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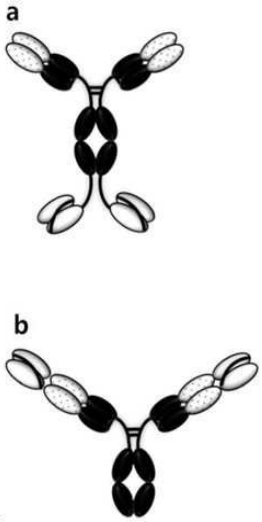
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(54) 발명의 명칭 **이중특이성 항체 및 이의 제조 및 사용 방법**

(57) 요 약

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.

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명 세 서

청구범위

청구항 1

중쇄 및 경쇄를 갖는 IgG 도메인, 및 중쇄의 C-말단 또는 경쇄의 N-말단에 연결되어있는 2개의 scFv 성분을 포함하는 이중특이성 항체(bispecific antibody)로서, 여기서 IgG 도메인이 제1 항원에 대한 제1 결합 특이성을 갖고, 여기서 scFv 성분이 제2 항원에 대한 제2 결합 특이성을 가지며, 여기서 제1 항원 및 제2 항원이 상이하고 α-CTLA4, α-PD-1 및 α-PD-L1으로부터 독립적으로 선택되는, 이중특이성 항체.

청구항 2

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

청구항 3

제2항에 있어서, 제1 항원이 α-CTLA4를 포함하고 제2 항원이 α-PD-1 또는 α-PD-L1을 포함하는, 이중특이성 항체.

청구항 4

제2항에 있어서, 제1 항원이 α-PD-1 또는 α-PD-L1을 포함하고 제2 항원이 α-CTLA4를 포함하는, 이중특이성 항체.

청구항 5

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

청구항 6

제5항에 있어서, 제 1항원이 α-PD-1 또는 α-PD-L1을 포함하고 제2 항원이 α-CTLA4를 포함하는, 이중특이성 항체.

청구항 7

제5항에 있어서, 제1 항원이 α-CTLA4를 포함하고 제2 항원이 α-PD-1 또는 α-PD-L1을 포함하는, 이중특이성 항체.

청구항 8

제1항에 있어서, 이중특이성 항체가 단리된 단일클론 항체인, 이중특이성 항체.

청구항 9

제1항에 있어서, 서열번호 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 또는 134와 적어도 98% 유사성(similarity)을 갖는 서열을 갖는 항원-결합 단편을 포함하는, 이중특이성 항체.

청구항 10

제1항에 있어서, α-CTLA4에 대한 제1 결합 특이성 및 α-PD-1 또는 α-PD-L1에 대한 제2 결합 특이성을 갖고, 여기서 제1 특이성과 제2 특이성 중 어느 것도 70nM 이상의 Kd를 갖지 않는, 이중특이성 항체.

청구항 11

제1항에 있어서, α-CTLA4에 대한 제1 결합 특이성 및 α-PD-1에 대한 제2 특이성을 갖고, 여기서 제1 특이성과 제2 특이성 중 어느 것도 70nM 이상의 Kd를 갖지 않는, 이중특이성 항체.

청구항 12

제1항에 있어서, α-CTLA4에 대한 제1 결합 특이성 및 α-PD-L1에 대한 제2 특이성을 갖고, 여기서 제1 결합 특이성과 제2 결합 특이성 중 어느 것도 70nM 이상의 Kd를 갖지 않는, 이중특이성 항체.

청구항 13

제1항에 있어서, 인간 프레임워크 영역(인간 framework region)을 포함하는, 이중특이성 항체.

청구항 14

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

청구항 15

제1항에 있어서, IgG 도메인이 IgG 불변 영역을 포함하고, 여기서 IgG1 불변 영역이 서열번호 136과 적어도 98% 유사성을 갖는 아미노산 서열을 포함하는, 이중특이성 항체.

청구항 16

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 98% 유사성을 갖는 아미노산 서열을 포함하는, IgG1 중쇄.

청구항 17

서열번호 04, 28, 32, 36, 40, 44, 48, 52, 56, 60, 및 64와 적어도 98% 유사성을 갖는 아미노산 서열을 포함하는, 카파(카파) 경쇄.

청구항 18

서열번호 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 또는 134와 적어도 98% 유사성을 갖는 아미노산 서열을 포함하는, 가변 경쇄.

청구항 19

서열번호 92, 96, 100, 104,108, 112, 116, 120, 124, 128, 또는 132와 적어도 98% 유사성을 갖는 아미노산 서열을 포함하는, 가변 중쇄.

청구항 20

제1항의 이중특이성 항체, 제16항의 IgG1 중쇄, 제17항의 카파 경쇄, 제18항의 가변 경쇄, 또는 제19항의 가변 중쇄를 암호화하는, 단리된 핵산.

청구항 21

제20항의 단리된 핵산을 포함하는, 발현 벡터.

청구항 22

제21항에 있어서, 벡터가 세포 내에서 발현가능한, 발현 벡터.

청구항 23

제20항의 핵산을 포함하는, 숙주 세포.

청구항 24

제21항의 발현 벡터를 포함하는, 숙주 세포.

청구항 25

제23항 또는 제24항에 있어서, 숙주 세포가 원핵 세포 또는 진핵 세포인, 숙주 세포.

청구항 26

제23항 내지 제25항 중 어느 한 항의 숙주 세포를 배양하는 단계를 포함하여 이중특이성 항체를 생산하는, 이중특이성 항체를 생산하는 방법.

청구항 27

제1항의 이중특이성 항체 및 세포독성제를 포함하는, 면역접합체(immunoconjugate).

청구항 28

제27항에 있어서, 세포독성제가 화학치료제(chemotherapeutic agent), 성장 억제제, 독소, 또는 방사성 동위원소를 포함하는, 면역접합체.

청구항 29

제1항의 이중특이성 항체 및 약학적으로 허용되는 담체를 포함하는, 약학 조성물.

청구항 30

제29항에 있어서, 방사성 동위원소, 방사성 핵종(radionuclide), 독소, 치료제, 화학치료제 또는 이의 조합을 추가로 포함하는, 약학 조성물.

청구항 31

제30항의 면역접합체 및 약학적으로 허용되는 담체를 포함하는, 약학 조성물.

청구항 32

대상체에게 유효량의 제1항의 이중특이성 항체를 투여하는 단계를 포함하는, 암을 가진 대상체를 치료하는 방법.

청구항 33

제32항에 있어서, 암이 PD-L1을 발현하는 세포를 포함하는, 방법.

청구항 34

제32항에 있어서, 암이 유방암, 결장직장암, 췌장암, 두경부암, 흑색종, 난소암, 전립선암, 비소세포폐암, 소세포폐암, 신경교종, 식도암, 비인두암, 신장암, 위암, 간암, 방광암, 자궁경부암, 뇌암, 림프종, 백혈병, 골수종을 포함하는, 방법.

청구항 35

제32항에 있어서, 유효량의 치료제를 공동 투여하는 단계를 추가로 포함하는, 방법.

청구항 36

제35항에 있어서, 치료제가 항체, 화학치료제, 효소, 또는 이의 조합을 포함하는, 방법.

청구항 37

제36항에 있어서, 치료제가 카페시타빈(capecitabine), 시스플라틴(cisplatin), 트라스투주맙(trastuzumab), 풀베스트란트(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), 납-팔리탁셀(nab-palitaxel), 이의 유도체 또는 조합을 포함하는, 방법.

청구항 38

제32항에 있어서, 대상체가 인간인, 방법.

청구항 39

유효 농도의 제1항의 이중특이성 항체를 포함하는 용액으로서, 여기서 용액이 대상체 내의 혈장인, 용액.

청구항 40

제1 항원에 대한 제1 결합 특이성 및 제2 항원에 대한 제2 결합 특이성을 갖는 이중특이성 항체로서, 여기서 제1 및 제2 항원 둘 모두가 체크 포인트(check point) 항원이고, 여기서 제1 특이성과 제2 특이성 중 어느 것도 70nM 이상의 Kd를 갖지 않는, 이중특이성 항체.

청구항 41

중쇄 및 경쇄를 갖는 IgG 도메인, 및 중쇄의 C 말단 또는 경쇄의 N 말단에 연결되어있는 2개의 scFv 성분을 포함하는 이중특이성 항체로서, 여기서 IgG 도메인이 제1 항원에 대해 제1 결합 특이성을 갖고, 여기서 scFv 성분이 제2 항원에 대해 제2 결합 특이성을 가지며, 여기서 제1 항원 및 제2 항원 둘 모두가 체크포인트 항원이고 여기서 제1 항원이 제 2항원과 상이한, 이중특이성 항체.

발명의 설명

기 술 분 야

[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.

배 경 기 술

[0005] 암 세포는 면역감시(immunosurveillance)를 피하기 위한 다양한 전략을 개발한다. 특정 종양 항원의 부재 및 주조직적합성 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 미세환경은 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 반응률을 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 조합

으로 구성된 치료에 비해 추가적인 작용 기전을 갖는다.

발명의 내용

해결하려는 과제

[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-CTLA4을 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(framework) 영역을 포함한다.

[0027] 한 실시양태에서, 이중특이성 항체는 인간화 항체, 키메라 항체(chimeric antibod), 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(immunoconjugate)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 개시한다. 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), 풀베스트란트(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), 납-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 숙련가에게 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 않아야한다는 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 다어그램을 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 IFNg 생산을 나타낸다;

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

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 예시로써 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 조작된 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 입스위치(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 팩키지(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 결찰되었다. 두 작제물 모두에 대해, 소량의 분취물을 *이. 콜라이* DH10b (Invitrogen, 미국 캘리포니아주 칼스배드(Carlsbad, CA) 소재)로 형질전환시키고 TB + 카르베니실린(carbenicillin) 100㎍/ml 플레이트(Teknova, 미국 캘리포니아주 홀리스터(Hollister, CA) 소재)에 플레이팅하고 37℃에서 밤새 배양(incubating)하였다. 생성된 콜로니를 선택하고 2ml의 밤샘 배양물을 TB + 카르베니실린에 접종하였다. 밤샘 배양물로부터 DNA를 제조하고(Thermo-Fisherm, 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 플라스몬 공명(Surface Plasmon Resonance)을 통해 평가하였다. 항원을 센서 칩 표면에 고정화하고 시험된 항체를 고정화된 항원 위에 흘렸다. 모든 분자는 예를 들어 **표 1**에 나타낸 바와 같이 항원에 대한 강한 결합을 나타냈다.

표 1

PD-L1 항원에 대한 항-PD-L1 항체의 결합

[0061]

	mAb			scFv-Fc			Fc-scFv		
샘플 ID	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

[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 접합된 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 자

극 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 루시퍼라아제(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 신호절달에서의 증가를 통해 평가하였다. 결과적으로 NFAT 신호전달을 루시퍼라아제 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).

[0070] **실시예 6: 수지상 세포 혼합된 백혈구 반응**

[0071] 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 IFNɣ를 통해 평가하였다. 도 6에 나타낸 바와 같이, 시험된 모든 이중특이성 항체는 IFNɣ의 생산을 증대시킬 수 있었다.

[0072] **실시예 7: 조절 T 세포에 의한 CD8 T 세포의 억제**

[0073] 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(써모피셔)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 IFNɣ(도 7b)를 통해 평가하였다.

[0074] **실시예 8: CD8 T 세포 탈과립화(degranulation)**

[0075] 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-IFNɣ 항체로 염색하고 유동 세포분석기 BD LSRFortessa 상에서 평가하였다. 도 8에 나타낸 바와 같이, 시험된 모든 이중특이성 항체는 세포독성 IFNɣ 양성 T 세포의 수를 증가시킬 수 있었다.

[0076] **실시예 9: 믹세노(MiXeno) 마우스 종양 모델**

[0077] 인간화 마우스 모델을 사용하여 생체내 종양 성장을 억제하는 이 부류의 이중특이성 항체의 능력을 평가하였다. 요약하면, NOG 마우스를 인간 PBMC (마우스 당 $5x10^6$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).

[0078] **실시예 10: Flu-특이적 T 세포의 증식**

[0079] 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 덱스트라머(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).

[0080] **실시예 11: CEFT 펩타이드 풀에 대한 PBMC 기억 반응**

[0081] 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 IFNɣ의 양을 정량화하였다. 도 11에 나타낸 바와 같이, 이중특이성 CT4 x PD224D1는 대조군 치료에 비해 IFNɣ의 생산을 수배 향상시킬 수 있었다.

[0082] **실시예 12: 방향전환된 T 세포 세포독성의 향상**

[0083] 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. 이중특이성 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 이중특이성 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] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTACAGCCTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACATTGGTGAT
ACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTCACCATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCCTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGC
GGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC
ATCACTTGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATCAGGCCTCCACTCTG
GCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGT
CAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0092] 서열번호 02: CT4 x PD224D1 아미노산 서열 (aa)

[0093] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN

HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKGLEYIGYIGD
TTGIAYASWANGRFTISKDNTKNTVDLQMNSLRAEDTAVYYCARGWSYLDIWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSALVMTQSPSSLSASVGDRVT
ITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISSLQPEDVATYYCQGGYYSAALNTFGGGTKVEIK

[0094] 서열번호 03: CT4 카파 경쇄 nt

[0095] GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTA
GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCT
GGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGG
ACCAAGGTGGAAATCAAA

[0096] CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCC
AGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
AACAGGGGAGAGTGT

[0097] 서열번호 04: CT4 카파 경쇄 aa

[0098] EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQG
TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS
PVTKSFNRGEC

[0099] 서열번호 05: CT4 x PL230C6 nt

[0100] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTC
TCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTTGGAATCATTACTTATAGT
GGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAGACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAG
GACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTTCCGGTGGAGGCGGTTCAGGC
GGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC
ATCAAGTGTCAGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTG
GCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGT
CAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0101] 서열번호 06: CT4 x PL230C6 aa

[0102] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYS
GSRYYANWAKGRFTISKDNTKNTVYLQMNSLRAEDTAVYYCARDYMSGSHLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGDRVT

IKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYGKNNVDNAFGGGTKVEIK

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

[0104] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCT
GCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
CTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCA
TCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTG
ATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGAT
GATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0105] 서열번호 08: CT4 x PL221G5 널 Fc aa

[0106] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIACIA
AGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSAFSFDYAMDLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSA
SVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQGYSWGNVDNVFGGGTKVEIK

[0107] 서열번호 09: CT4 x PL231H2 nt

[0108] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGA
CTCTCCTGTACAACTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTAT
GTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTCACCCTCTCCAAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCT

GAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCT
GGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTC
ACCATCAATTGTCAGGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTCTGCATCCACT
CTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTAT
TGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0109] 서열번호 10: CT4 x PL231H2 aa

[0110] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIISY
VGNTYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISGSHLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGDRV
TINCQASESISSFLSWYQQKPGKAPKLLIFSASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIK

[0111] 서열번호 11: CT4 x PL004B5 nt

[0112] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTGATACT
AATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAATGATGATTATATTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGA
GGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGA
GACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATC
TATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGAT
TTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0113] 서열번호 12: CT4 x PL004B5 aa

[0114] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFSLSSYWMSWVRQAPGKGLEWIGVIDT
NVYIYYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYVGNNDDYINLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVG
DRVTITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSFGGGTKVEIK

[0115] 서열번호 13: CT4 x PL004B9 nt

[0116] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG

GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCATCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTACTTAT
GTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGAC
ACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCATTCGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
AGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCA
TCCAATCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACT
TATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0117] **서열번호 14: CT4 x PL004B9 aa**

[0118] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITY
VGNTYYASWAKGRFTISKTSTTVDLKITSPTTEDTAVYYCARESGTIYYSYFNLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAFELTQSPSSLSASVGD
RVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQSYYGGGSAYTFGGGTKVEIK

[0119] **서열번호 15: CT4 x PD206F12 nt**

[0120] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTCGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTAT
GCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGCAGATTCACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTG
AGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGAC
AGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATGATAACAACTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTAT
ACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTT
GCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACTTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0121] 서열번호 16: CT4 x PD206F12 aa

[0122] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFDFSSGYWICWVRQAPGKGLELIACIY
AGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCARNLYTYNSLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGD
RVTITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQGTYYSSGWNFAFGGGTKVEIK

[0123] 서열번호 17: CT4 x PD215A1 nt

[0124] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACT
GGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATCTCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCT
GGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGC
AGTTGGTTGAGTGGTGCTGTTGGTAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0125] 서열번호 18: CT4 x PD215A1 aa

[0126] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITT
GSGSTYYASWAKRRFTISKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT
CQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIK

[0127] 서열번호 19: CT4 x PD220F6 nt

[0128] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC

CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTCACCATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCATTGATTTTTCCC
GGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTCACCCTCTCCAGCGACAACGCCCAGAACACTGTGGAACTGCAAATGAACAGCCTGAGA
GCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCACTCTGGCA
TCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCA
GGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0129] 서열번호 20: CT4 x PD220F6 aa

[0130] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQEQVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFP
GIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT
CQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCAGGYSSSTRAFGGGTKVEIK

[0131] 서열번호 21: CT4 x PD225G11 nt

[0132] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTAT
ACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
CTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCA
TCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTG
ATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCACCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAA
GATGTTGCAACTTATTACTGTCATGTTCATTATTGCAGTGGTGGTAGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0133] 서열번호 22: CT4 x PD225G11 aa

[0134] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACIY

TGSIDVFYYASWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAANTDTTYFNLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSLSA
SVGDRVTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWAFGGGTKVEIK

[0135] 서열번호 23: G4S x 4 nt

[0136] GGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCT

[0137] 서열번호 24: G4S x 4 aa

[0138] GGGGSGGGGSGGGGSGGGGS

[0139] 서열번호 25: PL230C6 x CT4 nt

[0140] CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATC
TCCAAAGACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCC
CACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGC
ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTC
TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC
CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCT
CCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAAC
AATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGAC
ACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGTTCAGGC
GGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC
CTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGC
AGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0141] 서열번호 26: PL230C6 x CT4 aa

[0142] QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYSGSRYYANWAKGRFTISKDNTKNTVYLQMNSLRAEDTAVYYCARDYMSGS
HLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP
SNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGN
NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERAT
LSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0143] 서열번호 27: PL230C6 카파 경쇄 nt

[0144] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTCAGGCCAGTGAGGACATTTATAGCTTCTTGGCC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0145] CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCC
AGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
AACAGGGGAGAGTGT

[0146] 서열번호 28: PL230C6 카파 경쇄 aa

[0147] AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYGKNNVDNAFG
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0148] 서열번호 29: PD224D1 x CT4 nt

[0149] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCCTCAGTAGCTATGCAATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTCACC
ATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCCTACTTA
GACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGC
ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCT
GTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTC
TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAG
TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC
CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCT
CCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAAC
AATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGAC
ACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGC
GGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC
CTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGC
AGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0150] 서열번호 30: PD224D1 x CT4 aa

[0151] EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKGLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVDLQMNSLRAEDTAVYYCARGWSYL
DIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP
SNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
LHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGN
NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERAT
LSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0152] 서열번호 31: PD224 경쇄 nt

[0153] GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCC
TGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATATGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA
CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCC
AGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTC
AACAGGGGAGAGTGT

[0154] 서열번호 32: PD224 경쇄 aa

[0155] ALVMTQSPSSLSASVGDRVTITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISSLQPEDVATYYCQGGYYSAALNTFGG
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

[0156] 서열번호 33: PL221G5 x CT4 널 Fc nt

[0157] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGAC
ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGC
CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCG
TTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC
TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC
TGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA
GCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGC
CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
CAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG
AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACA
TTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATG
AACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTG
TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC
CTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCT
GAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0158] 서열번호 34: PL221G5 x CT4 널 Fc aa

[0159] EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIACIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSA
FSFDYAMDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVT
FISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSL
SPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0160] 서열번호 35: PL221G5 경쇄 nt

[0161] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAAAC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTG
AGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0162] 서열번호 36: PL221G5 경쇄 aa

[0163] DIQMTQSPSTLSASVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQGYSWGNVDNVFG
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0164] 서열번호 37: PL231H2 x CT4 널 Fc nt

[0165] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAACTTCTGGAATCGACCTTAGTACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTCACC
CTCTCCAAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGT
TCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGG

GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCA
GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACC
GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGG
CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGC
GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAG
CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG
TCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC
TGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGA
AACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAG
GACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCT
GGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCC
ACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTC
AGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTAT
TACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0166] 서열번호 38: PL231H2 x CT4 널 Fc aa

[0167] QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIISYVGNTYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISG
SHLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDG
NNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERA
TLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0168] 서열번호 39: PL231H2 경쇄 nt

[0169] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTCAGGCCAGTGAGAGCATTAGTAGCTTCTTATCC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTG
AGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0170] 서열번호 40: PL231H2 경쇄 aa

[0171] AYDMTQSPSSVSASVGDRVTINCQASESISSFLSWYQQKPGKAPKLLIFSASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSKSNVDNAFG
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0172] 서열번호 41: PL004B5 x CT4 nt

[0173] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAAT
GATGATTATATTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGC
ACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC
ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGG
GCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGAC
CCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC

GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC
TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC
TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC
CTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTG
AGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCA
TATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
AGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGA
GGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGG
GAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTT
GCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0174] **서열번호 42: PL004B5 x CT4 aa**

[0175] EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYWMSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYVGNN
DDYINLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFIS
YDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPG
ERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0176] **서열번호 43: PL004B5 경쇄 nt**

[0177] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATAATGGCTACTGG
TTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0178] **서열번호 44: PL004B5 경쇄 aa**

[0179] DIQMTQSPSTLSASVGDRVTITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSF
GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

[0180] **서열번호 45: PL004B9 x CT4 nt**

[0182] *181GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCATCAA
TATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTACTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATT
CACCATCTCCAAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTA
TTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAG
CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCA
CACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT
GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGG
GGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGA
CCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAA
AGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTT
CTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG

CCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCT
GAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATC
ATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCT
GAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGG
AGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG
GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTA
TGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTT
TGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0183] **서열번호 46: PL004B9 x CT4 aa**

[0184] EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTISKTSTTVDLKITSPTTEDTAVYYCARESGTIYY
SYFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISY
DGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGE
RATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0185] **서열번호 47: PL004B9 경쇄 nt**

[0186] GCATTCGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTACTTATCC
TGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCGGCGGA
GGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC
CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGC
TCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0187] **서열번호 48: PL004B9 경쇄 aa**

[0188] AFELTQSPSSLSASVGDRVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQSYYGGGSAYTFGG
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

[0189] **서열번호 49: PD206F12 x CT4 nt**

[0190] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCGACTTCAGTAGCGGCTACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGC
AGATTCACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTAC
ACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC
TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC
CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT
AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC
TCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATAT
GATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA
GCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGC
GGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAA

AGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT
GCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCA
GTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0191] **서열번호 50: PD206F12 x CT4 aa**

[0193] *191EVQLVESGGGLVQPGGSLRLSCAASGFDFSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCA
RNLYTYNSLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVT
FISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSL
SPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0194] **서열번호 51: PD206F12 경쇄 nt**

[0195] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATGATAACAACTGG
TTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACTTTGCT
TTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCT
GTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAG
CAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAG
GGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0196] **서열번호 52: PD206F12 경쇄 aa**

[0197] DIQMTQSPSTLSASVGDRVTITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQGTYYSSGWNFA
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQ
GLSSPVTKSFNRGEC

[0198] **서열번호 53: PD215A1 x CT4 nt**

[0199] CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATG
TGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTC
ACCATCTCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTTGACTTG
TGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
ACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTC
TTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
GGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAA
TACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCT
ATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGCAGGGCC
ACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAG
CAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0200] 서열번호 54: PD215A1 x CT4 aa

[0201] QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTISKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDL
WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNK
YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLS
CRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0202] 서열번호 55: PD215A1 경쇄 nt

[0203] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAAC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGCTGTTGGTAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTG
AGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0204] 서열번호 56: PD215A1 경쇄 aa

[0205] DIQMTQSPSSLSASVGDRVTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQSSWLSGAVGNAFG
GGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL
SSPVTKSFNRGEC

[0206] 서열번호 57: PD220F6 x CT4 nt

[0207] CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCATCAGCAGCTATGGAGTG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCATTGATTTTTCCCGGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTC
ACCCTCTCCAGCGACAACGCCCAGAACACTGTGGAACTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTG
TGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG
GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
ACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTC
TTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCAC
CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGA
GAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
GGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCC
TCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAA
TACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCT
ATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGT
GGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGCAGGGCC
ACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAG
CAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0208] 서열번호 58: PD220F6 x CT4 aa

[0209] QEQVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDL
WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
QDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV

DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNK
YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLS
CRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0210] 서열번호 59: PD220F6 경쇄 nt

[0211] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTA
TCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCT
GGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC
CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC
AAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGC
TCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0212] 서열번호 60: PD220F6 경쇄 aa

[0213] DIQMTQSPSSLSASVGDRVTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCAGGYSSSTRAFGG
GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

[0214] 서열번호 61: PD225G11 x CT4 nt

[0215] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCAGCCACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGC
CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCT
AATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCC
TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC
TGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA
GCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGC
CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC
ATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
CAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGG
AGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACA
TTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATG
AACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCG
AGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTG
TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC
CTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCT
GAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

[0216] 서열번호 62: PD225G11 x CT4 aa

[0217] EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACIYTGSIDVFYYASWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAA
NTDTTYFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVT
FISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSL
SPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0218] 서열번호 63: PD225G11 경쇄 nt

[0219] GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCC

TGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCACCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTCATTATTGCAGTGGTGGTAGTTGTTTTTGGGCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAG
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

[0220] **서열번호 64: PD225G11 경쇄 aa**

[0221] AYDMTQSPSSLSASVGDRVTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWAF
GGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG
LSSPVTKSFNRGEC

[0222] **서열번호 65: CT4 중쇄 신호 펩타이드 뉴클레오타이드 서열 nt**

[0223] ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCC

[0224] **서열번호 66: CT4 중쇄 신호 펩타이드 뉴클레오타이드 서열 aa**

[0225] MKHLWFFLLLVAAPRWVLS

[0226] **서열번호 67: PL230/PD224 중쇄 신호 펩타이드 nt**

[0227] ATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCC

[0228] **서열번호 68: PL230/PD224 중쇄 신호 펩타이드 aa**

[0229] MAVLGLLFCLVTFPSCVLS

[0230] **서열번호 69: PL230/PD224 경쇄 신호 펩타이드 nt**

[0231] ATGAGGGCCCCTGCTCAGTTTCTTGGCTTCTTGCTTTTCTGGATTCCAGCCTCCAGAAGT

[0232] **서열번호 70: PL230/PD224 경쇄 신호 펩타이드 aa**

[0233] MRAPAQFLGFLLFWIPASRS

[0234] **서열번호 71: CT4 scFv nt**

[0235] CAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGC
GGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGC
TACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGC
CAAGGGACCAAGGTGGAAATCAAA

[0236] **서열번호 72: CT4 scFv aa**

[0237] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGS
GSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

[0238] **서열번호 73: PD224D1 scFv nt**

[0239] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGC

[0240] CTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACATTGGTGATACTACTGGCATAGC
CTACGCGAGCTGGGCGAATGGCAGATTCACCATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGT
GTATTACTGTGCGAGAGGCTGGTCCTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGG
CGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGC
CAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCC

ATCTCGGTTCAGTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTA
TAGTGCTGCCCTTAATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0241] 서열번호 74: PD224D1 scFv aa

[0242] EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKGLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVDLQMNSLRAEDTAVYYCARGWSYL
DIWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSALVMTQSPSSLSASVGDRVTITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGT
DFTLTISSLQPEDVATYYCQGGYYSAALNTFGGGTKVEIK

[0243] 서열번호 75: PD206F12 scFv nt

[0244] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCGACTTCAGTAGCGGCTACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGC
AGATTCACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTAC
ACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGC
GGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATGATAAC
AACTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGC
AGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAAC
TTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0245] 서열번호 76: PD206F12 scFv aa

[0246] EVQLVESGGGLVQPGGSLRLSCAASGFDFSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCARNLY
TYNSLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVTITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSG
SGSGTEFTLTISSLQPDDFATYYCQGTYYSSGWNFAFGGGTKVEIK

[0247] 서열번호 77: PD215A1 scFv nt

[0248] CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATG
TGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTC
ACCATCTCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTTGACTTG
TGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAG
ATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAACTGGTATCAG
CAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGACAGATTTC
ACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGCTGTTGGTAATGCTTTCGGCGGAGGGACC
AAGGTGGAGATCAAA

[0249] 서열번호 78: PD215A1 scFv aa

[0250] QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTISKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDL
WGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTDF
TLTISSLQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIK

[0251] 서열번호 79: PD225G11 scFv nt

[0252] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCAGCCACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGC
CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCT
AATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGC
TCCGGTGGAGGCGGCTCTGCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGC
ATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTC
ACCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTCATTATTGCAGTGGTGGT
AGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0253] 서열번호 80: PD225G11 scFv aa

[0254] EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACIYTGSIDVFYYASWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAA
NTDTTYFNLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSLSASVGDRVTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRF
TGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWAFGGGTKVEIK

[0255] 서열번호 81: PL230C6 scFv nt

[0256] CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATC
TCCAAAGACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCC
CACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTTCCGGTGGAGGCGGTTCAGGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGCC
TATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTCAGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGG
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACA
GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

[0257] 서열번호 82: PL230C6 scFv aa

[0258] QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYSGSRYYANWAKGRFTISKDNTKNTVYLQMNSLRAEDTAVYYCARDYMSGS
HLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGT
DFTLTISSLQPEDFATYYCQQGYGKNNVDNAFGGGTKVEIK

[0259] 서열번호 83: PL231H2 scFv nt

[0260] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAACTTCTGGAATCGACCTTAGTACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTCACC
CTCTCCAAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGT
TCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCT
GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTCAGGCCAGTGAGAGCATTAGTAGCTTCTTATCC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0261] 서열번호 84: PL231H2 scFv aa

[0262] QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIISYVGNTYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISG
SHLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAYDMTQSPSSVSASVGDRVTINCQASESISSFLSWYQQKPGKAPKLLIFSASTLASGVPSRFSGSGSG
TDFTLTISSLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIK

[0263] 서열번호 85: PL221G5 scFv nt

[0264] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGAC
ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGC
CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCG
TTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGC
TCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGC
ATTAGTTCCCACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTC
AGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAAT
GTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0265] 서열번호 86: PL221G5 scFv aa

[0266] EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIACIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSA
FSFDYAMDLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRF
SGSGSGTEFTLTISSLQPDDFATYYCQQGYSWGNVDNVFGGGTKVEIK

[0267] 서열번호 87: PL004B5 scFv nt

[0268] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAAT
GATGATTATATTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGA
GGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATAAT

GGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGC
GGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAG
AACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0269] **서열번호 88: PL004B5 scFv aa**

[0270] EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYWMSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYVGNN
DDYINLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGDRVTITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFS
GSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSFGGGTKVEIK

[0271] **서열번호 89: PL004B9 scFv nt**

[0272] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCATCAATATG
GGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTACTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTCACC
ATCTCCAAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTAC
AGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGC
GGCTCTGCATTCGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTAC
TTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGA
TCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA

[0273] **서열번호 90: PL004B9 scFv aa**

[0274] EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTISKTSTTVDLKITSPTTEDTAVYYCARESGTIYY
SYFNLWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSAFELTQSPSSLSASVGDRVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSG
SGTDFTLTISSLQPEDVATYYCQSYYGGGSAYTFGGGTKVEIK

[0275] **서열번호 91: CT4 VH nt**

[0276] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATG
CACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
GGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

[0277] **서열번호 92: CT4 VH aa**

[0278] QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
GPFDYWGQGTLVTVSS

[0279] **서열번호 93: CT4 VL nt**

[0280] GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTA
GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCT
GGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGG
ACCAAGGTGGAAATCAAA

[0281] **서열번호 94: CT4 VL aa**

[0282] EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQG
TKVEIK

[0283] **서열번호 95: PD224D1 VH nt**

[0284] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCCTCAGTAGCTATGCAATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTCACC
ATCTCCAAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCCTACTTA
GACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

[0285] **서열번호 96: PD224D1 VH aa**

[0286] EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKGLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVDL

[0287] QMNSLRAEDTAVYYCARGWSYLDIWGQGTLVTVSS

[0288] **서열번호 97: PD224D1 VL nt**

[0289] GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCC
TGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATATGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

[0290] **서열번호 98: PD224D1 VL aa**

[0291] ALVMTQSPSSLSASVGDRVTITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISSLQP

[0292] EDVATYYCQGGYYSAALNTFGGGTKVEIK

[0293] **서열번호 99: PD206F12 VH nt**

[0294] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCGACTTCAGTAGCGGCTACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGC
AGATTCACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTAC
ACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0295] **서열번호 100: PD206F12 VH aa**

[0296] EVQLVESGGGLVQPGGSLRLSCAASGFDFSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCARNLY
TYNSLWGQGTLVTVSS

[0297] **서열번호 101: PD206F12 VL nt**

[0298] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATGATAACAACTGG
TTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACTTTGCT
TTCGGCGGAGGGACCAAGGTGGAGATCAAA

[0299] **서열번호 102: PD206F12 VL aa**

[0300] DIQMTQSPSTLSASVGDRVTITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQGTYYSSGWNFA
FGGGTKVEIK

[0301] **서열번호 103: PD215A1 VH nt**

[0302] CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGGATG
TGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTC
ACCATCTCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTTGACTTG
TGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0303] **서열번호 104: PD215A1 VH aa**

[0304] QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTISKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDL
WGQGTLVTVSS

[0305] **서열번호 105: PD215A1 VL nt**

[0306] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAAC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGCTGTTGGTAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0307] **서열번호 106: PD215A1 VL aa**

[0308] DIQMTQSPSSLSASVGDRVTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQSSWLSGAVGNAFG
GGTKVEIK

[0309] **서열번호 107: PD225G11 VH nt**

[0310] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCAGCCACTGG
ATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGC
CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCT
AATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0311] **서열번호 108: PD225G11 VH aa**

[0312] EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACIYTGSIDVFYYASWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAA
NTDTTYFNLWGQGTLVTVSS

[0313] **서열번호 109: PD225G11 VL nt**

[0314] GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCC
TGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCACCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTCATTATTGCAGTGGTGGTAGTTGTTTTTGGGCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA

[0315] **서열번호 110: PD225G11 VL aa**

[0316] AYDMTQSPSSLSASVGDRVTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWAF
GGGTKVEIK

[0317] **서열번호 111: PL230C6 VH nt**

[0318] CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCTCTGGAATCGACCTTAATACCTACGACATGATC
TGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATC
TCCAAAGACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCC
CACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTTCC

[0319] **서열번호 112: PL230C6 VH aa**

[0320] QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYSGSRYYANWAKGRFTISKDNTKNTVYLQMNSLRAEDTAVYYCARDYMSGS
HLWGQGTLVTVSS

[0321] **서열번호 113: PL230C6 VL nt**

[0322] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTCAGGCCAGTGAGGACATTTATAGCTTCTTGGCC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0323] **서열번호 114: PL230C6 VL aa**

[0324] AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQP

[0325] EDFATYYCQQGYGKNNVDNAFGGGTKVEIK

[0326] **서열번호 115: PL231H2 VH nt**

[0327] CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAACTTCTGGAATCGACCTTAGTACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTCACC
CTCTCCAAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGT
TCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0328] **서열번호 116: PL231H2 VH aa**

[0329] QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIISYVGNTYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISG
SHLWGQGTLVTVSS

[0330] **서열번호 117: PL231H2 VL nt**

[0331] GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTCAGGCCAGTGAGAGCATTAGTAGCTTCTTATCC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0332] **서열번호 118: PL231H2 VL aa**

[0333] AYDMTQSPSSVSASVGDRVTINCQASESISSFLSWYQQKPGKAPKLLIFSASTLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYSKSNVDNAFG
GGTKVEIK

[0334] **서열번호 119: PL221G5 VH nt**

[0335] GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTACGAC
ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGC
CGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCG
TTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0336] **서열번호 120: PL221G5 VH aa**

[0337] EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIACIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSA
FSFDYAMDLWGQGTLVTVSS

[0338] **서열번호 121: PL221G5 VL nt**

[0339] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAAAC
TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGG
ACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

[0340] **서열번호 122: PL221G5 VL aa**

[0341] DIQMTQSPSTLSASVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQGYSWGNVDNVFG
GGTKVEIK

[0342] **서열번호 123: PL004B5 VH nt**

[0343] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCCTCAGTAGCTACTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTCACC
ATCTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAAT
GATGATTATATTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0344] **서열번호 124: PL004B5 VH aa**

[0345] EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYWMSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARYVGNN
DDYINLWGQGTLVTVSS

[0346] **서열번호 125: PL004B5 VL nt**

[0347] GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATAATGGCTACTGG
TTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGA
TCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA

[0348] **서열번호 126: PL004B5 VL aa**

[0349] DIQMTQSPSTLSASVGDRVTITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSF
GGGTKVEIK

[0350] **서열번호 127: PL004B9 VH nt**

[0351] GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCATCAATATG
GGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTACTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTCACC

ATCTCCAAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTAC
AGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

[0352] **서열번호 128: PL004B9 VH aa**

[0353] EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTISKTSTTVDLKITSPTTEDTAVYYCARESGTIYY
SYFNLWGQGTLVTVSS

[0354] **서열번호 129: PL004B9 VL nt**

[0355] GCATTCGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTACTTATCC
TGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGG
ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

[0356] **서열번호 130: PL004B9 VL aa**

[0357] AFELTQSPSSLSASVGDRVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQSYYGGGSAYTFGG
GTKVEIK

[0358] **서열번호 131: PD220F6 VH nt**

[0359] CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCATCAGCAGCTATGGAGTG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCATTGATTTTTCCCGGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTC
ACCCTCTCCAGCGACAACGCCCAGAACACTGTGGAACTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTG
TGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

[0360] **서열번호 132: PD220F6 VH aa**

[0361] QEQVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDL
WGQGTLVTVSS

[0362] **서열번호 133: PD220F6 VL nt**

[0363] GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTA
TCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCT
GGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

[0364] **서열번호 134: PD220F6 VL aa**

[0365] DIQMTQSPSSLSASVGDRVTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCAGGYSSSTRAFGG
GTKVEIK

[0366] **서열번호 135: 인간 IgG1 불변 영역 nt**

[0367] GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCT
TGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC
AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

[0368] **서열번호 136: 인간 IgG1 불변 영역 aa**

[0369] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC

KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPG

[0370] 서열번호 137: 인간 IgG1 효과기 널 nt

[0371] GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG
GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCT
TGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCC
AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
GCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC
AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

[0372] 서열번호 138: 인간 IgG1 효과기 널 aa

[0373] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS
CDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
AVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
SCSVMHEALHNHYTQKSLSLSPG

[0374] 서열번호 139: PD220F6 scFv nt

[0375] CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCATCAGCAGCTATGGAGTG
AGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCGCATTGATTTTTCCCGGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTC
ACCCTCTCCAGCGACAACGCCCAGAACACTGTGGAACTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTG
TGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAG
ATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTATCCTGGTAT
CAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGAT
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAG
GTGGAGATCAAA

[0376] 서열번호 140: PD220F6 scFv aa

[0377] QEQVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDL
WGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTD
FTLTISSLQPEDVATYYCAGGYSSSTRAFGGGTKVEIK

[0378] 서열번호 141: CT4 VH CDR1 aa

[0379] SSYTMH

[0380] 서열번호 142: CT4 VH CDR2 aa

[0381] FISYDGNNKYYADSVKG

[0382] 서열번호 143: CT4 VH CDR3 aa

[0383] TGWLGPFDY

[0384] 서열번호 144: CT4 VL CDR1 aa

[0385] RASQSVGSSYLA

[0386] 서열번호 145: CT4 VL CDR2 aa

[0387] GAFSRAT

[0388] 서열번호 146: CT4 VL CDR3 aa

[0389] QQYGSSPWT

[0390] **서열번호 147: PL230C6 VH CDR1 aa**

[0391] NTYDMI

[0392] **서열번호 148: PL230C6VH CDR2 aa**

[0393] IITYSGSRYYANWAKG

[0394] **서열번호 149: PL230C6VH CDR3 aa**

[0395] DYMSGSHL

[0396] **서열번호 150: PL230C6VL CDR1 aa**

[0397] QASEDIYSFLA

[0398] **서열번호 151: PL230C6VL CDR2 aa**

[0399] SASSLAS

[0400] **서열번호 152: PL230C6VL CDR3 aa**

[0401] QQGYGKNNVDNA

[0402] **서열번호 153: PD224D1 VH CDR1 aa**

[0403] NTYDMI

[0404] **서열번호 154: PD224D1 CDR2 aa**

[0405] IITYSGSRYYANWAKG

[0406] **서열번호 155: PD224D1 CDR3 aa**

[0407] DYMSGSHL

[0408] **서열번호 156: PD224D1 CDR1 aa**

[0409] QASEDIYSFLA

[0410] **서열번호 157: PD224D1 CDR2 aa**

[0411] SASSLAS

[0412] **서열번호 158: PD224D1 CDR3 aa**

[0413] QQGYGKNNVDNA

[0414] **서열번호 159: PL221G5 VH CDR1 aa**

[0415] SGYDMC

[0416] **서열번호 160: PL221G5 CDR2 aa**

[0417] CIAAGSAGITYDANWAKG

[0418] **서열번호 161: PL221G5 CDR3 aa**

[0419] SAFSFDYAMDL

[0420] **서열번호 162: PL221G5 CDR1 aa**

[0421] QASQSISSHLN

[0422] **서열번호 163: PL221G5 CDR2 aa**

[0423] KASTLAS

[0424] **서열번호 164: PL221G5 CDR3 aa**

[0425] QQGYSWGNVDNV

[0426] **서열번호 165: PL231H2 VH CDR1 aa**

[0427] STYDMI

[0428] **서열번호 166: PL231H2 VH CDR2 aa**

[0429] IISYVGNTYYASWAKG

[0430] **서열번호 167: PL231H2 VH CDR3 aa**

[0431] DFISGSHL

[0432] **서열번호 168: PL231H2 VL CDR1 aa**

[0433] QASESISSFLS

[0434] **서열번호 169: PL231H2 VL CDR2 aa**

[0435] SASTLAS

[0436] **서열번호 170: PL231H2 VL CDR3 aa**

[0437] QQGYSKSNVDNA

[0438] **서열번호 171: PL004B5 VH CDR1 aa**

[0439] SSYWMS

[0440] **서열번호 172: PL004B5 VH CDR2 aa**

[0441] VIDTNVYIYYANWAKG

[0442] **서열번호 173: PL004B5 VH CDR3 aa**

[0443] YVGNNDDYINL

[0444] **서열번호 174: PL004B5 VL CDR1 aa**

[0445] QSSQSVYNGWLS

[0446] **서열번호 175: PL004B5 VL CDR2 aa**

[0447] GASTLAS

[0448] **서열번호 176: PL004B5 VL CDR3 aa**

[0449] LGSYTSSTENS

[0450] **서열번호 177: PL004B9 VH CDR1 aa**

[0451] SVINMG

[0452] **서열번호 178: PL004B9 VH CDR2 aa**

[0453] TITYVGNTYYASWAKG

[0454] **서열번호 179: PL004B9 VH CDR3 aa**

[0455] ESGTIYYSYFNL

[0456] **서열번호 180: PL004B9 VL CDR1 aa**

[0457] QASESISNYLS

[0458] **서열번호 181: PL004B9 VL CDR2 aa**

[0459] YASNLAS

[0460] **서열번호 182: PL004B9 VL CDR3 aa**

[0461] QSYYGGGSAYT

[0462] **서열번호 183: PD206F12 VH CDR1 aa**

[0463] SGYWIC

[0464] **서열번호 184: PD206F12 VH CDR2 aa**

[0465] CIYAGTSGSTSYASWARG

[0466] **서열번호 185: PD206F12 VH CDR3 aa**

[0467] NLYTYNSL

[0468] **서열번호 186: PD206F12 VL CDR1 aa**

[0469] QSSQSVYDNNWLA

[0470] **서열번호 187: PD206F12 VL CDR2 aa**

[0471] TVSTLAS

[0472] **서열번호 188: PD206F12 VL CDR3 aa**

[0473] QGTYYSSGWNFA

[0474] **서열번호 189: PD215A1 VH CDR1 aa**

[0475] SSYWMC

[0476] **서열번호 190: PD215A1 VH CDR2 aa**

[0477] CITTGSGSTYYASWAKR

[0478] **서열번호 191: PD215A1 VH CDR3 aa**

[0479] AFDL

[0480] **서열번호 192: PD215A1 VL CDR1 aa**

[0481] QASQSIYSYLN

[0482] **서열번호 193: PD215A1 VL CDR2 aa**

[0483] GASNLAS

[0484] **서열번호 194: PD215A1 VL CDR3 aa**

[0485] QSSWLSGAVGNA

[0486] **서열번호 195: PD220F6 VH CDR1 aa**

[0487] SSYGVS

[0488] **서열번호 196: PD220F6 VH CDR2 aa**

[0489] LIFPGIGFKDYASWVNG

[0490] **서열번호 197: PD220F6 VH CDR3 aa**

[0491] DLDL

[0492] **서열번호 198: PD220F6 VL CDR1 aa**

[0493] QSSPSVYSNYLS

[0494] **서열번호 199: PD220F6 VL CDR2 aa**

[0495] YASTLAS

[0496] **서열번호 200: PD220F6 VL CDR3 aa**

[0497] AGGYSSSTRA

[0498] **서열번호 201: PD225G11 VH CDR1 aa**

[0499] SSHWIC

[0500] **서열번호 202: PD225G11 VH CDR2 aa**

[0501] CIYTGSIDVFYYASWAKG

[0502] **서열번호 203: PD225G11 VH CDR3 aa**

[0503] AANTDTTYFNL

[0504] **서열번호 204: PD225G11 VL CDR1 aa**

[0505] QASQSINNQLS

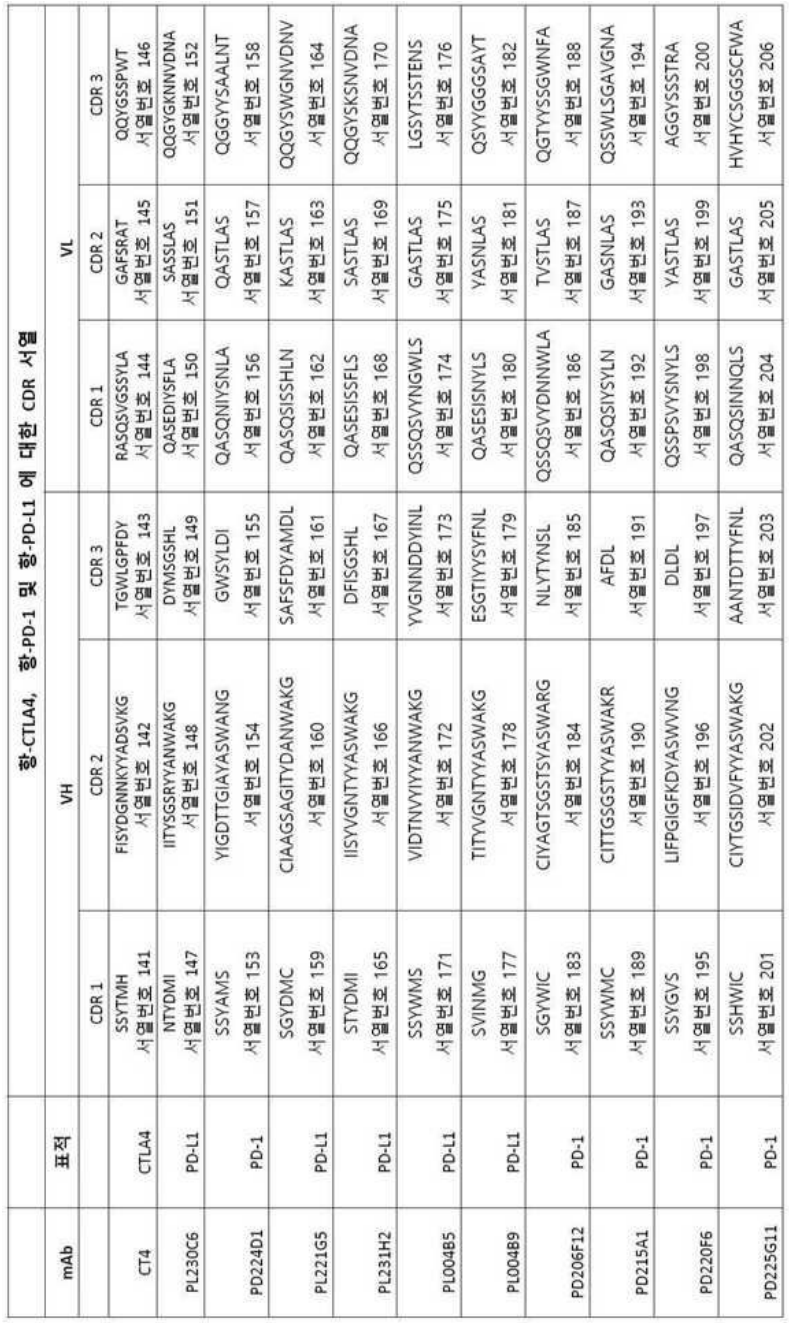
[0506] **서열번호 205: PD225G11 VL CDR2 aa**

[0507] GASTLAS

[0508] **서열번호 206: PD225G11 VL CDR3 aa**

[0509] HVHYCSGGSCFWA

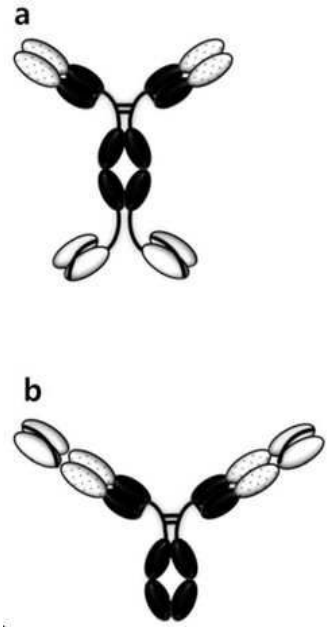
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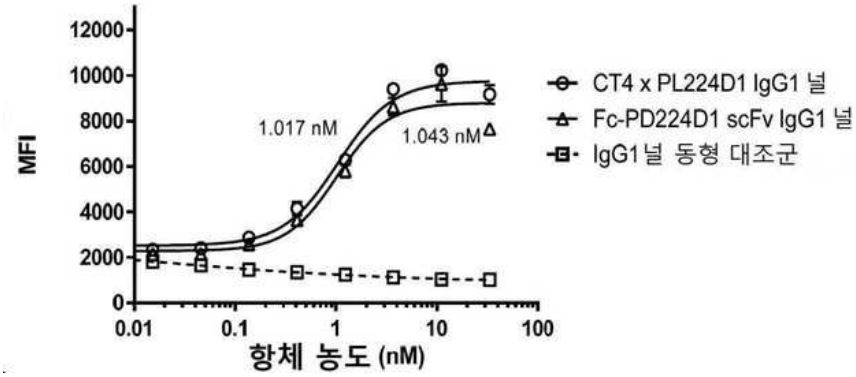
항-CTLA4, 항-PD-1 및 항-PD-L1 에 대한 CDR 서열									
mAb	표적	VH			VL				
		CDR 1	CDR 2	CDR 3	CDR 1	CDR 2	CDR 3		
CT4	CTLA4	SSYTMH 서열번호 141	FISYDGNNKYYADSVKG 서열번호 142	TGWLGPFDY 서열번호 143	RASQSVGSSYLA 서열번호 144	GAFSRAT 서열번호 145	QQYGSSPWT 서열번호 146		
PL230C6	PD-L1	NTYDMI 서열번호 147	IITYSGSRYYANWAKG 서열번호 148	DYMSGSHL 서열번호 149	QASEDIYSFLA 서열번호 150	SASSLAS 서열번호 151	QQGYGKNNVDNA 서열번호 152		
PD224D1	PD-1	SSYAMS 서열번호 153	YIGDTTGIAYASWANG 서열번호 154	GWSYLDI 서열번호 155	QASQNIYSNLA 서열번호 156	QASTLAS 서열번호 157	QGGYYSAALNT 서열번호 158		
PL221G5	PD-L1	SGYDMC 서열번호 159	CIAAGSAGITYDANWAKG 서열번호 160	SAFSFDYAMDL 서열번호 161	QASQSISSHLN 서열번호 162	KASTLAS 서열번호 163	QQGYSWGNVDNV 서열번호 164		
PL231H2	PD-L1	STYDMI 서열번호 165	IISYVGNTYYASWAKG 서열번호 166	DFISGSHL 서열번호 167	QASESISSFLS 서열번호 168	SASTLAS 서열번호 169	QQGYSKSNVDNA 서열번호 170		
PL00485	PD-L1	SSYWMS 서열번호 171	VIDTNVYIYYANWAKG 서열번호 172	YVGNNDDYINL 서열번호 173	QSSQSVYNGWLS 서열번호 174	GASTLAS 서열번호 175	LGSYTSSTENS 서열번호 176		
PL00489	PD-L1	SVINMG 서열번호 177	TITYVGNTYYASWAKG 서열번호 178	ESGTIYYSYFNL 서열번호 179	QASESISNYLS 서열번호 180	YASNLAS 서열번호 181	QSYYGGGSAYT 서열번호 182		
PD206F12	PD-1	SGYWIC 서열번호 183	CIYAGTSGSTSYASWARG 서열번호 184	NLYTYNSL 서열번호 185	QSSQSVYDNNWLA 서열번호 186	TVSTLAS 서열번호 187	QGTYYSSGWNFA 서열번호 188		
PD215A1	PD-1	SSYWMC 서열번호 189	CITTGSGSTYYASWAKR 서열번호 190	AFDL 서열번호 191	QASQSIYSYLN 서열번호 192	GASNLAS 서열번호 193	QSSWLSGAVGNA 서열번호 194		
PD220F6	PD-1	SSYGVS 서열번호 195	LIFPGIGFKDYASWVNG 서열번호 196	DLDL 서열번호 197	QSSPSVYSNYLS 서열번호 198	YASTLAS 서열번호 199	AGGYSSSTRA 서열번호 200		
PD225G11	PD-1	SSHWIC 서열번호 201	CIYTGSIDVFYYASWAKG 서열번호 202	AANTDTTYFNL 서열번호 203	QASQSINNQLS 서열번호 204	GASTLAS 서열번호 205	HVHYCSGGSCFWA 서열번호 206		

도면

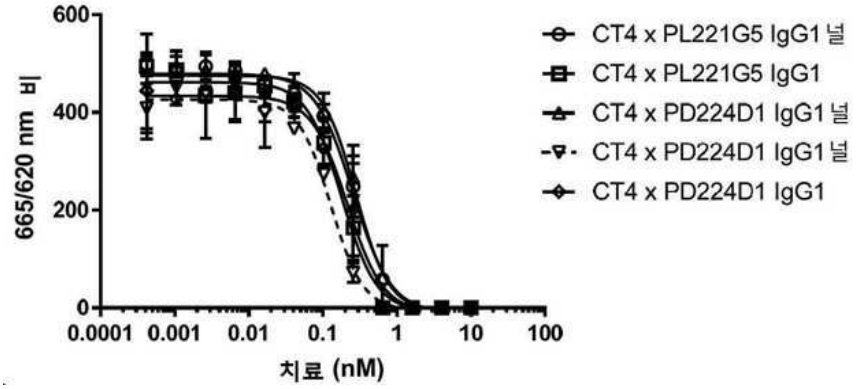
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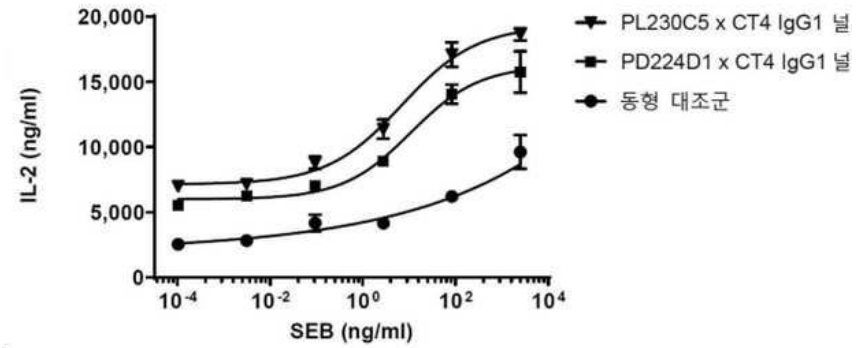
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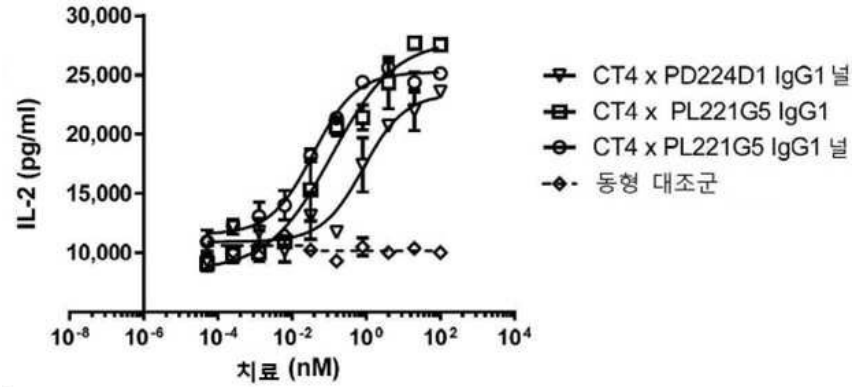
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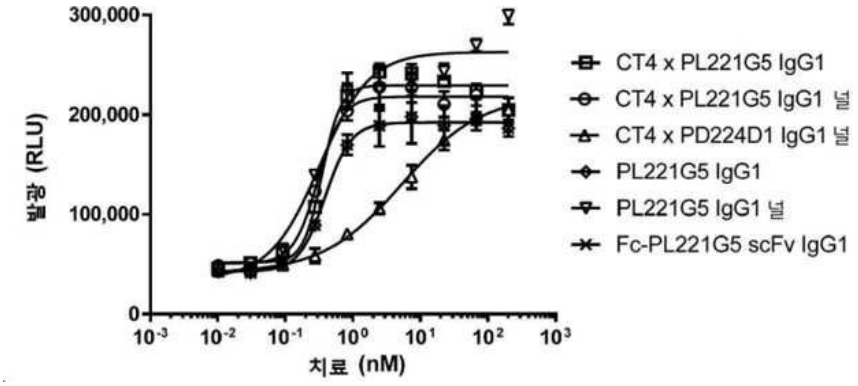
도면4a



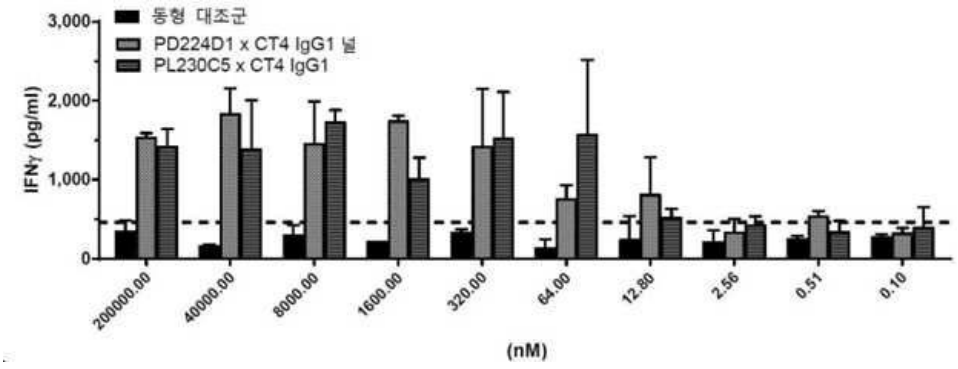
도면4b



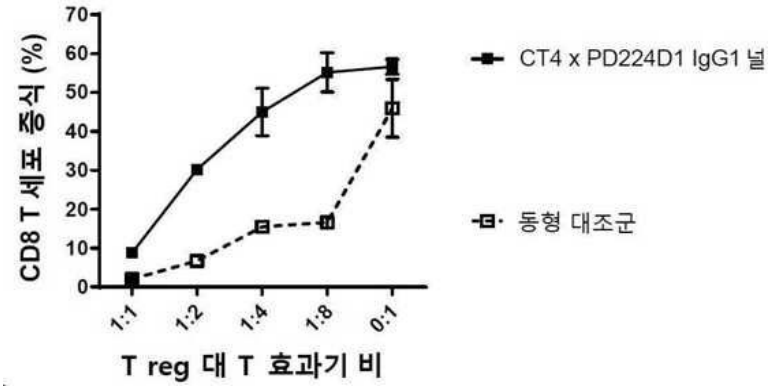
도면5



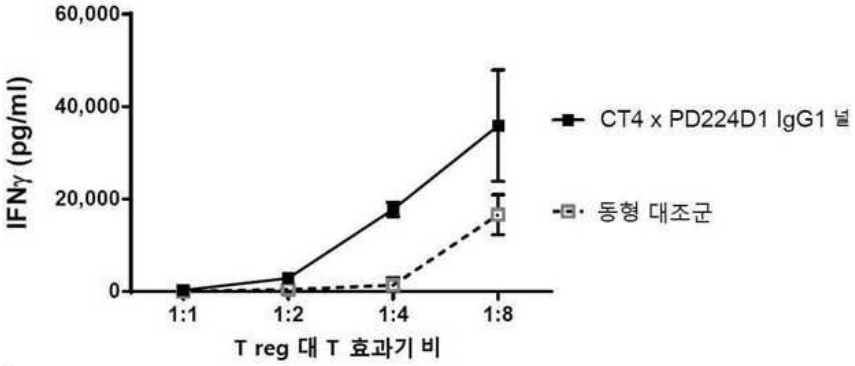
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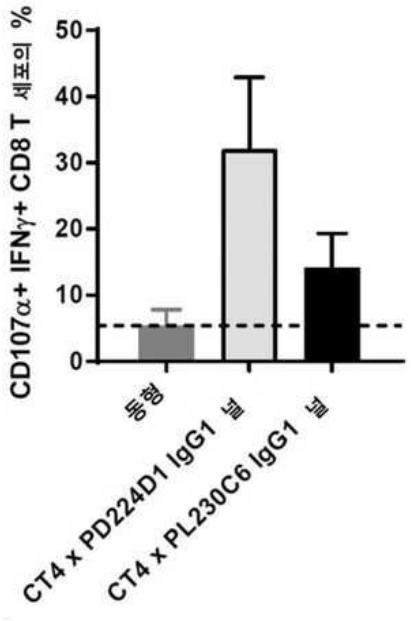
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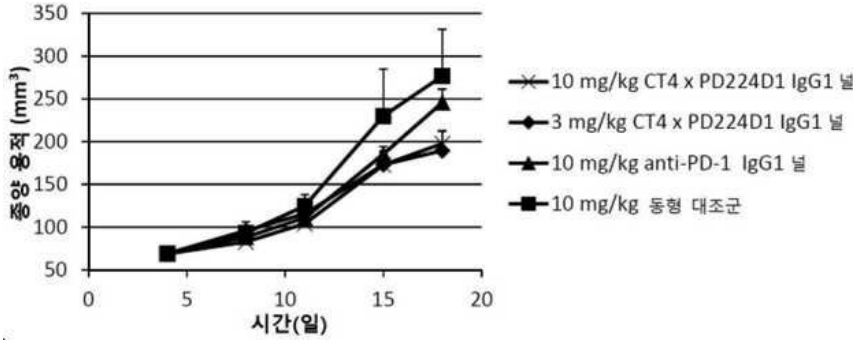
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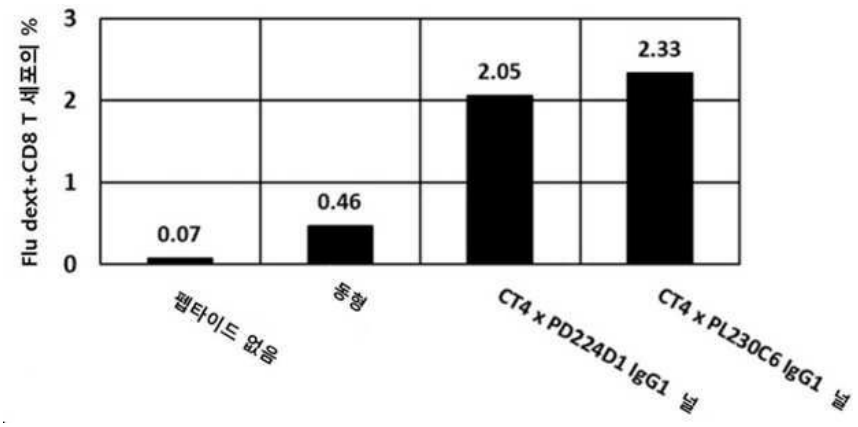
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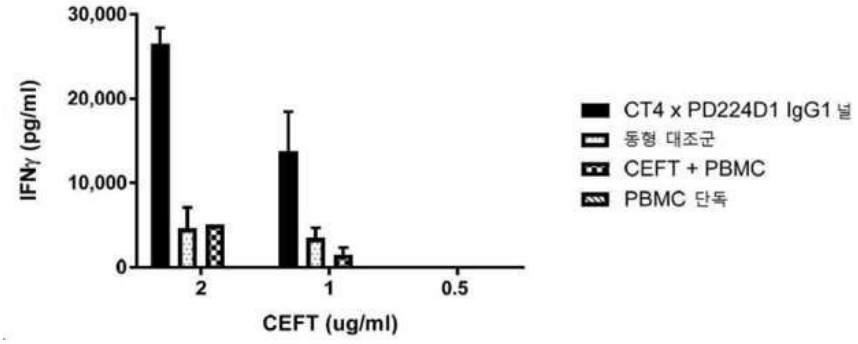
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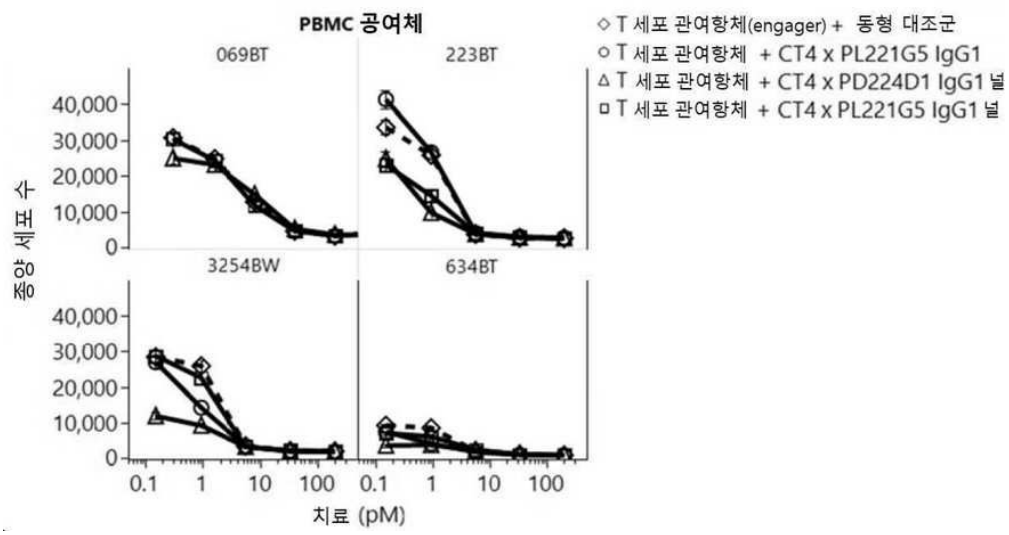
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도면11



도면12



서 열 목 록

SEQUENCE LISTING

<110> SYSTIMMUNE, INC.

SICHUAN BAILI PHARM CO., LTD.

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

<130> IPA191696-US-D1-1

<150> US 62/580,845

<151> 2017-11-02

<160> 206

<170> PatentIn version 3.5

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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

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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
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cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180

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tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 480

caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 540

acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag 600

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<211> 215

<212> PRT

<213> Artificial Sequence

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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

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Ser Phe Asn Arg Gly Glu Cys

210 215

<210> 5

<211> 2106

<212> DNA

<213> Artificial Sequence

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gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

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tggctggggc cctttgacta ctggggccag ggaaccctgg tcaccgtctc ctcagctagc 360

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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

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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

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545 550 555 560
Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
565 570 575
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580 585 590

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acttgccagg ccagtcagag cattagttcc cacttaaact ggtatcagca gaaaccaggg 1920

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ttcagcggca gtggatctgg gacagaattt actctcacca tcagcagcct gcagcctgat 2040

gattttgcaa cttattactg ccaacagggt tatagttggg gtaatgttga taatgttttc 2100

ggcggaggga ccaaggtgga gatcaaa 2127

<210> 8

<211> 709

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 8

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 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

<400> 9

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc acaggtgcag 1380

ctggtggagt ctgggggagg cctggtccag cctgggggct ccctgagact ctcctgtaca 1440

acttctggaa tcgaccttag tacctacgac atgatctggg tccgccaggc tccaggcaag 1500

gggctagagt gggtgggaat cattagttat gttggtaaca catactacgc gagctgggcg 1560

aaaggccgat tcaccctctc caaagacaat acctcgacca cggtggatct gcaaatgaac 1620

agcctgagag ctgaggacac ggctgtgtat tactgtgcga gagattttat tagtggttcc 1680

cacttgtggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcgga 1740

ggtggttccg gcggtggcgg ctccggtgga ggcggttctg cctatgatat gacccagtct 1800

ccatcttccg tgtctgcatc tgtaggagac agagtcacca tcaattgtca ggccagtgag 1860

agcattagta gcttcttatc ctggtatcag cagaaaccag ggaaagcccc taagctcctg 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

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc agaggtgcag 1380

ctggtggagt ctgggggagg cttggtccag cctgggggt ccctgagact ctcctgtgca 1440

gcctctggat tctccctcag tagctactgg atgagctggg tccgccaggc tccagggaag 1500

gggctggagt ggatcggagt cattgatact aatgtttata tactacgc gaactgggca 1560

aaaggcagat tcaccatctc cagagacaat tccaagaaca cgctgtatct tcaaatgaac 1620

agcctgagag ccgaggacac ggctgtgtat tactgtgcga gatatgtggg taataatgat 1680

gattatatta acttgtgggg ccagggaacc ctggtcaccg tctcgagcgg tggaggcgga 1740

tctggcggag gtggttccgg cggtggcggc tccggtggag gcggctctga catccagatg 1800

acccagtctc cttccaccct gtctgcatct gtaggagaca gagtcaccat cacttgccag 1860

tccagtcaga gtgtttataa tggctactgg ttatcctggt atcagcagaa accagggaaa 1920

gcccctaagc tcctgatcta tggtgcatcc actctggcat ctggggtccc atcaaggttc 1980

agcggcagtg gatctgggac agaattcact ctcaccatca gcagcctgca gcctgatgat 2040

tttgcaactt attactgcct aggcagttat actagtagta ctgagaactc tttcggcgga 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 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

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc agaggtgcag 1380

ctggtggagt ctgggggagg cttggtccag cctgggggt ccctgagact ctcctgtaca 1440

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gggctggagt ggatcggaac cattacttat gttggtaaca catattacgc gagctgggcg 1560

aaaggcagat tcaccatctc caaaacctcg accacggtgg atcttaaaat caccagtccg 1620

acaaccgagg acacggctgt gtattactgt gcgagagaat ctggtactat ttattacagt 1680

tactttaact tgtggggcca agggaccctg gtcaccgtct cgagcggtgg aggcggatct 1740

ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gctctgcatt cgaattgacc 1800

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcaa gtgccaggcc 1860

agtgaaagca ttagcaacta cttatcctgg tatcagcaga ttccagggaa agttcctaag 1920

ctcctgatct attatgcatc caatctggca tctggggtcc catctcggtt cagtggcagt 1980

ggatctggga cagatttcac tctcaccatc agcagcctgc agcctgaaga tgttgcaact 2040

tattactgtc aaagctatta tggtggtggt 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

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

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

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc agaggtgcag 1380

ctggtggagt ctgggggagg cttggtccag cctggggggt ccctgagact ctcctgtgca 1440

gcctctggat tcgacttcag tagcggctac tggatatgct gggtccgcca ggctccaggg 1500

aaggggctgg agttgatcgc atgcatttat gctggtacta gtggtagtac ttcctacgcg 1560

agctgggcga gaggcagatt caccatctcc gaaacctcca agaacacggt gactcttcaa 1620

atgaacagcc tgagagccga ggactcggct gtgtattact gtgcgagaaa tctttacact 1680

tacaatagct tgtggggcca gggaaccctg gtcaccgtct cgagcggtgg aggcggatct 1740

ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gctctgacat ccagatgacc 1800

cagtctcctt ccaccctgtc tgcatctgta ggagacagag tcaccatcac ttgccagtcc 1860

agtcagagtg tttatgataa caactggtta gcctggtatc agcagaaacc agggaaagcc 1920

cctaagctcc tgatctatac agtatccact ctggcatctg gggtcccatc aaggttcagc 1980

ggcagtggat ctgggacaga attcactctc 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

<210> 17

<211> 2100

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 17

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 840

gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 900

taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg caaggagtac 960

aagtgcgcgg tctccaacaa agccctccca gccccccatcg 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 ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc acaggagcag 1380

ctgttggagt ctgggggagg cttggtacag cctggggggt ccctgagact ctcctgtaca 1440

gcctctggat tctcctttag cagctactgg atgtgctggg tccgccaggc tccagggaag 1500

gggctggagt ggatcggatg cattacgact ggtagtggta gcacttacta cgcgagctgg 1560

gcgaagcgcc ggttcaccat ctccaaagac aattccaaga acacggtgac tctgcaaatg 1620

aacagcctga gagccgagga cacggccgta tattactgta cgagagcatt tgacttgtgg 1680

ggccagggaa ccctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740

ggcggtggcg gctccggtgg aggcggctct gacatccaga tgacccagtc tccatcctcc 1800

ctgtctgcat ctgtaggaga cagagtcacc atcacttgcc aggccagtca gagcatttac 1860

agctacttaa actggtatca gcagaaacca gggaaagccc ctaagctcct gatctatggt 1920

gcatccaatc tggcatctgg ggtcccatca aggttcagtg gcagtggatc tgggacagat 1980

ttcactctca ccatcagcag tctgcaacct gaagattttg caacttacta ctgtcaaagc 2040

agttggttga gtggtgctgt tggtaatgct ttcggcggag 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

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt cccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

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gtgaaggaga ccgggggagg cttggtacag cctggggggt ccctgagact ctcctgtgca 1440

gcctctggat tcaccatcag cagctatgga gtgagctggg tccgccaggc tccagggaag 1500

gggctggagt gggtcgcatt gatttttccc gggattggtt tcaaagacta cgcgagctgg 1560

gtgaatggcc ggttcaccct ctccagcgac aacgcccaga acactgtgga actgcaaatg 1620

aacagcctga gagccgagga cacggccgta tattactgtg cgagagattt ggacttgtgg 1680

ggccagggaa ccctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740

ggcggtggcg gctccggtgg aggcggctct gacatccaga tgacccagtc tccatcctcc 1800

ctgtctgcat ctgtaggaga cagagtcacc atcacttgcc agtccagtcc gagtgtttat 1860

agtaactact tatcctggta tcagcagaaa ccagggaaag ttcctaagct cctgatctat 1920

tatgcatcca ctctggcatc tggggtccca tctcggttca gtggcagtgg 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

caggtgcagc tggtggagtc 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 ctcagctagc 360

accaagggcc catcggtctt cccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc agaggtgcag 1380

ctgttggagt ctgggggagg cttggtacag cctgggggggt ccctgagact ctcctgtgca 1440

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 ctcgagcggt 1740

ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggctctgcc 1800

tatgatatga cccagtctcc atcctccctg tctgcatctg taggagacag agtcaccatc 1860

aattgccagg ccagtcagag cattaacaac caactatcct ggtatcagca gaaaccaggg 1920

aaagttccta agctcctgat ctatggtgca tccactctgg catctggggt cccatctcgg 1980

ttcaccggca gtggatctgg gacagatttc actctcacca tcagcagcct gcagcctgaa 2040

gatgttgcaa cttattactg tcatgttcat tattgcagtg gtggtagttg 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

ggtggaggcg gatctggcgg aggtggttcc ggcggtggcg gctccggtgg aggcggctct 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 aggagtctgg gggaggcttg gtccagcctg gggggtccct gagactctcc 60

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 gggaaccctg gtcaccgtct cgagcgctag caccaagggc 360

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagccgcgg gggcaccgtc agtcttcctc 720

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcgcg 960

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctatagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggcggtgg agggtccggc ggtggtggat cccaggtgca attggtggag 1380

tctgggggag gcgtggtcca gcctgggagg tccctgagac tctcctgtgc agcctctgga 1440

ttcaccttca gtagctatac tatgcactgg gtccgccagg ctccaggcaa ggggctggag 1500

tgggtgacat ttatatcata tgatggaaac aataaatact acgcagactc cgtgaagggc 1560

cgattcacca tctccagaga caattccaag aacacgctgt atctgcaaat gaacagcctg 1620

agagctgagg acacggctat atattactgt gcgaggaccg gctggctggg gccctttgac 1680

tactggggcc agggaaccct ggtcaccgtc tcgagcggtg gaggcggttc aggcggaggt 1740

ggaagtggtg gtggcggctc tggaggcggc ggatctgaaa ttgtgttgac gcagtctcca 1800

ggcaccctgt ctttgtctcc aggggaaaga gccaccctct 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 tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcatcctctc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta aaaataatgt tgataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct 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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtacag cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120

ccagggaagg ggctggagta catcggctac 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 ctgggggcac agcggccctg 420

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 480

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 540

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 600

aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa 660

actcacacat gcccaccgtg cccagcacct gaagccgcgg gggcaccgtc agtcttcctc 720

ttccccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 780

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcgcg 960

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctatagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1320

ctgtctccgg gtggcggtgg agggtccggc ggtggtggat cccaggtgca attggtggag 1380

tctgggggag gcgtggtcca gcctgggagg tccctgagac tctcctgtgc agcctctgga 1440

ttcaccttca gtagctatac tatgcactgg gtccgccagg ctccaggcaa ggggctggag 1500

tgggtgacat ttatatcata tgatggaaac aataaatact acgcagactc cgtgaagggc 1560

cgattcacca tctccagaga caattccaag aacacgctgt atctgcaaat gaacagcctg 1620

agagctgagg acacggctat atattactgt gcgaggaccg gctggctggg gccctttgac 1680

tactggggcc agggaaccct ggtcaccgtc tcgagcggtg gaggcggatc tggcggaggt 1740

ggttccggcg gtggcggctc cggtggaggc ggttctgaaa ttgtgttgac gcagtctcca 1800

ggcaccctgt ctttgtctcc aggggaaaga gccaccctct 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> 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

gcccttgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gaacatttac agcaatttag cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatcag gcctccactc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggata tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaggc ggttattata gtgctgccct taatactttc 300

ggcggaggga ccaaggtgga gatcaaacgt acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaaagagc 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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120
gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggtatcact 180

tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

tcggcgtttt cgttcgacta cgccatggac ctctggggcc agggaaccct ggtcaccgtc 360

tcgagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480

gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540

tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600

cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660

gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 720

ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960

ggcaaggagt acaagtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 1020

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc 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 atgaggctct gcacaaccac 1320

tacacgcaga agagcctctc cctgtctccg ggtggcggtg gagggtccgg cggtggtgga 1380

tcccaggtgc aattggtgga gtctgggggga ggcgtggtcc agcctgggag gtccctgaga 1440

ctctcctgtg cagcctctgg attcaccttc agtagctata ctatgcactg ggtccgccag 1500

gctccaggca aggggctgga gtgggtgaca tttatatcat atgatggaaa caataaatac 1560

tacgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 1620

tatctgcaaa tgaacagcct gagagctgag gacacggcta tatattactg tgcgaggacc 1680

ggctggctgg ggccctttga ctactggggc cagggaaccc tggtcaccgt ctcgagcggt 1740

ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggttctgaa 1800

attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc 1860

tcctgcaggg ccagtcagag tgttggcagc agctacttag cctggtacca gcagaaacct 1920

ggccaggctc ccaggctcct catctatggt gcattcagca gggccactgg catcccagac 1980

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 2040

gaagattttg cagtgtatta ctgtcagcag tatggtagct caccgtggac gttcggccaa 2100

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

gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gagcattagt tcccacttaa actggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa tttactctca ccatcagcag cctgcagcct 240

gatgattttg caacttatta ctgccaacag ggttatagtt ggggtaatgt tgataatgtt 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct 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

caggtgcagc tggtggagtc tgggggaggc ctggtccagc ctgggggctc cctgagactc 60

tcctgtacaa cttctggaat 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 ccagggaacc ctggtcaccg tctcgagcgc tagcaccaag 360
ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420
ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480
gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540
ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600
gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaagccg cgggggcacc gtcagtcttc 720
ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780
gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840
gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt 900
gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 960
gcggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg 1020
cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac 1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200
ggctccttct tcctctatag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320
tccctgtctc cgggtggcgg tggagggtcc ggcggtggtg gatcccaggt gcaattggtg 1380
gagtctgggg gaggcgtggt ccagcctggg aggtccctga gactctcctg tgcagcctct 1440
ggattcacct tcagtagcta tactatgcac tgggtccgcc aggctccagg caaggggctg 1500

gagtgggtga catttatatc atatgatgga aacaataaat actacgcaga ctccgtgaag 1560
ggccgattca ccatctccag agacaattcc aagaacacgc tgtatctgca aatgaacagc 1620
ctgagagctg aggacacggc tatatattac tgtgcgagga ccggctggct ggggcccttt 1680
gactactggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcgga 1740
ggtggttccg gcggtggcgg ctccggtgga ggcggttctg aaattgtgtt gacgcagtct 1800
ccaggcaccc tgtctttgtc tccaggggaa agagccaccc tctcctgcag ggccagtcag 1860
agtgttggca gcagctactt agcctggtac cagcagaaac ctggccaggc tcccaggctc 1920

ctcatctatg gtgcattcag cagggccact ggcatcccag acaggttcag tggcagtggg 1980

tctgggacag acttcactct caccatcagc agactggagc ctgaagattt tgcagtgtat 2040

tactgtcagc agtatggtag ctcaccgtgg acgttcggcc aagggaccaa 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 tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaattgtc aggccagtga gagcattagt agcttcttat cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatcttttct gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatagta aaagtaatgt ggataatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct ccaatcgggt 480

aactcccagg agagtgtcac agagcaggac agcaaggaca gcacctacag cctcagcagc 540

accctgacgc tgagcaaagc agactacgag aaacacaaag tctacgcctg cgaagtcacc 600

catcagggcc tgagctcgcc cgtcacaaag agcttcaaca ggggagagtg t 651

<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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc 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 ctcgagcgct 360

agcaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga 540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa 660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaagccgc gggggcaccg 720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 840

gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960

tacaagtgcg cggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa 1020

gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320

aagagcctct ccctgtctcc gggtggcggt ggagggtccg gcggtggtgg atcccaggtg 1380

caattggtgg agtctggggg aggcgtggtc cagcctggga ggtccctgag actctcctgt 1440

gcagcctctg gattcacctt cagtagctat actatgcact gggtccgcca 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 tggaggcgga 1740

tctggcggag gtggttccgg cggtggcggc tccggtggag gcggttctga aattgtgttg 1800

acgcagtctc caggcaccct gtctttgtct ccaggggaaa gagccaccct ctcctgcagg 1860

gccagtcaga gtgttggcag cagctactta gcctggtacc agcagaaacc tggccaggct 1920

cccaggctcc tcatctatgg tgcattcagc agggccactg gcatcccaga caggttcagt 1980

ggcagtgggt ctgggacaga cttcactctc accatcagca gactggagcc tgaagatttt 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

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atcacttgcc agtccagtca gagtgtttat aatggctact ggttatcctg gtatcagcag 120

aaaccaggga aagcccctaa gctcctgatc tatggtgcat ccactctggc atctggggtc 180

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240

cagcctgatg attttgcaac ttattactgc ctaggcagtt atactagtag tactgagaac 300

tctttcggcg 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

agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 600

acccatcagg 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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtacag tgtctggaat cgacctcagt gtcatcaata tgggctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180

agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240

accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tggtactatt 300

tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagcgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc ccaggtgcaa 1380

ttggtggagt ctgggggagg cgtggtccag cctgggaggt ccctgagact ctcctgtgca 1440

gcctctggat tcaccttcag tagctatact atgcactggg tccgccaggc tccaggcaag 1500

gggctggagt gggtgacatt tatatcatat gatggaaaca ataaatacta cgcagactcc 1560

gtgaagggcc gattcaccat ctccagagac aattccaaga acacgctgta tctgcaaatg 1620

aacagcctga gagctgagga cacggctata tattactgtg cgaggaccgg ctggctgggg 1680

ccctttgact actggggcca gggaaccctg gtcaccgtct cgagcggtgg aggcggatct 1740

ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gttctgaaat tgtgttgacg 1800

cagtctccag gcaccctgtc tttgtctcca ggggaaagag ccaccctctc ctgcagggcc 1860

agtcagagtg ttggcagcag ctacttagcc tggtaccagc agaaacctgg ccaggctccc 1920

aggctcctca tctatggtgc attcagcagg gccactggca tcccagacag 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

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atcaagtgcc aggccagtga aagcattagc aactacttat cctggtatca gcagattcca 120

gggaaagttc ctaagctcct gatctattat gcatccaatc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaagc tattatggtg gtggtagtgc ctatactttc 300

ggcggaggga ccaaggtgga gatcaaacgt acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaaagagc 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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggcgag aggcagattc accatctccg aaacctccaa gaacacggtg 240

actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300

ctttacactt acaatagctt gtggggccag ggaaccctgg tcaccgtctc gagcgctagc 360

accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420

gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600

tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agagagttga gcccaaatct 660

tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aagccgcggg ggcaccgtca 720

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 780

acatgcgtgg tggtggacgt gagccacgaa gaccctgagg 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 cccgagaacc acaggtgtac accctgcccc catcccggga tgagctgacc 1080

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct atcccagcga catcgccgtg 1140

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac 1200

tccgacggct ccttcttcct ctatagcaag ctcaccgtgg acaagagcag gtggcagcag 1260

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacgcagaag 1320

agcctctccc tgtctccggg tggcggtgga gggtccggcg gtggtggatc ccaggtgcaa 1380

ttggtggagt ctgggggagg cgtggtccag cctgggaggt ccctgagact ctcctgtgca 1440

gcctctggat tcaccttcag tagctatact atgcactggg tccgccaggc tccaggcaag 1500

gggctggagt gggtgacatt tatatcatat gatggaaaca ataaatacta cgcagactcc 1560

gtgaagggcc gattcaccat ctccagagac aattccaaga acacgctgta tctgcaaatg 1620

aacagcctga gagctgagga cacggctata tattactgtg cgaggaccgg ctggctgggg 1680

ccctttgact actggggcca gggaaccctg gtcaccgtct cgagcggtgg aggcggatct 1740

ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gttctgaaat tgtgttgacg 1800

cagtctccag gcaccctgtc tttgtctcca ggggaaagag ccaccctctc ctgcagggcc 1860

agtcagagtg ttggcagcag ctacttagcc tggtaccagc agaaacctgg ccaggctccc 1920

aggctcctca tctatggtgc attcagcagg gccactggca tcccagacag 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 tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtccagtca gagtgtttat gataacaact ggttagcctg gtatcagcag 120

aaaccaggga aagcccctaa gctcctgatc tatacagtat ccactctggc atctggggtc 180

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240

cagcctgatg attttgcaac ttattactgc caaggcactt attatagtag tggttggaac 300

tttgctttcg gcggagggac caaggtggag atcaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc 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 tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtacag cctctggatt ctcctttagc agctactgga tgtgctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggatgc attacgactg gtagtggtag cacttactac 180

gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300

gacttgtggg gccagggaac cctggtcacc gtctcgagcg ctagcaccaa gggcccatcg 360

gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 420

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480

agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 540

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 600

aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 660

acatgcccac cgtgcccagc acctgaagcc gcgggggcac cgtcagtctt cctcttcccc 720

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 780

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg cgcggtctcc 960

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctata gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

tgctccgtga tgcatgaggc 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 ccctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740

ggcggtggcg gctccggtgg aggcggttct gaaattgtgt tgacgcagtc tccaggcacc 1800

ctgtctttgt ctccagggga aagagccacc ctctcctgca gggccagtca gagtgttggc 1860

agcagctact tagcctggta ccagcagaaa cctggccagg ctcccaggct cctcatctat 1920

ggtgcattca gcagggccac tggcatccca gacaggttca gtggcagtgg gtctgggaca 1980

gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgta 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 tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gagcatttac agctacttaa actggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggt gcatccaatc tggcatctgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaaagc agttggttga gtggtgctgt tggtaatgct 300

ttcggcggag ggaccaaggt ggagatcaaa cgtacggtgg ctgcaccatc tgtcttcatc 360

ttcccgccat ctgatgagca gttgaaatct ggaactgcct ctgttgtgtg cctgctgaat 420

aacttctatc ccagagaggc caaagtacag tggaaggtgg ataacgccct 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 ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt 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

gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 420

ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 480

agcggcgtgc acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 540

gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 600

aagcccagca acaccaaggt ggacaagaga gttgagccca aatcttgtga caaaactcac 660

acatgcccac cgtgcccagc acctgaagcc gcgggggcac cgtcagtctt cctcttcccc 720

ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg 780

gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 840

cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 900

gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg cgcggtctcc 960

aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1020

gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1080

ctgacctgcc tggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1140

gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1200

ttcctctata gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1260

tgctccgtga tgcatgaggc 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 ccctggtcac cgtctcgagc ggtggaggcg gatctggcgg aggtggttcc 1740

ggcggtggcg gctccggtgg aggcggttct gaaattgtgt tgacgcagtc tccaggcacc 1800

ctgtctttgt ctccagggga aagagccacc ctctcctgca gggccagtca gagtgttggc 1860

agcagctact tagcctggta ccagcagaaa cctggccagg ctcccaggct cctcatctat 1920

ggtgcattca gcagggccac tggcatccca gacaggttca gtggcagtgg gtctgggaca 1980

gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgta ttactgtcag 2040

cagtatggta gctcaccgtg 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 agtccagtcc gagtgtttat agtaactact tatcctggta tcagcagaaa 120

ccagggaaag ttcctaagct cctgatctat tatgcatcca ctctggcatc tggggtccca 180

tctcggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 240

cctgaagatg ttgcaactta ttactgtgca ggcggttata gtagtagtac tcgtgctttc 300

ggcggaggga ccaaggtgga gatcaaacgt acggtggctg caccatctgt cttcatcttc 360

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 480

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 540

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 600

cagggcctga gctcgcccgt cacaaagagc 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 ctgggggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180

tactacgcga gctgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

gccgctaata ctgatactac ctactttaac ttgtggggcc agggaaccct ggtcaccgtc 360

tcgagcgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 420

tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 480
gtgtcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgcg 720
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 780
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 840

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960
ggcaaggagt acaagtgcgc ggtctccaac aaagccctcc cagccccat cgagaaaacc 1020
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc 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 atgaggctct gcacaaccac 1320
tacacgcaga agagcctctc cctgtctccg ggtggcggtg gagggtccgg cggtggtgga 1380
tcccaggtgc aattggtgga gtctgggggga ggcgtggtcc agcctgggag gtccctgaga 1440
ctctcctgtg cagcctctgg attcaccttc agtagctata ctatgcactg ggtccgccag 1500
gctccaggca aggggctgga gtgggtgaca tttatatcat atgatggaaa caataaatac 1560
tacgcagact ccgtgaaggg ccgattcacc atctccagag acaattccaa gaacacgctg 1620
tatctgcaaa tgaacagcct gagagctgag gacacggcta tatattactg tgcgaggacc 1680

ggctggctgg ggcctttga ctactggggc cagggaaccc tggtcaccgt ctcgagcggt 1740
ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggttctgaa 1800
attgtgttga cgcagtctcc aggcaccctg tctttgtctc caggggaaag agccaccctc 1860
tcctgcaggg ccagtcagag tgttggcagc agctacttag cctggtacca gcagaaacct 1920
ggccaggctc ccaggctcct catctatggt gcattcagca gggccactgg catcccagac 1980
aggttcagtg gcagtgggtc tgggacagac ttcactctca 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 tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aggccagtca gagcattaac aaccaactat cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatggt gcatccactc tggcatctgg ggtcccatct 180

cggttcaccg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcatgtt cattattgca gtggtggtag 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

agcaccctga 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

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 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

atgagggccc ctgctcagtt tcttggcttc 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

caggtgcaat tggtggagtc 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 gagcggtgga 360

ggcggatctg gcggaggtgg ttccggcggt ggcggctccg gtggaggcgg ttctgaaatt 420

gtgttgacgc agtctccagg caccctgtct ttgtctccag gggaaagagc caccctctcc 480

tgcagggcca gtcagagtgt tggcagcagc tacttagcct ggtaccagca gaaacctggc 540

caggctccca ggctcctcat ctatggtgca ttcagcaggg ccactggcat cccagacagg 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

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtacag cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120

ccagggaagg ggctggagta catcggctac attggtgata ctactggcat agcctacgcg 180

agctgggcga atggcagatt caccatctcc aaagacaata ccaagaacac ggtggatctt 240

caaatgaaca gcctgagagc cgaggacacg gctgtgtatt actgtgcgag aggctggtcc 300

tacttagaca tctggggcca agggaccctg gtcaccgtct cgagcggtgg aggcggatct 360

ggcggaggtg gttccggcgg tggcggctcc ggtggaggcg gctctgccct tgtgatgacc 420

cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccaggcc 480

agtcagaaca tttacagcaa tttagcctgg tatcagcaga aaccagggaa agttcctaag 540

ctcctgatct atcaggcctc cactctggca tctggggtcc catctcggtt cagtggcagt 600

ggatatggga cagatttcac tctcaccatc agcagcctgc agcctgaaga tgttgcaact 660

tattactgtc aaggcggtta ttatagtgct gcccttaata ctttcggcgg agggaccaag 720

gtggagatca aa 732

<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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggcgag aggcagattc accatctccg aaacctccaa gaacacggtg 240

actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300

ctttacactt acaatagctt gtggggccag ggaaccctgg tcaccgtctc gagcggtgga 360

ggcggatctg gcggaggtgg ttccggcggt ggcggctccg gtggaggcgg ctctgacatc 420

cagatgaccc agtctccttc 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

gatgattttg caacttatta ctgccaaggc acttattata gtagtggttg gaactttgct 720

ttcggcggag 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 ctgggggtc cctgagactc 60
tcctgtacag cctctggatt ctcctttagc agctactgga tgtgctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggatgc attacgactg gtagtggtag cacttactac 180
gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300
gacttgtggg gccagggaac cctggtcacc gtctcgagcg gtggaggcgg atctggcgga 360

ggtggttccg gcggtggcgg ctccggtgga ggcggctctg acatccagat gacccagtct 420

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcca ggccagtcag 480

agcatttaca gctacttaaa ctggtatcag cagaaaccag ggaaagcccc taagctcctg 540

atctatggtg catccaatct ggcatctggg gtcccatcaa ggttcagtgg cagtggatct 600

gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660

tgtcaaagca gttggttgag tggtgctgtt 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 ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180
tactacgcga gctgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240
ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300
gccgctaata ctgatactac ctactttaac ttgtggggcc agggaaccct ggtcaccgtc 360
tcgagcggtg gaggcggatc tggcggaggt ggttccggcg gtggcggctc cggtggaggc 420
ggctctgcct atgatatgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 480
gtcaccatca ttgccaggc cagtcagagc attaacaacc aactatcctg gtatcagcag 540

aaaccaggga aagttcctaa gctcctgatc tatggtgcat ccactctggc atctggggtc 600
ccatctcggt tcaccggcag tggatctggg acagatttca ctctcaccat cagcagcctg 660
cagcctgaag atgttgcaac ttattactgt catgttcatt attgcagtgg tggtagttgt 720

ttttgggctt tcggcggagg gaccaaggtg 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
cagtcggtgg aggagtctgg gggaggcttg gtccagcctg gggggtccct gagactctcc 60

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 gggaaccctg gtcaccgtct cttccggtgg aggcggttca 360
ggcggaggtg gaagtggtgg tggcggctct ggaggcggcg gatctgccta tgatatgacc 420
cagtctccat cttccgtgtc tgcatctgta ggagacagag tcaccatcaa gtgtcaggcc 480

agtgaggaca tttatagctt cttggcctgg tatcagcaga aaccagggaa agcccctaag 540
ctcctgatcc attctgcatc ctctctggca tctggggtcc 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 ccagggaacc 120

ctggtcaccg tctcgagcgg tggaggcgga tctggcggag gtggttccgg cggtggcggc 180

tccggtggag gcggttctgc ctatgatatg acccagtctc catcttccgt gtctgcatct 240

gtaggagaca gagtcaccat 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
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120
gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggtatcact 180

tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300
tcggcgtttt cgttcgacta cgccatggac ctctggggcc agggaaccct ggtcaccgtc 360
tcgagcggtg gaggcggatc tggcggaggt ggttccggcg gtggcggctc cggtggaggc 420
ggctctgaca tccagatgac ccagtctcct tccaccctgt ctgcatctgt aggagacaga 480
gtcaccatca cttgccaggc cagtcagagc attagttccc acttaaactg gtatcagcag 540
aaaccaggga aagcccctaa gctcctgatc tataaggcat ccactctggc atctggggtc 600
ccatcaaggt tcagcggcag tggatctggg acagaattta ctctcaccat cagcagcctg 660

cagcctgatg attttgcaac ttattactgc caacagggtt atagttgggg taatgttgat 720
aatgttttcg gcggagggac 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

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc 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 ctcgagcggt 360

ggaggcggat ctggcggagg tggttccggc ggtggcggct ccggtggagg cggctctgac 420

atccagatga cccagtctcc ttccaccctg tctgcatctg taggagacag agtcaccatc 480

acttgccagt ccagtcagag tgtttataat ggctactggt tatcctggta tcagcagaaa 540

ccagggaaag cccctaagct 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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtacag tgtctggaat cgacctcagt gtcatcaata tgggctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180

agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240

accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tggtactatt 300

tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagcggtgga 360

ggcggatctg gcggaggtgg ttccggcggt ggcggctccg gtggaggcgg ctctgcattc 420

gaattgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcaag 480

tgccaggcca gtgaaagcat tagcaactac ttatcctggt atcagcagat tccagggaaa 540

gttcctaagc tcctgatcta ttatgcatcc aatctggcat ctggggtccc atctcggttc 600

agtggcagtg gatctgggac agatttcact ctcaccatca gcagcctgca gcctgaagat 660

gttgcaactt attactgtca aagctattat ggtggtggta 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

caggtgcagc tggtggagtc 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 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 gggccagtca gagtgttggc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta 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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtacag cctctggatt ctccctcagt agctatgcaa tgagctgggt ccgccaggct 120

ccagggaagg ggctggagta catcggctac 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

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

115

<210> 97

<211> 327

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 97

gcccttgtga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gaacatttac agcaatttag cctggtatca gcagaaacca 120

gggaaagttc ctaagctcct gatctatcag gcctccactc tggcatctgg ggtcccatct 180

cggttcagtg gcagtggata tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaggc ggttattata gtgctgccct taatactttc 300

ggcggaggga ccaaggtgga gatcaaa 327

<210> 98

<211> 109

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 98

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

100 105

<210> 99

<211> 354

<212> DNA

<213> Artificial Sequence

<220><223> synthesized

<400> 99

gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cgacttcagt agcggctact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gttgatcgca tgcatttatg ctggtactag tggtagtact 180

tcctacgcga gctgggcgag aggcagattc accatctccg aaacctccaa gaacacggtg 240

actcttcaaa tgaacagcct gagagccgag gactcggctg tgtattactg tgcgagaaat 300

ctttacactt acaatagctt gtggggccag ggaaccctgg tcaccgtctc gagc 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 tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtccagtca gagtgtttat gataacaact ggttagcctg gtatcagcag 120

aaaccaggga aagcccctaa gctcctgatc tatacagtat ccactctggc atctggggtc 180

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240

cagcctgatg attttgcaac ttattactgc caaggcactt attatagtag tggttggaac 300

tttgctttcg gcggagggac 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 ctgggggggtc cctgagactc 60

tcctgtacag cctctggatt ctcctttagc agctactgga tgtgctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggatgc attacgactg gtagtggtag cacttactac 180

gcgagctggg cgaagcgccg gttcaccatc tccaaagaca attccaagaa cacggtgact 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtac gagagcattt 300

gacttgtggg gccagggaac 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 aggccagtca gagcatttac agctacttaa actggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggt gcatccaatc tggcatctgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca 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

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt cacctttagc agcagccact ggatatgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcatttata ctggtagtat tgatgtcttt 180

tactacgcga gctgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

gccgctaata ctgatactac ctactttaac ttgtggggcc agggaaccct 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 tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaattgcc aggccagtca gagcattaac aaccaactat cctggtatca gcagaaacca 120
gggaaagttc ctaagctcct gatctatggt gcatccactc tggcatctgg ggtcccatct 180
cggttcaccg gcagtggatc tgggacagat ttcactctca 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 gggggtccct gagactctcc 60

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 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 tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgtc aggccagtga ggacatttat agcttcttgg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatccattct gcatcctctc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag ggttatggta 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 tggtggagtc tgggggaggc ctggtccagc ctgggggctc cctgagactc 60

tcctgtacaa cttctggaat 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 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 tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcaattgtc aggccagtga gagcattagt agcttcttat cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatcttttct gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca 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 ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt ctccttcagt agcgggtacg acatgtgctg ggtccgccag 120

gctccaggga aggggctgga gtggatcgca tgcattgctg ctggtagtgc tggtatcact 180

tacgacgcga actgggcgaa aggccggttc accatctcca gagacaattc caagaacacg 240

ctgtatctgc aaatgaacag cctgagagcc gaggacacgg ccgtatatta ctgtgcgaga 300

tcggcgtttt cgttcgacta cgccatggac ctctggggcc agggaaccct ggtcaccgtc 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 tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc aggccagtca gagcattagt tcccacttaa actggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctataag gcatccactc tggcatctgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagaa tttactctca 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 ctgggggtc 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 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 tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc agtccagtca gagtgtttat aatggctact ggttatcctg gtatcagcag 120

aaaccaggga aagcccctaa gctcctgatc tatggtgcat ccactctggc atctggggtc 180

ccatcaaggt tcagcggcag tggatctggg acagaattca ctctcaccat cagcagcctg 240

cagcctgatg attttgcaac ttattactgc ctaggcagtt atactagtag tactgagaac 300

tctttcggcg 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 tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60

tcctgtacag tgtctggaat cgacctcagt gtcatcaata tgggctgggt ccgccaggct 120

ccagggaagg ggctggagtg gatcggaacc attacttatg ttggtaacac atattacgcg 180

agctgggcga aaggcagatt caccatctcc aaaacctcga ccacggtgga tcttaaaatc 240

accagtccga caaccgagga cacggctgtg tattactgtg cgagagaatc tggtactatt 300

tattacagtt actttaactt gtggggccaa gggaccctgg tcaccgtctc gagc 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 tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcaagtgcc aggccagtga aagcattagc aactacttat cctggtatca gcagattcca 120

gggaaagttc ctaagctcct gatctattat gcatccaatc tggcatctgg ggtcccatct 180
cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagatgttg caacttatta ctgtcaaagc tattatggtg 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 ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt 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 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 agtccagtcc gagtgtttat agtaactact tatcctggta tcagcagaaa 120

ccagggaaag ttcctaagct cctgatctat tatgcatcca ctctggcatc tggggtccca 180

tctcggttca gtggcagtgg atctgggaca gatttcactc tcaccatcag cagcctgcag 240

cctgaagatg ttgcaactta ttactgtgca ggcggttata 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 ctggcaccct cctccaagag cacctctggg 60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 360

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 420

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840

ctggactccg acggctcctt cttcctctat 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

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ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc cgcgggggca 360

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccct 420

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600

gagtacaagt gcgcggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 720

ctgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 900

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960

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<210> 138

<211> 329

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 138

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 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
325

<210> 139
<211> 726
<212> DNA
<213> Artificial Sequence
<220><223> Synthesized
<400> 139
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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 gtggaggcgg atctggcgga 360
ggtggttccg gcggtggcgg ctccggtgga ggcggctctg acatccagat gacccagtct 420
ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgcca gtccagtccg 480
agtgtttata gtaactactt atcctggtat cagcagaaac cagggaaagt tcctaagctc 540
ctgatctatt atgcatccac tctggcatct ggggtcccat ctcggttcag tggcagtgga 600
tctgggacag atttcactct caccatcagc agcctgcagc ctgaagatgt tgcaacttat 660
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atcaaa 726

<210> 140

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 140

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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 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

210 215 220

Gly Tyr Ser Ser Ser Thr Arg Ala Phe Gly Gly Gly Thr Lys Val Glu

225 230 235 240

Ile Lys

<210> 141

<211> 6

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 141

Ser Ser Tyr Thr Met His

1 5

<210> 142

<211> 17

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 142

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

1 5 10 15

Gly

<210> 143

<211

> 9

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 143

Thr Gly Trp Leu Gly Pro Phe Asp Tyr

1 5

<210> 144

<211> 12

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 144

Arg Ala Ser Gln Ser Val Gly Ser Ser Tyr Leu Ala

1 5 10

<210> 145

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 145

Gly Ala Phe Ser Arg Ala Thr

1 5

<210> 146

<211> 9

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 146

Gln Gln Tyr Gly Ser Ser Pro Trp Thr

1 5

<210> 147

<211> 6

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 147

Asn Thr Tyr Asp Met Ile

1 5

<210> 148

<211> 16

<212> PRT

<213> Artificial Sequence

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<400> 148

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

1 5 10 15

<210> 149

<211> 8

<212> PRT

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<220><223> Synthesized

<400> 149

Asp Tyr Met Ser Gly Ser His Leu

1 5

<210> 150

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 150

Gln Ala Ser Glu Asp Ile Tyr Ser Phe Leu Ala

1 5 10

<210> 151

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 151

Ser Ala Ser Ser Leu Ala Ser

1 5

<210> 152

<211> 12

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<400> 152

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

1 5 10

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<400> 153

Asn Thr Tyr Asp Met Ile

1 5

<210> 154

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<213> Artificial Sequence

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<400> 154

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

1 5 10 15

<210> 155

<211> 8

<212> PRT

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<220><223> synthesized

<400> 155

Asp Tyr Met Ser Gly Ser His Leu

1 5

<210> 156

<211> 11

<212> PRT

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<400> 156

Gln Ala Ser Glu Asp Ile Tyr Ser Phe Leu Ala

1 5 10

<210> 157

<211> 7

<212> PRT

<213> Artificial Sequence

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<400> 157

Ser Ala Ser Ser Leu Ala Ser

1 5

<210> 158

<211> 12

<212> PRT

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<400> 158

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

1 5 10

<210> 159

<211> 6

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 159

Ser Gly Tyr Asp Met Cys

1 5

<210> 160

<211> 18

<212> PRT

<213> Artificial Sequence

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<400> 160

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

1 5 10 15

Lys Gly

<210> 161

<211> 11

<212> PRT

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<400> 161

Ser Ala Phe Ser Phe Asp Tyr Ala Met Asp Leu

1 5 10

<210> 162

<211> 11

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<213> Artificial Sequence

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<400> 162

Gln Ala Ser Gln Ser Ile Ser Ser His Leu Asn

1 5 10

<210> 163

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 163

Lys Ala Ser Thr Leu Ala Ser

1 5

<210> 164

<211> 12

<212> PRT

<213> Artificial Sequence

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<400> 164

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

1 5 10

<210> 165

<211> 6

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<

400> 165

Ser Thr Tyr Asp Met Ile

1 5

<210> 166

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 166

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

1 5 10 15

<210> 167

<211> 8

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 167

Asp Phe Ile Ser Gly Ser His Leu

1 5

<210> 168

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 168

Gln Ala Ser Glu Ser Ile Ser Ser Phe Leu Ser

1 5 10

<210> 169

<211> 7

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<213> Artificial Sequence

<220><223> synthesized

<400> 169

Ser Ala Ser Thr Leu Ala Ser

1 5

<210> 170

<211> 12

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<400> 170

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

1 5 10

<210> 171

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<213> Artificial Sequence

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<400> 171

Ser Ser Tyr Trp Met Ser

1 5

<210> 172

<211> 16

<212> PRT

<213> Artificial Sequence

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<400> 172

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

1 5 10 15

<210> 173

<211> 11

<212> PRT

<213> Artificial Sequence

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<400> 173

Tyr Val Gly Asn Asn Asp Asp Tyr Ile Asn Leu

1 5 10

<210> 174

<211> 12

<212> PRT

<213> Artificial Sequence

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<400> 174

Gln Ser Ser Gln Ser Val Tyr Asn Gly Trp Leu Ser

1 5 10

<210> 175

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 175

Gly Ala Ser Thr Leu Ala Ser

1 5

<210> 176

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 176

Leu Gly Ser Tyr Thr Ser Ser Thr Glu Asn Ser

1 5 10

<210> 177

<211> 6

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 177

Ser Val Ile Asn Met Gly

1 5

<210> 178

<211> 16

<212> PRT

<213> Artificial Sequence

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<400> 178

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

1 5 10 15

<210> 179

<211> 12

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 179

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

1 5 10

<210> 180

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 180

Gln Ala Ser Glu Ser Ile Ser Asn Tyr Leu Ser

1 5 10

<210> 181

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 181

Tyr Ala Ser Asn Leu Ala Ser

1 5

<210> 182

<211> 11

<212> PRT

<213> Artificial Sequence

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<400> 182

Gln Ser Tyr Tyr Gly Gly Gly Ser Ala Tyr Thr

1 5 10

<210> 183

<211> 6

<212> PRT

<213> Artificial Sequence

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<400> 183

Ser Gly Tyr Trp Ile Cys

1 5

<210> 184

<211> 18

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 184

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

1 5 10 15

Arg Gly

<210> 185

<211> 8

<212> PRT

<213> Artificial Sequence

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<400> 185

Asn Leu Tyr Thr Tyr Asn Ser Leu

1 5

<210> 186

<211> 13

<212> PRT

<213> Artificial Sequence

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Gln Ser Ser Gln Ser Val Tyr Asp Asn Asn Trp Leu Ala

1 5 10

<210> 187

<211> 7

<212> PRT

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<400> 187

Thr Val Ser Thr Leu Ala Ser

1 5

<210> 188

<211> 12

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<400> 188

Gln Gly Thr Tyr Tyr Ser Ser Gly Trp Asn Phe Ala

1 5 10

<210> 189

<211> 6

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 189

Ser Ser Tyr Trp Met Cys

1 5

<210> 190

<211> 17

<212> PRT

<213> Artificial Sequence

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<400> 190

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

1 5 10 15

Arg

<210> 191

<211> 4

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<400> 191

Ala Phe Asp Leu

1

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<211> 11

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<400> 192

Gln Ala Ser Gln Ser Ile Tyr Ser Tyr Leu Asn

1 5 10

<210> 193

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 193

Gly Ala Ser Asn Leu Ala Ser

1 5

<210> 194

<211> 12

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<213> Artificial Sequence

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<400> 194

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

1 5 10

<210> 195

<211> 6

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<220><223> synthesized

<

400> 195

Ser Ser Tyr Gly Val Ser

1 5

<210> 196

<211> 17

<212> PRT

<213> Artificial Sequence

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<400> 196

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

1 5 10 15

Gly

<210> 197

<211> 4

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<213> Artificial Sequence

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<400> 197

Asp Leu Asp Leu

1

<210> 198

<211> 12

<212> PRT

<213> Artificial Sequence

<220><223> synthesized

<400> 198

Gln Ser Ser Pro Ser Val Tyr Ser Asn Tyr Leu Ser

1 5 10

<210> 199

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 199

Tyr Ala Ser Thr Leu Ala Ser

1 5

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 200

Ala Gly Gly Tyr Ser Ser Ser Thr Arg Ala

1 5 10

<210> 201

<211

> 6

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 201

Ser Ser His Trp Ile Cys

1 5

<210> 202

<211> 18

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 202

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

1 5 10 15

Lys Gly

<210> 203

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 203

Ala Ala Asn Thr Asp Thr Thr Tyr Phe Asn Leu

1 5 10

<210> 204

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 204

Gln Ala Ser Gln Ser Ile Asn Asn Gln Leu Ser

1 5 10

<210> 205

<211> 7

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 205

Gly Ala Ser Thr Leu Ala Ser

1 5

<210> 206

<211> 13

<212> PRT

<213> Artificial Sequence

<220><223> Synthesized

<400> 206

His Val His Tyr Cys Ser Gly Gly Ser Cys Phe Trp Ala

1 5 10