAGTGGGCAAAAGGAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGTAATAATGATGATTATATTAAGTGTGGGGCCAGGGAACCTGGTACCGTCTCGAGCGGTGGA
GGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGA
GACAGAGTCAACATCACTTGCCAGTCCAGTCAAGTGTATATAATGGTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATC
TATGGTGCATCCACTCTGGCATCTGGGTCCCATCAAGGTTACGCGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGAT
TTTGAACCTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAATCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0113] 서열번호 12: CT4 x PL004B5 aa

[0114] QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLY
SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWIGVIDT
NVYIYYANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARYVGNNDYINLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVG
DRVITTCQSSQSVYNGYWLSWYQQKPKGAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISLQPDFATYYCLGSYTSSTENSFGGGTKVEIK

[0115] 서열번호 13: CT4 x PL004B9 nt

[0116] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTG

GGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGGTGCACACC
TTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGCA
CCGTCACTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTACCGTCTGCACCAGGACTGGTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCTTCTTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCTGTACAGTGTCTGGAATCGACCTCAGTGTATCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTAATCTAT
GTTGTAACACATATTACGCGAGCTGGGCGAAAGGAGATTACCATCTCCAAAACCTCGACCAGGTGGATCTTAAATCACCAGTCCGACAACCGAGGAC
ACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCAAGGGACCCCTGGTCACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCATTGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
AGAGTCAACATCAAGTGCAGGCCAGTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAGGTTCTTAAGCTCCTGATCTATTATGCA
TCCAATCTGGCATCTGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACT
TATTACTGTCAAAGCTATTATGTTGGTGGTAGTGCCTATACTTTCCGCGGAGGGACCAAGGTGGAGATCAAA

[0117] 서열번호 14: CT4 x PL004B9 aa

[0118] QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQYICNVN
HKPSNTKVKDRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKLSLSPGGGGSGGGSEVQLVESGGGLVQPGSLRLSCTVSGIDL~~SVINMG~~WVRQAPGKLEWIGTITY
VGNTYYASWAKGRFTISKSTSTVDLKITSPPTTEDAVYYCARESGTIYYSYFNLWGQGLTVTVSSGGGGSGGGSGGGSGGGSAFELTQSPSSLASVGD
RVTIKCQASESISNLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQSYGGGSAYTFGGGTKEIK

[0119] 서열번호 15: CT4 x PD206F12 nt

[0120] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATT
ACCATCTCCAGAGACAATTCCAAGAACCGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGCGCGGTGCACACC
TTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGCA
CCGTCACTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTACCGTCTGCACCAGGACTGGTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCTTCTTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCTGTGCAGCCTCTGGATTGCACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGTATGCATGCATTTAT
GCTGGTACTAGTGGTAGTACTTCTACGCGAGCTGGGCGAGAGGAGATTACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTG
AGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCCTGGTACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCGTGTCTGCATCTGTAGGAGAC
AGAGTCAACATCACTTGCAGTCCAGTCAGAGTGTATTATGATAACAACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTAT
ACAGTATCCACTCTGGCATCTGGGTCCCATCAAGGTTACGCGGAGTGGATCTGGGACAGAATTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTT
GCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACCTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0121] 서열번호 16: CT4 x PD206F12 aa

[0122] QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY
SKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFDSSGYWICWVRQAPGKLEL IACIY
AGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCARNLYTYNSLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGSDIQMTQSPSTLSASVGD
RVTITCQSSQSVYDNNWLAWYQKPGKAPKLLIYTVSTLASGVP SRFSGSGSGTEFTLTITSSLPQPDFATYYCQGTYYSSGWNAFAGGGTKVEIK

[0123] 서열번호 17: CT4 x PD215A1 nt

[0124] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCTGTGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTAGGCGCCCTGACCAGCGCGTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCA
CCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGC CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCTCTCCAAAGCC
AAAGGGCAGCCCGAGAACACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCGGAGAACAACTACAAGACCAGCCTCCCGTGCTGGACTCCGACGGCTCTTCTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCACAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGA
CTCTCTGTACAGCCTCTGGATTCTCTTTAGCAGTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACT
GGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCGGTTACCATCTCCAAGACAAATTCCAAGAACACGGTGACTCTGCAATGAACAGCCTGAGA
GCCGAGGACACGGCGTATATTACTGTACGAGAGCATTTGACTTGTGGGGCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCGGCGGTGGCGGCTCCGGTGGAGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACT
TGCCAGGCCAGTCAGAGCATTTACAGTACTTAACTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCT
GGGTCCCATCAAGTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGC
AGTTGGTTGAGTGGTGTGTTGGTAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0125] 서열번호 18: CT4 x PD215A1 aa

[0126] QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY
SKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSGEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKLEWIGCIT
GSGSTYYASWAKRRFTISKDN SKNTVTLQMNSLRAEDTAVYYCTRAFDLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGSDIQMTQSPSSLASVGD
RVTITCQASQSIYSYLNWYQKPGKAPKLLIYGASNLASGVP SRFSGSGSGTDFTLTITSSLPQPDFATYYCQSSWLSGAVGNFAFGGGTKVEIK

[0127] 서열번호 19: CT4 x PD220F6 nt

[0128] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCTGTGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTAGGCGCCCTGACCAGCGCGTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCA
CCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC

CTCACGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGAGCAGGTGAAGGAGACCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTACCATCAGCAGCTATGGAGTGGAGTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGTGCATTGATTTTTCCC
GGGATTGGTTTCAAAGACTACGCAGCTGGGTGAATGGCCGTTACCCCTCTCCAGCGACAACGCCCAGAACACTGTGGAAGTCAAATGAACAGCCTGAGA
GCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGAACCCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACT
TGCCAGTCCAGTCCGAGTGTATTATAGTAACCTATTATCCTGGTATCAGCAGAAACCAGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCACTCTGGCA
TCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTGCAACTATTACTGTGCA
GGCGGTATAGTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0129] 서열번호 20: CT4 x PD220F6 aa

[0130] QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKDRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEQVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKLEWVALIFP
GIGFKDYASVWNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDL DLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGSDIQMTQSPSSLASVGDRTIT
CQSSPSVYSNYLSWYQKPGKVPKLLIYYASTLASGVPSRFSGSGSGDTFTLTISSLQPEDVATYYCAGGYSSSTRAFGGGTKVEIK

[0131] 서열번호 21: CT4 x PD225G11 nt

[0132] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACCGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAACCCAAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGCATGCATTAT
ACTGGTAGTATTGATGTCTTTACTACGCGAGCTGGGCGAAAGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGC
CTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGTAATACTGATACTACCTACTTAACTTGTGGGGCCAGGAACCCCTGGTCACCGTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCTATGATATGACCAGTCTCCATCCTCCCTGTCTGCA
TCTGTAGGAGACAGAGTCAACATCAATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGAAAGTTCCTAAGCTCCTG
ATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCCGCACTGGATCTGGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAA
GATGTTGCAACTATTACTGTATGTTCAATTATTGAGTGGTGGTAGTTGTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0133] 서열번호 22: CT4 x PD225G11 aa

[0134] QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKDRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKLEWIACTIY

TGSIDVFYYASWAKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARAANTDTTYFNLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSLSA
SVGDRVTINCQASQSINNQLSWYQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISLQPEDVATYYCHVHYCSGGSCFWAFGGGTKVEIK

[0135] 서열번호 23: G4S x 4 nt

[0136] GGTGGAGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGCGGCTCT

[0137] 서열번호 24: G4S x 4 aa

[0138] GGGGSGGGGSGGGGSGGGGS

[0139] 서열번호 25: PL230C6 x CT4 nt

[0140] CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATC
TCCAAAGACAATACCAAGAACACGGTGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCC
CACTTGTGGGGCCAGGGAACCCCTGGTACCGTCTCGAGCGCTAGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC
ACAGCGGCCCTGGGTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGT
GTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCCGAGCACCTGAAGCCGCGGGGACCGTCAGTC
TTCCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTACCGTC
CTGCACCGAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCTGCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGAC
ATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCT
CCGGGTGGCGGTGGAGGGTCCGCGGTGGTGGATCCAGGTGAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGAAAA
AATAAATACTACGACAGCTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGAC
ACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGGGGCAGGGAACCCCTGGTCAACGTCTCGAGCGGTGGAGGCGGTTCAGGC
GGAGGTGGAAGTGGTGGTGGCGCTCTGGAGGCGCGGATCTGAAAATTGTGTGACGAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGGCCACC
CTCTCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAACTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTACGC
AGGGCCACTGGCATCCAGACAGGTTAGTGGCAGTGGGTCTGGGACAGACTTACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTCAGTGTATTAC
TGTCAGCAGTATGTTAGCTACCGTGGACGTTCCGGCCAAGGGACCAAGGTGGAATCAAA

[0141] 서열번호 26: PL230C6 x CT4 aa

[0142] QSVESGGGLVQPGSLRLSCTASGIDLNTYDMIWVRQAPGKLEWVGIIITYSGSRYYANWAKGRFTISKDNTKNTVYLQMN SLRAEDTAVYYCARDYMSG
HLWGQGLVTVSSASTKGPSVFLAPSSKSTSGGTAAALGLVKDYFPEPVTVSWNSGALTSVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP
SNTKVDKRVEPKSCDKTHTPCPAPEAAGAPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSGVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGN
NKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPGERAT
LSCRASQSVGSSYLAWYQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSSPWTFGQGTKEIK

[0143] 서열번호 27: PL230C6 카파 경쇄 nt

[0144] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTGAGGCCAGTGAGGACATTTATAGCTTCTTGCC
TGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0145] CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGTGTAATAACTTCTATCCC
AGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGCGCTGAGCTCGCCGCTCACAAAGAGCTTC
AACAGGGGAGAGTGT

[0146] 서열번호 28: PL230C6 카파 경쇄 aa

[0147] AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYGKNNVDNAFG
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0148] 서열번호 29: PD224D1 x CT4 nt

[0149] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCCTCAGTAGCTATGCAATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCC
ATCTCCAAGACAATACCAAGAACACGGTGGATCTTCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCTACTTA
GACATCTGGGGCCAAGGGACCCTGGTACCGCTCTCGAGCGCTAGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGG
ACAGCGGCCCTGGGTGCTGGTCAAGGACTACTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCCCGGT
GTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTC
TTCCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAG
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCCTC
CTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGGCAAGGGGAG
CCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTCTCTATAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACGAGAAGAGCTCTCCCTGTCT
CCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCAGTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGAAAC
AATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGAC
ACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGGGATCTGGC
GGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCGTGCTTTGTCTCCAGGGGAAAGAGCCACC
CTCTCTGCAGGGCCAGTCAGAGTGTGGCAGCAGTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTACAGC
AGGGCCACTGGCATCCAGACAGGTTAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAGCTACCGTGGACGTTCCGGCAAGGGACCAAGGTGGAATCAAA

[0150] 서열번호 30: PD224D1 x CT4 aa

[0151] EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKLEYIGYIGDTTGIAIASWANGRFTISKDNTKNTVDLQMSLRAEDTAVYYCARGWSYL
DIWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP
SNTKVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVSCSMHEALHNHYTQKLSLSLPGGGGGSGGGGSQVQLVESGGGVVQPGRSRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGN
NKYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERAT
LSCRASQSVGSSYLAWYQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFTGQGTKEIK

[0152] 서열번호 31: PD224 경쇄 nt

[0153] GCCCTTGTGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCC
TGGTATCAGCAGAAACCAGGAAAGTTCTAAGCTCCTGATCTATCAGGCTCCACTCTGGCATCTGGGTCCCATCTCGGTTTCAGTGGCAGTGGATATGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTATTACTGTCAAGCGGTTATTATAGTGCTGCCCTTAATACTTTCCGGCGGA
GGGACCAAGGTGGAGATCAAA
CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCC
AGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGCGCTGAGCTCGCCGTCACAAAGAGCTTC
AACAGGGGAGAGTGT

[0154] 서열번호 32: PD224 경쇄 aa

[0155] ALVMTQSPSSLASVGDRVTITCQASQNIYSNLAWYQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISSLQPEDVATYYCQGGYYSAAALNTFGG
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

[0156] 서열번호 33: PL221G5 x CT4 널 Fc nt

[0157] GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGAC
ATGTGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGTGGTATCACTTACGACGCGAACTGGGCGAAAGGC
CGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCG
TTTTCGTTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCTGGTACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCC
TCCAAGAGACCTCTGGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAAGTCAAGCGCCCTGACCAGC
GGCGTGCACACCTTCCCCGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC
TGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTACACATGCCCACCGTGCCAGCACCTGAA
GCCGCGGGGGCACCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGC
CACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGT
GTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACAGCTGACCTGCCTGGTC
AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCC
TTCTTCTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCTACACG
CAGAAGAGCCTCTCCCTGTCTCCGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG
AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGACA
TTTATATCATATGATGAAAACAATAACTACGCAGACTCCGTGAAGGGCCGATACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATG
AACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTCCGGCGGTGGCGCTCCGGTGGAGGCGGTCTGAAATTTGTGTTGACGCGCTCCAGGCACCTGTCTTTG
TCTCCAGGGGAAAGGCCACCTCTCTGCAGGGCCAGTCAGAGTGTGGCAGCAGTACTTAGCCTGGTACCAGCAGAACTGGCCAGGCTCCAGGCTC
CTCATCTATGGTGCATTACGAGGGCCACTGGCATCCAGACAGGTTAGTGGCAGTGGGTCTGGGACAGACTTCACTCTACCATCAGCAGACTGGAGCCT
GAAGATTTGCAGTGTATTACTGTACGAGTATGGTAGCTACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAATCAAA

[0158] 서열번호 34: PL221G5 x CT4 널 Fc aa

[0159] EVQLLESGGGLVQPGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAICIAAGSAGITYDANWAKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCARSA
FSFDYAMD^LWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSPGGGGSGGGGSGVQVLESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVT
FI SYDGNKYYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSTL
SPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS^{SP}PTWTFGQGTKEIK

[0160] 서열번호 35: PL221G5 경쇄 nt

[0161] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTCCCCTTAAAC
TGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGG
ACAGAATTTACTCTACCATCAGCAGCTGCAGCCTGATGATTTTGCACTTATTACTGCCAACAGGGTTATAGTTGGGGTAAATGTTGATAATGTTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGCTTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCGCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTG
AGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0162] 서열번호 36: PL221G5 경쇄 aa

[0163] DIQMTQSPSTLSASVGRVITTCQASQSISSHLN^{WY}QKPKGAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTITSSLPDDFATYYCQQGYSWGNVDN^{VFG}
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN^{FY}PREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSITLTKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0164] 서열번호 37: PL231H2 x CT4 널 Fc nt

[0165] CAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGGGTCCTGAGACTCTCCTGTACAACCTTCTGGAATCGACCTTAGTACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGCTAGAGTGGGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACC
CTCTCCAAAGACAATACCTCGACCACGGTGGATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGT
TCCCCTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGG

GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACCTAGGCGCCCTGACCAGCGCGTGCACACCTTCCCG
GCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCGTCA
GTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTG
AAGTTCAACTGGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACGCGTCTCACC
GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGG
CAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGC
GACATCGCCGTGGAGTGGAGAGCAATGGGAGCCGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTATAGCAAG
CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
TCTCCGGTGGCGGTGGAGGTCGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTATATCATATGATGGA
AACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGTGTATCTGCAATGAACAGCCTGAGAGCTGAG
GACACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTACCGTCTCGAGCGGTGGAGGCGGATCT
GGCGGAGGTGGTTCGCGGTGGCGGTCCCGTGGAGGCGGTCTGAAATTGTGTTGACGAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCC
ACCTCTCTGCAGGGCCAGTCAAGTGTGGCAGCAGTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTC
AGCAGGGCCACTGGCATCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTGCACTGTAT
TACTGTCAGCAGTATGGTAGCTACCGTGGACGTTCCGCCAAGGACCAAGGTGGAATCAAA

[0166] 서열번호 38: PL231H2 x CT4 념 Fc aa

[0167] QVQLVESGGGLVQPGGSLRLSCTTSIGIDLSYDMLVWRQAPGKGLEWVGIISYVGNYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISG
SHLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK
PSNTKVDKRVKPEKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSLT
VLHQDWLNGKEYKCAVSKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVSCFVSMEALHNHYTQKSLSLPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGL
NNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLSPGERA
TLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWFQGQTKVEIK

[0168] 서열번호 39: PL231H2 경쇄 nt

[0169] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTCAGGCCAGTGAGAGCATTAGTAGCTTCTTATCC
TGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGATCTTTCTGCATCCACTCTGGCATCTGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTACCATCAGCAGCTGCAGCCTGAAGATTTTGCACTTACTATTGTCAACAGGGTTATAGTAAAGTAATGTGGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATCGCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAATCCCAGGAGAGTGTACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGACCCCTGACGTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAAGTACCCATCAGGGCCTG
AGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0170] 서열번호 40: PL231H2 경쇄 aa

[0171] AYDMTQSPSSVSASVGDVITINQASESISFLSWYQQKPGKAPKLLIFASASTLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYYSKSNVDNAFG
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0172] 서열번호 41: PL004B5 x CT4 nt

[0173] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGTGGAGTGGATCGGAGTCAATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTACCC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGTAATAAT
GATGATTATATTAACCTTGTGGGGCCAGGGAACCTGGTCAACGCTCTCGAGCGTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGC
ACCTCTGGGGGCACAGCGGCCCTGGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGTGCAC
ACCTTCCCGGTGTCTACAGTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGG
GCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCACGAAGAC
CCTGAGGTCAAGTTCACTAGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC

GTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACAGCTGCCTGGTCAAAGGCTTC
TATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCCTC
TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGC
CTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTG
AGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTATATCA
TATGATGGAAACAATAAATACTACGCACTCCGTGAAGGGCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTG
AGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTACCGTCTCGAGCGGTGGA
GGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGAGTCTCCAGGCACCTGTCTTGTCTCCAGGG
GAAAGAGCCACCTCTCTGCAAGGGCAGTCAGAGTGTGGCAGCAGTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGTCCAGGCTCCTCATCTAT
GGTGCATTACAGCAGGGCCACTGGCATCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT
GCAGTGATTACTGTCAGCAGTATGGTAGCTACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAATCAAA

[0174] 서열번호 42: PL004B5 x CT4 aa

[0175] EVQLVESGGGLVQPGSLRLSCAASGFSLSYWMSWVRQAPGKLEWIGV IDTNVYIYYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYVGN
DDYINLWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV
NHKPSNTKVDKRVEPKSCKDTHTCPPCPAPEAAGAPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGGSGVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFIS
YDGNKKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLPFDYWGQGLVTVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPG
ERATLSCRASQSVGSYLAWYQQKPGQAPRLIYGAFSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQYGSSPWTFGQGTKEIK

[0176] 서열번호 43: PL004B5 경쇄 nt

[0177] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACTTGCCAGTCCAGTCCAGTGTATTATAATGGCTACTGG
TTATCTCGGTATCAGCAGAAACCAGGGAAGCCCCAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGCAGTGGGA
TCTGGGACAGAATCACTCTCACCATCAGCAGCTGCAGCCTGATGATTTTGAACCTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATCGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAGTCTACGCCTGCGAAGTACCCATCAGGGC
CTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0178] 서열번호 44: PL004B5 경쇄 aa

[0179] DIQMTQSPSTLSASVGDRTVITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISSLQPDFATYYCLGSYTSSTENSF
GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

[0180] 서열번호 45: PL004B9 x CT4 nt

[0181] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCTGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCAATATG
GGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCACTTATGTTGGTAACATATTACGCGAGCTGGGCGAAAGGCAGATTACC
ATCTCCAAAACCTCGACCACGGTGGATCTTAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTATTAC
AGTTACTTTAACTTGTGGGGCAAGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCA
CCGTGAGTCTTCTCTTCCCCCAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTT
GAGGTCAAGTTAACTGTTACGTGGACGGCTGGAGGTGATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCGTGC
CTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCGGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA

CTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATAT
GATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCTGAGGACACGGCTATATATTAAGTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCGTGTCTTTGTCTCCAGGGGAA
AGAGCCACCTCTCTGCAAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT
GCATTACAGAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGA
GTGTATTACTGTACAGTATGGTAGCTACCGTGGACGTTCCGCCAAGGACCAAGGTGGAATCAAA

[0182] 서열번호 46: PL004B9 x CT4 aa

[0183] EVQLVESGGGLVQPGGSLRLSCTVSGIDL~~SVINMGWVRQAPGKGLEWIGTITYVGN~~TYIASWAKGRFTISKSTSTVDLKITSPPTEDTAVVYCARESGTIIY
SYFNLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVN
HKPSNTKVKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTI~~SKAKGQPREPQVYTLPPSRDEL~~TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKLSLSPGGGGSGGGGSGVQLVESGGGVQPGRSLRLSCAASGFTF~~SSYTMH~~WVRQAPGKLEWVTFISY
DGNKYIADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIIYCARTGWLGPFDYWGQGLTVTVSSGGGGSGGGGSGGGGSGGGSEIVLTQSPGTLSPGGE
RATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGA~~FSRATG~~IPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0184] 서열번호 47: PL004B9 경쇄 nt

[0185] GCATTGCAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTACTTATCC
TGGTATCAGCAGATTCCAGGAAAGTTCTTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGTCCCATCTCGGTCAGTGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCCGGCGGA
GGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCACTCTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCCTCTGTTGTGTGC
CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCATCAGGCCTGAGC
TCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT

[0186] 서열번호 48: PL004B9 경쇄 aa

[0187] AFELTQSPSSLSASVGDVRIKQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTIS~~SLQPED~~VATYYCQSYGGGSAYTFGG
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

[0188] 서열번호 49: PD206F12 x CT4 nt

[0189] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTGCACTTCAGTAGCGGCTACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCTACGCGAGCTGGCGGAGAGGC
AGATTACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTAC
ACTTACAATAGCTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCTCTCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACC
TTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCAAATCTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGCA
CCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTACCGTCTGCACAGGACTGGTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACATCTCCAAAGCC
AAAGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGAGCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATAT
GATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCTGAGGACACGGCTATATATTAAGTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCGTGTCTTTGTCTCCAGGGGAA
AGAGCCACCTCTCTGCAAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT

GCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGCTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCA
GTGTATTACTGTACAGCAGTATGGTAGCTACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAATCAAA

[0190] 서열번호 50: PD206F12 x CT4 aa

[0191] EVQLVESGGGLVQPGGSLRLSCAASGFD~~FSSGYW~~ICWVRQAPGKLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLMNSLRAEDSAVYYCARNLY
T~~YN~~SLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN
HKPSNTKVDKRVPEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI~~SRT~~PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTI~~SKAKGQ~~PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFC~~SVM~~HEALHNHYTQKSLSPGGGGSGGGGSQVQLVESGGGVQPG~~RS~~LRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISY
DGNKY~~YADSVKGRFT~~ISRDNSKNTLYLMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTL~~SL~~SPGE
RATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQY~~GSSPWTF~~GQGTKVEIK

[0192] 서열번호 51: PD206F12 경쇄 nt

[0193] GACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTCCAGTCCAGTCAGAGTGTATTATGATAACAACCTGG
TTAGCCTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGCAGTGGA
TCTGGGACAGAATCACTCTCACCATCAGCAGCCTGACGCTGATGATTTTGCAACTTATTACTGCCAAGGCACCTATTATAGTAGTGGTTGGAACCTTGCT
TTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCT
GTTGTGTGCTGTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACACAGAG
CAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTCGCAAGTCACCCATCAG
GGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0194] 서열번호 52: PD206F12 경쇄 aa

[0195] DIQMTQSPSTLSASVGD~~RV~~ITTCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTIS~~SL~~QPDFATYYCQGTYYSSGWNFA
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNFIYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQ
GLSSPVTKSFNRGEC

[0196] 서열번호 53: PD215A1 x CT4 nt

[0197] CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATG
TGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTC
ACCATCTCCAAAGACAATTCCAAGAACACGGTGA~~CT~~CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTGACTTG
TGGGGCCAGGGAACCTGGTCAACGCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCAAGAGCACCTCTGGGGGCACAGCG
GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA~~ACT~~CAGGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGTGTCTTA
CAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
ACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAA~~ACT~~CACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCACCCTGAGTCTTCTCTC
TTCCCCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC
TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACGCGTCTCACCGTCTGCAC
CAGGACTGGCTGAATGGCAAGGAGTACAAGTGC~~CGGT~~TCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGA
GAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTATAGCAAGCTACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
GGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAA
TACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCT
ATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCGGCGCGGTGGCGGTCCGGTGGAGGCGGTCTGAAATTTGTGTGACGAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGGCCACCCCTCTCC
TGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGTTGCATTACAGAGGGCC
ACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTGCACTGTATTACTGTACAG
CAGTATGGTAGCTACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAATCAAA

[0198] 서열번호 54: PD215A1 x CT4 aa

[0199] QEQLLES~~GGGLVQPGGSLRLSCTASGFSSSYW~~MCWVRQAPGKLEWIGCITTGSGSTYYASWAKRRFTISKDN~~SKNTVTLMNSLRAEDT~~AVYYCTRAFDL
WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSN

TKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCAVSNKALPAPI EKT I SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNK
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEI VLTQSPGTLSLSPGERATLS
CRASQSVGSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0200] 서열번호 55: PD215A1 경쇄 nt

[0201] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAAC
TGGTATCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCACTGGCAGTGGATCTGGG
ACAGATTTCACTCTACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGTCTTGGTAATGCTTTCGGC
GGAGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTG
AGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0202] 서열번호 56: PD215A1 경쇄 aa

[0203] DIQMTQSPSSLASVGDRTVITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQSSWLSGAVGNFAG
GGTKVEIKRTVAAPSVFIFPPSPDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0204] 서열번호 57: PD220F6 x CT4 nt

[0205] CAGGAGCAGGTGAAGGAGACCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGCAGCTATGGAGTG
AGCTGGGTCCGCCAGGCTCCAGGAAGGGGTGGAGTGGTGCATTGATTTTCCCGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTC
ACCTCTCCAGCGACAACGCCGAGAACACTGTGAACTGCAATGAACAGCCTGAGAGCCGAGGACACGCCGTATATTACTGTGCGAGAGATTGGACTTG
TGGGGCCAGGAACCTGGTACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCTTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCG
GCCCTGGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGTGTCTTA
CAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAAC
ACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTACACATGCCCACCGTGCCAGCACCTGAAGCCGCGGGGGACCGTCAGTCTTCTCT
TTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC
TGGTACGTGGAGCGGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTACAGCTCCTACCGTCTGCAC
CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCC
GTGGAGTGGGAGACAATGGGCAGCGGAGAACTACAAGACCAGCCTCCCGTGTGGACTCCGACGGCTCTTCTTCTCTATAGCAAGCTACCGGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGT
GGCGGTGGAGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGCGGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCTGTGCAGCC
TCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGTCCAGGCAAGGGGTGGAGTGGGTGACATTTATATCATATGATGAAACAATAAA
TACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCT
ATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGGGGCAGGGAACCTGGTACCGTCTCGAGCGGTGGAGCGGATCTGGCGGAGGT
GGTTCCGGCGGTGGCGGTCCGGTGGAGCGGTCTGAAATTTGTGTTGACGAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTACAGAGGGCC
ACTGGCATCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTACAG
CAGTATGGTAGCTACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAATCAAA

[0206] 서열번호 58: PD220F6 x CT4 aa

[0207] QEQVKETGGGLVQPGGLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDL
WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSN
TKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCAVSNKALPAPI EKT I SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNK
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEI VLTQSPGTLSLSPGERATLS
CRASQSVGSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0208] 서열번호 59: PD220F6 경쇄 nt

[0209] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTATAGTAACTACTTA
TCCTGGTATCAGCAGAAACCAGGAAAGTTCTTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGTCCCATCTCGGTTCACTGGCAGTGATCT
GGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCACTTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTTCGGCGGA
GGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGC
CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAACCATCAGGGCCTGAGC
TCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0210] 서열번호 60: PD220F6 경쇄 aa

[0211] DIQMTQSPSSLSASVGDRTITCQSSPVSYNYLSWYQKPKVPKLLIYYASTLASGVPSRFSGSGSGTDFLTITISLQPEDVATYYCAGGYSSSTRAFGG
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

[0212] 서열번호 61: PD225G11 x CT4 nt

[0213] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCAGCCACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCACTTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGC
CGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCT
AATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCTTGGTACCGCTCTCGAGCGCTAGCACAAGGGCCCATCGGCTTCCCCCTGGCACCTCC
TCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAGC
GGCGTGCACACCTTCCCGGTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACATC
TGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAA
GCCGCGGGGGACCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGC
CACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
GTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAAACC
ATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTGC
AAAGGCTTCTATCCAGCGACATCGCGGTGGAGTGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCC
TTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
CAGAAGACCTCTCCCTGTCTCCGGTGGCGGTGGAGGTCCGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG
AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACA
TTTATATCATATGATGGAACAATAAATACTACGACAGCTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATG
AACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCAACGCTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTCCGGCGGTGGCGCTCCGGTGGAGGCGGTCTGAAATTTGTTGACGCAGTCTCCAGGCACCTGTCTTTG
TCTCCAGGGGAAAGGCCACCTCTCTGCAGGGCCAGTCAGAGTGTGGCAGCAGTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTC
CTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCAGACAGGTTAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCT
GAAGATTTTCAGTGTATTACTGTGACAGTATGGTAGCTCACCCTGGACGTTCCGCCAAGGGACCAAGGTGGAATCAAA

[0214] 서열번호 62: PD225G11 x CT4 aa

[0215] EVQLLESQGLVQPGSLRLSCAASGFTFSSSHWICWVRQAPGKLEWIACIYTGSDIVFYASWAKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCARAA
NTDITYFNLWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVPEPKCDKHTHTPPCPAPEAAGAPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGS
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSPGGGGGSGGGGSGVQVLESQGLVQPGSLRLSCAASGFTFSSSYTMHWVRQAPGKLEWVT
FISYDGNKYYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSL
SPGERATLSCRASQSVGSSYLAWYQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFLTISRLEPEDFAVYYCQQYGSPPWTFGQGTKEIK

[0216] 서열번호 63: PD225G11 경쇄 nt

[0217] GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCC
TGGTATCAGCAGAAACCAGGAAAGTTCTTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGTCCCATCTCGGTTACCGGCAGTGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCACTTATTACTGTATGTTTATTGAGTGGTGGTAGTTGTTTTGGGCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTT

GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0218] 서열번호 64: PD225G11 경쇄 aa

[0219] AYDMTQSPSSLASVGDVRTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWAF
GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

[0220] 서열번호 65: CT4 중쇄 신호 펩타이드 뉴클레오타이드 서열 nt

[0221] ATGAAACACCTGTGGTTCTTCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCC

[0222] 서열번호 66: CT4 중쇄 신호 펩타이드 뉴클레오타이드 서열 aa

[0223] MKHLWFFLLLVAAAPRWLS

[0224] 서열번호 67: PL230/PD224 중쇄 신호 펩타이드 nt

[0225] ATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCC

[0226] 서열번호 68: PL230/PD224 중쇄 신호 펩타이드 aa

[0227] MAVLGLLFCLVTFPSCVLS

[0228] 서열번호 69: PL230/PD224 경쇄 신호 펩타이드 nt

[0229] ATGAGGGCCCTGCTCAGTTTCTTGGCTTCTTGCTTTTCTGGATTCCAGCCTCCAGAAGT

[0230] 서열번호 70: PL230/PD224 경쇄 신호 펩타이드 aa

[0231] MRAPAQFLGFLFWIPASRS

[0232] 서열번호 71: CT4 scFv nt

[0233] CAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGC
GGTTCTGAAATTGTGTGACGAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGC
TACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGAGGGCCACTGGCATCCAGACAGGTTCACTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTGTCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCCGGC
CAAGGGACCAAGGTGGAATCAAA

[0234] 서열번호 72: CT4 scFv aa

[0235] QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGS
GSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0236] 서열번호 73: PD224D1 scFv nt

[0237] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACAGC

[0238] CTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACATTGGTGATACTACTGGCATAGC
CTACGCGAGCTGGGCGAATGGCAGATTACCATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGT
GTATTACTGTGCGAGAGGCTGGTCTACTTAGACATCTGGGGCAAGGGACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGG
CGGTGGCGGTCCGGTGGAGGCGGCTCTGCCCTTGTGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGC
CAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACAGGGAAGTTTCTAAGCTCCTGATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCC
ATCTCGGTTCACTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTA
TAGTGCTGCCCTTAATACTTTCCGGCGGAGGGACCAAGGTGGAGATCAAA

- [0239] 서열번호 74: PD224D1 scFv aa
- [0240] EVQLVESGGGLVQPGGSLRLSCTASGFSLSYAMS~~W~~VRQAPGKGL~~E~~YIGYIGD~~T~~TG~~I~~AYASWANG~~R~~FTISKDNTKNTVDLQMNSLRAEDTAVYYCARGW~~S~~YLDI~~W~~GQGT~~L~~VTVSSGGGSGGGGSGGGGSGGGGSALVMTQSPSSLSASVGD~~R~~VTITCQASQNIYSNLAWYQKPKGKVPKLLIYQASTLASGVPSRFSGSGYGTDFLT~~I~~SSLPEDVATYYCQGGYSAALNTFGGGTKVEIK
- [0241] 서열번호 75: PD206F12 scFv nt
- [0242] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGCAGATTACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTATTGATAAACAACTGGTTAGCCTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGCAGTGGATCTGGGACAGAATTCATCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACTTTGCTTTCGGCGGAGGACCAAGGTGGAGATCAAA
- [0243] 서열번호 76: PD206F12 scFv aa
- [0244] EVQLVESGGGLVQPGGSLRLSCAASGDFSSGYWIC~~W~~VRQAPGKGL~~E~~L~~I~~ACIYAGTSGSTSYASWARG~~R~~FTISETSKNTVTLQMNSLRAEDSAVYYCARNLYTYNSLWGQGT~~L~~VTVSSGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGD~~R~~VTITCQSSQSVYDNNWLAWYQKPKGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLT~~I~~SSLPDDFATYYCQGTYYSSGWNFAFGGGTKVEIK
- [0245] 서열번호 77: PD215A1 scFv nt
- [0246] CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATCTCCAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGCGGTATATTACTGTACAGAGCATTTGACTTGTGGGGCCAGGAACCTGGTACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAACTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAAGTGGCAGTGGATCTGGGACAGATTCCTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGTGTTGGTAATGCTTTCGGCGGAGGGACC AAGGTGGAGATCAAA
- [0247] 서열번호 78: PD215A1 scFv aa
- [0248] QEQLLES~~G~~GGGLVQPGGSLRLSCTASGFSFSSY~~W~~MC~~W~~VRQAPGKGL~~E~~WIGCIT~~T~~SGSGSTYYASWAK~~R~~RFTISKD~~N~~SKNTVTLQMNSLRAEDTAVYYCTR~~A~~FDLWGQGT~~L~~VTVSSGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGD~~R~~VTITCQASQS~~I~~YSYLNWYQKPKGKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLT~~I~~SSLPEDFATYYCQSSWL~~S~~GAVGNAFAGGGTKVEIK
- [0249] 서열번호 79: PD225G11 scFv nt
- [0250] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTACTACGCGAGCTGGGCGAAAGGC CGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGCGGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGAACCTGGTACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGC TCCGGTGGAGGCGGCTCTGCCTATGATATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGC ATTAACAACCAACTATCTGGTATCAGCAGAAACAGGGAAGTTCTAAGCTCCTGATCTATGGTGCATCCACTTGGCATCTGGGGTCCCATCTCGGTTCCGGTCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTATTACTGTGATGTTTATTATGTCAGTGGTGGT AGTTGTTTTTGGGCTTTCGGCGGAGGACCAAGGTGGAGATCAAA
- [0251] 서열번호 80: PD225G11 scFv aa
- [0252] EVQLLES~~G~~GGGLVQPGGSLRLSCAASGFTFSSSH~~W~~IC~~W~~VRQAPGKGL~~E~~W~~I~~ACIYTGSDIVFY~~Y~~ASWAK~~G~~RFTISRDN~~S~~KNTLYLQMNSLRAEDTAVYYCARAA~~N~~TD~~T~~TYFNLWGQGT~~L~~VTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSLSASVGD~~R~~VTINCQASQS~~I~~NNQLSWYQKPKGKVPKLLIYGASTLASGVPSRFTGSGSGTDFLT~~I~~SSLPEDVATYYCHVHYCSGGSCFWAFGGGTKEIK
- [0253] 서열번호 81: PL230C6 scFv nt

- [0254] CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATC
TCCAAAGACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTATTACTGTGCGAGAGATTATATGAGTGGTTCC
CACTTGTGGGGCCAGGGAACCTTGGTACCCTCTCTCCGGTGGAGGCGGTTACAGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGCC
TATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAACATCAAGTGTCAAGCCAGTGGAGACATTTATAGTCTCTTGGCCTGG
TATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGTCCCATCAAGGTTACAGCGGAGTGGATCTGGGACA
GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA
- [0255] 서열번호 82: PL230C6 scFv aa
- [0256] QSVESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIIITYSGSRYANWAKGRFTISKDNTKNTVYLQMNSLRAEDTAVYYCARDYMSG
HLWGQTLVTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGDRTIKCQASEDIYSFLAWYQKPKGKAPKLLIHSASSLASGVPSRFSGSGSGT
DFTLTISLQPEDFATYYCQQGYGKNNVDNAFGGGTKVEIK
- [0257] 서열번호 83: PL231H2 scFv nt
- [0258] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACAACCTTCTGGAATCGACCTTAGTACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACCC
CTCTCCAAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTATAGTGGT
TCCCATTGTGGGGCCAGGGAACCTTGGTACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCT
GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAACATCAATGTCAAGCCAGTGGAGCATTAGTAGCTTCTTATCC
TGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTTTTCTGCATCCACTCTGGCATCTGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAAATGTGGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA
- [0259] 서열번호 84: PL231H2 scFv aa
- [0260] QVQLVESGGGLVQPGGSLRLSCTTSIDLSTYDMIWVRQAPGKGLEWVGIIISYVGNYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISG
SHLWGQTLVTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGDRTINCQASESISSEFLSWYQKPKGKAPKLLIFSASTLASGVPSRFSGSGSG
TDFTLTISLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIK
- [0261] 서열번호 85: PL221G5 scFv nt
- [0262] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGAC
ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGC
CGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCGTATATTACTGTGCGAGATCGGCG
TTTTCTGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCTTGGTACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGC
TCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCAACATCACTTCCAGGCCAGTCAGAGC
ATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGTCCCATCAAGGTTT
AGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAAT
GTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA
- [0263] 서열번호 86: PL221G5 scFv aa
- [0264] EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIIACIAAGSAGITYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSA
FSFDYAMDHLWGQTLVTVSSGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRTITCQASQSISSHLNWWYQKPKGKAPKLLIYKASTLASGVPSR
SGSGSGTEFTLTISLQPDFFATYYCQQGYSWGNVDNVFGGGTKVEIK
- [0265] 서열번호 87: PL004B5 scFv nt
- [0266] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCAATGATACTAATGTTTATATACTACGCGAACTGGGCGAAAGGCAGATTACCC
ATCTCCAGAGACAATCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTTGGTAATAAT
GATGATTATATTAAGTTGTGGGGCCAGGGAACCTTGGTACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGG
GGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCAACATCACTTCCAGTCCAGTCAGAGTGTTTATAAT
GGCTACTGGTTATCTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTATGTTGCATCCACTCTGGCATCTGGGTCCCATCAAGGTTTACG
GGCAGTGGATCTGGGACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAG

AACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0267] 서열번호 88: PL004B5 scFv aa

[0268] EVQLVESGGGLVQPGGSLRLSCAASGFSLSYWMSSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARYVGNNDYINLWGQGLTVTVSSGGGSGGGSGGGSGGGSDIQMTQSPSTLSASVGDRTITCQSSQSVYNGYWL SWYQKPGKAPKLLIYGASTLASGVP SRFS GSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSFSGG TKVEIK

[0269] 서열번호 89: PL004B9 scFv nt

[0270] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGCATCAATATG GGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGGAACCATTA CTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTCACC ATCTCCAAAACCTCGACCACGGTGGATCTTAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTATTAC AGTTACTTTAACTTGTGGGGCCAAGGACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGGCGGTGGCGGCTCCGGTGGAGGC GGCTCTGCATTGCAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCCACATCAAGTCCAGGCCAGTGAAGCATTAGCAACTAC TTATCTGGTATCAGCAGATTCCAGGAAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGGA TCTGGGACAGATTTCACTCTACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTC GCGGAGGGACCAAGGTGGAGATCAAA

[0271] 서열번호 90: PL004B9 scFv aa

[0272] EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNYYASWAKGRFTISKSTSTVDLKITSPPTEDTAVYYCARESGTIYY SYFNLWGQGLTVTVSSGGGSGGGSGGGSGGGSAFELTQSPSSLASVGDRTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVP SRFSGSG SGTDFTLTISSLQPEDVATYYCQSYYGGSAYTFGGG TKVEIK

[0273] 서열번호 91: CT4 VH nt

[0274] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATG CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC ACCATCTCCAGAGACAATTCCAAGAACCGCTGTATCTGCAATGAACGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCAGGACCGGCTGGCTG GGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCA

[0275] 서열번호 92: CT4 VH aa

[0276] QVQLVESGGGVVQGRSLRLSCAASGFTFSYTMHWVRQAPGKLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWL GPFDYWGQGLTVTVSS

[0277] 서열번호 93: CT4 VL nt

[0278] GAAATGTGTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCT GGGACAGACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGCAGCAGTATGGTAGCTACCGTGGACGTTCCGCCAAGGG ACCAAGGTGGAAATCAAA

[0279] 서열번호 94: CT4 VL aa

[0280] EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFVAVYYCQQYGS SPWTFGQG TKVEIK

[0281] 서열번호 95: PD224D1 VH nt

[0282] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCCTCAGTAGCTATGCAATG AGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTACATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTCACC ATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCTACTTA GACATCTGGGGCCAAGGGACCTGGTCACCGTCTCGAGC

[0283] 서열번호 96: PD224D1 VH aa

[0284] EVQLVESGGGLVQPGGSLRLSCTASGFSLSYAMS WVRQAPGKGLEWIGYIGDTTGIAVASWANGRFTISKDN TKNTVDL

[0285] QMNSLRAEDTAVYYCARGWSYLDI WGQGLTVTVSS

- [0286] 서열번호 97: PD224D1 VL nt
- [0287] GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCC
TGGTATCAGCAGAAACCAGGGAAGTTCTTAAGCTCCTGATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATATGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA
- [0288] 서열번호 98: PD224D1 VL aa
- [0289] ALVMTQSPSSLSASVGDRTITCQASQNIYSNLAWYQQKPKVPKLLIYQASTLASGVPSRFSGSGYGTDFLTISSLQP
- [0290] EDVATYYCQGGYSAALNTFGGGTKVEIK
- [0291] 서열번호 99: PD206F12 VH nt
- [0292] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTGACTTCAGTAGCGGCTACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCTACGCGAGCTGGGCGAGAGGC
AGATTACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTAC
ACTTACAATAGCTTGTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGC
- [0293] 서열번호 100: PD206F12 VH aa
- [0294] EVQLVESGGGLVQPGGSLRLSCAASGFDSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCARNLY
TYNLSLWGQGLVTVSS
- [0295] 서열번호 101: PD206F12 VL nt
- [0296] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTATGATAACAACCTGG
TTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGGA
TCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACCTTTGCT
TTCGGCGGAGGGACCAAGGTGGAGATCAAA
- [0297] 서열번호 102: PD206F12 VL aa
- [0298] DIQMTQSPSTLSASVGDRTITCQSSQSVYDNNLAWYQQKPKGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTISSLQPDFFATYYCQGTYYSSGWNFA
FGGGTKVEIK
- [0299] 서열번호 103: PD215A1 VH nt
- [0300] CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATG
TGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTC
ACCATCTCCAAGACAATTCCAAGAACACGGTGACTCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTTGACTTG
TGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGC
- [0301] 서열번호 104: PD215A1 VH aa
- [0302] QEQLLESGGGLVQPGGSLRLSCTASGFSFYWMCVVRQAPGKGLEWIGCITGSGSTYYASWAKRRFTISKDN SKNTVTLQMNSLRAEDTAVYYCTR AFDL
WGQGLVTVSS
- [0303] 서열번호 105: PD215A1 VL nt
- [0304] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAAC
TGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGGTGATCCAATCTGGCATCTGGGGTCCCATCAAGGTTTCAGTGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGAACCTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGCTGTTGGTAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA
- [0305] 서열번호 106: PD215A1 VL aa
- [0306] DIQMTQSPSSLSASVGDRTITCQASQSIYSYLNWYQQKPKGKAPKLLIYGASNLASGVPSRFSGSGSGTDFLTISSLQPEDFATYYCQSSWLSGAVGN AFG
GGTKVEIK
- [0307] 서열번호 107: PD225G11 VH nt

- [0308] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCAGCCACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTACTACGCGAGCTGGGCGAAAGGC
CGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCT
AATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC
- [0309] 서열번호 108: PD225G11 VH aa
- [0310] EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACIYTGSDIVFYASWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARAA
NTDITYFNLWGQGLVTVSS
- [0311] 서열번호 109: PD225G11 VL nt
- [0312] GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCC
TGGTATCAGCAGAAACCAGGGAAGTTCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCGGCAGTGGATCTGGG
ACAGATTCTACTCTACCATCAGCAGCCTGCAGCCTGAAGATGTGCAACTTATTACTGTATGTCATTATTGCAGTGGTGGTAGTGTGTTTTGGGCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA
- [0313] 서열번호 110: PD225G11 VL aa
- [0314] AYDMTQSPSSLASVGDRTINCAQSQINNQLSWYQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWAF
GGGKVEIK
- [0315] 서열번호 111: PL230C6 VH nt
- [0316] CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATC
TGGGTCCGCCAGGCTCCAGGCAAGGGCTAGAGTGGGTTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATC
TCCAAAGACAATAACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCC
CACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTTCC
- [0317] 서열번호 112: PL230C6 VH aa
- [0318] QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIIITYSGSRYYANWAKGRFTISKDN TKNTVYLQMNSLRAEDTAVYYCARDYMSG
SHLWGQGLVTVSS
- [0319] 서열번호 113: PL230C6 VL nt
- [0320] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTGAGGCCAGTGAGGACATTTATAGCTTCTTGCC
TGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGCAGTGGATCTGGG
ACAGATTCTACTCTACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA
- [0321] 서열번호 114: PL230C6 VL aa
- [0322] AYDMTQSPSSVSASVGDRTIKCAQASEDIYSFLAWYQKPGKAPKLLIHSASSLASGVPSRFTGSGSGTDFTLTISSLQP
- [0323] EDFATYYCQQGYGKNNVDNAFGGKVEIK
- [0324] 서열번호 115: PL231H2 VH nt
- [0325] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAACCTCTGGAATCGACCTTAGTACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTATGTTGGTAACATACTACGCGAGCTGGGCGAAAGGCCGATTACCC
CTCTCAAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGT
TCCCCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC
- [0326] 서열번호 116: PL231H2 VH aa
- [0327] QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIIISYVGNITYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFI
SHLWGQGLVTVSS
- [0328] 서열번호 117: PL231H2 VL nt
- [0329] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTGAGGCCAGTGAGAGCATTAGTAGCTTCTTATCC
TGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGGCAGTGGATCTGGG

ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0330] 서열번호 118: PL231H2 VL aa

[0331] AYDMTQSPSSVSASVGDVRTINCQASESISSFLSWYQKPGKAPKLLIFSASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQOQYKSNVDNAFG
GGTKVEIK

[0332] 서열번호 119: PL221G5 VH nt

[0333] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGAC
ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGC
CGGTTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCG
TTTTCGTTTCCACTACGCCATGGACCTCTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGC

[0334] 서열번호 120: PL221G5 VH aa

[0335] EVQLLESGLLVQPGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAICIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMSLRAEDTAVYYCARSA
FSFDYAMDLYWGQGLTVTVSS

[0336] 서열번호 121: PL221G5 VL nt

[0337] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAAAC
TGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGG
ACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0338] 서열번호 122: PL221G5 VL aa

[0339] DIQMTQSPSTLSASVGDVRTITCQASQSISSHLNWIYQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQOQYKSNVDNVFG
GGTKVEIK

[0340] 서열번호 123: PL004B5 VH nt

[0341] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTGATACTAATGTTTATATACTACGCGAACTGGGCAAAAGGCAGATTACCC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAAT
GATGATTATATTAACCTGTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGC

[0342]

[0343] 서열번호 124: PL004B5 VH aa

[0344] EVQLVESGGLVQPGSLRLSCAASGFSLSYWMWSVVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTISRDN SKNTLYLQMSLRAEDTAVYYCARYVGN
DDYINLWGQGLTVTVSS

[0345] 서열번호 125: PL004B5 VL nt

[0346] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTATAATGGCTACTGG
TTATCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACGCGGCAGTGGA
TCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA

[0347] 서열번호 126: PL004B5 VL aa

[0348] DIQMTQSPSTLSASVGDVRTITCQSSQSVYNGYWLSWYQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCLGSYTSSTENSF
GGGTKVEIK

[0349] 서열번호 127: PL004B9 VH nt

[0350] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCAATATG
GGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTACTTATGTTGGTAACATATTACGCGAGCTGGGCGAAAGGCAGATTACCC
ATCTCCAAAACCTCGACCACGGTGGATCTTAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTAC

AGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

[0351] 서열번호 128: PL004B9 VH aa

[0352] EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYIASWAKGRFTISKSTSTVDLKITSPTTEDTAVYYCARESGTIYY
SYFNLWGQGLTVTVSS

[0353] 서열번호 129: PL004B9 VL nt

[0354] GCATTGGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTCCAGGCCAGTGAAAGCATTAGCAACTACTTATCC
TGGTATCAGCAGATTCCAGGGAAGTTCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGG
ACAGATTTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

[0355] 서열번호 130: PL004B9 VL aa

[0356] AFELTQSPSSLSASVGDRTIKQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQSYGGGSAYTFGG
GTKVEIK

[0357] 서열번호 131: PD220F6 VH nt

[0358] CAGGAGCAGGTGAAGGAGACCGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCAACATCAGCAGCTATGGAGTG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTGCGATTGATTTTCCCGGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTC
ACCTCTCCAGCGACAACGCCGAGAACACTGTGGAAGTGAACAGCCTGAGAGCCGAGGACACGCCGTATATTACTGTGCGAGAGATTGGACTTG
TGGGGCCAGGGAACCTGGTCACCGTCTCGAGC

[0359] 서열번호 132: PD220F6 VH aa

[0360] QEQVKETGGGLVQPGGSLRLSCAASGFTISYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDL
WGQGLTVTVSS

[0361] 서열번호 133: PD220F6 VL nt

[0362] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCAGTGTATTATAGTAACTACTTA
TCCTGGTATCAGCAGAAACCAGGGAAGTTCTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCT
GGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

[0363] 서열번호 134: PD220F6 VL aa

[0364] DIQMTQSPSSLSASVGDRTITCQSSPSVSYNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISLQPEDVATYYCAGGYSSSTRAFGG
GTKVEIK

[0365] 서열번호 135: 인간 IgG1 불변 영역 nt

[0366] GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTGCTGGAAGTCAAGCGCCCTGACCAGCGCGTGACACCTTCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGTTAGCCCCAAATCT
TGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATC
TCCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTCAACTGGTACGTGACGCGGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGACGCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGG
GATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGACCCGGAGAAC
AACTACAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCTTCTTCTCTATAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTTC
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGACCTCTCCTGTCTCCGGGT

[0367] 서열번호 136: 인간 IgG1 불변 영역 aa

[0368] ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
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- [0369] 서열번호 137: 인간 IgG1 효과기 널 nt
- [0370] GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
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- [0371] 서열번호 138: 인간 IgG1 효과기 널 aa
- [0372] ASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKS
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- [0373] 서열번호 139: PD220F6 scFv nt
- [0374] CAGGAGCAGGTGAAGGAGACCGGGGAGGCTTGGTACAGCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGCAGCTATGGAGTG
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GTGGAGATCAAA
- [0375] 서열번호 140: PD220F6 scFv aa
- [0376] QEQVKETGGGLVQPGSLRLSCAASGFTI SSYGVSWVRQAPGKLEWVAL IFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDL
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- [0377] 서열번호 141: CT4 VH CDR1 aa
- [0378] SSYTMH
- [0379] 서열번호 142: CT4 VH CDR2 aa
- [0380] FISYDGNKYYADSVKG
- [0381] 서열번호 143: CT4 VH CDR3 aa
- [0382] TGWLGPFDY
- [0383] 서열번호 144: CT4 VL CDR1 aa
- [0384] RASQSVGSSYLA
- [0385] 서열번호 145: CT4 VL CDR2 aa
- [0386] GAFSRAT
- [0387] 서열번호 146: CT4 VL CDR3 aa
- [0388] QQYGSSPWT

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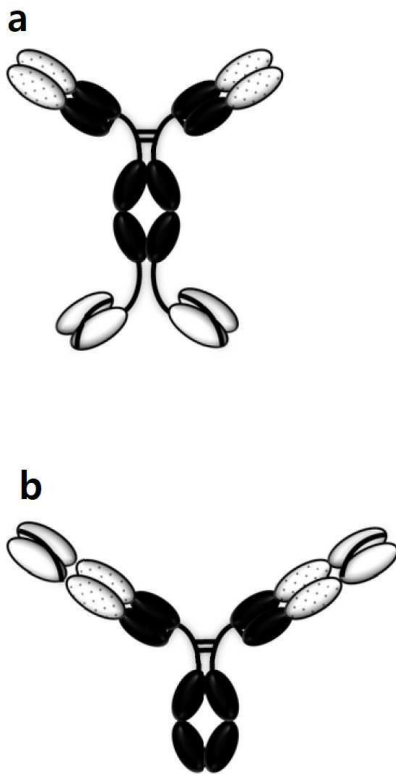
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		NTYDMI 서열번호 147	IITYSGSRYYANWAKG 서열번호 148	DYMSGHL 서열번호 149	QASEDIYSFLA 서열번호 150	SASLIAS 서열번호 151
PL230C6	PD-L1	SSYAMS 서열번호 153	YIGDTTGIAYASWANG 서열번호 154	GWSYLDI 서열번호 155	QASQNIYSNLA 서열번호 156	QASTLAS 서열번호 157
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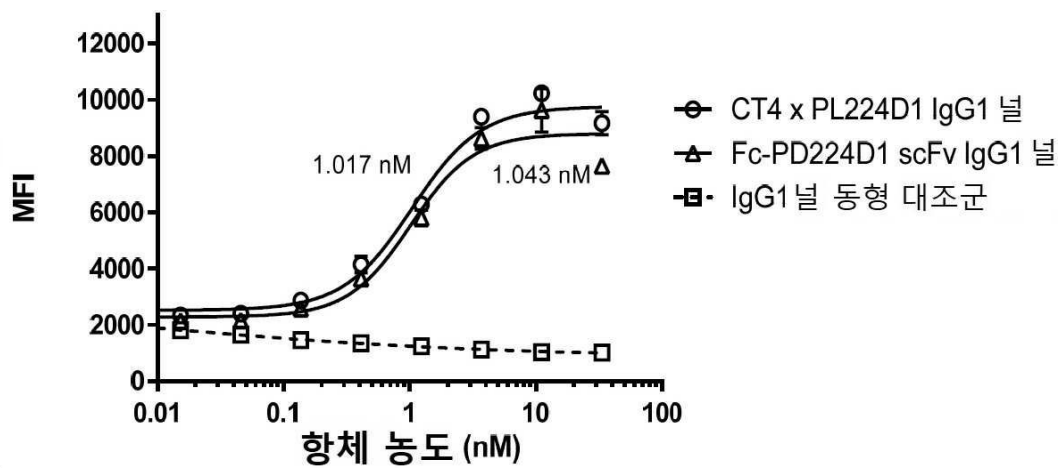
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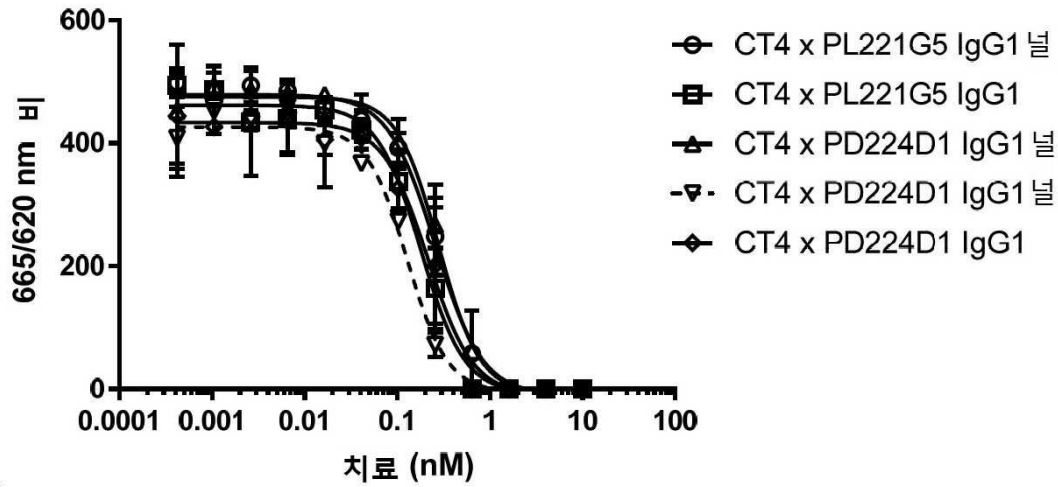
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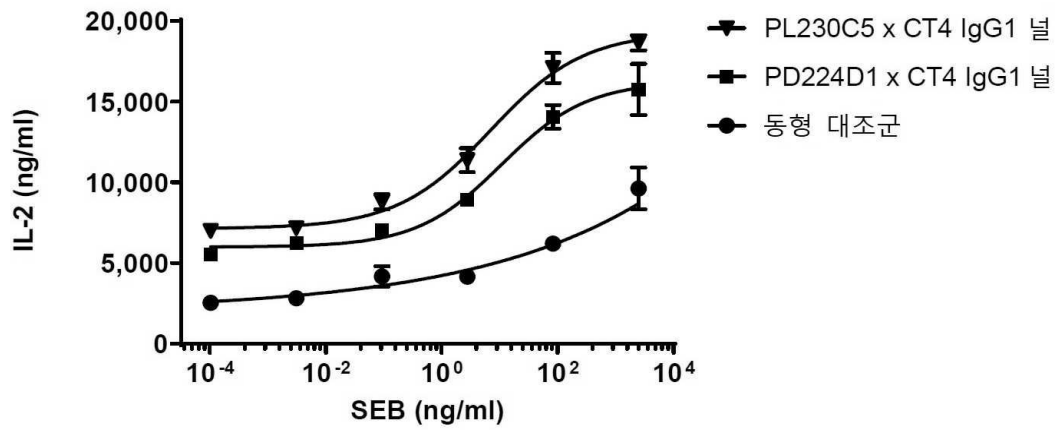
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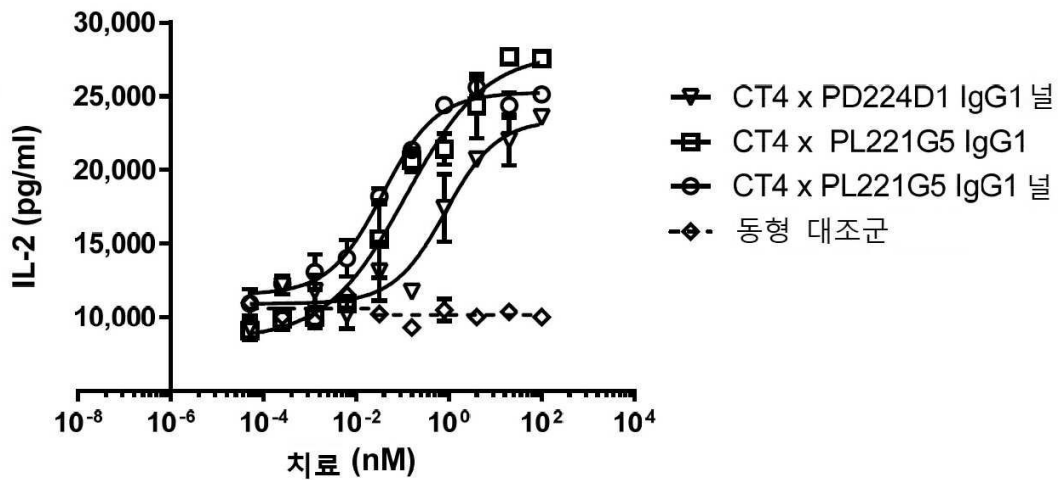
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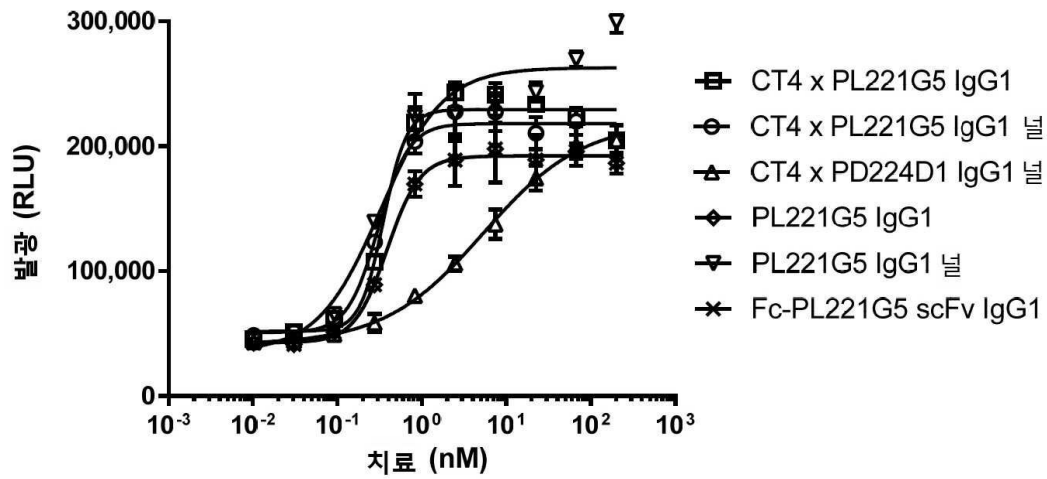
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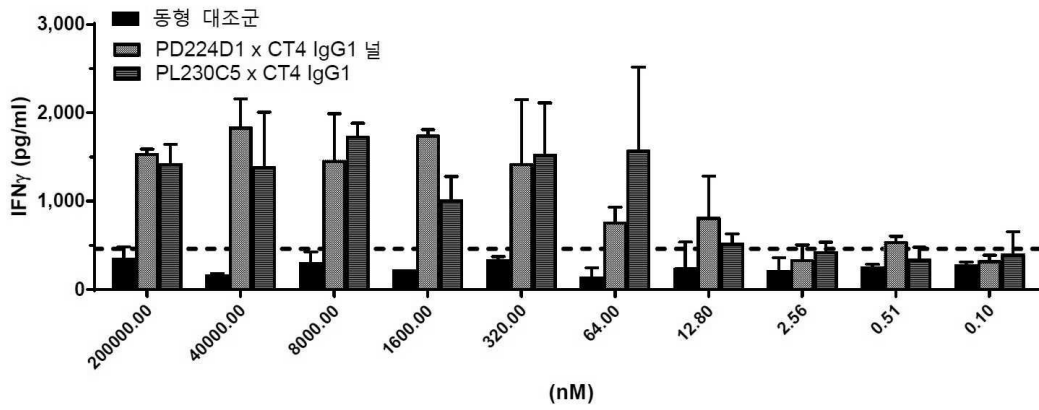
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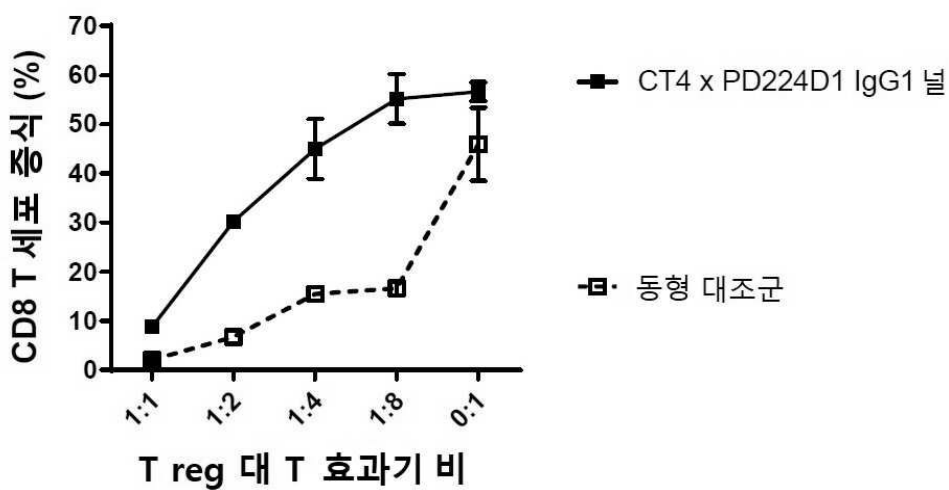
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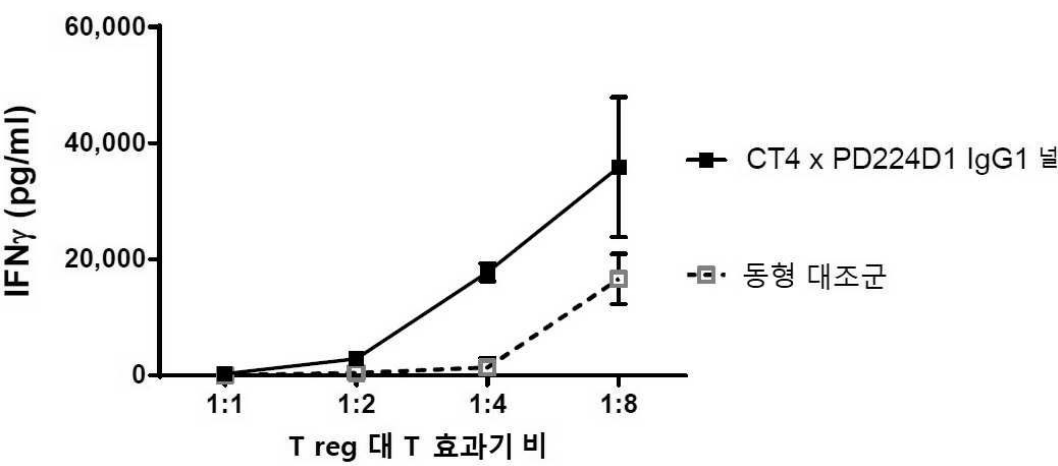
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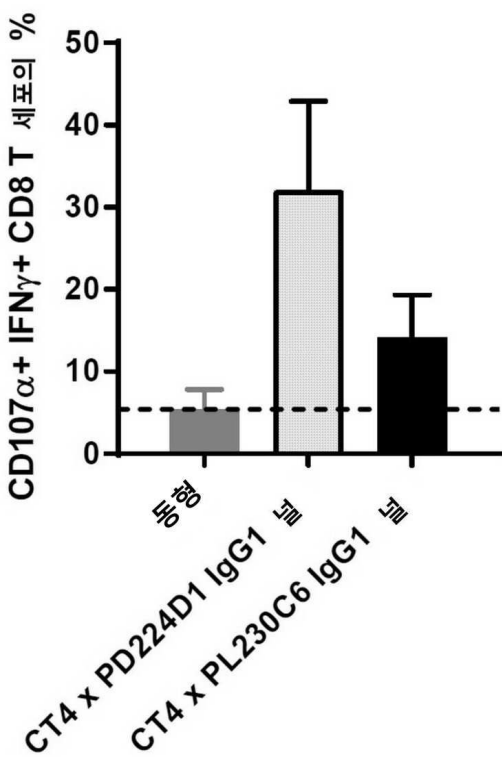
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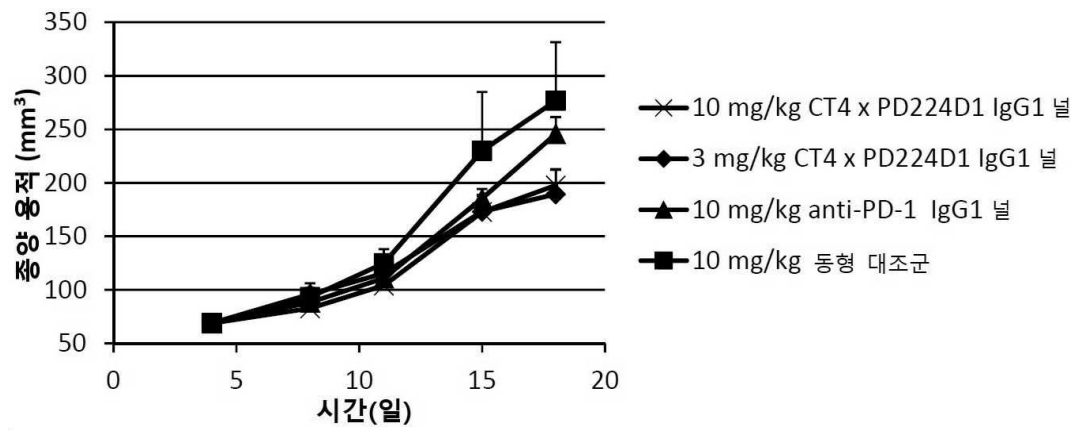
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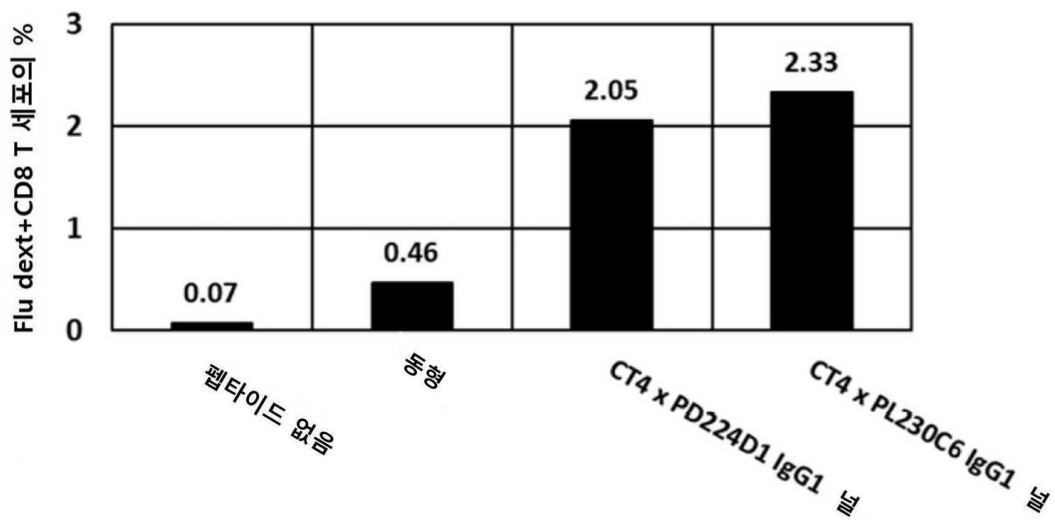
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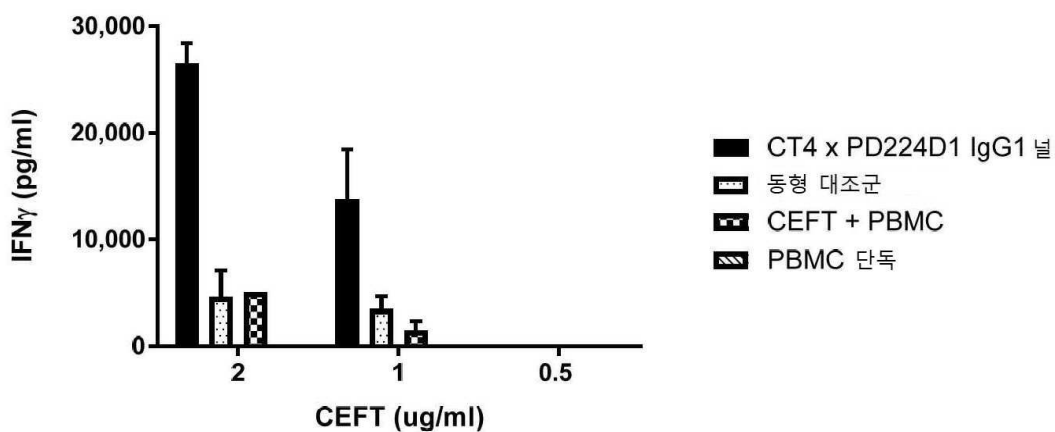
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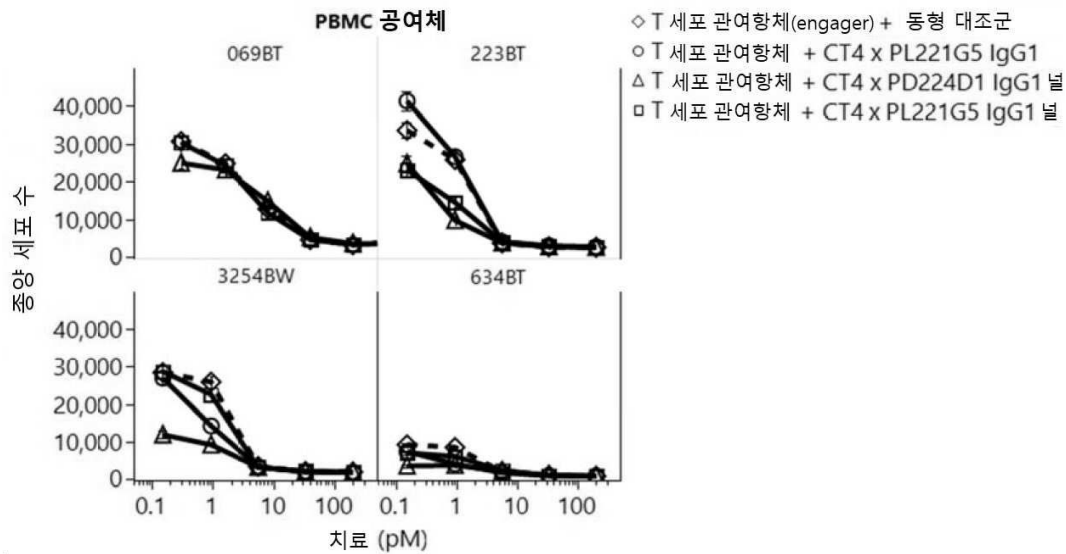
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서열 목록

SEQUENCE LISTING

<110> SYSTIMMUNE, INC.

SICHUAN BAILI PHARM CO., LTD.

<120> BISPECIFIC ANTIBODIES AND METHODS OF MAKING AND USING THEREOF

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<151> 2017-11-02

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<210> 2

<211> 701

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 2

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195	200	205	
Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr			
210	215	220	
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser			
225	230	235	240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg			
245	250	255	
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro			
260	265	270	
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala			
275	280	285	
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val			
290	295	300	
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr			
305	310	315	320
Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr			
325	330	335	
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu			
340	345	350	
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys			
355	360	365	
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser			
370	375	380	
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp			
385	390	395	400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser			
405	410	415	
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala			
420	425	430	
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly			
435	440	445	

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr
465 470 475 480

Ala Ser Gly Phe Ser Leu Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
485 490 495

Ala Pro Gly Lys Gly Leu Glu Tyr Ile Gly Tyr Ile Gly Asp Thr Thr
500 505 510

Gly Ile Ala Tyr Ala Ser Trp Ala Asn Gly Arg Phe Thr Ile Ser Lys
515 520 525

Asp Asn Thr Lys Asn Thr Val Asp Leu Gln Met Asn Ser Leu Arg Ala
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Trp Ser Tyr Leu Asp
545 550 555 560

Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
580 585 590

Ala Leu Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
595 600 605

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asn Ile Tyr Ser Asn
610 615 620

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
625 630 635 640

Tyr Gln Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
645 650 655

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
660 665 670

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gly Gly Tyr Tyr Ser Ala Ala
675 680 685

Leu Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
690 695 700

<210>

3

<211> 645

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 3

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cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca      180
gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag      240
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc      300
caagggacca aggtggaaat caaacgtacg gtggctgcac catctgtctt catcttcccg      360

ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc      420
tatccagag aggccaaagt acagtgggaag gtggataacg cctccaatc gggtaactec      480
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcacctg      540
acgtgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag      600
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<210> 4

<211> 215

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 4

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

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

```

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

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

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

100 105 110

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

115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys

195 200 205

Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 5

<211> 2106

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 5

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tcctgtgcag ccctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagccctgag agctgaggac acggctatat attactgtgc gaggaccggc 300

tggtggggc cctttgacta ctggggccag ggaacctgg tcaccgtctc ctcagctagc	360
accaagggcc catcgttctt ccccttgga cctctctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
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tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattc	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca	720
gttttctct tcccccaaa acccaaggac accctcatga tctcccgac cctgaggtc	780
acatgcgtgg tggtagcgt gagccacgaa gacctgagg tcaagttcaa ctggtacgtg	840
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taccgtgtgg tcagcgtcct caccgtctg caccaggact ggctgaatgg caaggagtac	960
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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atccagcga catgccgtg	1140
gagtgggaga gcaatggga gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag	1260
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acagatttca ctctacat cagcagcctg cagcctgaag attttgcaac ttactattgt	2040
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<210> 6

<211> 702

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 6

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195	200	205
Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr		
210	215	220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser		
225	230	235
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg		
245	250	255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro		
260	265	270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala		
275	280	285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val		
290	295	300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr		
305	310	315
Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr		
325	330	335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu		
340	345	350
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys		
355	360	365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser		
370	375	380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp		
385	390	395
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser		
405	410	415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
420	425	430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly		
435	440	445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Glu Glu Ser Gly
450 455 460

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr Ala
465 470 475 480

Ser Gly Ile Asp Leu Asn Thr Tyr Asp Met Ile Trp Val Arg Gln Ala
485 490 495

Pro Gly Lys Gly Leu Glu Trp Val Gly Ile Ile Thr Tyr Ser Gly Ser
500 505 510

Arg Tyr Tyr Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Lys Asp
515 520 525

Asn Thr Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
530 535 540

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Met Ser Gly Ser His
545 550 555 560

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
565 570 575

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
580 585 590

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
595 600 605

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
610 615 620

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
625 630 635 640

His Ser Ala Ser Ser Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
645 650 655

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
660 665 670

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Gly Lys Asn Asn
675 680 685

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

690	695	700	
<210> 7			
<211> 2127			
<212> DNA			
<213> Artificial Sequence			
<220><223> synthesized			
<400> 7			
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ttcagcggca gtggatctgg gacagaattt actctacca tcagcagcct gcagcctgat 2040
gattttgcaa cttattactg ccaacagggt tatagtggg gtaatgttga taatgttttc 2100
ggcggaggga ccaaggtgga gatcaaa 2127

<210> 8

<211> 709

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 8

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr

210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser

225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro

260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

305 310 315 320

Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

325 330 335

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

340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys

355 360 365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser

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

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

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

565 570 575
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
580 585 590
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
595 600 605

Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala

610 615 620

Ser Gln Ser Ile Ser Ser His Leu Asn Trp Tyr Gln Gln Lys Pro Gly

625 630 635 640

Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ala Ser Thr Leu Ala Ser Gly

645 650 655

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

660 665 670

Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln

675 680 685

Gln Gly Tyr Ser Trp Gly Asn Val Asp Asn Val Phe Gly Gly Gly Thr

690 695 700

Lys Val Glu Ile Lys

705

<210> 9

<211> 2109

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgtgtat	240

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tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720
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tccgacggct ccttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag 1260
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ctggtggagt ctgggggagg cctggtccag cctgggggct ccctgagact ctctgtaca 1440
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agcattagta gcttcttacc ctggtatcag cagaaaccag ggaaagcccc taagtcctg 1920

atcttttctg catccactct ggcatctggg gtcccatcaa ggttcagcgg cagtggatct 1980
gggacagatt tcactctcac catcagcagc ctgcagcctg aagattttgc aacttactat 2040
tgtcaacagg gttatagtaa aagtaatgtg gataatgctt tcggcggagg gaccaaggtg 2100
gagatcaaa 2109

<210> 10

<211> 703

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 10

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

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

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

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

 Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr
465 470 475 480

Thr Ser Gly Ile Asp Leu Ser Thr Tyr Asp Met Ile Trp Val Arg Gln
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Ile Ile Ser Tyr Val Gly

500 505 510
 Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr Leu Ser Lys
 515 520 525

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

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

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

<210> 11

<211> 2121

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 11

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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300

tggctggggc cctttgacta ctggggccag ggaaccttgg tcaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccttggca cctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600

tgcaactga atcacaagcc cagcaacacc aaggtggaca agagagttga gccc aaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttctct tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780

acatgcgtgg tgggtggacgt gagccacgaa gacctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtctg caccaggact ggctgaatgg caaggagtac 960

aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcttggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggtctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcgggtgga gggtccggcg gtggtggatc agagggtcag 1380

ctggtggagt ctgggggagg cttggtccag cctgggggggt ccctgagact ctctgtgca 1440

gcctctggat tctccctcag tagctactgg atgagctggg tccgccaggc tccagggaag 1500

gggctggagt ggtacggagt cattgatact aatgtttata tatactacgc gaactgggca 1560

aaaggcagat tcaccatctc cagagacaat tccaagaaca cgctgtatct tcaaatgaac 1620

agcctgagag ccgaggacac ggctgtgtat tactgtgcga gatatgtggg taataatgat 1680

gattatatta acttgtgggg ccagggaacc ctggtcaccg tctcgagcgg tggaggcggg 1740

tctggcggag gtggttccgg cggtggcggc tccggtggag gcggtctga catccagatg 1800
 acccagtctc ctccaccct gtctgcatct gtaggagaca gattcaccat cacttgccag 1860
 tccagtcaga gtgtttataa tggctactgg ttatcctggt atcagcagaa accagggaaa 1920
 gcccctaagc tcttgatcta tggatcatcc actctggcat ctgggggtccc atcaaggttc 1980
 agcggcagtg gatctgggac agaattcact ctccaccatca gcagcctgca gcctgatgat 2040
 ttgcaactt attactgcct aggcagttat actagtagta ctgagaactc tticggcgga 2100
 gggaccaagg tggagatcaa a 2121

<210> 12

<211> 707

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 12

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

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

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

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

 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
465 470 475 480

Ala Ser Gly Phe Ser Leu Ser Ser Tyr Trp Met Ser Trp Val Arg Gln
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Val Ile Asp Thr Asn Val
500 505 510

Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg
515 520 525

Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
530 535 540

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Val Gly Asn Asn Asp
545 550 555 560

Asp Tyr Ile Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
580 585 590

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
595 600 605

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser
610 615 620

Val Tyr Asn Gly Tyr Trp Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys
625 630 635 640

Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val

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

690 695 700
Glu Ile Lys

705

<210> 13

<211> 2112

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 13

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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac	180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc	300
tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc	360
accaagggcc catcggctct ccccttgcca cctcctcca agagcacctc tgggggcaca	420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcgcgc tgaccagcgg cgtgcacacc ttcccggctg tctacagtc ctcaggactc	540
tactccctca gcagcgtggt gaccgtgcc tccagcagct tgggcacca gacctacatc	600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagtga gcccaaatct	660
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca	720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccggac cctgaggtc	780
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaaccat ctccaaagcc	1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200
tccgacggct ccttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260
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aaaggcagat tcaccatctc caaaacctcg accacgtgg atcttaaaat caccagtccg 1620
acaaccgagg acacggctgt gtattactgt gcgagagaat ctggtactat ttattacagt 1680
tactttaact tgtggggcca agggacctg gtcaccgtct cgagcggagg aggcggatct 1740
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cagtctccat cctccctgct tgcactgtga ggagacagag tcaccatcaa gtgccaggec 1860
agtgaagca ttagcaacta cttatcctgg tatcagcaga ttccaggga agttcctaag 1920
ctctgatct attatgcac caatctggca tctggggtcc catctcggtt cagtggcagt 1980

ggatctggga cagatttcac tctcaccatc agcagcctgc agcctgaaga tgttgcaact 2040
tattactgtc aaagctatta tgggtggtgt agtgcctata ctttcggcgg agggaccaag 2100
gtggagatca aa 2112

<210> 14
<211> 704
<212> PRT
<213> Artificial Sequence
<220><223> synthesized
<400> 14

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
 85 90 95
 Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 260 265 270
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 275 280 285
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

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

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

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

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

 530 535 540

Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ser Gly Thr Ile Tyr Tyr Ser
 545 550 555 560
 Tyr Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 580 585 590
 Gly Gly Ser Ala Phe Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala

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

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

<210> 15

<211> 2121

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 15

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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300

tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360

accaagggcc catcggtctt ccccttgga cctctctcca agagcacctc tgggggcaca 420
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtagcggg gtcgtggaac 480

 tcaggcgccc tgaccagcgg cgtgcacacc ttccccgctg tctacagtc ctcaggactc 540
 tactcctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600
 tgcaactga atcacaagcc cagcaacacc aagggtgaca agagagttga gccc aaatct 660
 tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720
 gtcttctct tcccccaaa acccaaggac accctcatga tctcccgac cctgaggtc 780
 acatgcgtgg tggtagcgt gagccacgaa gacctgagg tcaagttcaa ctggtacgtg 840
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 taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1020
 aaagggcagc cccgagaacc acaggtgtac accctgccc catcccggga tgagctgacc 1080
 aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140
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 atgaacagcc tgagagccga ggactcggt gtgtattact gtgcgagaaa tctttacact 1680
 tacaatagct tgtggggcca gggaacctg gtcaccgtct cgagcggtag aggcggatct 1740

 ggcgagggtg gttccggcgg tggcggtccc ggtggaggcg gctctgacat ccagatgacc 1800
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 ggcatggat ctgggacaga attcactct accatcagca gcctgcagcc tgatgatttt 2040
 gcaacttatt actgccaagg cacttattat agtagtggtt ggaactttgc tttcggcgga 2100

gggaccaagg tggagatcaa a

2121

<210> 16

<211> 707

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 16

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly

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

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

 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 580 585 590
 Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala
 595 600 605
 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val
 610 615 620
 Tyr Asp Asn Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala

 625 630 635 640
 Pro Lys Leu Leu Ile Tyr Thr Val Ser Thr Leu Ala Ser Gly Val Pro
 645 650 655
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
 660 665 670
 Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Thr
 675 680 685

Tyr Tyr Ser Ser Gly Trp Asn Phe Ala Phe Gly Gly Gly Thr Lys Val

690	695	700	
Glu Ile Lys			
705			
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<211> 2100			
<212> DNA			
<213> Artificial Sequence			
<220><223> synthesized			
<400> 17			
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tgactcgggt	ccgccaggct	120	
ccaggcaagg	ggctggagtg	ggtgacattt	atatcatatg
atggaaacaa	taaatactac	180	
gcagactccg	tgaagggccg	attcaccatc	tccagagaca
attccaagaa	cacgctgtat	240	
ctgcaaatga	acagcctgag	agctgaggac	acggctatat
attactgtgc	gaggaccggc	300	
tggtcggggc	cttttgacta	ctggggccag	ggaaccctgg
tcaccgtctc	ctcagctagc	360	
accaagggcc	catcggctct	ccccctggca	ccctcctcca
agagcacctc	tggtgggcaca	420	
gcggccctgg	gctgcctggt	caaggactac	ttccccgaac
cggcgacggg	gtcgtggaac	480	
tcaggcgccc	tgaccagcgg	cgtgcacacc	ttcccggctg
tctacagtc	ctcaggactc	540	
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tggtggcacca	gacctacatc	600	
tgcaactgta	atcacaagcc	cagcaacacc	aaggtggaca
agagagttga	gccccaatct	660	
tgtgacaaaa	ctcacacatg	cccaccgtgc	ccagcacctg
aagccgcggg	ggcacctgca	720	
gtcttctctt	tcccccaaaa	acccaaggac	accctcatga
tctcccgac	ccctgaggtc	780	
acatgcgtgg	tggtggacgt	gagccacgaa	gacctgagg
tcaagttcaa	ctggtacgtg	840	
gacggcgtgg	aggtgcataa	tgccaagaca	aagccgcggg
aggagcagta	caacagcacg	900	
taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact
ggctgaatgg	caaggagtac	960	
aagtgcgcgg	tctccaacaa	agccctccca	gcccccatcg
agaaaaccat	ctccaaagcc	1020	
aaagggcagc	cccagaaacc	acaggtgtac	accctgcccc
catcccggga	tgagctgacc	1080	
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct
atcccagcga	catcgccgtg	1140	
gagtgggaga	gcaatgggca	gccggagaa	aactacaaga
ccacgcctcc	cgtgctggac	1200	
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acaagagcag	gtggcagcag	1260	

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 agctacttaa actggtatca gcagaaacca gggaaagccc ctaagtcct gatctatggt 1920
 gcatccaatc tggcatctgg ggtcccatca aggttcagtg gcagtggatc tgggacagat 1980

ttcactctca ccatcagcag tctgcaacct gaagattttg caacttacta ctgtcaaagc 2040
 agttggttga gtggtgctgt tggtaatgct ttggcgggag ggaccaaggt ggagatcaaa 2100

<210> 18

<211> 700

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 18

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys

85

90

95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr

100

105

110

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

115

120

125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130

135

140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145

150

155

160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165

170

175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

180

185

190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195

200

205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr

210

215

220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser

225

230

235

240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

245

250

255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro

260

265

270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala

275

280

285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

290

295

300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr

305

310

315

320

Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr

325

330

335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Glu Gln Leu Leu Glu Ser
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Thr
465 470 475 480

Ala Ser Gly Phe Ser Phe Ser Ser Tyr Trp Met Cys Trp Val Arg Gln
485 490 495

Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Cys Ile Thr Thr Gly Ser
500 505 510

Gly Ser Thr Tyr Tyr Ala Ser Trp Ala Lys Arg Arg Phe Thr Ile Ser
515 520 525

Lys Asp Asn Ser Lys Asn Thr Val Thr Leu Gln Met Asn Ser Leu Arg
530 535 540

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Ala Phe Asp Leu Trp
545 550 555 560

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile

580 585 590
Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
595 600 605

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

Phe Ala Thr Tyr Tyr Cys Gln Ser Ser Trp Leu Ser Gly Ala Val Gly
675 680 685
Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
690 695 700

<210> 19

<211> 2097

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 19

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ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300
tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360
accaagggcc catcggtctt ccccttgcca cctcctcca agagcacctc tgggggcaca 420
gcggcccttg gctgcctggt caaggactac ttcccgaac cggtagcggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tctacagtc ctcaggactc 540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaattct 660
 tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720
 gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgac ccctgaggtc 780
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 gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900
 tacctgtggt tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960
 aagtgcgcgg tctccaacaa agccctccca gcccctatcg agaaaacat ctccaaagcc 1020

aaaggcagc cccgagaacc acaggtgtac accctgcccc catcccgga tgagctgacc 1080
 aagaaccagg tcagcctgac ctgcctggc aaaggcttct atccagcga catcgccgtg 1140
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 gggaacgtct tctcatgctc cgtgatgcat gaggtctctg acaaccacta cacgcagaag 1320
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gcctctggat tcaccatcag cagctatgga gtgagctggg tccgccaggc tccagggaag 1500
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 ggccaggga cctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740
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agtaactact tatcctggtg tcagcagaaa ccagggaag ttctaagct cctgatctat 1920
 tatgcatcca ctctggcatc tgggtccca tctcggttca gtggcagtg atctgggaca 1980
 gatttcactc tcaccatcag cagcctgcag cctgaagatg ttgcaactta ttactgtgca 2040
 ggcggttata gtagtagtac tcgtgctttc ggcggaggga ccaaggtgga gatcaaa 2097

<210> 20

<211> 699

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 20

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

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

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

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

 Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
 225 230 235 240
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Glu Gln Val Lys Glu Thr
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
465 470 475 480

Ala Ser Gly Phe Thr Ile Ser Ser Tyr Gly Val Ser Trp Val Arg Gln
485 490 495

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

500 505 510
 Gly Phe Lys Asp Tyr Ala Ser Trp Val Asn Gly Arg Phe Thr Leu Ser
 515 520 525

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

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

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

<210> 21

<211> 2130

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 21

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ccaggcaagg ggcctggagt ggtgacattt atatcatatg atggaacaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300

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gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacca gacctacatc 600

tgcaactga atcacaagcc cagcaacacc aagggtggaca agagagttga gccc aaatct 660

tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttctct tcccccaaa acccaaggac accctcatga tctcccgac cctgaggtc 780

acatgcgtgg tgggtggact gagccacgaa gacctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtctg caccaggact ggctgaatgg caaggagtac 960

aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc 1020

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgctgtgtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttct ctatagcaag ctaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgtc cgtgatgcat gaggtctgc acaaccacta cacgcagaag 1320

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gcctctggat tcacctttag cagcagccac tggatatgct gggtccgcca ggctccaggg 1500

aaggggctgg agtggatcgc atgcatttat actggtagta ttgatgtctt ttactacgcg 1560

agctgggcga aaggccggtt caccatctcc agagacaatt ccaagaacac gctgtatctg 1620

caaatgaaca gcctgagagc cgaggacacg gccgtatatt actgtgcgag agccgctaat 1680

actgatacta cctactttaa cttgtggggc cagggaaccc tggtcaccgt ctcgagcggg 1740

ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggctctgcc 1800
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ttcaccggca gtggatctgg gacagatttc actctcacca tcagcagcct gcagcctgaa 2040
gatgttgcaa cttattactg tcatgttcat tattgcagtg gtggtagtgt tttttgggct 2100
ttcggcggag ggaccaaggt ggagatcaaa 2130

<210> 22

<211> 710

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 22

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr

20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

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

50 55 60

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

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys

85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

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

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

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

 370 375 380
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
435 440 445

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser
450 455 460

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
465 470 475 480

Ala Ser Gly Phe Thr Phe Ser Ser Ser His Trp Ile Cys Trp Val Arg
485 490 495

Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ala Cys Ile Tyr Thr Gly
500 505 510

Ser Ile Asp Val Phe Tyr Tyr Ala Ser Trp Ala Lys Gly Arg Phe Thr
515 520 525

Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
530 535 540

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ala Asn
545 550 555 560

Thr Asp Thr Thr Tyr Phe Asn Leu Trp Gly Gln Gly Thr Leu Val Thr
565 570 575

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
580 585 590

Gly Ser Gly Gly Gly Gly Ser Ala Tyr Asp Met Thr Gln Ser Pro Ser
595 600 605

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln Ala
610 615 620

Ser Gln Ser Ile Asn Asn Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly
625 630 635 640

Lys Val Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Leu Ala Ser Gly

645 650 655
Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
660 665 670
Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys His
675 680 685
Val His Tyr Cys Ser Gly Gly Ser Cys Phe Trp Ala Phe Gly Gly Gly
690 695 700
Thr Lys Val Glu Ile Lys
705 710
<210> 23
<211> 60
<212> DNA
<213> Artificial Sequence
<220><223> synthesized
<400> 23
gggtggaggcgg gatctggcgg aggtggttcc ggcggtggcg gctccggtgg aggcggtctt 60
<210> 24
<211> 20
<212> PRT
<213> Artificial Sequence
<220><223> synthesized
<400> 24
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser
20
<210> 25
<211> 2100
<212> DNA
<213> Artificial Sequence
<220><223> synthesized
<400> 25
cagtcggtgg aggagtcctgg gggaggcttg gtccagcctg gggggtcctt gagactctcc 60

tgtaccgcct ctggaatcga ccttaataacc tacgacatga tctgggtccg ccaggctcca 120
 ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac 180
 tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa 240
 atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt 300

 ggttcccact tgtggggcca gggaaccctg gtcaccgtct cgagcgctag caccaagggc 360
 ccatcgggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420
 ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480
 ctgaccagcg gcgtgcacac cttcccggtc gtctacagt cctcaggact ctactcctc 540
 agcagcgtag tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600
 aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatac ttgtgacaaa 660
 actcacacat gccccaccgtg cccagcacct gaagccgcgg gggcaccgtc agtcttcctc 720

 ttcccccaa aaccaagga caccctcatg atctcccga cccctgaggt cacatgcgtg 780
 gtggtggacg tgagccacga agaccctgag gtcaagtcca actggtacgt ggacggcgtg 840
 gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900
 gtcagcgctc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcgcg 960
 gtctccaaca aagccctccc agccccatc gagaaaacca tctccaaagc caaagggcag 1020
 ccccgagaac cacaggtgta caccctgccc ccatcccggtg atgagctgac caagaaccag 1080
 gtcagcctga cctgcctggt caaaggcttc tatccagcg acatcgccgt ggagtgggag 1140

 agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200
 tccttcttcc tctatagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260
 ttctcatgct ccgtgatgca tgaggtcttg cacaaccact acacgcagaa gacccctcctc 1320
 ctgtctccgg gtggcggtgg agggctccgc ggtgggtgat cccaggtgca attggtggag 1380
 tctgggggag gcgtggtcca gcctgggagg tcctgagac tctcctgtgc agcctctgga 1440
 ttcaccttca gtagctatac tatgcactgg gtccgccagg ctccaggcaa ggggctggag 1500
 tgggtgacat ttatatcata tgatggaaac aataaatact acgcagactc cgtgaagggc 1560

 cgattcacca tctccagaga caattccaag aacacgtgt atctgcaaat gaacagcctg 1620
 agagctgagg acacggctat atattactgt gcgaggaccg gctggctggg gccctttgac 1680
 tactggggcc agggaaacct ggtcaccgtc tcgagcgttg gaggcggttc aggcggaggt 1740
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 ggcacctgt ctttgtctcc aggggaaaga gccacctct cctgcagggc cagtcagagt 1860
 gttggcagca gctacttagc ctggtaccag cagaaacctg gccaggctcc caggctcctc 1920

atctatggtg cattcagcag ggccactggc atcccagaca ggttcagtgg cagtgggtct 1980

gggacagact tcactctcac catcagcaga ctggagcctg aagattttgc agtgtattac 2040

tgtcagcagt atggtagctc accgtggacg ttcggccaag ggaccaaggt ggaaatcaaa 2100

<210> 26

<211> 700

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 26

Gln Ser Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

85 90 95

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr

100 105 110

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

115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val

130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala

145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly

165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
 180 185 190
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 195 200 205
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 210 215 220

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

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

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

 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn

420	425	430	
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly			
435	440	445	
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly			
450	455	460	
Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly			
465	470	475	480
Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly			
485	490	495	
Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys			
500	505	510	
Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn			
515	520	525	
Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp			
530	535	540	
Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp			
545	550	555	560
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly			
565	570	575	
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
580	585	590	
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly			
595	600	605	
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser			
610	615	620	
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu			
625	630	635	640
Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser			
645	650	655	
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu			
660	665	670	

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

675 680 685

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

690 695 700

<210> 27

<211> 651

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 27

gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcaccccttc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcaactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacgggtg ctgcaccatc tgtcttcac 360

ttcccgcct ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagagcg caaagtacag tggaaggtgg ataacgcct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 28

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 28

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1 5 10 15

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

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
His Ser Ala Ser Ser Leu Ala 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 Gln Gln Gly Tyr Gly Lys Asn Asn
85 90 95
Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr

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

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

<210> 29

<211> 2100

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 29

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
tcctgtacag ccctctggatt ctccctcagt agctatgcaa tgagctgggt cgcagggt 120
ccagggaagg ggctggagta catcggtac attggtgata ctactggcat agcctacgcg 180

agctgggcga atggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt 240
 caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggctggtcc 300
 tacttagaca tctggggcca agggaccctg gtcaccgtct cgagcgctag caccaagggc 360
 ccatcggtct tccccctggc accctcctcc aagagcacct ctggggggcac agcggccctg 420

 ggctgcctgg tcaaggacta ctccccgaa cgggtgacgg tgtcgtggaa ctgagcgcc 480
 ctgaccagcg gcgtgcacac ctccccggt gtcctacagt cctcaggact ctactccctc 540
 agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600
 aatcacaagc ccagcaacac caaggtggac aagagagtgt agcccaaatt ttgtgacaaa 660
 actcacacat gccaccgtg cccagcacct gaagcccgcg gggcacccgtc agtcttcctc 720
 tccccccaa aaccaagga caccctcatg atctccgga cccctgaggt cacatgcgtg 780
 gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

 gaggtgcata atgccaagac aaagcccgcg gaggagcagt acaacagcac gtaccgtgtg 900
 gtcagcgtec tcaccgtcct gcaccaggac tggtgtaatg gcaaggagta caagtgcgcg 960
 gtctccaaca aagccctccc agcccccatc gagaaaaacca tctccaaagc caaagggcag 1020
 ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080
 gtcagcctga cctgcctggt caaaggcttc tatccagcg acatcgccgt ggagtgggag 1140
 agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200
 tccttcttcc tctatagca gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

 ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320
 ctgtctccgg gtggcggtgg agggccggc ggtggtggat cccaggtgca attggtggag 1380
 tctgggggag gcgtggtcca gcctgggagg tcctgagac tctctgtgc agcctctgga 1440
 ttcacattca gtagctatac tatgcactgg gtccgccagg ctccaggcaa ggggctggag 1500
 tgggtgacat ttatatcata tgatggaaac aataaatact acgcagactc cgtgaagggc 1560
 cgattacca tctccagaga caattccaag aacacgtgt atctgcaaat gaacagcctg 1620
 agagctgagg acacggctat atattactgt gcgaggaccg gctggctggg gccctttgac 1680

 tactggggcc agggaaccct ggtcaccgtc tcgagcggtg gaggcggatc tggcggaggt 1740
 ggttccggcg gtggcggtc cgggtggaggc ggttctgaaa ttgtgttgac gcagtctcca 1800
 ggcaccctgt ctttgtctcc aggggaaaga gccaccctct cctgcagggc cagtcagagt 1860
 gttggcagca gctacttagc ctggtaccag cagaaacctg gccaggtcc caggctcctc 1920
 atctatggtg cattcagcag ggccactggc atcccagaca ggttcagtgg cagtgggtct 1980
 gggacagact tcactctcac catcagcaga ctggagcctg aagattttgc agtgtattac 2040

tgtcagcagt atggtagctc accgtggacg ttcggccaag ggaccaaggt ggaaatcaaa 2100

<210> 30

<211> 700

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 30

Glu Val Gln Leu Val 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 Leu Ser Ser Tyr

20 25 30

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

35 40 45

Gly Tyr Ile Gly Asp Thr Thr Gly Ile Ala Tyr Ala Ser Trp Ala Asn

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Gly Trp Ser Tyr Leu Asp Ile Trp Gly Gln Gly Thr Leu Val Thr

100 105 110

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

115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val

130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala

145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly

165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly

180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
 195 200 205
 Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
 210 215 220
 Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu
 225 230 235 240
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 245 250 255
 Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 260 265 270
 Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 275 280 285
 Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 290 295 300
 Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala
 305 310 315 320
 Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 325 330 335
 Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
 340 345 350
 Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 355 360 365
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 370 375 380
 Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 385 390 395 400
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 405 410 415
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 420 425 430
 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly

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

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

 565 570 575
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 580 585 590
 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 595 600 605
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
 610 615 620
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

 625 630 635 640
 Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
 645 650 655
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 660 665 670
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 675 680 685

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

690 695 700

<210> 31

<211> 648

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 31

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atcacttgcc aggccagtc gaacatttac agcaatttag cctggtatca gcagaaacca 120

gggaaagtgc ctaagctcct gatctatcag gcctccactc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggata tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaggc ggttattata gtgctgcct taatactttc 300

ggcggaggga ccaaggtgga gatcaaactg acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgcccctca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacagaaaa cacaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaagagc ttcaacaggg gagagtgt 648

<210> 32

<211> 216

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 32

Ala Leu Val 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 Gln Asn Ile Tyr Ser Asn

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

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

50	55	60	
Ser Gly Tyr 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 Gln Gly Gly Tyr Tyr Ser Ala Ala			
	85	90	95
Leu Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val			
	100	105	110
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys			
	115	120	125
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg			
	130	135	140
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn			
145	150	155	160
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser			
	165	170	175
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys			
	180	185	190
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr			
	195	200	205
Lys Ser Phe Asn Arg Gly Glu Cys			
	210	215	
<210>	33		
<211>	2121		
<212>	DNA		
<213>	Artificial Sequence		
<220><223>	synthesized		
<400>	33		
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tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag		120	
gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggatcact		180	
tacgacgcga actgggcgaa aggccgggttc accatctcca gagacaattc caagaacacg		240	

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300
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 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
 gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggtc tgcctacag 540
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag ctgggcacc 600

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 gagcccaaat ctgtgacaa aactcacaca tgcccaccgt gcccgacc tgaagccg 720
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 tcctgcaggg ccagtcagag tggtggcagc agctacttag cctggtacca gcagaaacct 1920
 ggccaggctc ccaggctcct catctatggt gattcagca gggccactgg catcccagac 1980
 aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct 2040
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gggaccaagg tggaaatcaa a

2121

<210> 34

<211> 707

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<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 Ser Phe Ser Ser Gly

20 25 30
Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

35 40 45
Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn

50 55 60
Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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
Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp

100 105 110
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

115 120 125
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr

130 135 140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr

145 150 155 160
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

165 170 175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn

195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser

210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala

225 230 235 240

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

245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

260 265 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr

290 295 300

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

305 310 315 320

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro

325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val

370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro

385 390 395 400

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

405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

420 425 430

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

435 440 445
Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln

450 455 460
Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg

465 470 475 480
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His

485 490 495
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile

500 505 510
Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg

515 520 525
Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met

530 535 540
Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr

545 550 555 560
Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

565 570 575
Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

580 585 590
Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly

595 600 605
Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala

610 615 620
Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro

625 630 635 640
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr

645 650 655
Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

660 665 670
Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys

675 680 685

Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val

690

695

700

Glu Ile Lys

705

<210> 35

<211> 651

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 35

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gggaaagccc ctaagctcct gatctataag gcattcactc tggcatctgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagaa ttactctca ccatcagcag cctgcagcct 240
gatgatattg caacttatta ctgccaacag ggttatagtt ggggtaatgt tgataatgtt 300
ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcac 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420
aacttctatc ccagagagcg caaagtacag tggaagggtg ataacgcct ccaatcgggt 480
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 36

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly

1

5

10

15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser His

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45
Tyr Lys Ala Ser Thr Leu Ala 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
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Trp Gly Asn
85 90 95
Val Asp Asn Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
115 120 125
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro

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

195 200 205
Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 37

<211> 2103

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 37

cagggtgcagc tgggtggagtc tggggggaggc ctggtccagc ctgggggctc cctgagactc 60
tcctgtacaa ctcttggaat cgaccttagt acctacgaca tgatctgggt ccgccaggct 120
ccaggcaagg ggctagagtg ggtgggaatc attagttatg ttggtaacac atactacgcg 180

agctgggcga aaggccgatt caccctctcc aaagacaata cctcgaccac ggtggatctg 240

caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agattttatt 300

agtggttccc acttgtgggg ccaggggaacc ctggtcaccg tctcgagcgc tagcaccaag 360

ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtaagga ctacttcccc gaaccggtga cgggtgctg gaactcaggc 480

gccctgacca gggcggtgca caccttcccc gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tggtagaccg gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaagggtg gacaagagag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagccg cgggggcacc gtcagtcctc 720

ctcttcccc caaaacccaa ggacaccctc atgatctccc ggaccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagacct gaggtcaagt tcaactggta cgtggacggc 840

gtggagggtgc ataatgcaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900

gtggtcagcg tcttcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960

gcggtctcca acaaagccct cccagcccc atcgagaaaa ccatctccaa agccaaaggg 1020

cagccccgag aaccacaggt gtacaccctg ccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgect ggtcaaaggc ttctatccca ggcacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgctgt ggactccgac 1200

ggctccttct tctctatag caagctcacc gtggacaaga gcaggtggca gcagggggaa 1260

gtcttctcat gtcctgtgat gcatgaggt ctgcacaacc actacacgca gaagagcctc 1320

tccctgtctc cgggtggcgg tggagggtcc ggcggtggtg gatcccaggt gcaattggtg 1380

gagtcctggg gaggcgtggt ccagcctggg aggtccctga gactctctg tgcagcctct 1440

ggattcacct tcagtagcta tactatgcac tgggtccgcc aggtccagg caaggggctg 1500

gagtgggtga catttatatc atatgatgga aacaataaat actacgcaga ctccgtgaag 1560

ggccgattca ccatctccag agacaattcc aagaacacgc tgtatctgca aatgaacagc 1620

ctgagagctg aggacacggc tataatattac tgtcgagga ccggttggt ggggcctttt 1680

gactactggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcgga 1740

ggtggttccg gcggtggcgg ctccggtgga ggcggttctg aaattgtgtt gacgcagtct 1800

ccaggcacc tgictttgtc tccaggggaa agagccacc tctcctgcag ggccagtcag 1860

agtgttgga gcagctactt agcctggtac cagcagaaac ctggccaggc tcccaggctc 1920

ctcatctatg gtgcattcag cagggccact ggcatcccag acaggttcag tggcagtggg 1980
tctgggacag acttcactct caccatcagc agactggagc ctgaagattt tgcagtgtat 2040
tactgtcagc agtatggtag ctcaccgtgg acgttcggcc aagggaacaa ggtggaaatc 2100
aaa 2103

<210> 38

<211> 701

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 38

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Ile Asp Leu 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

Gly Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Phe Ile Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val

100 105 110

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

115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu

130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly

145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser

165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

420 425 430
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly
 435 440 445
 Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly
 450 455 460

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

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

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

 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu
 660 665 670

Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser

675 680 685

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

690 695 700

<210> 39

<211> 651

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 39

gcctatgata tgaccacgtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaattgtc aggccagtga gagcattagt agcttcttat cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatcttttct gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttactcttca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatagta aaagtaatgt ggataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacgggtg ctgcaccatc tgtcttcac 360

ttcccgcct ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggg caaagtacag tggaaggtgg ataacgcct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

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<210> 40

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 40

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser Ile Ser Ser Phe

20 25 30

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

35 40 45
Phe Ser Ala Ser Thr Leu Ala 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 Gln Gln Gly Tyr Ser Lys Ser Asn

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

145 150 155 160
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
165 170 175
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
180 185 190
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
195 200 205
Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 41

<211> 2112

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 41

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag ccctctggatt ctccctcagt agctactgga tgagctgggt ccgccaggct 120
ccaggaagg ggctggagtg gatcggagtc attgatacta atgtttatat atactacgcg 180

aactgggcaa aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt	240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag atatgtgggt	300
aataatgatg attatattaa cttgtggggc cagggaaccc tggtcaccgt ctcgagcgct	360
agcaccaagg gcccatcggt cttcccccig gcaccctcct ccaagagcac ctctgggggc	420
acagcgggcc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	480
aactcaggcg cctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga	540
ctctactccc tcagcagcgt ggtgaccgtg cctccagca gcttgggcac ccagacctac	600
atctgaacg tgaatcaca gccagcaac accaaggtgg acaagagagt tgagcccaaa	660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagccgc gggggcaccg	720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gaccctgag	780
gtcacatgcg tgggtgtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac	840
gtggacggcg tggagggtga taatgccaag acaaagccgc gggaggagca gtacaacagc	900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	960
tacaagtgcg cgggtctcaa caaagccctc ccagccccca tcgagaaaaac catctccaaa	1020
gccaaagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggatgagctg	1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc	1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1200
gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag cagggtggcag	1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgag	1320
aagagcctct cctgtctcc ggggtggcgggt ggagggtccg gcggtggtgg atcccagggtg	1380
caattggtgg agtctggggg aggcgtggtc cagcctggga ggtccctgag actctcctgt	1440
gcagcctctg gattcacctt cagtagctat actatgcact gggtcgcca ggctccaggc	1500
aaggggctgg agtgggtgac atttatatca tatgatggaa acaataaata ctacgcagac	1560
tccgtgaagg gccgattcac catctccaga gacaattcca agaacacgct gtatctgcaa	1620
atgaacagcc tgagagctga ggacacggct atatattact gtgcgaggac cggctggctg	1680
gggccctttg actactgggg ccagggaacc ctggtcaccg tctcgagcgg tggaggcggga	1740
tctggcggag gtggttccgg cgggtggcggc tccggtggag gcggttctga aattgtgttg	1800
acgcagtctc caggcacctt gtctttgtct ccaggggaaa gagccacct ctctgcagg	1860
gccagtcaga gtgttggcag cagctactta gcctgtgacc agcagaaaacc tggccaggct	1920
cccaggctcc tcattatgg tgcatcagc agggccactg gcattcccaga caggttcagt	1980

ggcagtggtggt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatatt 2040

gcagtgtatt actgtcagca gtatggtagc tcaccgtgga cgttcggcca agggaccaag 2100

gtggaaatca aa 2112

<210> 42

<211> 704

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 42

Glu Val Gln Leu Val Glu Ser 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 Leu Ser Ser Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu Trp Gly Gln Gly

100 105 110

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

115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu

130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

145 150 155 160

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

165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu

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

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

 Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu
 545 550 555 560
 Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 565 570 575
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 580 585 590
 Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
 595 600 605

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

Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr

675 680 685

Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

690 695 700

<210> 43

<211> 654

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 43

gacatccaga tgaccagtc tcttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtcagtc gagtggttat aatggctact gggtatcctg gtatcagcag 120

aaaccagga aagcccctaa gctcctgac tatgtgcat ccactctggc atctggggtc 180

ccatcaaggc tcagcggcag tggatctggg acagaattca ctctaccat cagcagcctg 240

cagcctgatg attttgcaac ttattactgc ctaggcagtt atactagtag tactgagaac 300

tctttcggcg gagggaccaa ggtggagac aaacgtacgg tggctgcacc atctgtcttc 360

atcttcccg catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtg cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcacctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acctatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 44

<211> 218

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 44

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val Tyr Asn Gly

20 25 30

Tyr Trp Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu

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

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

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

<210> 45

<211> 2109

<212>

> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 45

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
 tcctgtacag tgcttggaat cgacctcagt gtcatcaata tgggctgggt ccgccaggct 120
 ccaggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180

agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc	240
accagtccga caaccgagga caggctgtg tattactgtg cgagagaatc tggtagtatt	300
tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagcgctagc	360
accaagggcc catcggctctt ccccttggca ccttcctcca agagcacctc tgggggcaca	420
gcggcccttg gctgcctggt caaggactac ttccccgaac cggtagcggg gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaactga atcacaagcc cagcaacacc aaggtggaca agagagtga gcccaaatct	660
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca	720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgac cctgaggtc	780
acatgcgtgg tggtagcgtg gagccacgaa gacctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac	960
aagtgcgcgg tctccaacaa agccctccca gccccatcg agaaaacat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc	1080
aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttct ctatagcaag ctacacgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgtc cgtgatgat gaggtctgc acaaccacta cacgcagaag	1320
agcctctccc tgctccggg tggcgtgga gggccggcg gtggtggatc ccaggtgcaa	1380
ttggtggagt ctgggggagg cgtggtccag cctgggaggt ccctgagact ctctgtgca	1440
gcctctggat tcaccttcag tagctatact atgcactggg tccgccaggc tccaggcaag	1500
gggctggagt gggtagatt tataatcata gatggaaca ataaatacta cgcagactcc	1560
gtgaagggcc gattccat ctccagagac aattccaaga acacgtgta tctgcaaatg	1620
aacagcctga gagctgagga cacggctata tattactgtg cgaggaccgg ctggctgggg	1680
ccctttgact actggggcca gggaacctg gtcaccgtct cgagcggtag aggcggatct	1740
ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gttctgaaat tgtgttgacg	1800
cagtctccag gcacctgtc tttgtctcca ggggaaagag ccacctctc ctgcagggcc	1860
agtcagagtg ttggcagcag ctacttagcc tggtagcagc agaaacctgg ccaggctccc	1920
aggctctca tctatggtgc attcagcagg gccactggca tccagacag gttcagtggc	1980

agtgggtctg ggacagactt cactctcacc atcagcagac tggagcctga agattttgca 2040

gtgtattact gtcagcagta tggtagctca ccgtggacgt tcggccaagg gaccaaggtg 2100

gaaatcaaa 2109

<210> 46

<211> 703

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Ile Asp Leu Ser Val Ile

20 25 30

Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
260 265 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

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

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

 Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly
 545 550 555 560
 Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 580 585 590
 Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
 595 600 605

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

Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly

675

680

685

Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

690

695

700

<210> 47

<211> 648

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 47

gcattcgaat tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgcc aggccagtga aagcattagc aactacttat cctggtatca gcagattcca 120

gggaaagttc ctaagctcct gatctattat gcatccaatc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaagc tattatgggtg gtggtagtc ctatactttc 300

ggcggaggga ccaaggtgga gatcaaagc acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aagggtggata acgcctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacagaaaa cacaagctct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaagagc ttcaacaggg gagagtgt 648

<210> 48

<211> 216

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 48

Ala Phe Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1

5

10

15

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

20

25

30

Leu Ser Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45
Tyr Tyr Ala Ser Asn Leu Ala 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 Gln Ser Tyr Tyr Gly Gly Gly Ser
85 90 95

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

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

<210> 49

<211> 2109

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 49

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
tcctgtgcag ccctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120
gtccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggcgag aggcagattc accatctccg aaacctccaa gaacacggtg	240
actcttcaaa tgaacagcct gagagccgag gactcggtg tgtattactg tgcgagaaat	300
ctttacattt acaatagctt gtggggccag ggaaccttgg tcaccgtctc gagcgctagc	360
accaagggcc catcggtctt ccccttggca cctctctcca agagcacctc tgggggcaca	420
gcggcccttg gctgccttgt caaggactac ttccccgaac cggtgacggt gtcgtggaac	480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc	540
tactccctca gcagcgttgt gaccgtgccc tccagcagct tgggcaccca gacctacatc	600
tgcaactga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct	660
tgtgacaaaa ctacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca	720
gtcttctctt tcccccaaa acccaaggac accctcatga tctcccgac cctgaggtc	780
acatgcgtgg tgggtggact gagccacgaa gacctgagg tcaagttcaa ctggtacgtg	840
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg	900
taccgtgtgg tcagcgtcct caccgtctg caccaggact ggctgaatgg caaggagtac	960
aagtgcgcgg tctccaacaa agccttccca gccccatcg agaaaacat ctccaaagcc	1020
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc	1080
aagaaccagg tcagcctgac ctgcctgttc aaaggcttct atcccagcga catcgccgtg	1140
gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac	1200
tccgacggct ctttcttct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag	1260
gggaacgtct tctcatgtc cgtgatgat gaggtcttgc acaaccacta cagcagaag	1320
agcctctccc tgtctccggg tggcgttga gggtccggcg gtggtggatc ccagggtcaa	1380
ttggtggagt ctgggggagg cgtgtgtccag cctgggaggt ccctgagact ctctgtgca	1440
gcctctggat tcaccttcag tagctatact atgcactggg tccgccaggc tccaggcaag	1500
gggctggagt gggtagacatt tatacataat gatggaaca ataaatacta cgcagactcc	1560
gtgaagggcc gattcccat ctccagagac aattccaaga acacgtgtg tctgcaaatg	1620
aacagcctga gagctgagga cacggtata tattactgtg cgaggaccgg ctggctgggg	1680
ccctttgact actggggcca gggaacctg gtcaccgtct cgagcgttg aggcggtct	1740
ggcggagggt gttccggcgg tggcggctcc ggtggaggcg gttctgaaat tgtgttgacg	1800
cagtctccag gcacctgtc tttgtctcca ggggaaagag ccacctctc ctgcagggcc	1860
agtcagagtg ttggcagcag ctacttagcc tggtagcagc agaaacctgg ccaggctccc	1920
aggctctca tctatggtgc attcagcagg gccactggca tccagacag gttcagtggc	1980
agtgggtctg ggacagactt cactctcacc atcagcagac tggagcctga agattttgca	2040

gtgtattact gtcagcagta tggtagctca ccgtggacgt tcggccaagg gaccaaggtg 2100

gaaatcaaa 2109

<210> 50

<211> 703

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 50

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Ser Gly

20 25 30

Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu

35 40 45

Ile Ala Cys Ile Tyr Ala Gly Thr Ser Gly Ser Thr Ser Tyr Ala Ser

50 55 60

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

65 70 75 80

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

85 90 95

Cys Ala Arg Asn Leu Tyr Thr Tyr Asn Ser Leu Trp Gly Gln Gly Thr

100 105 110

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

115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly

130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn

145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln

165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser

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

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

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

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

 420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly
 435 440 445
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser
 450 455 460
 Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
 465 470 475 480
 Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His Trp Val Arg Gln
 485 490 495
 Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile Ser Tyr Asp Gly
 500 505 510
 Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 515 520 525
 Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 530 535 540
 Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr Gly Trp Leu Gly
 545 550 555 560
 Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 580 585 590
 Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu
 595 600 605
 Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
 610 615 620
 Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
 625 630 635 640
 Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp
 645 650 655
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 660 665 670
 Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly

675 680 685
 Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 690 695 700
 <210> 51
 <211> 657
 <212> DNA
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 51
 gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc agtccagtc gagtggttat gataacaact ggtagcctg gtatcagcag 120
 aaaccaggga aagccctaa gctcctgac tatacagtat ccactctggc atctggggtc 180

 ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240
 cagcctgatg attttgcaac ttattactgc caaggcactt attatagtag tggttggaac 300
 ttgtctttcg gcggaggag caaggtggag atcaaacgta cggtagcctgc accatctgtc 360
 ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatccag agaggccaaa gtacagtga agtggataa cgccctcaa 480
 tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540
 agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa 600

 gtcacccatc agggcctgag ctgccccgc acaaagagct tcaacagggg agagtgt 657
 <210> 52
 <211> 219
 <212> PRT
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 52
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val Tyr Asp Asn
 20 25 30
 Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu

35 40 45

Leu Ile Tyr Thr Val Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe
 50 55 60
 Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu
 65 70 75 80
 Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Thr Tyr Tyr Ser
 85 90 95
 Ser Gly Trp Asn Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 180 185 190
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 53

<211> 2094

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 53

caggagcagc tgitggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtacag cctctggatt ctcttttagc agctactgga tgtgctgggt ccgccaggct	120
ccagggaagg ggctggagtg gatcgatgc attacgactg gtagtggttag cacttactac	180
gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact	240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300
 gacttgtggg gccagggaac cctgtgcacc gtctcgagcg ctagcaccaa gggcccatcg 360
 gtcttcccc tggcacctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 420

 ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480
 agcggcgtgc acaccttccc ggctgtccta cagtctcag gactctactc cctcagcagc 540
 gtggtgaccg tgcctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 600
 aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 660
 acatgccac cgtgcccagc acctgaagcc gcgggggcac cgtcagctt cctcttcccc 720
 ccaaaaccca aggacacct catgatctcc cggaccctg aggtcacatg cgtggtggtg 780
 gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 900
 gtctcaccg tctgcacca ggactggctg aatggcaagg agtacaagtg cgcggtctcc 960
 aacaaagccc tccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020
 gaaccacagg tgtacacct gcccctatcc cgggatgagc tgaccaagaa ccaggtcagc 1080
 ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140
 gggcagccgg agaacaacta caagaccacg cctcccgctg tggactccga cggtccttc 1200
 ttctctata gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

 tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1320
 ccgggtggcg gtggagggtc cggcgggtgt ggatcccagg tgcaattggt ggagtctggg 1380
 ggaggcgtgg tccagcctgg gaggtccctg agactctcct gtgcagcctc tggattcacc 1440
 ttcagtagct atactatgca ctgggtccgc caggctccag gcaaggggct ggagtgggtg 1500
 acatttatat catatgatgg aaacaataaa tactacgcag actccgtgaa gggccgattc 1560
 accatctcca gagacaattc caagaacacg ctgtatctgc aaatgaacag cctgagagct 1620
 gaggacacgg ctatatatta ctgtcgagg accggctggc tggggccctt tgactactgg 1680

 ggccagggaa ccctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740
 ggcggtggcg gctccggtgg aggcggttct gaaattgtgt tgacgcagtc tccaggcacc 1800
 ctgtctttgt ctccaggga aagagccacc ctctctgca gggccagtca gagtgttggc 1860
 agcagctact tagcctggtg ccagcagaaa cctggccagg ctcccaggct cctcatctat 1920
 ggtgcattca gcaggccac tggcatcca gacaggttca gtggcagtgg gtctgggaca 1980
 gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgtg ttactgtcag 2040

cagtatggta gctcaccgtg gacgttcggc caagggacca aggtggaaat caaa

2094

<210> 54

<211> 698

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 54

Gln 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 Ser Phe Ser Ser Tyr

20 25 30

Trp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Cys Ile Thr Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala

50 55 60

Lys Arg Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Thr

65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Thr Arg Ala Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

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

115 120 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr

145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr

165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln

180 185 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 195 200 205
 Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 210 215 220
 Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
 225 230 235 240
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 245 250 255
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 260 265 270
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser
 305 310 315 320
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 340 345 350
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 355 360 365
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 370 375 380
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 405 410 415
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 420 425 430
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly

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

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

 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile
 580 585 590
 Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
 595 600 605
 Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu
 610 615 620
 Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr

 625 630 635 640
 Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
 645 650 655
 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
 660 665 670
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Trp Thr
 675 680 685
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

690

695

<210> 55

<211> 651

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 55

gacatccaga tgaccacgtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc aggccagtc gagcatttac agctacttaa actggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatggt gcatccaatc tggcatctgg ggtcccatca 180
aggttcagt gtcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttacta ctgtcaaagc agttgggtga gtggtgctgt tggtaatgct 300
ttcggcggag ggaccaaggt ggagatcaaa cgtacgggtg ctgcaccatc tgtcttcac 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttggtg cctgctgaat 420
aacttctatc ccagagagcg caaagtacag tggaagggtg ataacgcct ccaatcgggt 480
aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540
accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600
catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<210> 56

<211> 217

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 56

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	Gln	Ser
Ile	Tyr	Ser	Tyr
20	25	30	
Leu	Asn	Trp	Tyr
Gln	Gln	Lys	Pro
Gly	Lys	Ala	Pro
Lys	Leu	Leu	Ile
35	40	45	
Tyr	Gly	Ala	Ser
Asn	Leu	Ala	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 Gln Ser Ser Trp Leu Ser Gly Ala
 85 90 95
 Val Gly Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110
 Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
 115 120 125
 Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro

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

195 200 205
 Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 57

<211> 2094

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 57

caggagcagg tgaaggagac cgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag ccctctggatt caccatcagc agctatggag tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtcgcattg atttttcccg ggattggttt caaagactac	180
gcgagctggg tgaatggccg gttcaccctc tccagcgaca acgcccagaa cactgtggaa	240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatttg	300

gacttgtggg gccagggaac cctggtcacc gtctcgagcg ctagcaccaa gggcccatcg 360
gtcttcccc tggcaccttc ctcaagagc acctctgggg gcacagcggc cctgggctgc 420
ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480
agcggcgtgc acaccttccc ggctgtccta cagtccctcag gactctactc cctcagcagc 540
gtggtgaccg tgcctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 600
aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 660

acatgcccac cgtgcccagc acctgaagcc gcggggggcac cgtcagtcct cctcttcccc 720
ccaaaaccca aggacacctt catgatctcc cggacccttg aggtcacatg cgtggtggtg 780
gacgtgagcc acgaagacc ttaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 900
gtcctcaccg tctgcacca ggactggctg aatggcaagg agtacaagt gcggtctcc 960
aacaagccc tccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020
gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtaaaagg ctctctatcc agcgacatcg ccgtggagtg ggagagcaat 1140
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggtccttc 1200
ttctctata gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1260
tgctccgtga tgcatgagcg tctgcacaac cactacacgc agaagagcct ctccctgtct 1320
ccgggtggcg gtggagggtc cggcggtggt ggatcccagg tgcaattggt ggagtctggg 1380
ggaggcgtgg tccagcctgg gaggtccctg agactctcct gtgcagcctc tggattcacc 1440
ttcagtagct atactatgca ctgggtccgc caggctccag gcaaggggct ggagtgggtg 1500

acatttatat catatgatgg aaacaataaa tactacgcag actccgtgaa gggccgattc 1560
accatctcca gagacaattc caagaacacg ctgtatctgc aaatgaacag cctgagagct 1620
gaggacacgg ctatatatta ctgtgcgagg accggctggc tggggccctt tgactactgg 1680
ggccagggaa ccttggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740
ggcgggtggcg gctccggtgg aggcgggttct gaaatttgtt tgacgcagtc tccaggcacc 1800
ctgtctttgt ctccagggga aagagccacc ctctcctgca gggccagtca gagtgttggc 1860
agcagctact tagcctggta ccagcagaaa cctggccagg ctcccaggt cctcatctat 1920

ggtgcattca gcagggccac tggcatccca gacaggttca gtggcagtgg gtctgggaca 1980
gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgtt ttactgtcag 2040
cagtatggta gtcaccgtg gacgttcggc caagggacca aggtggaaat caaa 2094

<210> 58

<211> 698

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 58

Gln Glu Gln Val Lys 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 Ile Ser Ser Tyr

20 25 30

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

35 40 45

Ala Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val

50 55 60

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

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 Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

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

115 120 125

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

130 135 140

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr

145 150 155 160

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr

165 170 175

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln

180 185 190

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp

195 200 205

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro

210

215

220

Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro

225

230

235

240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

245

250

255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn

260

265

270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg

275

280

285

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

290

295

300

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

305

310

315

320

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

325

330

335

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

340

345

350

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

355

360

365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu

370

375

380

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

385

390

395

400

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

405

410

415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr

420

425

430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gly Gly Gly Gly Ser Gly

435

440

445

Gly Gly Gly Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val

450 455 460
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr

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

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

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

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

<210> 59

<211> 648

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 59

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc agtccagtc gagtggttat agtaactact taccctggta tcagcagaaa 120

ccagggaag ttctaagct cctgatctat tatgcatcca ctctggcatc tgggggccca 180
tctcggttca gtggcagtg atctgggaca gatttcactc tcaccatcag cagcctgcag 240
cctgaagatg ttgcaactta ttactgtgca ggcggttata gtagtagtac tcgtgctttc 300
ggcggaggga ccaaggtgga gatcaaacgt acggtggctg caccatctgt ctcatcttc 360
ccgcatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacagaaaa cacaaagtct acgcctgcga agtcacccat 600
cagggcctga gctcgcccggt cacaagagc ttcaacaggg gagagtgt 648

<210> 60

<211> 216

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 60

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 Ser Ser Pro Ser Val Tyr Ser Asn

20 25 30

Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu

35 40 45

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

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln

65 70 75 80
 Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Ser Ser Ser
 85 90 95

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

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

<210> 61

<211> 2121

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 61

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60
tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag	120
gtccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt	180
tactacgcga gctgggcgaa aggccgggtc accatctcca gagacaattc caagaacacg	240
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga	300
gccgctaata ctgatactac ctactttaac ttgtggggcc aggggaaccct ggtcacgcgc	360

tcgagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctctc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg	480
gtgtcgtgga actcaggcgc cctgaccagc ggcggtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tciactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaa cccagcaaca ccaaggtgga caagagagtt	660
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg	720
ggggcaccgt cagtcttctt cttccccca aaaccaagg acacctcat gatctcccgg	780
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagacctga ggtcaagttc	840
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	900
tacaacagca cgtaccgtgt ggtcagcgtc ctaccgtcc tgcaccagga ctggctgaat	960
ggcaaggagt acaagtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc	1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acacctgcc cccatcccgg	1080
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	1200
cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc	1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggtctt gcacaaccac	1320
tacacgcaga agagcctctc cctgtctccg ggtggcgggtg gagggctccg cggtggtgga	1380
tcccaggtgc aattggtgga gtctggggga ggcgtggtcc agcctgggag gtccctgaga	1440
ctctcctgtg cagcctctgg attcaccttc agtagctata ctatgactg ggtccgccag	1500
gtctcaggca aggggctgga gtgggtgaca ttatatacat atgatgaaa caataatac	1560
tacgcagact ccgtgaaggg ccgattcacc atctccagag acaattcaa gaacacgtg	1620
tatctgcaaa tgaacagcct gagagctgag gacacggcta tatattactg tgcgaggacc	1680
ggctggctgg gccctttga ctactggggc cagggaaacc tggtcaccgt ctcgagcgg	1740
ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggttctgaa	1800
attgtgttga cgcagtctcc aggcaccttg tctttgtctc caggggaaag agccaccctc	1860
tcctgcaggg ccagtcagag tgttggcagc agctacttag cctggtacca gcagaaacct	1920
ggccaggtct ccaggtcct catctatggt gcattcagca gggccactgg catcccagac	1980
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag actggagcct	2040
gaagattttg cagtgtatta ctgtcagcag tatggtagct caccgtggac gttcggccaa	2100

gggaccaagg tggaaatcaa a

2121

<210> 62

<211> 707

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<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 Ser Ser Ser

20 25 30

His Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

35 40 45

Ile Ala Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser

50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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

Tyr Cys Ala Arg Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro

115 120 125

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

130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr

145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro

165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn

195 200 205
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala

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

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

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

 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 435 440 445

Ser Pro Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
 450 455 460
 Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
 465 470 475 480
 Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Thr Met His
 485 490 495
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Thr Phe Ile
 500 505 510
 Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg
 515 520 525
 Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
 530 535 540
 Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Thr
 545 550 555 560
 Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 565 570 575
 Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 580 585 590
 Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly
 595 600 605
 Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala
 610 615 620
 Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 625 630 635 640
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Phe Ser Arg Ala Thr
 645 650 655
 Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 660 665 670
 Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 675 680 685
 Gln Gln Tyr Gly Ser Ser Pro Trp Thr Phe Gly Gln Gly Thr Lys Val

690 695 700

Glu Ile Lys

705

<210> 63

<211> 654

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 63

gcctatgata tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aggccagtc gagcattaac aaccaactat cctggtatca gcagaaacca 120

gggaaagtgc ctaagtcct gatctatggt gcatccactc tggcatctgg ggtcccatct 180

cggttcaccg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcatgtt cattattgca gtggtggttag ttgtttttgg 300

gctttcggcg gagggaccaa ggtggagatc aaacgtacgg tggctgcacc atctgtcttc 360

atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 420

aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 480

ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 540

agcacctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgt 654

<210> 64

<211> 218

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 64

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asn Asn Gln

20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile

Tyr Gly Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Thr 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 His Val His Tyr Cys Ser Gly Gly
 85 90 95
 Ser Cys Phe Trp Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 65

<211> 57

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400

> 65

atgaaacacc tgtggttctt cctcctcctg gtggcagctc ccagatgggt cctgtcc

57

<210> 66

<211> 19

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 66

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1 5 10 15

Val Leu Ser

<210> 67

<211> 57

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 67

atggctgtct tggggctgct cttctgcctg gtgacattcc caagctgtgt cctatcc 57

<210> 68

<211> 19

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 68

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys

1 5 10 15

Val Leu Ser

<210> 69

<211> 60

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 69

atgagggcc cgtctcagtt tcttggttc ttgcttttct ggattccagc ctccagaagt 60

<210> 70

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 70

Met Arg Ala Pro Ala Gln Phe Leu Gly Phe Leu Leu Phe Trp Ile Pro

1 5 10 15

Ala Ser Arg Ser

20

<210> 71

<211> 738

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 71

cagggtgcaat tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300

tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc gagcgggtgga 360

ggcggatctg gcggaggtgg ttccggcggg ggcggtccg gtggaggcgg ttctgaaatt 420

gtgttgacgc agtctccagg caccctgtct ttgtctccag gggaaagagc caccctctcc 480

tgcagggccca gtcagagtgt tggcagcagc tacttagcct ggtaccagca gaaacctggc 540

caggctccca ggctcctcat ctatggtgca ttcagcaggg cactggcat ccagacagg 600

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa 660

gattttgcag tgtattactg tcagcagtat ggtagctcac cgtggacgtt cggccaaggg 720

accaaggtgg aaatcaaa 738

<210> 72

<211> 246

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 72

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

245

<210> 73

<211> 732

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 73

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gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc      60
tcctgtacag cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct      120
ccaggaagg ggctggagta catcggtac attggtgata ctactggcat agcctacgcg      180

agctgggcga atggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt      240
caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggctggtcc      300
tacttagaca tctggggcca agggaccctg gtcaccgtct cgagcgttg aggcggtatct      360
ggcggagggtg gttccggcgg tggcggtcc ggtggaggcg gctctgccct tgtgatgacc      420
cagtctccat cctccctgtc tgcctctgta ggagacagag tcaccatcac ttgccaggcc      480
agtcagaaca ttacagcaa ttagcctgg tatcagcaga aaccaggga agttcctaag      540
ctctgatct atcaggcctc cactctggca tctgggtcc catctcggtt cagtggcagt      600

ggatatggga cagatttcac tctcaccatc agcagcctgc agcctgaaga tgttgcaact      660
tattactgtc aaggcggtta ttatagtgt gcccttaata ctttcggcgg agggaccaag      720
gtggagatca aa      732

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<210> 74

<211> 244

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 74

```

Glu Val Gln Leu Val 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 Leu Ser Ser Tyr

20           25           30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile
35           40           45

```

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

<210> 75

<211> 750

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 75

gaggtgcagc tggtaggagtc tgggggaggc ttggtccagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120
 gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggcgag aggcagattc accatctccg aaacctcaa gaacacggtg 240
 actcttcaaa tgaacagcct gagagccgag gactcgctg tgtattactg tgcgagaaat 300
 ctttacactt acaatagctt gtggggccag ggaacctgg tcaccgtctc gagcggtgga 360
 ggcggtatctg gcggagggtg ttccggcggt ggcggtctcg gtggaggcgg ctctgacatc 420
 cagatgacct agtctcttc caccctgtct gcatctgtag gagacagagt caccatcact 480
 tgccagtcca gtcagagtgt ttatgataac aactggttag cctggtatca gcagaaacca 540
 gggaaagccc ctaagctcct gatctataca gtatccactc tggcatctgg ggtcccatca 600

aggttcagcg gcagtggatc tgggacagaa ttcactctca ccatcagcag cctgcagcct 660
 gatgatattg caacttatta ctgccaaggc acttattata gtagtggttg gaactttgct 720
 ttcggcgag ggaccaaggt ggagatcaaa 750

<210> 76

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 76

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Ser Gly

20 25 30

Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu

35 40 45

Ile Ala Cys Ile Tyr Ala Gly Thr Ser Gly Ser Thr Ser Tyr Ala Ser

50 55 60

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

65 70 75 80

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

85

90

95

Cys Ala Arg Asn Leu Tyr Thr Tyr Asn Ser Leu Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
 130 135 140
 Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr

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

210 215 220
 Thr Tyr Tyr Cys Gln Gly Thr Tyr Tyr Ser Ser Gly Trp Asn Phe Ala
 225 230 235 240
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 245 250

<210> 77

<211> 729

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 77

caggagcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60

tcctgtacag cctctggatt ctccctttagc agctactgga tgtgctgggt ccgccagget 120

ccaggggaagg ggctggagtg gatcgatgc attacactg gtagtggtag cacttactac 180

gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300

gacttgtggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcgga 360

ggtgggttccg gcggtggcgg ctccggtgga ggcggctctg acatccagat gacccagtct 420
ccatctctcc tgtctgcac tgtaggagac agagtcacca tcacttgcca ggccagtcag 480
agcatttaca gctacttaaa ctggtatcag cagaaaccag ggaaagcccc taagtcctg 540

atctatgggtg catccaatct ggcatctggg gtcccatcaa ggttcagtgg cagtggatct 600
gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660
tgtcaaagca gttggttgag tgggtctgtt ggtaatgctt tcggcggagg gaccaaggtg 720
gagatcaaa 729

<210> 78

<211> 243

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 78

Gln 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 Ser Phe Ser Ser Tyr
20 25 30

Trp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Cys Ile Thr Thr Gly Ser Gly Ser Thr Tyr Tyr Ala Ser Trp Ala
50 55 60

Lys Arg Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Thr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Ala Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
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 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

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

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Ser Ser
 210 215 220
 Trp Leu Ser Gly Ala Val Gly Asn Ala Phe Gly Gly Gly Thr Lys Val
 225 230 235 240
 Glu Ile Lys

<210> 79

<211> 759

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 79

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag 120

gtccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180
 tactacgcga gctgggcgaa aggccgggtc accatctcca gagacaattc caagaacacg 240
 ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300
 gccgctaata ctgatactac ctactttaac ttgtggggcc aggggaaccct ggtcaccgtc 360
 tcgagcgggtg gaggcggatc tggcggaggt ggttccggcg gtggcggctc cgggtggaggc 420
 ggctctgcct atgatatgac ccagtctcca tcttccctgt ctgcatctgt aggagacaga 480
 gtcacatca attgccaggc cagtcagagc attaacaacc aactatcctg gtatcagcag 540

aaaccaggga aagttcctaa gtccttgatc tatggtgcat ccactctggc atctggggtc 600
 ccatctcggg tcaccggcag tggatctggg acagatttca ctctcacat cagcagcctg 660
 cagcctgaag atgttgcaac ttattactgt catgttcatt attgcagtgg tggtagttgt 720

ttttgggctt tcggcggagg gaccaagggtg gagatcaaa

759

<210> 80

<211> 253

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 80

Glu Val Gln Leu Leu Glu Ser Gly Gly 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

His Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

35 40 45

Ile Ala Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser

50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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

Tyr Cys Ala Arg Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Tyr

130 135 140

Asp Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

145 150 155 160

Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Asn Asn Gln Leu Ser

165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr Gly

180 185 190

Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Thr Gly Ser Gly

195	200	205	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp			
210	215	220	
Val Ala Thr Tyr Tyr Cys His Val His Tyr Cys Ser Gly Gly Ser Cys			
225	230	235	240
Phe Trp Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys			
245	250		
<210> 81			
<211> 735			
<212> DNA			
<213> Artificial Sequence			
<220><223> synthesized			
<400> 81			
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tgtaccgcct ctggaatcga ccttaatacc tacgacatga tctgggtccg ccaggctcca			120
ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac			180
tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa			240
atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt			300
ggttcccact tgtggggcca gggaacctg gtcaccgtct cttccggtgg aggcggttca			360
ggcggaggtg gaagtgtgtg tggcggctct ggaggcggcg gatctgccta tgatatgacc			420
cagtcctcat cttccgtgtc tgcactgtga ggagacagag tcaccatcaa gtgtcaggcc			480
agtgaggaca tttatagctt cttggcctgg tatcagcaga aaccaggga agcccctaag			540
ctcctgatcc attctgcac ctctctggca tctgggtcc catcaaggtt cagcggcagt			600
ggatctggga cagatttcac tctcaccatc agcagcctgc agcctgaaga ttttgcaact			660
tactattgtc aacagggtta tggtaaaaat aatgttgata atgctttcgg cggagggacc			720
aaggtggaga tcaaa			735
<210> 82			
<211> 245			
<212> PRT			
<213> Artificial Sequence			
<220><223> synthesized			
<400> 82			

Gln Ser Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser

1 5 10 15

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

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

85 90 95

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr

100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

115 120 125

Gly Ser Gly Gly Gly Gly Ser Ala Tyr Asp Met Thr Gln Ser Pro Ser

130 135 140

Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Lys Cys Gln Ala

145 150 155 160

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

165 170 175

Lys Ala Pro Lys Leu Leu Ile His Ser Ala Ser Ser Leu Ala Ser Gly

180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln

210 215 220

Gln Gly Tyr Gly Lys Asn Asn Val Asp Asn Ala Phe Gly Gly Gly Thr

225 230 235 240

Lys Val Glu Ile Lys

245

<210> 83

<211> 528

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 83

aaagacaata cctcgaccac ggtggatctg caaatgaaca gcctgagagc tgaggacacg 60

gctgtgtatt actgtgcgag agattttatt agtggttccc acttgtgggg ccagggaaacc 120

ctggtcaccg tctcgagcgg tggaggcggg tctggcggag gtggttccgg cgggtggcggc 180

tccggtggag gcggttctgc ctatgatatg acccagtctc catcttccgt gtctgcatct 240

gtaggagaca gagtacccat caattgtcag gccagtgaga gcattagtag cttcttatcc 300

tggtatcagc agaaaccagg gaaagcccct aagctcctga tcttttctgc atccactctg 360

gcatctgggg tcccatcaag gttcagcggc agtggatctg ggacagattt cactctcacc 420

atcagcagcc tgcagcctga agattttgca acttactatt gtcaacaggg ttatagtaaa 480

agtaatgtgg ataatgcttt cggcggaggg accaaggtgg agatcaaa 528

<210> 84

<211> 246

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 84

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Ile Asp Leu 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

Gly Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

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

130 135 140

Ser Ser Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Asn Cys Gln

145 150 155 160

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

165 170 175

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

180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys

210 215 220

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

225 230 235 240

Thr Lys Val Glu Ile Lys

245

<210> 85

<211> 756

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 85

gagggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120

gtccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggatatcact 180

tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

tcggcgTTTT cgttcgacta cgccatggac ctctggggcc agggaaacct ggtcacctc 360

tcgagcgggtg gaggcggatc tggcggaggt ggttccggcg gtggcggctc cggtaggagc 420

ggctctgaca tccagatgac ccagtctcct tccacctgt ctgcatctgt aggagacaga 480

gtcaccatca cttgccaggc cagtcagagc attagttccc acttaactg gtatcagcag 540

aaaccagga aagcccctaa gctcctgac tataaggcat ccactctggc atctggggtc 600

ccatcaaggt tcagcggcag tggatctggg acagaattta ctctcaccat cagcagcctg 660

cagcctgatg attttgcaac ttattactgc caacagggtt atagtgggg taatgttgat 720

aatgttttcg gcggaggac caaggtggag atcaaa 756

<210> 86

<211> 252

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<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 Ser Phe Ser Ser Gly

20 25 30

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

35 40 45

Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn

50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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

Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

115 120 125
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 130 135 140
 Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg
 145 150 155 160

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

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

<210> 87

<211> 750

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 87

gagggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt ctccctcagt agctactgga tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg gatcggagtc attgatacta atgtttatat atactacgcg 180

aactgggcaa aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
 caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag atatgtgggt 300
 aataatgatg attatattaa cttgtggggc cagggaaccc tggtcaccgt ctgcagcgggt 360
 ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggtctgac 420
 atccagatga cccagtcctc ttccacctg tctgcatctg taggagacag agtcaccatc 480
 acttgccagt ccagtcagag tgtttataat ggctactggt tatcctggta tcagcagaaa 540

ccagggaag ccctaagct cctgatctat ggtgcatcca ctctggcatc tggggtccca 600

tcaaggttca gcggcagtgg atctgggaca gaattcactc tcaccatcag cagcctgcag 660

cctgatgatt ttgcaactta ttactgccta ggcagttata ctagtagtac tgagaactct 720

ttcggcggag ggaccaaggt ggagatcaaa 750

<210> 88

<211> 250

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 88

Glu Val Gln Leu Val Glu Ser 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 Leu Ser Ser Tyr

20 25 30

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

35 40 45

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

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr

130 135 140

Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile

145 150 155 160

Thr Cys Gln Ser Ser Gln Ser Val Tyr Asn Gly Tyr Trp Leu Ser Trp

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

210 215 220
Ala Thr Tyr Tyr Cys Leu Gly Ser Tyr Thr Ser Ser Thr Glu Asn Ser
225 230 235 240
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 89

<211> 741

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 89

gaggtgcagc tgggtggagtc tgggggaggc ttgggtccagc ctgggggggtc cctgagactc 60
tcctgtacag tgtctggaat cgacctcagt gtcacatcaata tgggctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180
agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240
accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tgggtactatt 300
tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagcgggtgga 360
ggcggatctg gcggagggtg ttccggcggt ggcggctccg gtggaggcgg ctctgcattc 420
gaattgacct agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcaag 480
tgccaggcca gtgaaagcat tagcaactac ttatcctgggt atcagcagat tccagggaaa 540

gttctaagc tctgatcta ttatgcatcc aatctggcat ctgggggtccc atctcggttc 600
agtggcagtg gatctgggac agatttcaact ctacacatca gcagcctgca gcctgaagat 660
gttgcaactt attactgtca aagctattat ggtgggtgga gtgcctatac tttcggcgga 720
gggaccaagg tggagatcaa a 741

<210> 90

<211> 247

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 90

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Ile Asp Leu Ser Val Ile

20 25 30

Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35 40 45

Gly Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

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

130 135 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Lys

145 150 155 160

Cys Gln Ala Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln

165 170 175

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

180 185 190

Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

195 200 205

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

210 215 220
Tyr Cys Gln Ser Tyr Tyr Gly Gly Gly Ser Ala Tyr Thr Phe Gly Gly
225 230 235 240
Gly Thr Lys Val Glu Ile Lys
245
<210> 91
<211> 354
<212> DNA
<213> Artificial Sequence
<220><223> synthesized
<400> 91
cagggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctatacta tgcactgggt cgcgcaggct 120

ccaggcaagg ggctggagtg ggtgacattt atatcatatg atggaaacaa taaatactac 180
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agctgaggac acggctatat attactgtgc gaggaccggc 300
tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctca 354
<210> 92
<211> 118
<212> PRT
<213> Artificial Sequence
<220><223> synthesized
<400> 92
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

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

65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys			
85	90	95	
Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr			
100	105	110	
Leu Val Thr Val Ser Ser			
115			
<210>	93		
<211>	324		
<212>	DNA		
<213>	Artificial Sequence		
<220><223>	synthesized		
<400>	93		
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60			
ctctcctgca gggccagtc gagtgttggc agcagctact tagcctggta ccagcagaaa 120			
cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180			
gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240			
cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300			
caagggacca aggtggaaat caaa 324			
<210>	94		
<211>	108		
<212>	PRT		
<213>	Artificial Sequence		
<220><223>	synthesized		
<400>	94		
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly			
1	5	10	15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser			
20	25	30	
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu			
35	40	45	
Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser			

50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 95
 <211> 345
 <212> DNA
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 95

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60
 tcctgtacag ccctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120
 ccaggaagg ggctggagta catcggtac attggtgata ctactggcat agcctacgcg 180

agctgggcga atggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt 240
 caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggctggtcc 300
 tacttagaca tctggggcca agggaccctg gtcaccgtct cgagc 345

<210> 96
 <211> 115
 <212> PRT
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 96

Glu Val Gln Leu Val 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 Leu Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Ile
 35 40 45

Gly Tyr Ile Gly Asp Thr Thr Gly Ile Ala Tyr Ala Ser Trp Ala Asn

[illegible]

35 40 45
Tyr Gln Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Tyr 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 Gln Gly Gly Tyr Tyr Ser Ala Ala

85 90 95
Leu Asn Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 99

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 99

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggcgag aggcagattc accatctccg aaacctcaa gaacacggtg 240

actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300

ctttacactt acaatagctt gtggggccag ggaacctgg tcaccgtctc gaggc 354

<210> 100

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 100

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Ser Gly

20 25 30

Tyr Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu

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

Cys Ala Arg Asn Leu Tyr Thr Tyr Asn Ser Leu Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

<210> 101

<211> 336

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 101

gacatccaga tgaccagtc tcttccacc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc agtccagtc gagtggttat gataacaact ggtagcctg gtatcagcag 120
 aaaccaggga aagccctaa gctcctgac tatacagtat ccactctggc atctggggtc 180

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240
 cagcctgatg attttgcaac ttattactgc caaggcactt attatagtag tggttggaac 300
 ttgcttttcg gcggaggac caaggtggag atcaaa 336

<210> 102

<211> 112

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 102

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Val Tyr Asp Asn

20	25	30	
Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu			
35	40	45	
Leu Ile Tyr Thr Val Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe			
50	55	60	
Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu			
65	70	75	80
Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Thr Tyr Tyr Ser			
85	90	95	
Ser Gly Trp Asn Phe Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys			
100	105	110	
<210> 103			
<211> 339			
<212> DNA			
<213> Artificial Sequence			
<220><223> synthesized			
<400> 103			
caggagcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc	60		
tcctgtacag cctctggatt ctcttttagc agctactgga tgtgctgggt ccgccaggct	120		
ccaggaagg ggctggagtg gatcggatgc attacgactg gtagtggtag cacttactac	180		
gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact	240		
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt	300		
gacttgtggg gccaggaac cctggtcacc gtctcgagc	339		
<210> 104			
<211> 113			
<212> PRT			
<213> Artificial Sequence			
<220><223> synthesized			
<400> 104			
Gln 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 Ser Phe Ser Ser Tyr			

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

85 90 95
 Thr Arg Ala Phe Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 100 105 110
 Ser

<210> 105

<211> 330

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 105

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc aggccagtc gagcatttac agctacttaa actggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatggt gcatccaatc tggcatctgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttacta ctgtcaaagc agttggttga gtggtgctgt tggtaatgct 300
 ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 106

<211> 110

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 106

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 Gln Ser Ile Tyr Ser Tyr

20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Asn Leu Ala 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 Gln Ser Ser Trp Leu Ser Gly Ala

85 90 95
Val Gly Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 107

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 107

gagggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60
tcctgtgcag cccttgatt cacccttagc agcagccact ggatatgctg ggtccgccag 120
gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180

tactacgcga gctgggcgaa aggccgggtc accatctcca gagacaattc caagaacacg 240
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300
gccgctaata ctgatactac ctactttaac ttgtggggcc aggggaaccct ggtcaccgtc 360
tcgagc 366

<210> 108

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<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 Ser Ser Ser

20 25 30

His Trp Ile Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp

35 40 45

Ile Ala Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser

50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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

Tyr Cys Ala Arg Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu Trp

100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 109

<211> 333

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 109

gcctatgata tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aggccagtc gagcattaac aaccaactat cctggtatca gcagaaacca 120

gggaaagtgc ctaagctcct gatctatggt gcatccactc tggcatctgg ggtcccatct 180

cggttcaccg gcagtggatc tgggacagat ttcactetca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcatgtt cattattgca gtggtggtag ttgtttttgg 300

gctttcggcg gagggaccaa ggtggagatc aaa 333

<210> 110

<211> 111

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 110

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

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

<210> 111

<211> 345

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 111

cagtcggtgg aggagtctgg gggaggcttg gtccagcctg gggggtcct gagactctcc 60
tgtaccgcct ctggaatcga ccttaatacc tacgacatga tctgggtccg ccaggtccca 120

ggcaaggggc tagagtgggt tggaatcatt acttatagtg gtagtagata ctacgcgaac 180
tgggcgaaag gccgattcac catctccaaa gacaatacca agaacacggt gtatctgcaa 240
atgaacagcc tgagagctga ggacacggct gtgtattact gtgcgagaga ttatatgagt 300
ggttcccact tgtggggcca gggaaccctg gtcaccgtct cttcc 345

<210> 112

<211> 115

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 112

Gln Ser Val Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
1 5 10 15

Leu Arg Leu Ser Cys Thr Ala Ser Gly Ile Asp Leu Asn Thr Tyr Asp
20 25 30

Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly
35 40 45

Ile Ile Thr Tyr Ser Gly Ser Arg Tyr Tyr Ala Asn Trp Ala Lys Gly
50 55 60

Arg Phe Thr Ile Ser Lys Asp Asn Thr Lys Asn Thr Val Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Asp Tyr Met Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 113

<211> 330

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 113

gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcacaccttc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggatatggta aaaataatgt tgataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 114

<211> 110

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 114

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Lys Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

His Ser Ala Ser Ser Leu Ala 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 Gln Gln Gly Tyr Gly Lys Asn Asn
85 90 95

Val Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 115

<211> 348

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 115

caggtgcagc tgggtggagtc tgggggaggc ctggtccagc ctgggggctc cctgagactc 60
tcctgtacaa cttctggaat cgaccttagt acctacgaca tgatctgggt ccgccaggct 120
ccaggcaagg ggctagagtg ggtgggaatc attagttatg ttgtaaacac atactacgcg 180

agctgggcga aaggccgatt caccctctcc aaagacaata cctcgaccac ggtggatctg 240
caaatgaaca gcctgagagc tgaggacacg gctgtgtatt actgtgcgag agattttatt 300
agtgggtccc acttgtgggg ccagggaacc ctggtcaccg tctcgagc 348

<210> 116

<211> 116

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 116

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Thr Ser Gly Ile Asp Leu 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

Gly Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys

50 55 60

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

65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Phe Ile Ser Gly Ser His Leu Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

<210> 117

<211> 330

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 117

gcctatgata tgaccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaattgtc aggccagtga gagcattagt agcttcttat cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatcttttct gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatagta aaagtaatgt ggataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa 330

<210> 118

<211> 110

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 118

Ala Tyr Asp Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Glu Ser Ile Ser Ser Phe

20 25 30

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

35 40 45

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

85 90 95

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

100 105 110

<210> 119

<211> 366

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 119

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggatatcact 180

tacgacgcga actgggcgaa aggccgggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

tcggcgtttt cgttcgacta cgccatggac ctcctggggcc aggggaaccct ggtcacccgtc 360

tcgagc 366

<210> 120

<211> 122

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<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 Ser Phe Ser Ser Gly
20 25 30

Tyr Asp Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Ala Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn
50 55 60

Trp Ala Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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

Tyr Cys Ala Arg Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 121

<211> 330

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 121

gacatccaga tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtc gagcattagt tccacttaa actggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa ttactctca ccatcagcag cctgcagcct 240

gatgatTTTg caacttatta ctgccaacag ggttatagtt ggggtaatgt tgataatgtt 300
 TTCggcggag ggaccaaggt ggagatcaaa 330

<210> 122
 <211> 110
 <212> PRT
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 122

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly

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

<210> 123
 <211> 357
 <212> DNA
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 123

gaggtgcagc tggTggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60
 tcctgtgcag cctctggatt ctccctcagt agctactgga tgagctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcgagtc attgatacta atgtttatat atactacgcg 180
 aactgggcaa aaggcagatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgagc atatgtgggt 300
 aataatgatg attatattaa cttgtggggc cagggaaccc tggtcaccgt ctcgagc 357
 <210> 124
 <211> 119
 <212> PRT
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 124
 Glu Val Gln Leu Val Glu Ser 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 Leu Ser Ser Tyr
 20 25 30
 Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Val Ile Asp Thr Asn Val Tyr Ile Tyr Tyr Ala Asn Trp Ala Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115
 <210> 125
 <211> 333
 <212> DNA
 <213> Artificial Sequence
 <220><223> synthesized
 <400> 125
 gacatccaga tgacccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
 atcacttgcc agtcaggatc gagtggttat aatggctact gggtatcctg gtatcagcag 120

aaaccaggga aagcccctaa gctcctgac tatggtgcat ccactctggc atctggggtc 180
ccatcaagg tccagcgagc tggatctggg acagaattca ctctcaccat cagcagcctg 240
cagcctgatg attttgcaac ttattactgc ctaggcagtt atactagtag tactgagaac 300
tccttcggcg gagggaccaa ggtggagatc aaa 333

<210> 126

<211> 111

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 126

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

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

Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Leu Gly Ser Tyr Thr Ser
85 90 95
Ser Thr Glu Asn Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 127

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 127

gaggtgcagc tgggtggagtc tgggggaggc ttggtccagc ctggggggtc cctgagactc 60
tcctgtacag tgctctggaat cgacctcagt gtcacataa tgggctgggt ccgccaggct 120

ccaggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180
agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240
accagtccga caaccgagga caggctgtg tattactgtg cgagagaatc tggactatt 300
tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gage 354

<210> 128

<211> 118

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 128

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Val Ser Gly Ile Asp Leu Ser Val Ile
20 25 30

Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu Lys Ile
65 70 75 80

Thr Ser Pro Thr Thr Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu
85 90 95

Ser Gly Thr Ile Tyr Tyr Ser Tyr Phe Asn Leu Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 129

<211> 327

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 129

gcattcgaat tgaccacgtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgcc aggccagtga aagcattagc aactacttat cctggtatca gcagattcca 120

gggaaagttc ctaagctcct gatctattat gcatccaatc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttcactetca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaagc tattatgggtg gtggtagtgc ctatactttc 300

ggcggaggga ccaaggtgga gatcaaa 327

<210> 130

<211> 109

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 130

Ala Phe Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

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

20 25 30

Leu Ser Trp Tyr Gln Gln Ile Pro Gly Lys Val Pro Lys Leu Leu Ile

35 40 45

Tyr Tyr Ala Ser Asn Leu Ala 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 Gln Ser Tyr Tyr Gly Gly Gly Ser

85 90 95

Ala Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

100 105

<210> 131

<211> 339

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 131

caggagcagg tgaaggagac cgggggaggc ttggtacagc ctggggggtc cctgagactc 60

tcctgtgcag cctctggatt caccatcagc agctatggag tgagctgggt ccgccaggct 120
ccaggaagg ggctggagtg ggtcgcattg atttttcccg ggattggttt caaagactac 180

gcgagctggg tgaatggccg gttcacctc tccagcgaca acgcccagaa cactgtggaa 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagatttg 300
gacttgtggg gccaggaac cctggtcacc gtctcgagc 339

<210> 132

<211> 113

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 132

Gln Glu Gln Val Lys 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 Ile Ser Ser Tyr

20 25 30

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

35 40 45

Ala Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val

50 55 60

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

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 Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser

100 105 110

Ser

<210> 133

<211> 327

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 133

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtccagtc gagtggttat agtaactact tatcctggta tcagcagaaa 120

ccagggaag ttctaagct cctgatctat tatgcatcca ctctggcatc tggggtccca 180

tctcggttca gtggcagtg atctgggaca gatttcactc tcaccatcag cagcctgcag 240

cctgaagatg ttgcaactta ttactgtgca ggcgggtata gtagtagtac tcgtgctttc 300

ggcggaggga ccaaggtgga gatcaaa 327

<210> 134

<211> 109

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 134

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 Ser Ser Pro Ser Val Tyr Ser Asn

20 25 30

Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu

35 40 45

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

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln

65 70 75 80

Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly Gly Tyr Ser Ser Ser

85 90 95

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

100 105

<210> 135

<211> 987

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 135

gctagcacca agggcccatc ggtcttcccc ctggcacctt cctccaagag cacctctggg	60
ggcacagcgg ccttgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg	120
tggaaactcag gcgccctgac cagcggcgtg cacaccttcc cggtgtcct acagtctca	180
ggactctact cctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc	240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc	300
aaatcttgtg acaaaactca cacatgccc cctgtcccag cacctgaact cctgggggga	360
ccgtcagtct tctcttccc cccaaaacc aaggacaccc tcatgatctc ccggaccctt	420
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg	480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac	540
agcacgtacc gtgtggtcag cgtcctcacc gtctgcacc aggactggct gaatggcaag	600
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc	660
aaagccaaag ggcagcccg agaaccacag gtgtacacc tgccccatc ccgggatgag	720
ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc	780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg	840
ctggactccg acggctcctt ctctctctat agcaagctca ccgtggacaa gagcaggtgg	900
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg	960
cagaagagcc tctccctgtc tccgggt	987

<210> 136

<211> 329

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 136

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

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

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

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

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

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

305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly

325

<210> 137

<211> 987

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 137

gctagcacca agggcccatc ggtcttcccc ctggcacccct cctccaagag cacctctggg 60
ggcacagcgg ccttgggctg cctggtaag gactacttcc ccgaaccggt gacgggtgctg 120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggtctgctt acagtctca 180
ggactctact cctcagcag cgtggtgacc gtgcctcca gcagcttggg caccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300
aaatcttgtg aaaaaactca cacatgcca cctgcccag cacctgaagc gcggggggca 360
ccgtcagtct tctcttccc ccaaaaacc aaggacacce tcatgatctc ccggaccct 420
gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc gcggggagga gcagtacaac 540
agcacgtacc gtgtggtcag cgtcttcacc gtctgcacc aggactggct gaatggcaag 600
gagtacaagt gcgcggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660

aaagccaaag ggcagccccc agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720
ctgaccaaga accaggtcag cctgacctgc ctggtaaaag gcttctatcc cagcgacatc 780
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840
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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr

65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys

100 105 110

Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro

115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys

130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp

145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu

165 170 175

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

180 185 190

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

195 200 205

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

210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu

225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
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tctgggacag atttactct caccatcagc agcctgcagc ctgaagatgt tgcaacttat 660
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20 25 30

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

35 40 45

Ala Leu Ile Phe Pro Gly Ile Gly Phe Lys Asp Tyr Ala Ser Trp Val

50 55 60

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

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 Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser

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 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu

130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro

145 150 155 160

Ser Val Tyr Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys

165 170 175

Val Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser Gly Val

180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gly

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Gly Tyr Ser Ser Ser Thr Arg Ala Phe Gly Gly Gly Thr Lys Val Glu

225

230

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Ile Lys

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Ser Ser Tyr Thr Met His

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Thr Gly Trp Leu Gly Pro Phe Asp Tyr

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Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala

1 5 10

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Gly Ala Phe Ser Arg Ala Thr

1 5

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Gln Gln Tyr Gly Ser Ser Pro Trp Thr

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Asn Thr Tyr Asp Met Ile

1 5

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Asp Tyr Met Ser Gly Ser His Leu

1 5

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Ser Ala Ser Ser Leu Ala Ser

1 5

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Ser Ala Ser Ser Leu Ala Ser

1 5

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Ser Gly Tyr Asp Met Cys

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Cys Ile Ala Ala Gly Ser Ala Gly Ile Thr Tyr Asp Ala Asn Trp Ala

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Lys Gly

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Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu

1 5 10

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Lys Ala Ser Thr Leu Ala Ser

1 5

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Gln Gln Gly Tyr Ser Trp Gly Asn Val Asp Asn Val

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Ser Thr Tyr Asp Met Ile

1 5

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Ile Ile Ser Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

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Asp Phe Ile Ser Gly Ser His Leu

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Ser Ala Ser Thr Leu Ala Ser

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Ser Ser Tyr Trp Met Ser

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Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu

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Gly Ala Ser Thr Leu Ala Ser

1 5

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Leu Gly Ser Tyr Thr Ser Ser Thr Glu Asn Ser

1 5 10

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Ser Val Ile Asn Met Gly

1 5

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Thr Ile Thr Tyr Val Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly

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Tyr Ala Ser Asn Leu Ala Ser

1 5

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1 5 10

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Ser Gly Tyr Trp Ile Cys

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Thr Val Ser Thr Leu Ala Ser

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Ser Ser Tyr Trp Met Cys

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Gly Ala Ser Asn Leu Ala Ser

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Ser Ser Tyr Gly Val Ser

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Tyr Ala Ser Thr Leu Ala Ser

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Ala Gly Gly Tyr Ser Ser Ser Thr Arg Ala

1 5 10

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<211

> 6

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Ser Ser His Trp Ile Cys

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Cys Ile Tyr Thr Gly Ser Ile Asp Val Phe Tyr Tyr Ala Ser Trp Ala

1 5 10 15

Lys Gly

<210> 203

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Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu

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His Val His Tyr Cys Ser Gly Gly Ser Cys Phe Trp Ala

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