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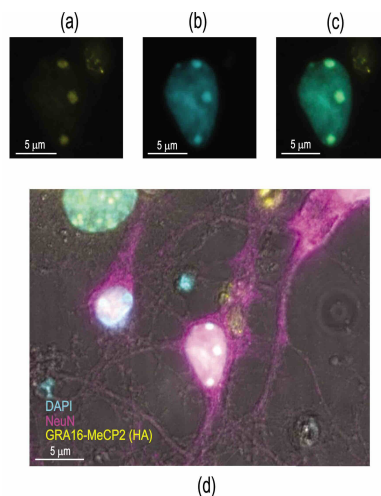
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(54) 발명의 명칭 중추신경계(CNS)에 단백질을 전달하기 위한 조작된 기생충

(57) 요약

CNS와 같은 개체의 목적조직(tissue-of-interest)에 목적단백질을 전달하고, 나아가 개체의 중추신경계 내 치료용 폴리펩티드의 투여에 의해 치료가능한 병리를 치료하기 위한, 핵산 구조물, 이를 포함하는 독소플라스마, 이를 포함하는 약학적 조성물 및 이를 이용한 방법이 제공된다.

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명세서

청구범위

청구항 1

약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 톡소플라즈마(*Toxoplasma*) 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물로 형질전환된 톡소플라즈마로서, 상기 이중 폴리뉴클레오티드는 톡소플라즈마에서 상기 이중 폴리뉴클레오티드의 전사를 유도하기 위한 프로모터에 작동가능하게 연결되며, 상기 프로모터는 전신발현 프로모터, 유도 프로모터, 잠복기-특이적 프로모터, 및 톡소필린(*Toxofilin*) 프로모터가 아닌 톡소플라즈마 내인성 프로모터:로 구성된 군에서 선택되며, 상기 톡소플라즈마 분비 단백질은 GRA16 및 GRA24로 구성된 군에서 선택되는 밀집 과립 단백질이고 숙주세포로 분비되며, 중추신경계의 병리의 치료에 사용하기 위한 톡소플라즈마.

청구항 2

제1항에 있어서, 상기 톡소플라즈마는 감염된 상기 숙주세포에서 지속되는, 톡소플라즈마.

청구항 3

약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 톡소플라즈마(*Toxoplasma*) 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물로 형질전환된 톡소플라즈마로서, 상기 이중 폴리뉴클레오티드는 톡소플라즈마에서 상기 이중 폴리뉴클레오티드의 전사를 유도하기 위한 프로모터에 작동가능하게 연결되며, 상기 프로모터는 전신발현 프로모터, 유도 프로모터, 잠복기-특이적 프로모터, 및 톡소필린(*Toxofilin*) 프로모터가 아닌 톡소플라즈마 내인성 프로모터:로 구성된 군에서 선택되며, 상기 톡소플라즈마 분비 단백질은 비-곤봉체 단백질이고 숙주세포로 분비되며, 중추신경계의 병리의 치료에 사용하기 위한 톡소플라즈마.

청구항 4

제3항에 있어서, 상기 톡소플라즈마는 감염된 상기 숙주세포에서 지속되는, 톡소플라즈마.

청구항 5

제3항에 있어서, 상기 톡소플라즈마 분비 단백질은 미세간상체 단백질 및 톡소플라즈마 곤디 대식세포 이동 저해 인자(*TgMIF*)로 구성된 군에서 선택되는, 톡소플라즈마.

청구항 6

제5항에 있어서, 상기 미세간상체로부터 분비되는 상기 단백질은 서열번호 280 내지 322로 구성된 군에서 선택된 아미노산 서열을 포함하는, 톡소플라즈마.

청구항 7

제1항에 있어서, 상기 핵산 구조물은 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열을 추가로 포함하는, 톡소플라즈마.

청구항 8

제3항에 있어서, 상기 핵산 구조물은 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열을 추가로 포함하는, 특소플라즈마.

청구항 9

제1항에 있어서, 단 상기 핵산 구조물은 Cre-재조합효소 코딩 서열을 포함하지 않는, 특소플라즈마.

청구항 10

제7항에 있어서, 상기 유도성 자기-파괴 요소는 약물에 반응하여 활성화인, 특소플라즈마.

청구항 11

제8항에 있어서, 상기 유도성 자기-파괴 요소는 약물에 반응하여 활성화인, 특소플라즈마.

청구항 12

제1항에 있어서, 상기 핵산 구조물은 상기 특소플라즈마 분비 단백질로부터 상기 약학적 폴리펩티드의 분리를 허용하는 적어도 하나의 프레임 내 절단 부위를 추가로 포함하는, 특소플라즈마.

청구항 13

제3항에 있어서, 상기 핵산 구조물은 상기 특소플라즈마 분비 단백질로부터 상기 약학적 폴리펩티드의 분리를 허용하는 적어도 하나의 프레임 내 절단 부위를 추가로 포함하는, 특소플라즈마.

청구항 14

제1항에 있어서, 약독화되지 않은, 특소플라즈마.

청구항 15

제3항에 있어서, 약독화되지 않은, 특소플라즈마.

청구항 16

제1항에 있어서, 숙주 세포에서 상기 특소플라즈마의 증식을 촉진시키는 특소플라즈마 요소가 존재하지 않는, 특소플라즈마.

청구항 17

제3항에 있어서, 숙주 세포에서 상기 특소플라즈마의 증식을 촉진시키는 특소플라즈마 요소가 존재하지 않는, 특소플라즈마.

청구항 18

제1항에 있어서, 개체의 중추신경계(CNS)로의 목적단백질(protein-of-interest)의 전달에 필요하지 않은 독성 유전자가 없는, 독소플라즈마.

청구항 19

제3항에 있어서, 개체의 중추신경계(CNS)로의 목적단백질(protein-of-interest)의 전달에 필요하지 않은 독성 유전자가 없는, 독소플라즈마.

청구항 20

제1항 내지 제19항 중 어느 한 항의 독소플라즈마 및 약학적으로 허용가능한 담체를 포함하는 약학적 조성물.

청구항 21

삭제

청구항 22

삭제

청구항 23

삭제

청구항 24

삭제

청구항 25

삭제

청구항 26

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청구항 37

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청구항 38

삭제

청구항 39

삭제

청구항 40

삭제

발명의 설명

기술 분야

[0001] 본 발명은 이의 일부 구현예에서, 톡소플라즈마 곤디(*Toxoplasma gondii*) 분비 폴리펩티드에 융합된 약학적 폴리펩티드의 분비를 위한 핵산 구조물, 및 이를 포함하는 톡소플라즈마에 관한 것으로, 보다 구체적으로, 베타적인 것은 아니나, 개체를 치료하기 위해 이를 이용한 약학적 조성물 및 방법에 관한 것이다.

배경 기술

[0002] 단백질 치료제의 전달을 위한 확실한 방법의 부족은 그의 임상 치료로의 번역에서 현재의 병목 현상을 크게 약화시킨다. 단백질은 종종 단순한 화합물에 의해 모방할 수 없는, 고도로 특이적이고 복잡한 일련의 기능을 제공한다(Nat Rev Drug Discov. 2008; 7(1):21-39. Protein therapeutics: a summary and pharmacological classification. Leader B, Baca QJ, and Golan DE); 그러나, 그의 거대분자 본성으로 인해, 치료용 단백질의 신체 내 표적 부위에서의 전달은 매우 어렵다. 생물학적 장벽에 의한 낮은 침투성과 함께, 투여 후 또는 저장 중의 낮은 기능적 안정성 및 활성의 급격한 감소는 활성 단백질의 전달을 제한한다. 화학적 변형체, 접합체 및 담체 시스템의 개발의 진행으로 일부 치료용 단백질의 전달을 도왔으나, 대부분이 여전히 "접근가능한 표적 공간" 내 - 혈관 구역 내 또는 세포 표면 상의 표적에 제한되어 있다(Mitragotri 2014, Nat. Rev. Drug. Discov. 13(9):655-72). 효율적인 전달은, 뇌로의 분자의 수송은 엄격히 조절하는 반면, 표적이 세포 내에 있는 경우 더욱 복잡해지는, 혈뇌 장벽(BBB)에 의한 신경질환 분야에서 특히 어렵다.

[0003] CNS 내 세포에 보충 단백질을 전달하기 위하여, BBB를 관통하고 CNS 내로 특정 세포를 표적으로 하는 메커니즘을 개발할 필요가 있다.

- [0004] 현재, 특정 단백질의 결핍으로 인한 상태를 치료하기 위한 주요 접근법은 유전자 치료법, 줄기세포 치료법 및 효소 대체요법이 있다.
- [0005] 유전자 치료법은 단백질의 기능적 복사체의 발현을 증가시키기 위한, 치료용 단백질을 코딩하는 유전자의 기능적 복사체를 삽입하는 것이다(Cox, D. B. T., et al., 2015). 유전자 치료법은 유전자의 정확한 서열을 제공하는 반면, 번역 메커니즘 또는 번역 후 변형에서의 결함에 의해 유발되거나 동반되는 단백질 기능의 상실은 다루지 않는다. 게다가, 삽입 돌연변이 유발(Persons, D. A. & Baum, C. 2011), 동원, 생식선 전염, 면역원성 및 제한된 전이유전자 능력(Schambach, A., et al., 2013; Al-Dosari et al., 2009)에 의한 암 발병의 위험을 부담한다. CNS를 표적으로 하기 위하여, 유전자 치료법은 가장 일반적으로 헤르페스 단클론 바이러스 1형(HSV-1), 아데노바이러스, AAV, HIV-1과 같은 렌티바이러스, 고양이 면역결핍성 바이러스 또는 말 전염성 빈혈 바이러스로부터 유래된 것을 포함하는 바이러스 벡터의 사용으로 매개되며, 최근에는 SV40-AAV 및 렌티바이러스가 가장 많이 사용된다. 일부 바이러스 벡터는 다른 것들 보다 안전하지만, 그것들은 단백질 조작 결함을 다루지 않으며, 임상 효용이 제한적이다.
- [0006] 줄기세포 치료법은 단백질의 결함있는 내인성 합성을 보충할 수 있는 이식 세포의 단백질 합성 메커니즘에 의존한다. 이러한 접근법을 임상적으로 구현하기 위한 수많은 노력에도 불구하고, 이러한 치료법의 효용성은 이식된 세포의 거부 및 환자-특이적 줄기세포의 이용의 낮은 비용-효율성에 의해 감소한다. 아울러, 줄기세포 치료에 관련된 위험은 이식된 세포의 거부를 줄이기 위해 요구되는 면역억제와 관련된 합병증, 및 암의 발생을 포함한다(Dimmeler, S., et al., 2014).
- [0007] 보충 단백질이 외부에서 합성된 후 CNS로 전달되는, 단백질- 또는 효소 대체요법(ERT)은 임상적으로 적합하도록 BBB의 불침투성을 극복하고 정밀한 표적을 개발하여야만 한다. 단백질 전달에 대한 이러한 접근법 중 하나는 단백질이 낮은 효율성으로 확산되는, 뇌 또는 인접 기관에 직접적으로 주입하는 것이다. 따라서, 이러한 접근법의 위험 외에도, 필요한 양으로 CNS 내 특정 부위를 표적으로 하는 능력이 제한적이다. 이러한 접근법의 또 다른 문제는 반복적 투약의 필요이며, 이는 보통 임상적으로 비실용적이다(Abbott, N. J. 2013).
- [0008] ERT는 치료용 단백질이 보다 효율적으로 CNS로 확산되도록, BBB 투과성 증가와 결합될 수 있다(Malhotra, M. & Prakash, S. 2011). 이는 BBB를 구성하는 세포의 축소 또는 BBB를 통한 수송 메커니즘의 조작을 통해 이루어진다. 그러나, 이러한 접근법은 오프타겟작용으로 인해 효율적이지 않으며, 원하지 않는 물질이 관심 보충 단백질과 함께 CNS로 확산되는 위험을 부담한다(Bradbury, M. W. B. 2012).
- [0009] 대안적인 접근법은 BBB를 통과하는 고유의 능력을 이용하기 위해 CNS로 들어가는 요소에 치료용 단백질을 부착하는 것이다. BBB를 통한 운행을 매개할 수 있는 제제는 융합 단백질, 덴드리머, 고체 지질 나노입자, 리포솜 및 나노입자를 포함한다(Solaro, R., 2010). 그러나, 이러한 접근법은 추가 개발이 필요하며, 임상시험에도 도달하지 못하였다.
- [0010] 톡소플라즈마 곤디(*Toxoplasma gondii*)는 접복포자충문(phylum apicomplexa)의 단일세포 세포내 원생 기생충이다. 이의 일차적인 숙주는 고양이과이고, 그것에서만 그 생활주기의 유성단계를 밟을 수 있다. 그러나, 이차적인 숙주로서 인간을 포함한, 많은 온혈 유기체를 감염시킬 수 있다. 설치류에서와 같이, 인간에서, 숙주가 기생충과 접촉한 후(일반적으로 감염성 조직 낭포 또는 접합자 섭취 후), 기생충은 빠르게 번식하는 급분열소체(tachyzoite) 단계로 분화한다. 톡소플라즈마 곤디 급분열소체는 활성 침투에 의해 유핵 숙주세포에 침입하고, 내부이분(endodyogeny)에 의해 복제하는 액포를 형성한다. 급분열소체는 장 상피를 통해 이동하고, 면역세포에 대한 "히치 하이킹(hitch-hiking)" 및 자율적 동원에 의해, 원위 조직에 도착하고, 혈뇌 장벽을 파괴하며, 뇌에 퍼진다[Harker 2015, Parasite Immunol. 37(3):141-9]. 따라서, 급분열소체는 순환계로 들어가 이차 조직으로 전파된다. 복제는 전파, 및 감염의 급성 단계에서 원위 조직에의 도달에 있어서 중요하다. 일단 뇌의 독특한 환경으로 들어가면, T. 곤디는 뇌에서 세포로 침투하여(주로 뉴런 뿐만 아니라, 낮은 비율의 신경교세포), 면역압력을 가하면, 잠복 느린분열소체(bradyzoite) 단계와 구별되며, 세포질 세포간 낭포에 존재한다. 이는 만성 감염을 특징으로 한다(Cabral et al. 2016, PLoS Pathog. 12(2):e1005447). 느린분열세포를 보유하고 있는 조직 낭포는 숙주의 평생동안 지속되며, 매우 천천히 번식하고 휴지기의 대사 과정을 가진다(Parasite Immunol. 2015, 37(3):141-9. "Toxoplasma gondii dissemination: a parasite's journey through the infected host").
- [0011] 비록 T. 곤디가 세계 인구의 약 3분의 1을 감염시키지만, 건강한 사람에게는 감염이 증상이 없으며(Montoya, J. G. & Liesenfeld, O. 2004), 면역체계가 불규칙적으로 손상된 사람들에게만 주로 위험하다. 가장 중요한 것은, 감염 시 T. 곤디가 세포 침입 동안 및 세포내 T. 곤디가 세 가지 유형의 전자고밀도(electrodense) 분비성 세포기관: 미세간상체(micronemes), 곤봉체(rhoptries) 및 밀집 과립(dense granules)을 가지면서, 숙주 세포로 단

백질을 분비한다는 것이다. 숙주세포 침입은 기생충이 숙주세포를 침입할 때와 그 내부에 머무를 때 정점 영역으로부터 세포외유출되는, 세 개의 세포 기관의 내용물을 순차적으로 분비함으로써 매개된다(Dlugonska, H. 2008). 미세간상체는 T. 곤디의 부착 및 침투에 관여하는 반면, 곤봉체는 일시적인 구조의 형성, 접합부 이동 및 PV의 형성에 필요하다. 곤봉체 단백질은 "키스와 침(kiss and spit)"이라고 불리는 과정에서 숙주와의 초기 접촉시 분비된다(Boothroyd, J. C. et al., 2008). 밀집 파립은 대부분의 기생충 단계에 걸쳐 단백질을 분비한다. 분비 과정은 액포내 네트워크의 형성과 일치하고, T. 곤디의 세포내 거주 동안 계속된다(Dlugonska, H. 2008; Carruthers, V. B. & Sibley, L. D. 1997).

[0012] 추가적인 배경 기술은 Koshy, A. A. et al. 2010; US8673289; US20120045477 A1; Lodoen M.B., et al. 2010. Cellular Microbiology, 12: 55-66; WO 2016/046321 A1; Sibley L.D., 2011 (Immunological Reviews 240: 72-91; Invasion and intracellular survival by protozoan parasites); Stanislaus MS and Cheng CL 2002 (Genetically engineered self-destruction: an alternative to herbicides for cover crop systems. Weed Science 50: 794-801)을 포함한다.

발명의 내용

[0013] 본 발명의 일부 구현예의 일 측면에 따르면, 약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 톡소플라즈마(*Toxoplasma*) 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물로서, 상기 이중 폴리뉴클레오티드는 톡소플라즈마에서 상기 이중 폴리뉴클레오티드의 전사를 유도하기 위한 프로모터에 작동가능하게 연결되며, 상기 프로모터는 전신발현 프로모터(constitutive promoter), 유도 프로모터(inducible promoter), 잠복기-특이적 프로모터(latent period-specific promoter), 및 톡소필린(*Toxofilin*) 프로모터가 아닌 톡소플라즈마 내인성 프로모터(*Toxoplasma* endogenous promoter)로 구성된 군에서 선택된, 핵산 구조물이 제공된다.

[0014] 본 발명의 일부 구현예의 일 측면에 따르면, 적어도 2개의 핵산 구조물을 포함하는 핵산 구조물 시스템으로서, 상기 적어도 2개의 핵산 구조물의 제1 핵산 구조물은 제1항 내지 제19항 중 어느 한 항의 핵산 구조물이고, 상기 적어도 2개의 핵산 구조물의 제2 핵산 구조물은 선택 마커를 코딩하는 폴리뉴클레오티드를 포함하는, 핵산 구조물 시스템이 제공된다.

[0015] 본 발명의 일부 구현예의 일 측면에 따르면, 본 발명의 일부 구현예의 핵산 구조물 또는 본 발명의 일부 구현예의 핵산 구조물 시스템으로 형질전환된 톡소플라즈마가 제공된다.

[0016] 본 발명의 일부 구현예의 일 측면에 따르면, 본 발명의 일부 구현예의 톡소플라즈마 및 약학적으로 허용가능한 담체를 포함하는 약학적 조성물이 제공된다.

[0017] 본 발명의 일부 구현예의 일 측면에 따르면, 개체의 중추신경계에 목적단백질(protein-of-interest)을 투여하는 방법으로서, 상기 방법은: 본 발명의 일부 구현예의 톡소플라즈마, 또는 본 발명의 일부 구현예의 약학적 조성물을 투여하여, 개체의 중추신경계에 목적단백질을 투여하는 것을 포함하는, 방법이 제공된다.

[0018] 본 발명의 일부 구현예의 일 측면에 따르면, 본 발명의 일부 구현예의 톡소플라즈마, 또는 본 발명의 일부 구현예의 약학적 조성물을 투여하여 이를 필요로 하는 개체를 치료하는 것을 포함하는, 이를 필요로 하는 개체를 치료하는 방법으로서, 상기 개체는 개체의 중추신경계에 상기 약학적 폴리펩티드를 투여하여 치료가능한 병리로 진단된, 방법이 제공된다.

[0019] 본 발명의 일부 구현예의 일 측면에 따르면, 약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 톡소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물을 포함하는 톡소플라즈마를 개체에 투여하여 이를 필요로 하는 개체를 치료하는 것을 포함하는, 이를 필요로 하는 개체를 치료하는 방법으로서, 상기 이중 폴리뉴클레오티드는 톡소플라즈마에서 상기 이중 폴리뉴클레오티드의 전사를 유도하기 위한 프로모터에 작동가능하게 연결되며, 상기 개체는 개체의 중추신경계에 상기 약학적 폴리펩티드를 투여하여 치료가능한 병리로 진단된, 방법이 제공된다.

[0020] 본 발명의 일부 구현예에 따르면, 상기 프로모터는 전신발현 프로모터, 유도 프로모터, 잠복기-특이적 프로모터, 및 톡소필린(*Toxofilin*) 프로모터가 아닌 톡소플라즈마 내인성 프로모터:로 구성된 군에서 선택된다.

[0021] 본 발명의 일부 구현예에 따르면, 상기 내인성 프로모터는 곤봉체(rhoptry) 단백질의 것이 아니다.

- [0022] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마는 약독화되지 않는다.
- [0023] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마 분비 단백질은 상기 톡소플라즈마의 곤봉체로부터 분비된다.
- [0024] 본 발명의 일부 구현예에 따르면, 상기 곤봉체로부터 분비되는 톡소플라즈마 분비 단백질은 톡소필린(Toxofilin) 및/또는 ROP1을 포함한다.
- [0025] 본 발명의 일부 구현예에 따르면, 상기 곤봉체로부터 분비되는 톡소플라즈마 분비 단백질은 서열번호 344 내지 465로 구성된 군에서 선택된 아미노산 서열을 포함한다.
- [0026] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마 분비 단백질은 비-곤봉체 단백질이다.
- [0027] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마 분비 단백질은 미세간상체(microneme) 단백질 및 밀집 과립 단백질로 구성된 군에서 선택된다.
- [0028] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마 분비 단백질은 톡소플라즈마의 밀집 과립(dense granule)으로부터 분비된다.
- [0029] 본 발명의 일부 구현예에 따르면, 상기 밀집 과립으로부터 분비되는 토곳플라즈마 분비 단백질은 GRA16 및/또는 GRA24를 포함한다.
- [0030] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마 분비 단백질은 톡소플라즈마의 미세간상체로부터 분비된다.
- [0031] 본 발명의 일부 구현예에 따르면, 상기 미세간상체로부터 분비되는 단백질은 서열번호 280 내지 322로 구성된 군에서 선택된 아미노산 서열을 포함한다.
- [0032] 본 발명의 일부 구현예에 따르면, 상기 밀집 과립으로부터 분비되는 단백질은 서열번호 234 내지 279로 구성된 군에서 선택된 아미노산 서열을 포함한다.
- [0033] 본 발명의 일부 구현예에 따르면, 상기 톡소플라즈마 분비 단백질은 톡소플라즈마 곤디 대식세포 이동 저해 인자(TgMIF)를 포함한다.
- [0034] 본 발명의 일부 구현예에 따르면, 상기 이중 폴리뉴클레오티드는 톡소플라즈마 분비 단백질 개방형 해독 프레임의 톡소플라즈마 비번역 부위(UTR) 핵산 서열 상류 및/또는 하류를 추가로 포함한다.
- [0035] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 5'-비번역 부위(5'-UTR)는 톡소플라즈마 분비 단백질 개방형 해독 프레임의 상류에 위치한다.
- [0036] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 3'-비번역 부위(3'-UTR)는 톡소플라즈마 분비 단백질 개방형 해독 프레임의 하류에 위치한다.
- [0037] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 3'-비번역 부위(3'-UTR) 핵산 서열은 3'-UTR GRA2 3'-UTR, GRA16 3'-UTR, GRA24 3'-UTR, SAG1 3'-UTR, 또는 DHFR이다.
- [0038] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 5'-비번역 부위(5'-UTR) 핵산 서열은 GRA2 5'-UTR, GRA16 5'-UTR, GRA24 5'-UTR, SAG1 5'-UTR, or the DHFR 5'-UTR이다.
- [0039] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 내인성 프로모터는 GRA2 프로모터, GRA16 프로모터, GRA24 프로모터, SAG1 프로모터, 또는 DHFR 프로모터이다.
- [0040] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 비번역 부위(UTR) 핵산 서열은 톡소필린 3'-UTR이다.
- [0041] 본 발명의 일부 구현예에 따르면, 상기 핵산 구조물은 유도성 자기-파괴 요소(inducible self-destruction element)를 코딩하는 제3 핵산 서열을 추가로 포함한다.
- [0042] 본 발명의 일부 구현예에 따르면, 상기 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열은 약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 톡소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 동일한 핵산 구조물 내에 포함된다.
- [0043] 본 발명의 일부 구현예에 따르면, 상기 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열은 약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 톡소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을

포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물과 별개의 핵산 구조물 내에 포함된다.

- [0044] 본 발명의 일부 구현예에 따르면, 상기 핵산 구조물은 Cre-재조합효소 코딩 서열을 포함하지 않는다.
- [0045] 본 발명의 일부 구현예에 따르면, 상기 핵산 구조물은 베타 (b)-락타마제 (BLA) 코딩 서열을 포함하지 않는다.
- [0046] 본 발명의 일부 구현예에 따르면, 상기 핵산 구조물은 독소플라스마의 게놈에 통합하기에 적합하다.
- [0047] 본 발명의 일부 구현예에 따르면, 상기 유도성 자기-파괴 요소는 약물에 반응하여 활성이다.
- [0048] 본 발명의 일부 구현예에 따르면, 상기 약물은 항생제를 포함한다.
- [0049] 본 발명의 일부 구현예에 따르면, 상기 핵산 구조물은 소플라스마 분비 단백질로부터 상기 약학적 폴리펩티드의 분리를 허용하는 적어도 하나의 프레임 내 절단 부위를 추가로 포함한다.
- [0050] 본 발명의 일부 구현예에 따르면, 상기 독소플라스마는 숙주 세포에서 상기 독소플라스마의 증식을 촉진시키는 요소가 없다.
- [0051] 본 발명의 일부 구현예에 따르면, 상기 독소플라스마는 개체의 CNS로의 목적단백질의 전달에 필요하지 않은 독성 유전자가 없다.
- [0052] 본 발명의 일부 구현예에 따르면, 상기 이중 폴리뉴클레오티드는 선택 마커를 코딩하는 핵산 서열을 추가로 포함한다.
- [0053] 본 발명의 일부 구현예에 따르면, 상기 선택 마커는 클로람페니콜 아세틸전달효소(CAT), DHFR-TS, BLE, HXGPRT, UPRT, TK, CD, 형광 단백질(GFP, YFP, RFP, mCherry 또는 그 외와 같은) 또는 에피토프 태그(HA, Myc, Ty-1, FLAG 또는 그 외와 같은)를 포함한다.
- [0054] 본 발명의 일부 구현예에 따르면, 상기 약학적 조성물은 개체의 중추신경계 내 결합있는 내인성 단백질을 특징으로 하는 병리로 진단된 개체를 치료하기 위한 것이다.
- [0055] 본 발명의 일부 구현예에 따르면, 상기 약학적 조성물은 개체의 중추신경계 내 상기 약학적 폴리펩티드의 투여에 의해 치료가능한 병리로 진단된 개체를 치료하기 위한 것이다.
- [0056] 본 발명의 일부 구현예에 따르면, 상기 약학적 조성물은 면역억제제를 추가로 포함한다.
- [0057] 본 발명의 일부 구현예에 따르면, 상기 방법은 개체에 상기 독소플라스마의 투여 전 및/또는 상기 독소플라스마의 투여 후 및/또는 상기 독소플라스마의 투여와 동시에, 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0058] 본 발명의 일부 구현예에 따르면, 상기 방법은 개체에 상기 독소플라스마의 투여 전에 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0059] 본 발명의 일부 구현예에 따르면, 상기 방법은 개체에 상기 독소플라스마의 투여 후에 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0060] 본 발명의 일부 구현예에 따르면, 상기 방법은 개체에 상기 독소플라스마의 투여와 동시에, 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0061] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 병리를 치료할 수 있는 상기 내인성 단백질에 상응하는 야생형 아미노산 서열을 포함한다.
- [0062] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 병리를 치료할 수 있는 항체를 포함한다.
- [0063] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 병리를 치료할 수 있는 항원을 포함한다.
- [0064] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 병리를 치료할 수 있는 독소를 포함한다.
- [0065] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 효소, 구조 폴리펩티드, 운동성 폴리펩티드, 조절 폴리펩티드, 저장 폴리펩티드, 신호/리간드 폴리펩티드, 수용체 폴리펩티드, 감각 폴리펩티드, 항체, 단백질 채널 및/또는 수송 폴리펩티드를 포함한다.
- [0066] 본 발명의 일부 구현예에 따르면, 투여는 말초 투여에 의해 수행된다.

- [0067] 본 발명의 일부 구현예에 따르면, 말초 투여는 정맥 투여를 포함한다.
- [0068] 본 발명의 일부 구현예에 따르면, 말초 투여는 경구 투여를 포함한다.
- [0069] 본 발명의 일부 구현예에 따르면, 투여는 중추신경계로의 직접 투여에 의해 수행된다.
- [0070] 본 발명의 일부 구현예에 따르면, 결핍 내인성 단백질은 내인성 단백질의 야생형 아미노산 서열과 비교하여, 적어도 하나의 내인성 단백질의 아미노산의 결실, 삽입 및/또는 치환을 포함한다.
- [0071] 본 발명의 일부 구현예에 따르면, 결핍 내인성 단백질은 병리가 없는 건강한 개체 내 내인성 단백질의 수준과 비교할 때, 감소된 수준의 내인성 단백질을 포함한다.
- [0072] 본 발명의 일부 구현예에 따르면, 결핍 내인성 단백질은 병리로 진단된 개체 내의 내인성 단백질이 없다.
- [0073] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 갈락토세레브로시다제(Galactocerebrosidase, GALC)이다.
- [0074] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 갈락토세레브로시다제(GLAC) 이소폼 1, 이소폼 2, 이소폼 3, 이소폼 4 또는 이소폼 5이다.
- [0075] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 메틸-CpG 결합 단백질 2(MECP2) 이소폼 1 또는 MECP2 이소폼 2이다.
- [0076] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 신경교세포 유도 신경영양 인자(Glial Cell Derived Neurotrophic Factor, GDNF)이다.
- [0077] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 신경교세포 유도 신경영양 인자(GDNF) 이소폼 1, 이소폼 2, 이소폼 3, 이소폼 4 또는 이소폼 5이다.
- [0078] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 아스파르토아실라제(Aspartoacylase, ASPA)이다.
- [0079] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 생존 운동 신경원 단백질(Survival Motor Neuron Protien, SMN1)이다.
- [0080] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 생존 운동 신경원 단백질 SMN, 이소폼 SMN-델타5, 이소폼 SMN-델타7 또는 이소폼 SMN-델타57이다.
- [0081] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 파킨(Parkin, PARK2)이다.
- [0082] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 파킨(PARK2) 이소폼 1, 이소폼 2, 이소폼 3, 이소폼 4, 이소폼 5, 이소폼 6, 이소폼 7 또는 이소폼 8이다.
- [0083] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 전사 인자 EB(Transcription Factor EB, TFEB)이다.
- [0084] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 전사 인자 EB(TFEB) 이소폼 1 또는 이소폼 2이다.
- [0085] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 TALEN(TALE 뉴클레아제)이다.
- [0086] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 TALE TF(TALE 전사 인자)이다.
- [0087] 본 발명의 일부 구현예에 따르면, 상기 개체는 크라베 질환으로 진단된 개체이다.
- [0088] 본 발명의 일부 구현예에 따르면, 상기 개체는 레트 증후군으로 진단된 개체이다.
- [0089] 본 발명의 일부 구현예에 따르면, 상기 개체는 카나반 질환으로 진단된 개체이다.
- [0090] 본 발명의 일부 구현예에 따르면, 상기 개체는 척수근위축증으로 진단된 개체이다.
- [0091] 본 발명의 일부 구현예에 따르면, 상기 개체는 파킨슨병으로 진단된 개체이다.
- [0092] 본 발명의 일부 구현예에 따르면, 상기 개체는 저산소/허혈성 또는 신경염증성 CNS 장애로 진단된 개체이다.
- [0093] 본 발명의 일부 구현예에 따르면, 상기 개체는 알츠하이머병으로 진단된 개체이다.
- [0094] 본 발명의 일부 구현예에 따르면, 상기 개체는 근위축성 측색 경화증으로 진단된 개체이다.

- [0095] 본 발명의 일부 구현예에 따르면, 상기 개체는 헌팅틴병으로 진단된 개체이다.
- [0096] 본 발명의 일부 구현예에 따르면, 상기 개체는 리소좀 축적병으로 진단된 개체이다.
- [0097] 본 발명의 일부 구현예에 따르면, 상기 개체는 MECP2-중복 증후군으로 진단된 개체이다.
- [0098] 본 발명의 일부 구현예에 따르면, 상기 방법은 개체에 자기-파괴 요소를 유도할 수 있는 약물을 투여하는 것을 추가로 포함한다.
- [0099] 본 발명의 일부 구현예에 따르면, 상기 방법은 개체에 숙주세포 및/또는 신체 내 독소플라스마를 지속시키는데 필요한 분자를 투여하는 것을 추가로 포함한다.
- [0100] 본 발명의 일부 구현예에 따르면, 상기 독소플라스마를 지속시키는데 필요한 분자는 항생제이다.
- [0101] 본 발명의 일부 구현예에 따르면, 상기 독소플라스마를 지속시키는데 필요한 분자는 소분자이다.
- [0102] 본 발명의 일부 구현예에 따르면, 상기 독소플라스마를 지속시키는데 필요한 분자는 대사물질이다.
- [0103] 달리 정의되지 않는 한, 본 명세서에서 사용되는 모든 기술적 및/또는 과학적 용어는 당업자에 의해 일반적으로 이해되는 것과 동일한 의미를 가진다. 비록 본 명세서에서 기술된 것과 유사하거나 동일한 방법 및 물질이 본 발명의 구현예를 실시 또는 시험하는데 사용될 수 있으나, 예시적인 방법 및/또는 물질을 후술한다. 충돌이 있는 경우, 정의를 포함하여 본 명세서가 우선한다. 아울러, 물질, 방법 및 실시예는 오로지 예시적인 것이며, 반드시 제한하려는 의도는 없다.

도면의 간단한 설명

- [0104] 본 발명의 일부 구현예는 첨부된 도면을 참조하여 단지 예시적으로 설명된다. 도면을 상세하게 특정하게 참조하면, 도시된 세부 사항은 예시로서, 그리고 본 발명의 구현예에 대한 설명을 목적으로 한 것이다. 이와 관련하여, 도면과 함께 기재된 설명은 본 발명의 구현예가 실시될 수 있는 방법을 당업자에게 명백하게 한다.

도면에서:

도 1은 본 발명의 일부 구현예의 임상적 개념의 도식 표현이다. (1) 선택되는 약학적 폴리펩티드 코딩 서열은 독소플라스마 곤디 분비가능 폴리펩티드 코딩 서열에 융합된다; (2) 핵산 구조물은 독소플라스마로 도입된다; (3) 융합 단백질은 기생충 내에서 발현되고, 기생충의 분비 세포 기관(예로서, 곤봉체)에 위치한다; (4) 기생충은 개체의 CNS로 들어가 병리 부위에 도달한다; (5) 단백질은 개체의 세포로 분비되고 병리학적 표현형을 구출한다.

도 2는 pGRA 백본 기반의 치료용 유전자 이식(transgenic) T. 곤디 주(line)의 발생에 사용되는 구조물의 도식도를 묘사한다. 핵산 구조물은 프레임 내 치료용 폴리펩티드 코딩 서열과 T. 곤디 독소필린 코딩 서열의 융합, 및 "HA" 태그로 구성된 개방형 해독 프레임(ORF)을 포함한다. ORF의 상류는 독소필린 유전자의 내인성 5' UTR (비번역 부위) (프로모터로 작용하는 독소필린 5'-UTR)이고, ORF의 하류는 풍부한 밀집 과립 단백질 GRA2의 3' UTR (GRA2 3'-UTR)이다. 구조물은 또한, DHFR-TS의 내인성 5' UTR 및 3' UTR 사이에 내포된 HXGPRT 유전자로 구성된 선택 마커 카세트를 포함한다. 또한, 구조물에 선택 항생제 저항을 포함하는 박테리아 발현 카세트가 포함된다.

도 3은 pGRA 백본 기반의 치료용 유전자 이식 T. 곤디 주의 발생에 사용되는 구조물의 도식도를 묘사한다. 핵산 구조물은 프레임 내 치료용 폴리펩티드 코딩 서열과 T. 곤디 독소필린 코딩 서열의 융합, 및 HA 태그로 구성된 ORF를 포함한다. ORF의 상류는 GRA16 유전자의 내인성 5' UTR(프로모터로 작용하는 GRA16 5'-UTR)이고, ORF의 하류는 풍부한 밀집 과립 단백질 GRA2의 3' UTR (GRA2 3'-UTR)이다. 구조물은 또한, DHFR-TS의 내인성 5' UTR 및 3' UTR 사이에 내포된 HXGPRT 유전자로 구성된 선택 마커 카세트를 포함한다. 또한, 구조물에 선택 항생제 저항을 포함하는 박테리아 발현 카세트가 포함된다.

도 4A 내지 I는 포유류 세포(HFF) 내 신규한 기생충 균주를 묘사한 것으로, 여기서 독소필린-융합 치료용 단백질 아스파르트아실라제(ASPA), 생존 운동 신경원 단백질(SMN1), 메틸-CpG 결합 단백질 2(MECP2) 및 갈락토세레브로시다제-TAT Δ 43(일반 물질 및 실험 방법 부분에 "변이 GALC-TAT"라고도 함)을 발현하는 기생충 균주가 기생충의 분비 곤봉체 세포 기관에 특이적 위치를 나타낸다. 도 4A - 곤봉체를 하이라이트한, 세포내 T. 곤디의 도식 구조. 붉은색: 내막 복합체(IMC), 푸른색: DNA(숙주세포 핵 및 T. 곤디 핵), 녹색: 곤봉체 단백질; 도 4B-I - 항-HA 항체(모든 패널에서 초록색)를 이용하여 변이된, 항-IMC1 항체(붉은색) 및 DAPI(푸른색)를 이용하여

내막 복합체 IMC1으로 공-염색된, 또는 세포의 편광 이미지의 상부에 나타낸(흑백), HA-태그 독소필린-ASPA(도 4B 및 4C), HA-태그 독소필린-SMN1(도 4D 및 4E), HA-태그 독소필린-MECP2(도 4F 및 4G) 및 HA-태그 독소필린-GALC-TAT(도 4H 및 4I)를 내인성으로 발현하는, HFF 세포 상에 성장한 기생충의 형광 현미경 분석. 기생충은 혼합된 집단으로 나타냈지만, 녹색 염색을 보이는 기생충만이 유전자 이식 단백질을 발현한다. 도 4B-I에 나타낸 모든 이미지에서 스케일 바 = 5 μ M.

도 5A 내지 I는 포유류 세포(HFF) 내 신규한 기생충 균주를 묘사한 것으로, 여기서 GRA16-융합 치료용 단백질 아스파르트아실라제(ASPA), 생존 운동 신경원 단백질(SMN1) 및 메틸-CpG 결합 단백질 2(MECP2)를 발현하는 기생충 균주가 숙주세포 핵 뿐만 아니라 기생충 액포(PV) 공간에의 특이적 위치를 나타낸다. 도 5A - 분비된 밀집 과립 이펙터 단백질의 분포를 하이라이트한, 숙주세포(섬유아세포)의 기생충 액포 내 세포내 T. 곤디 기생충의 도식 표현. 붉은색: 내막 복합체(IMC), 푸른색: DNA(숙주세포 핵 및 T. 곤디 핵), 노란색: 밀집 과립 분비 이펙터 단백질, 주황색: 기생충 액포. 도 5B-I - 항-HA 항체(모든 패널에서 초록색)를 이용하여 변이된, 항-IMC1 항체(붉은색) 및 DAPI(푸른색)를 이용하여 내막 복합체 IMC1으로 공-염색된, 또는 세포의 편광 이미지의 상부에 나타낸, HA-태그 GRA16-ASPA(도 5B 및 5C), HA-태그 GRA16-SMN1(도 5D 및 5E), HA-태그 GRA16-MECP2(100x 확대 도 5B-G 및 40x 확대 도 5H-I)를 내인성으로 발현하는, HFF 세포 상에 성장한 기생충의 형광 현미경 분석. 기생충은 혼합된 집단으로 나타냈지만, 녹색 염색을 보이는 기생충만이 유전자 이식 단백질을 발현한다. 스케일 바 = 5 μ M(도 5B-G). 스케일 바 = 20 μ M(도 5H-I).

도 6A-B는 "TACGTACG" (서열번호: 4505) 표적 서열의 예로서 설계된, TALE 뉴클레아제(도 6A) 및 TALE 전사 인자(도 6B)의 개략도이다. TALE 반복은 표적 서열 내 뉴클레오타이드의 순서에 따라 나타난다. TALE의 본질 때문에, 첫번째 뉴클레오타이드는 항상 T이어야만 하며(따라서 TAL N-말단에 통합되고, 주석이 달려있지 않다), 마지막 뉴클레오타이드(이 경우 G)는 반-단량체로 나타낸다(따라서 "반 반복(Half repeat)"로 주석을 달았다). 본 발명의 일부 구현예의 독소플라즈마에 의해 발현되고 분비되기 위하여, 이들 구조물의 개방형 해독 프레임(ORF)은 본 발명의 일부 구현예의 핵산 구조물에 삽입된다. TALE_{Nuc}(TALE 뉴클레아제)의 경우, ORF는 FokI 후까지 NLS로부터 유래한다(예를 들어, 서열번호 4506으로 기재된 폴리뉴클레오타이드의 뉴클레오타이드 2113-4104). TALE-TF(TALE 전사 인자)의 경우, ORF는 EGFP 후 TALE N 말단(N-말단)으로부터 유래한다(예를 들어, 서열번호 4507로 기재된 폴리뉴클레오타이드의 뉴클레오타이드 2120-5005). "TALE-TF" = TALE 전사 인자; "TALEN" = TALE 뉴클레아제. "NI", "NG", "NN" 및 "HD" = 하기 실시예 5에 기재된 단량체.

도 7은 치료용 유전자 이식 T. 곤디 주의 발생에 사용되는 구조물의 도식도를 묘사한다. 핵산 구조물은 프레임 내 치료용 폴리펩티드 코딩 서열과 T. 곤디 독소필린 코딩 서열의 융합, 및 "HA" 태그로 구성된 개방형 해독 프레임(ORF)을 포함한다. ORF의 상류는 독소필린 유전자의 내인성 5' UTR(비번역 부위) ("독소필린 5'-UTR")이고, ORF의 하류는 풍부한 밀집 과립 단백질 GRA2("GRA2 3-UTR")의 3' UTR이다. 구조물은 또한, DHFR-TS의 내인성 5' UTR 및 3' UTR 사이에 내포된 HXGPRT 유전자, DHFR-TS 유전자 또는 mCherry 유전자로 구성된 선택 마커 카세트를 포함한다. 또한, 구조물에 분자 클로닝에 사용되는 선택 항생제 저항을 포함하는 박테리아 발현 카세트가 포함된다.

도 8은 치료용 유전자 이식 T. 곤디 주의 발생에 사용되는 구조물의 도식도를 묘사한다. 핵산 구조물은 프레임 내 치료용 폴리펩티드 코딩 서열과 T. 곤디 GRA16 코딩 서열의 융합, 및 HA 태그로 구성된 ORF를 포함한다. ORF의 상류는 GRA16 유전자의 내인성 5' UTR(비번역 부위) ("GRA16 5'-UTR")이고, ORF의 하류는 풍부한 밀집 과립 단백질 GRA2("GRA2 3-UTR")의 3' UTR이다. 구조물은 또한, DHFR-TS의 내인성 5' UTR 및 3' UTR 사이에 내포된 HXGPRT 유전자, DHFR-TS 유전자 또는 mCherry 유전자로 구성된 선택 마커 카세트를 포함한다. 또한, 구조물에 분자 클로닝에 사용되는 선택 항생제 저항을 포함하는 박테리아 발현 카세트가 포함된다.

도 9A-N은 포유류 세포(HFF) 내 유전자 이식 기생충 균주를 묘사한 것으로, 여기서 기생충 균주는 12개의 신규한 독소필린-융합 치료용 단백질을 발현시킨다. 도 9A- 곤봉체를 하이라이트한, 세포내 T. 곤디의 도식 구조. 자홍색: 내막 복합체(IMC), 청록색: DNA(숙주세포 핵 및 T. 곤디 핵), 노란색: 곤봉체 단백질; 도 9B- 곤봉체 마커 ROP2/4로 면역염색한(노란색), HFF 세포에서 성장한 T. 곤디의 대표적인 형광 현미경 이미지. 왼쪽: DAPI(청록색)으로 공-염색, 오른쪽: 세포의 편광 이미지의 상부에 덮어씌움(흑백). 도 9C-N- HA-태그 독소필린-융합 치료용 단백질을 발현시키는 유전자 이식 기생충의 이미지: 도 9C: 아스파르트아실라제(ASPA), 도 9D- 코돈-최적화된 아스파르트아실라제(ASPAopt), 도 9E- 갈락토세레브로시다제(GALC), 도 9F- 코돈-최적화된 갈락토세레브로시다제(GALCopt), 도 9G- 갈락토세레브로시다제-TAT(GLAC-TAT), 도 9H- 갈락토세레브로시다제-TAT Δ 43(GALC-TAT Δ 43- 일반 물질 및 실험 방법 부분에 "변이 GALC-TAT"라고도 함). 도 9I- 신경아세포 유도 신경영양 인자(GDNF), 도 9J- 메틸-CpG 결합 단백질(SMN1) 및 도 9N- 코돈-최적화된 전사 인자 EB(TFEBopt). 독소필린-

ASPAopt, 독소필린-GALC-TAT Δ 43, 독소필린-GDNF, 독소필린-MeCP2opt, 독소필린-PARK2, 독소필린-SMN1 및 독소필린-TFEB를 발현하는 기생충의 예시적 이미지는 기생충의 분비 곤봉체 세포 기관으로의 위치화를 나타낸다. 독소필린 융합 단백질은 항-HA 항체를 이용하여 면역염색한다(노란색). 왼쪽: DAPI(청록색) 및 기생충 마커 항-IMC-1(자홍색)으로 공-염색, 오른쪽: 세포의 편광 이미지의 상부에 덮어씌움(흑백). 기생충은 혼합된 집단으로 나타냈지만, 노란색 염색을 보이는 기생충만이 유전자 이식 단백질을 발현한다. 스케일 바 = 5 μ M.

도 10A-J는 포유류 세포(HFF) 내 유전자 이식 기생충 균주를 묘사한 것으로, 여기서 기생충 균주는 8개의 신규한 GRA16-융합 치료용 단백질을 발현시킨다. 도 10A- 분비된 밀집 과립 이펙터 단백질의 분포를 하이라이트한, 숙주세포에서 기생충 액포 내 세포내 T. 곤디 기생충의 도식 표현. 자홍색: 내막 복합체(IMC), 청록색: DNA(숙주세포 핵 및 T. 곤디 핵), 노란색: 밀집 과립 분비 이펙터 단백질, 주황색: 기생충 액포; 도 10B- HA-태그 GRA16 단백질을 발현시키고, 항-HA로 면역염색한(노란색), HFF 세포에서 성장한 T. 곤디의 대표적인 형광 현미경 이미지. 왼쪽: DAPI(청록색)으로 공-염색, 오른쪽: 세포의 편광 이미지의 상부에 덮어씌움(흑백). 도 10C-J- HA-태그 GRA16-융합 치료용 단백질을 발현시키는 유전자 이식 기생충의 이미지: 도 10C: 아스파르트아실라제(ASPA), 도 10D- 생존 운동 신경원 단백질(SMN1), 도 10E- 갈락토세레브로시다제(GALC), 도 10F- 갈락토세레브로시다제-TAT(GLAC-TAT), 도 10G- 코돈-최적화된 아스파르트아실라제(ASPAopt), 도 10H- 코돈-최적화된 갈락토세레브로시다제(GALCopt), 도 10I- 코돈-최적화된 메틸-CpG 결합 단백질 2(MECP2opt) 및 도 10J- 코돈-최적화된 전사 인자 EB(TFEBopt). GRA16-ASPA, GRA16-SMN1, GRA16-ASPAopt, GRA16-MeCP2opt 및 GRA16-TFEBopt는 기생충 액포로의 위치화를 나타낸다. GRA16-MECP2opt 및 GRA16-TFEBopt는 또한 숙주세포 핵으로의 위치화를 나타낸다. GRA16 융합 단백질은 항-HA 항체를 이용하여 면역염색한다(노란색). 왼쪽: DAPI(청록색) 및 기생충 마커 항-IMC-1(자홍색)으로 공-염색, 오른쪽: 세포의 편광 이미지의 상부에 덮어씌움(흑백). 기생충은 혼합된 집단으로 나타냈지만, 노란색 염색을 보이는 기생충만이 유전자 이식 단백질을 발현한다. 스케일 바 = 5 μ M.

도 11A-C- 시간의 흐름에 따른 균주 RH GRA16-HAstop, GRA16-MECP2opt 및 GRA16-TFEBopt의 급분열소체에 의한 HFF 세포의 핵으로의 단백질 전달의 동역학 미 감염의 다양성(MOI). 감염된 세포 및 핵 전달은 GE IN Cell Investigator 소프트웨어(GE 헬스케어, 시카고, IL, USA)를 이용한 자동화된 이미지 분석에 의해 계산하였다. 그래프는 3개의 균주로부터의 결과를 함께 종합하여 나타낸다.

도 12A-C- T. 곤디 균주 RH GRA16-HAstop(도 12A), GRA16-MECP2opt(도 12B) 및 GRA16-TFEBopt(도 12C)의 급분열소체에 의한 감염 16-22시간 후 시험관 내-분화된 LUHMES 인간 신경세포의 대표적 이미지. GRA16 융합 단백질은 항-HA 항체를 이용하여 면역염색하고(노란색), DAPI(청록색) 및 성숙 뉴런 항-NeuN 마커(자홍색)으로 공-염색한다. 각 도면의 왼쪽의 삽입은 항-HA 단독(위, 노란색), 항-HA 및 DAPI(중간, 노란색 및 청록색) 및 항-HA 및 NeuN(아래, 노란색 및 자홍색)으로 가시화한 감염된 세포를 나타낸다. 모든 균주는 인간 뉴런의 핵에 대한 융합 단백질의 명확한 분비 및 표적화를 나타낸다.

도 13A-D- 유전자 이식 주 RH GRA16-MECP2opt의 급분열소체에 의한 감염 12시간 후, P1 새끼 쥐의 피질 및 해마 유래의 면역조직학적으로 염색된 뉴런-풍부 일차 배양물의 대표적 이미지. GRA16 융합 단백질은 항-HA 항체를 이용하여 면역염색한다(노란색). 도 13A- GRA16-MeCP2 단독(노란색). 13B- DAPI 단독(청록색). 도 13C- GRA16-MeCP2 및 DAPI 염색의 병합. 도 13D- 세포의 편광 이미지의 상부에 덮어씌움(흑백), GRA16-MeCP2(노란색), DAPI(청록색) 및 NeuN(자홍색)의 병합. 전달된 GRA16-MeCP2opt는 신경의 핵 내 응축된 이질염색질(heterochromatic) DNA의 영역과 함께 공동-위치화하는 특징적 패턴을 나타내는데, 이는 전달된 MeCP2의 이질염색질(heterochromatin)에의 효과적인 결합을 시사한다.

도 14는 RH GRA16-MeCP2opt 유전자 이식 T. 곤디 균주의 MOI=1로 감염된, MeCP2-특이적 항체로 면역침전되고 블롯팅된, R306C MeCP2-변이 인간 LUHMES 뉴런의 핵 추출물의 웨스턴 블롯이다. 블롯은 내인성 변이된 MeCP2 및 T. 곤디-전달 MeCP2와 일치하는 두 개의 밴드를 나타낸다. T. 곤디-전달된 MeCP2는 GRA16에의 융합으로 인해 더 큰 분자량을 가진다.

도 15A-C는 HFF 세포 내 유전자 이식 T. 곤디 균주 Pru GRA16-MECP2opt의, 시험관 내 분화된 느린분열소체의 예시적 이미지를 나타낸다. GRA16 융합 단백질은 항-HA 항체를 이용하여 면역염색한다(붉은색). 도 15A- GRA16-MeCP2 단독. 도 15B- 느린분열소체 낭포-벽 마커 돌리코스 비플로루스 응집소(Dolichos Biflorus Agglutinin, DBA) (초록색) 및 DAPI(청록색)으로 공-염색, 낭포를 포함하는 숙주 섬유아세포의 핵 내 HA-염색된(붉은색) GRA16-MeCP2 융합 단백질과 함께, 기생충 낭포를 초록색으로, 숙주 섬유아세포(HFF)의 핵을 푸른색으로 나타냄. 도 15C- DBA로 공-염색하고, 세포의 편광 이미지의 상부에 덮어씌움(흑백). 표시된 낭포는 느린분열소체 단계에서, 연속된 GRA16-MeCP2의 발현, 숙주세포의 핵으로의 융합 단백질의 분비 및 표적화를 나타낸다. 하얀색 화살

축은 느린분열소체 낭포를 포함하는 세포의 핵을 가리키며, 이는 전달된 단백질 GRA16-McCP2를 포함한다.

발명을 실시하기 위한 구체적인 내용

- [0105] 본 발명은, 그 일부 구현예에서, 약학적 폴리펩티드에 융합된 독소플라즈마 분비 단백질의 분비를 위한 핵산 구조물, 및 이를 포함하는 독소플라즈마, 및, 보다 구체적으로, 배타적인 것은 아니나, 개체를 치료하기 위해 이를 사용한 약학적 조성물 및 방법에 관한 것이다.
- [0106] 본 발명의 적어도 하나의 구현예를 상세히 설명하기 전에, 본 발명은 그 적용에 있어서 하기 설명에 기재되거나 실시예에 의해 예시된 세부 사항으로 제한되는 것이 아님을 이해하여야 한다. 본 발명은 다른 구현예가 가능하고, 또는 다양한 방법으로 실시되거나 수행될 수 있다.
- [0107] 본 발명자들은 이중 폴리펩티드를 코딩하는 유전적 구조물로 형질전환된 독소플라즈마 기생충이 이중 폴리펩티드를 포유류 세포로 합성하고 전달한다는 것을 밝혀내었다(도 4B-I, 5B-I, 9B-N, 10B-J, 11A-C, 12A-C, 13A-D, 14 및 15A-C 및 하기 실시예 부분). 포유류 세포 내에서, 이중 폴리펩티드는 세포 내 활성 영역으로 이동하는데, 여기서 내인성 약학적 단백질의 알려진 기능에 관련된 세포 과정을 증가시킬 수 있다. 예를 들어, 본 발명자들은 포유류 단백질 McCP2 및 TFEB를 발현시키고 전달하는, 타입 I 및 타입 II 독소플라즈마 균주를 생성시키고, 독소플라즈마 분비 단백질 GRA16에 번역으로 융합시키고, 독소플라즈마로 생체의 처리된 포유류 세포 내에서 바람직한 세포 위치(핵)로 융합된 치료용 단백질을 분비하여, 개체의 치료용 폴리펩티드의 특이적 전달 및 개체의 치료를 위한, 구조물, 독소플라즈마 및 방법의 타당성을 증명하였다.
- [0108] 본 발명의 일부 구현예의 일 측면에 따르면, 약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 독소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물로서, 상기 이중 폴리뉴클레오티드는 독소플라즈마에서 상기 이중 폴리뉴클레오티드의 전사를 유도하기 위한 프로모터에 작동가능하게 연결되며, 상기 프로모터는 전신발현 프로모터, 유도 프로모터, 잠복기-특이적 프로모터, 및 독소필린 프로모터가 아닌 독소플라즈마 내인성 프로모터로 구성된 군에서 선택된, 핵산 구조물이 제공된다.
- [0109] 본 발명의 일부 구현예에 따르면, 핵산 구조물은 독소플라즈마 내 발현에 적합하다.
- [0110] 본 발명의 일부 구현예에 따르면, 핵산 구조물은 Cre-재조합효소 코딩 서열을 포함하지 않는다.
- [0111] 본 발명의 일부 구현예에 따르면, 핵산 구조물은 베타 (b)-락타마제(BLA) 코딩 서열을 포함하지 않는다.
- [0112] 본 발명의 일부 구현예에 따르면, 핵산 구조물은 독소플라즈마의 게놈에의 통합에 적합하다.
- [0113] 본 발명의 일부 구현예에 따르면, 독소플라즈마는 내인성 기능적 CPSII를 포함하는, 숙주세포 내 독소플라즈마의 증식을 촉진시키는 효소가 없다(예를 들어, 숙주의 면역 체계를 피하는데 중요한 요소, 특정한 대사물질의 생성 또는 이용에 필수적인 요소, 특정한 독소 또는 항생제를 제거하는데 중요한 요소).
- [0114] 본 발명의 일부 구현예에 따르면, 독소플라즈마는 개체의 CNS로의 목적단백질의 전달에 필수적이지 않은 독성 유전자가 없다.
- [0115] 핵산 구조물은 독소플라즈마 세포 내 폴리뉴클레오티드 서열의 전사를 항시적, 일시적, 규칙적 또는 유도적 방식으로 지시하는 프로모터 서열을 포함한다.
- [0116] 기술한 바와 같이, 이중 폴리뉴클레오티스는 독소플라즈마 내 이중 폴리뉴클레오티드의 전사를 지시하는 프로모터에 작동가능하게 연결된다.
- [0117] 코딩 핵산 서열은 조절 서열이 그에 연결된 코딩 서열에 조절 효과를 미칠 수 있다면, 조절 서열(예를 들어, 프로모터)에 "작동가능하게 연결된"다.
- [0118] 본원에서 사용된, 용어 "프로모터"는 RNA 중합효소가 RNA의 전사를 개시하기 위하여 결합한 유전자의 전사 개시 부위의 상류에 높은 DNA 영역을 말한다. 프로모터는 유전자의 발현의 시기 및 강도, 예를 들어, 유전자가 발현되는 기생충 및/또는 숙주세포의 일생의 단계 또는 상태,를 조절한다.
- [0119] 본 발명의 일부 구현예에 따르면, 프로모터는 핵산 구조물의 발현에 사용되는 독소플라즈마에 이종이다.
- [0120] 본 발명의 일부 구현예에 따르면, 프로모터는 전신발현 프로모터이다.
- [0121] 본 발명의 일부 구현예에 따르면, 프로모터는 유도 프로모터이다.

- [0122] 본 발명의 일부 구현예에 따르면, 프로모터는 잠복기-특이적 프로모터이다.
- [0123] 본 발명의 일부 구현예에 따르면, 프로모터는 독소필린 프로모터가 아닌 독소플라즈마 내인성 프로모터이다.
- [0124] 본 발명의 일부 구현예에 따르면, 프로모터는 독소필린 내인성 프로모터가 아니다. 이는 예상되는 독소필린 프로모터(예상되는 유전자 ID=TGME49_214080의 프로모터; 서열번호 3689)가 실시예 부분의 일부 실험에서 사용되는 독소필린 프로모터(서열번호 4482) 및 추가 뉴클레오티드 상류를 포함한다는 것을 나타낸다.
- [0125] 일부 구현예에 따르면, 프로모터는 서열번호 3689 및/또는 서열번호 4482로 기재된 핵산 서열을 포함하지 않는다.
- [0126] 본 발명의 일부 구현예에 따르면, 내인성 프로모터는 곤봉체 단백질의 것이 아니다.
- [0127] 본 발명의 일부 구현예에 따르면, 독소플라즈마 내인성 프로모터는 GRA2 프로모터, GRA16 프로모터, GRA24 프로모터, SAG1 프로모터, 또는 DHFR 프로모터이다.
- [0128] 본 발명의 일부 구현예에 따르면, 독소플라즈마 내인성 프로모터는 GRA2 프로모터이다.
- [0129] 본 발명의 일부 구현예에 따르면, 독소플라즈마 내인성 프로모터는 GRA16 프로모터이다.
- [0130] 본 발명의 일부 구현예에 따르면, 독소플라즈마 내인성 프로모터는 GRA24 프로모터이다.
- [0131] 본 발명의 일부 구현예에 따르면, 독소플라즈마 내인성 프로모터는 SAG1 프로모터이다.
- [0132] 본 발명의 일부 구현예에 따르면, 독소플라즈마 내인성 프로모터는 DHFR 프로모터이다.
- [0133] 하기 본원의 표 1은 독소플라즈마 내 이중 폴리뉴클레오티드의 발현을 유도하기 위하여, 본 발명의 일부 구현예의 핵산 구조물로 클로닝될 수 있는 적합한 내인성 프로모터를 열거한 것이다.
- [0134] [표1] 적합한 내인성 프로모터

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	601871 4	6021975	-	ID=TGME49_278580;길이=326 1	467
TGME49_chr XI	464581 6	4647664	+	ID=TGME49_315320;길이=184 8	468
TGME49_chr XI	597572 5	5979863	-	ID=TGME49_216670;길이=413 8	469
TGME49_chr Ia	602877	607895	+	ID=TGME49_293850;길이=501 8	470
TGME49_chr VIIa	155162 6	1554994	+	ID=TGME49_205190;길이=336 8	471
TGME49_chr VIIb	561320	563366	+	ID=TGME49_263420;길이=204 6	472
TGME49_chr XII	279516 2	2799102	+	ID=TGME49_246485;길이=394 0	473
TGME49_chr Ib	904562	908487	+	ID=TGME49_208850;길이=392 5	474
TGME49_chr VIII	444932 9	4451277	-	ID=TGME49_271610;길이=194 8	475
TGME49_chr VIII	304478 8	3047633	+	ID=TGME49_274060;길이=284 5	476
TGME49_chr VIIb	361219 5	3614194	+	ID=TGME49_258060;길이=199 9	477

[0135]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	654961 3	6551657	+	ID=TGME49_277730;길이=204 4	478
TGME49_chr VIII	197364	199295	-	ID=TGME49_229350;길이=193 1	479
TGME49_chr XI	514331 9	5145850	+	ID=TGME49_316130;길이=253 1	480
TGME49_chr VIIa	247130 2	2472989	+	ID=TGME49_203490;길이=168 7	481
TGME49_chr V	111776 1	1121481	+	ID=TGME49_213530;길이=372 0	482
TGME49_chr XII	564098 3	5642416	-	ID=TGME49_251880;길이=143 3	483
TGME49_chr Ib	112092 6	1123894	+	ID=TGME49_209210;길이=296 8	484
TGME49_chr VIII	499601 8	4997934	-	ID=TGME49_270790;길이=191 6	485
TGME49_chr VIII	426647 7	4270885	-	ID=TGME49_271960;길이=440 8	486
TGME49_chr X	725098 6	7254222	+	ID=TGME49_275430;길이=323 6	487
TGME49_chr VIIb	393313 2	3934570	+	ID=TGME49_257640;길이=143 8	488
TGME49_chr Ib	120704 4	1211342	-	ID=TGME49_209410;길이=429 8	489
TGME49_chr VIIb	384933 7	3853482	+	ID=TGME49_257750;길이=414 5	490
TGME49_chr VIII	706425	708192	+	ID=TGME49_230230;길이=176 7	491
TGME49_chr II	210869 7	2112820	+	ID=TGME49_297920;길이=412 3	492
TGME49_chr IX	367810 5	3679325	-	ID=TGME49_290270;길이=122 0	493
TGME49_chr V	246954 9	2471470	-	ID=TGME49_285272;길이=192 1	494
TGME49_chr VIIb	219752 2	2200500	+	ID=TGME49_260500;길이=297 8	495
TGME49_chr XII	450076 6	4502482	-	ID=TGME49_249370;길이=171 6	496

[0136]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	231352 1	2315991	-	ID=TGME49_203705;길이=247 0	497
TGME49_chr VIIb	499361 8	4998625	+	ID=TGME49_255215;길이=500 7	498
TGME49_chr II	210025 7	2103772	+	ID=TGME49_297900;길이=351 5	499
TGME49_chr VIIa	279911 3	2803405	-	ID=TGME49_203135;길이=429 2	500
TGME49_chr IX	138964 4	1391469	-	ID=TGME49_265990;길이=182 5	501
TGME49_chr IX	518297 4	5185461	-	ID=TGME49_305030;길이=248 7	502
TGME49_chr VIII	50367	52586	-	ID=TGME49_229140;길이=221 9	503
TGME49_chr X	307200 6	3074113	-	ID=TGME49_224350;길이=210 7	504
TGME49_chr XII	320314 0	3205868	-	ID=TGME49_247260;길이=272 8	505
TGME49_chr VI	131650 2	1318224	+	ID=TGME49_240550;길이=172 2	506
TGME49_chr VIIb	490383 8	4908769	+	ID=TGME49_255310;길이=493 1	507
TGME49_chr VIIa	689060	693095	+	ID=TGME49_304760;길이=403 5	508
TGME49_chr VIII	150896 0	1513678	-	ID=TGME49_231625;길이=471 8	509
TGME49_chr XII	190321 6	1907934	+	ID=TGME49_217555;길이=471 8	510
TGME49_chr XI	609657 6	6098700	-	ID=TGME49_216530;길이=212 4	511
TGME49_chr XII	430075 3	4303035	-	ID=TGME49_249010;길이=228 2	512
TGME49_chr VIII	529885 4	5300947	+	ID=TGME49_270270;길이=209 3	513
TGME49_chr VIII	218402 3	2186702	+	ID=TGME49_232600;길이=267 9	514
TGME49_chr IV	143298 4	1435042	-	ID=TGME49_318300;길이=205 8	515

[0137]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	570824 3	5710982	+	ID=TGME49_305990;길이=273 9	516
TGME49_chr X	268926 2	2692060	+	ID=TGME49_224910;길이=279 8	517
TGME49_chr IX	871380	874729	-	ID=TGME49_266960;길이=334 9	518
TGME49_chr IX	158049 8	1583961	+	ID=TGME49_265390;길이=346 3	519
TGME49_chr VI	110743 3	1112442	+	ID=TGME49_240250;길이=500 9	520
TGME49_chr XI	461860 2	4621016	-	ID=TGME49_315270;길이=241 4	521
TGME49_chr IX	123894 1	1239596	-	ID=TGME49_266290;길이=655	522
TGME49_chr Ib	65733	70002	-	ID=TGME49_207440;길이=426 9	523
TGME49_chr VIIa	107838 9	1081603	-	ID=TGME49_206300;길이=321 4	524
TGME49_chr VIII	162884 8	1630628	+	ID=TGME49_231910;길이=178 0	525
TGME49_chr Ia	556012	557885	+	ID=TGME49_293780;길이=187 3	526
TGME49_chr Ia	128648 1	1288807	+	ID=TGME49_294960;길이=232 6	527
TGME49_chr XII	209872 0	2101108	-	ID=TGME49_217760;길이=238 8	528
TGME49_chr IX	335658 0	3358813	-	ID=TGME49_289620;길이=223 3	529
TGME49_chr XII	643221 0	6433693	-	ID=TGME49_277920;길이=148 3	530
TGME49_chr IX	144083 1	1443406	+	ID=TGME49_265810;길이=257 5	531
TGME49_chr VIIb	250506 8	2506652	-	ID=TGME49_260150;길이=158 4	532
TGME49_chr VIIa	251349 0	2515244	+	ID=TGME49_203400;길이=175 4	533
TGME49_chr IX	433878 6	4341883	-	ID=TGME49_291680;길이=309 7	534

[0138]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	184420 3	1845704	+	ID=TGME49_232085;길이=150 1	535
TGME49_chr XI	430329 3	4303677	+	ID=TGME49_314800;길이=384	536
TGME49_chr VIIa	394995 7	3952927	-	ID=TGME49_201240;길이=297 0	537
TGME49_chr Ia	106138 3	1062031	-	ID=TGME49_294680;길이=648	538
TGME49_chr XI	509059 3	5094613	+	ID=TGME49_315950;길이=402 0	539
TGME49_chr VIIa	244116 6	2446197	-	ID=TGME49_203540;길이=503 1	540
TGME49_chr IX	501264 8	5015438	-	ID=TGME49_307605;길이=279 0	541
TGME49_chr VIIb	390630 4	3910432	-	ID=TGME49_257690;길이=412 8	542
TGME49_chr XII	365273 0	3655440	-	ID=TGME49_247980;길이=271 0	543
TGME49_chr VIII	673256 8	6737516	+	ID=TGME49_267990;길이=494 8	544
TGME49_chr IX	362887	364364	-	ID=TGME49_267790;길이=147 7	545
TGME49_chr V	219744 0	2202168	+	ID=TGME49_285810;길이=472 8	546
TGME49_chr X	736001 5	7363002	-	ID=TGME49_207050;길이=298 7	547
TGME49_chr Ib	107385 6	1076422	+	ID=TGME49_209150;길이=256 6	548
TGME49_chr VIIb	274709 4	2748845	+	ID=TGME49_259630;길이=175 1	549
TGME49_chr Ib	4351	6355	-	ID=TGME49_207350;길이=200 4	550
TGME49_chr X	289909 2	2901603	+	ID=TGME49_224660;길이=251 1	551
TGME49_chr X	697594	700161	+	ID=TGME49_227970;길이=256 7	552
TGME49_chr XI	206962 2	2070833	-	ID=TGME49_311430;길이=121 1	553

[0139]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	297580 8	2977909	+	ID=TGME49_274150;길이=210 1	554
TGME49_chr VIIb	163376 4	1635885	+	ID=TGME49_261600;길이=212 1	555
TGME49_chr IX	477892 3	4783666	-	ID=TGME49_210450;길이=474 3	556
TGME49_chr XII	170916	172799	-	ID=TGME49_300180;길이=188 3	557
TGME49_chr VI	903242	908079	-	ID=TGME49_239760;길이=483 7	558
TGME49_chr XII	525691 3	5260639	+	ID=TGME49_250840;길이=372 6	559
TGME49_chr X	260946 7	2612329	+	ID=TGME49_224980;길이=286 2	560
TGME49_chr X	580629 5	5808296	+	ID=TGME49_237250;길이=200 1	561
TGME49_chr VI	548569	552854	-	ID=TGME49_239320;길이=428 5	562
TGME49_chr VIIb	145601 4	1458169	+	ID=TGME49_261960;길이=215 5	563
TGME49_chr XII	838987	840604	+	ID=TGME49_219590;길이=161 7	564
TGME49_chr IX	600361	602779	-	ID=TGME49_267530;길이=241 8	565
TGME49_chr V	307235 6	3074734	+	ID=TGME49_283550;길이=237 8	566
TGME49_chr IV	165370 2	1657375	+	ID=TGME49_211630;길이=367 3	567
TGME49_chr XI	634357 5	6348246	+	ID=TGME49_216190;길이=467 1	568
TGME49_chr XII	383564 7	3837281	-	ID=TGME49_248400;길이=163 4	569
TGME49_chr VI	613254	616583	+	ID=TGME49_239400;길이=332 9	570
TGME49_chr X	286419 2	2865912	-	ID=TGME49_224710;길이=172 0	571
TGME49_chr II	404894	406860	-	ID=TGME49_221500;길이=196 6	572

[0140]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	636407 9	6366025	+	ID=TGME49_268685;길이=194 6	573
TGME49_chr IX	341308 2	3417820	-	ID=TGME49_289730;길이=473 8	574
TGME49_chr IX	441154 8	4413465	+	ID=TGME49_291940;길이=191 7	575
TGME49_chr X	739515 7	7398234	-	ID=TGME49_207100;길이=307 7	576
TGME49_chr IX	424518 7	4246860	+	ID=TGME49_291330;길이=167 3	577
TGME49_chr V	142207 0	1425388	+	ID=TGME49_213910;길이=331 8	578
TGME49_chr IX	376679 4	3768071	-	ID=TGME49_290605;길이=127 7	579
TGME49_chr X	428335 2	4285324	-	ID=TGME49_234280;길이=197 2	580
TGME49_chr X	695646 2	6958294	-	ID=TGME49_215430;길이=183 2	581
TGME49_chr V	186946	188803	+	ID=TGME49_220175;길이=185 7	582
TGME49_chr XII	271977 0	2724408	-	ID=TGME49_246182;길이=463 8	583
TGME49_chr X	727312 7	7275437	-	ID=TGME49_275440;길이=231 0	584
TGME49_chr VIII	225013 3	2251577	+	ID=TGME49_232760;길이=144 4	585
TGME49_chr IX	211323 5	2114688	-	ID=TGME49_264680;길이=145 3	586
TGME49_chr Ib	150362 4	1507993	+	ID=TGME49_209880;길이=436 9	587
TGME49_chr VIIa	165392 0	1656907	-	ID=TGME49_205050;길이=298 7	588
TGME49_chr VIII	161412 2	1617638	-	ID=TGME49_231880;길이=351 6	589
TGME49_chr VIII	682303 5	6824629	+	ID=TGME49_200360;길이=159 4	590
TGME49_chr IV	392225	396143	+	ID=TGME49_320290;길이=391 8	591

[0141]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	172505 1	1727020	-	ID=TGME49_311010;길이=196 9	592
TGME49_chr IX	157081 3	1573290	+	ID=TGME49_265410;길이=247 7	593
TGME49_chr IV	258575	263510	+	ID=TGME49_320550;길이=493 5	594
TGME49_chr VIIb	343262 6	3435118	+	ID=TGME49_258410;길이=249 2	595
TGME49_chr X	443347 1	4435962	-	ID=TGME49_234510;길이=249 1	596
TGME49_chr XI	469568 7	4699361	-	ID=TGME49_315410;길이=367 4	597
TGME49_chr X	194415 3	1947194	+	ID=TGME49_225905;길이=304 1	598
TGME49_chr VIIb	207287 0	2074965	-	ID=TGME49_260670;길이=209 5	599
TGME49_chr XII	265195 8	2655687	+	ID=TGME49_246090;길이=372 9	600
TGME49_chr VIIa	122549 0	1226911	+	ID=TGME49_205662;길이=142 1	601
TGME49_chr VIIa	524618	528076	+	ID=TGME49_304500;길이=345 8	602
TGME49_chr VIII	290167 1	2903828	-	ID=TGME49_233925;길이=215 7	603
TGME49_chr VIII	471537 3	4717272	+	ID=TGME49_271100;길이=189 9	604
TGME49_chr XI	475083 6	4752746	-	ID=TGME49_315480;길이=191 0	605
TGME49_chr X	342895 4	3431481	-	ID=TGME49_223960;길이=252 7	606
TGME49_chr IX	119535 2	1197540	-	ID=TGME49_266368;길이=218 8	607
TGME49_chr II	179874 2	1800245	+	ID=TGME49_297465;길이=150 3	608
TGME49_chr IX	607760 2	6080932	-	ID=TGME49_306430;길이=333 0	609
TGME49_chr VIIa	740498	744501	+	ID=TGME49_206660;길이=400 3	610

[0142]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	313567 1	3138592	-	ID=TGME49_224280;길이=292 1	611
TGME49_chr VIIb	355374 1	3554846	-	ID=TGME49_258140;길이=110 5	612
TGME49_chr IX	535274 8	5353735	-	ID=TGME49_305315;길이=987	613
TGME49_chr VIII	469808 7	4702028	-	ID=TGME49_271115;길이=394 1	614
TGME49_chr IX	793986	798309	+	ID=TGME49_267060;길이=432 3	615
TGME49_chr VIIb	320259 0	3203934	+	ID=TGME49_258760;길이=134 4	616
TGME49_chr X	379796	381741	+	ID=TGME49_228350;길이=194 5	617
TGME49_chr X	463958 0	4641831	+	ID=TGME49_235150;길이=225 1	618
TGME49_chr IX	345871 3	3461263	+	ID=TGME49_289800;길이=255 0	619
TGME49_chr VIIa	250025 5	2501767	-	ID=TGME49_203450;길이=151 2	620
TGME49_chr XII	469211 2	4694534	+	ID=TGME49_249620;길이=242 2	621
TGME49_chr VIII	435112 6	4354140	-	ID=TGME49_271810;길이=301 4	622
TGME49_chr VIIa	130517 3	1307774	-	ID=TGME49_205570;길이=260 1	623
TGME49_chr XI	571006 2	5711311	+	ID=TGME49_217040;길이=124 9	624
TGME49_chr Ia	876889	879930	-	ID=TGME49_294390;길이=304 1	625
TGME49_chr VIIa	397518 2	3977201	+	ID=TGME49_201200;길이=201 9	626
TGME49_chr VIIb	287008 4	2871524	-	ID=TGME49_259220;길이=144 0	627
TGME49_chr VI	108434 8	1088618	+	ID=TGME49_240230;길이=427 0	628
TGME49_chr VIIb	338572 1	3387496	+	ID=TGME49_258490;길이=177 5	629

[0143]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	528457	531919	+	ID=TGME49_263480; 길이=3462	630
TGME49_chr II	757384	761699	+	ID=TGME49_222020; 길이=4315	631
TGME49_chr VIII	1358289	1362306	-	ID=TGME49_231350; 길이=4017	632
TGME49_chr IX	2802162	2802980	-	ID=TGME49_288900; 길이=818	633
TGME49_chr X	2467589	2469875	-	ID=TGME49_225130; 길이=2286	634
TGME49_chr VIIb	2251666	2252571	-	ID=TGME49_260460; 길이=905	635
TGME49_chr VIIa	2091486	2095749	+	ID=TGME49_203950; 길이=4263	636
TGME49_chr IX	6058657	6060999	+	ID=TGME49_306410; 길이=2342	637
TGME49_chr V	198241	200161	+	ID=TGME49_220200; 길이=1920	638
TGME49_chr II	1356741	1359871	-	ID=TGME49_222980; 길이=3130	639
TGME49_chr X	2206505	2209526	+	ID=TGME49_225490; 길이=3021	640
TGME49_chr XII	2096828	2099495	+	ID=TGME49_217770; 길이=2667	641
TGME49_chr VIIa	2970014	2971521	+	ID=TGME49_202870; 길이=1507	642
TGME49_chr VIIb	322918	324659	-	ID=TGME49_263800; 길이=1741	643
TGME49_chr VIIb	2953991	2955320	-	ID=TGME49_259140; 길이=1329	644
TGME49_chr VIIa	1469449	1473570	+	ID=TGME49_205320; 길이=4121	645
TGME49_chr XI	461912	464423	+	ID=TGME49_309060; 길이=2511	646
TGME49_chr IX	1224097	1225515	-	ID=TGME49_266320; 길이=1418	647
TGME49_chr II	2142037	2146242	+	ID=TGME49_297970; 길이=4205	648

[0144]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	104259 4	1045138	-	ID=TGME49_240070;길이=254 4	649
TGME49_chr V	130908 6	1311333	-	ID=TGME49_213770;길이=224 7	650
TGME49_chr II	102344 7	1025166	-	ID=TGME49_222305;길이=171 9	651
TGME49_chr XI	150041 7	1504291	-	ID=TGME49_310640;길이=387 4	652
TGME49_chr XI	437837 8	4379028	+	ID=TGME49_314890;길이=650	653
TGME49_chr X	738524	740600	+	ID=TGME49_227910;길이=207 6	654
TGME49_chr IX	604551 2	6047246	+	ID=TGME49_306390;길이=173 4	655
TGME49_chr X	193523 2	1938008	-	ID=TGME49_225920;길이=277 6	656
TGME49_chr VI	144126 7	1443761	-	ID=TGME49_240770;길이=249 4	657
TGME49_chr VIIa	200150 8	2005367	-	ID=TGME49_204090;길이=385 9	658
TGME49_chr Ia	654666	657455	-	ID=TGME49_294025;길이=278 9	659
TGME49_chr VIIb	217469 2	2176915	+	ID=TGME49_260530;길이=222 3	660
TGME49_chr XII	711702	713805	+	ID=TGME49_219700;길이=210 3	661
TGME49_chr Ia	130470 1	1306918	+	ID=TGME49_295000;길이=221 7	662
TGME49_chr IX	568139	569234	+	ID=TGME49_267560;길이=109 5	663
TGME49_chr VIII	539782 9	5399254	-	ID=TGME49_270110;길이=142 5	664
TGME49_chr XII	284410 2	2846241	+	ID=TGME49_246550;길이=213 9	665
TGME49_chr XII	493492 6	4937491	+	ID=TGME49_249900;길이=256 5	666
TGME49_chr X	488005 3	4884161	+	ID=TGME49_235470;길이=410 8	667

[0145]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	586859 5	5871618	-	ID=TGME49_216820;길이=302 3	668
TGME49_chr XII	640425 1	6407186	-	ID=TGME49_277940;길이=293 5	669
TGME49_chr IX	957423	959519	+	ID=TGME49_266800;길이=209 6	670
TGME49_chr XII	577498 9	5777401	-	ID=TGME49_278900;길이=241 2	671
TGME49_chr VIII	395975 1	3962176	+	ID=TGME49_272450;길이=242 5	672
TGME49_chr VIII	370067 5	3704469	-	ID=TGME49_273030;길이=379 4	673
TGME49_chr VIIb	353255 5	3534514	+	ID=TGME49_258170;길이=195 9	674
TGME49_chr IX	533864 5	5340540	-	ID=TGME49_305290;길이=189 5	675
TGME49_chr IX	380735 1	3810696	+	ID=TGME49_290645;길이=334 5	676
TGME49_chr XII	562578 6	5628283	+	ID=TGME49_251855;길이=249 7	677
TGME49_chr VI	300420 4	3006660	+	ID=TGME49_244070;길이=245 6	678
TGME49_chr VIIa	394860 2	3952191	+	ID=TGME49_201230;길이=358 9	679
TGME49_chr VIII	15020	16940	+	ID=TGME49_229005;길이=192 0	680
TGME49_chr Ia	429247	432726	-	ID=TGME49_293570;길이=347 9	681
TGME49_chr II	192728 1	1932126	+	ID=TGME49_297710;길이=484 5	682
TGME49_chr XI	263701 0	2638757	+	ID=TGME49_312370;길이=174 7	683
TGME49_chr XII	346902 0	3473396	-	ID=TGME49_247660;길이=437 6	684
TGME49_chr XI	491615 7	4920214	-	ID=TGME49_315700;길이=405 7	685
TGME49_chr Ib	629071	630918	+	ID=TGME49_208360;길이=184 7	686

[0146]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	6755827	6757330	+	ID=TGME49_277050;길이=1503	687
TGME49_chr VIIb	4411300	4413757	-	ID=TGME49_256840;길이=2457	688
TGME49_chr X	7049221	7051104	-	ID=TGME49_215610;길이=1883	689
TGME49_chr XII	6528538	6533549	+	ID=TGME49_277760;길이=5011	690
TGME49_chr VIIa	3427921	3430094	+	ID=TGME49_202310;길이=2173	691
TGME49_chr X	6689399	6691360	+	ID=TGME49_215030;길이=1961	692
TGME49_chr VI	2874483	2876334	+	ID=TGME49_243900;길이=1851	693
TGME49_chr VIII	83739	85719	-	ID=TGME49_229180;길이=1980	694
TGME49_chr IV	2119015	2122018	-	ID=TGME49_210715;길이=3003	695
TGME49_chr VIIb	3259075	3262189	+	ID=TGME49_258680;길이=3114	696
TGME49_chr V	125975	128008	+	ID=TGME49_220100;길이=2033	697
TGME49_chr VI	3354392	3358777	-	ID=TGME49_244550;길이=4385	698
TGME49_chr V	1810497	1813699	+	ID=TGME49_286490;길이=3202	699
TGME49_chr Ib	1306317	1308410	+	ID=TGME49_209530;길이=2093	700
TGME49_chr V	2062700	2065738	+	ID=TGME49_286000;길이=3038	701
TGME49_chr IX	2762545	2764943	+	ID=TGME49_288840;길이=2398	702
TGME49_chr X	995784	1000191	+	ID=TGME49_227350;길이=4407	703
TGME49_chr Ib	1537215	1542214	-	ID=TGME49_209890;길이=4999	704
TGME49_chr VI	2985954	2988613	+	ID=TGME49_244050;길이=2659	705

[0147]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	518708 5	5189714	-	ID=TGME49_316200;길이=262 9	706
TGME49_chr VIIa	256167 0	2565986	+	ID=TGME49_203340;길이=431 6	707
TGME49_chr V	222631 5	2231159	+	ID=TGME49_285790;길이=484 4	708
TGME49_chr IX	404524	405991	+	ID=TGME49_267725;길이=146 7	709
TGME49_chr IX	694704	696929	+	ID=TGME49_267360;길이=222 5	710
TGME49_chr XII	377734 5	3780569	+	ID=TGME49_248290;길이=322 4	711
TGME49_chr VIIa	309240 6	3094459	-	ID=TGME49_202720;길이=205 3	712
TGME49_chr XI	245560 0	2459938	+	ID=TGME49_312150;길이=433 8	713
TGME49_chr II	220920	223578	+	ID=TGME49_221295;길이=265 8	714
TGME49_chr XII	208416 9	2087144	-	ID=TGME49_217730;길이=297 5	715
TGME49_chr Ib	100779 1	1010351	-	ID=TGME49_209045;길이=256 0	716
TGME49_chr X	526570 2	5266555	-	ID=TGME49_236070;길이=853	717
TGME49_chr VIIb	345746 5	3460841	-	ID=TGME49_258360;길이=337 6	718
TGME49_chr VIII	219290 3	2195917	-	ID=TGME49_232610;길이=301 4	719
TGME49_chr VIIb	110948 3	1111172	+	ID=TGME49_262640;길이=168 9	720
TGME49_chr X	385365 7	3855793	-	ID=TGME49_223430;길이=213 6	721
TGME49_chr XI	423919 8	4243862	+	ID=TGME49_314720;길이=466 4	722
TGME49_chr VIIb	269786 9	2700279	+	ID=TGME49_259710;길이=241 0	723
TGME49_chr VIIa	147173 0	1473919	-	ID=TGME49_205330;길이=218 9	724

[0148]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr V	2711878	2714132	-	ID=TGME49_284570;길이=2254	725
TGME49_chr VIII	388717	391218	-	ID=TGME49_229700;길이=2501	726
TGME49_chr IX	1538973	1542213	+	ID=TGME49_265455;길이=3240	727
TGME49_chr XI	763730	767625	-	ID=TGME49_309610;길이=3895	728
TGME49_chr XI	2544365	2546425	+	ID=TGME49_312250;길이=2060	729
TGME49_chr VIII	5643590	5647253	-	ID=TGME49_269730;길이=3663	730
TGME49_chr IX	3584012	3585263	-	ID=TGME49_290005;길이=1251	731
TGME49_chr VIIa	3971108	3972217	-	ID=TGME49_201215;길이=1109	732
TGME49_chr IX	5666852	5669401	-	ID=TGME49_305910;길이=2549	733
TGME49_chr VIIa	1726778	1728368	+	ID=TGME49_204540;길이=1590	734
TGME49_chr IX	5763619	5766671	-	ID=TGME49_306030;길이=3052	735
TGME49_chr IX	5211532	5213996	-	ID=TGME49_305080;길이=2464	736
TGME49_chr II	1002441	1005482	+	ID=TGME49_222270;길이=3041	737
TGME49_chr XII	82314	83922	+	ID=TGME49_300320;길이=1608	738
TGME49_chr XI	4112813	4117560	+	ID=TGME49_314470;길이=4747	739
TGME49_chr VIII	6338649	6340670	-	ID=TGME49_268740;길이=2021	740
TGME49_chr IX	4955341	4957346	-	ID=TGME49_210220;길이=2005	741
TGME49_chr X	1176693	1177745	-	ID=TGME49_226980;길이=1052	742
TGME49_chr XII	1656412	1659890	-	ID=TGME49_218240;길이=3478	743

[0149]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	603391 9	6035646	-	ID=TGME49_278550;길이=172 7	744
TGME49_chr VIIa	296097 8	2963669	-	ID=TGME49_202890;길이=269 1	745
TGME49_chr XII	608758 5	6092290	+	ID=TGME49_278450;길이=470 5	746
TGME49_chr VIII	101229	104465	+	ID=TGME49_229230;길이=323 6	747
TGME49_chr IV	102717 6	1029320	-	ID=TGME49_319330;길이=214 4	748
TGME49_chr V	927001	929683	+	ID=TGME49_213325;길이=268 2	749
TGME49_chr VIIa	197927 8	1981377	-	ID=TGME49_204120;길이=209 9	750
TGME49_chr VIIa	216840 0	2170024	-	ID=TGME49_203875;길이=162 4	751
TGME49_chr V	805784	808589	+	ID=TGME49_213040;길이=280 5	752
TGME49_chr XI	325766 4	3259999	+	ID=TGME49_313310;길이=233 5	753
TGME49_chr XI	422592 1	4227690	-	ID=TGME49_314690;길이=176 9	754
TGME49_chr XI	246924 9	2471186	-	ID=TGME49_312160;길이=193 7	755
TGME49_chr VIIa	306939 6	3071264	-	ID=TGME49_202740;길이=186 8	756
TGME49_chr VIIb	398250 5	3984582	-	ID=TGME49_257550;길이=207 7	757
TGME49_chr VI	235240 5	2356464	-	ID=TGME49_242850;길이=405 9	758
TGME49_chr VIIa	136468 2	1367044	-	ID=TGME49_205510;길이=236 2	759
TGME49_chr IX	329028 0	3294112	-	ID=TGME49_289530;길이=383 2	760
TGME49_chr X	650976 4	6512159	+	ID=TGME49_214820;길이=239 5	761
TGME49_chr X	581261	582904	-	ID=TGME49_228110;길이=164 3	762

[0150]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	2990065	2994627	+	ID=TGME49_259040;길이=4562	763
TGME49_chr XI	2072060	2077000	+	ID=TGME49_311450;길이=4940	764
TGME49_chr VIII	2876231	2878765	-	ID=TGME49_233880;길이=2534	765
TGME49_chr V	1940852	1943237	+	ID=TGME49_286160;길이=2385	766
TGME49_chr Ib	737486	739366	+	ID=TGME49_208510;길이=1880	767
TGME49_chr X	7427442	7429460	+	ID=TGME49_207180;길이=2018	768
TGME49_chr XI	4517672	4520283	+	ID=TGME49_315150;길이=2611	769
TGME49_chr VI	2075613	2077679	-	ID=TGME49_242570;길이=2066	770
TGME49_chr XII	5792779	5795081	-	ID=TGME49_278878;길이=2302	771
TGME49_chr XI	6607068	6609847	+	ID=TGME49_298630;길이=2779	772
TGME49_chr II	1309836	1311957	+	ID=TGME49_222920;길이=2121	773
TGME49_chr VI	3254059	3255822	-	ID=TGME49_244420;길이=1763	774
TGME49_chr VI	1733335	1738338	+	ID=TGME49_241840;길이=5003	775
TGME49_chr XII	51579	55519	+	ID=TGME49_300350;길이=3940	776
TGME49_chr IX	4278507	4279338	-	ID=TGME49_291580;길이=831	777
TGME49_chr X	537261	540449	-	ID=TGME49_228160;길이=3188	778
TGME49_chr VIII	2637897	2639548	+	ID=TGME49_233430;길이=1651	779
TGME49_chr X	6320461	6322071	-	ID=TGME49_214490;길이=1610	780
TGME49_chr VIIa	1438969	1442993	+	ID=TGME49_205360;길이=4024	781

[0151]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	423314	427457	+	ID=TGME49_267710;길이=414 3	782
TGME49_chr XII	330533 8	3310175	-	ID=TGME49_247380;길이=483 7	783
TGME49_chr V	110712 1	1109784	+	ID=TGME49_213510;길이=266 3	784
TGME49_chr IX	392824 7	3930598	-	ID=TGME49_290900;길이=235 1	785
TGME49_chr XII	173725 4	1738814	-	ID=TGME49_218070;길이=156 0	786
TGME49_chr X	129759 3	1300223	+	ID=TGME49_226840;길이=263 0	787
TGME49_chr VI	329891 7	3303680	+	ID=TGME49_244480;길이=476 3	788
TGME49_chr XII	681432	686187	+	ID=TGME49_219730;길이=475 5	789
TGME49_chr VIIb	115439 8	1159261	+	ID=TGME49_262564;길이=486 3	790
TGME49_chr VIIb	252091 8	2523507	+	ID=TGME49_260020;길이=258 9	791
TGME49_chr VIIa	438343 9	4388493	+	ID=TGME49_282130;길이=505 4	792
TGME49_chr VIII	635787 8	6362199	-	ID=TGME49_268710;길이=432 1	793
TGME49_chr V	306285 8	3064646	-	ID=TGME49_283698;길이=178 8	794
TGME49_chr Ib	185665	190405	+	ID=TGME49_207650;길이=474 0	795
TGME49_chr XII	311395 3	3117617	-	ID=TGME49_247025;길이=366 4	796
TGME49_chr IV	266213 6	2664273	+	ID=TGME49_317705;길이=213 7	797
TGME49_chr XI	620410 2	6206390	-	ID=TGME49_216375;길이=228 8	798
TGME49_chr VIIa	197145 1	1974609	-	ID=TGME49_204130;길이=315 8	799
TGME49_chr II	137864 5	1380471	-	ID=TGME49_223030;길이=182 6	800

[0152]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	294956	296317	-	ID=TGME49_228480;길이=136 1	801
TGME49_chr VIIa	332591 2	3327698	-	ID=TGME49_202445;길이=178 6	802
TGME49_chr VIIa	530623	533507	+	ID=TGME49_304520;길이=288 4	803
TGME49_chr V	187853 0	1880133	-	ID=TGME49_286265;길이=160 3	804
TGME49_chr XI	595557 0	5956873	-	ID=TGME49_216700;길이=130 3	805
TGME49_chr II	209454 2	2097582	-	ID=TGME49_297880;길이=304 0	806
TGME49_chr X	682194 9	6825368	+	ID=TGME49_215220;길이=341 9	807
TGME49_chr VIII	658617 4	6591203	-	ID=TGME49_268280;길이=502 9	808
TGME49_chr V	234687 0	2349052	+	ID=TGME49_285520;길이=218 2	809
TGME49_chr VIIa	318295 6	3184488	-	ID=TGME49_202600;길이=153 2	810
TGME49_chr II	195987 3	1961931	-	ID=TGME49_297730;길이=205 8	811
TGME49_chr VIII	221336 7	2216028	-	ID=TGME49_232660;길이=266 1	812
TGME49_chr VIII	147259 3	1474572	+	ID=TGME49_231590;길이=197 9	813
TGME49_chr VIIb	407034	411993	+	ID=TGME49_263650;길이=495 9	814
TGME49_chr XII	604041 0	6041868	+	ID=TGME49_278522;길이=145 8	815
TGME49_chr VI	128832	133066	+	ID=TGME49_238210;길이=423 4	816
TGME49_chr VIII	235131 2	2353449	-	ID=TGME49_233020;길이=213 7	817
TGME49_chr XII	367567 0	3678134	+	ID=TGME49_248130;길이=246 4	818
TGME49_chr XI	175130 5	1754114	+	ID=TGME49_311060;길이=280 9	819

[0153]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	382092 0	3824021	-	ID=TGME49_272650; 길이=310 1	820
TGME49_chr IX	395819 7	3961023	-	ID=TGME49_290940; 길이=282 6	821
TGME49_chr VIII	392730 6	3931495	+	ID=TGME49_272500; 길이=418 9	822
TGME49_chr VIIb	455736 5	4559435	-	ID=TGME49_256030; 길이=207 0	823
TGME49_chr VIIa	327620 4	3279186	-	ID=TGME49_202500; 길이=298 2	824
TGME49_chr VIII	631889 6	6321304	-	ID=TGME49_268780; 길이=240 8	825
TGME49_chr VIIb	479812	483399	+	ID=TGME49_263550; 길이=358 7	826
TGME49_chr IX	429028 3	4293221	+	ID=TGME49_291620; 길이=293 8	827
TGME49_chr VI	28927	31927	+	ID=TGME49_238050; 길이=300 0	828
TGME49_chr IV	478540	480420	-	ID=TGME49_320140; 길이=188 0	829
TGME49_chr VIIa	625928	629635	-	ID=TGME49_304690; 길이=370 7	830
TGME49_chr XI	548533 8	5489618	-	ID=TGME49_316670; 길이=428 0	831
TGME49_chr VIIa	153984 1	1542075	+	ID=TGME49_205210; 길이=223 4	832
TGME49_chr XII	634097	638220	+	ID=TGME49_219800; 길이=412 3	833
TGME49_chr V	182285 1	1827597	-	ID=TGME49_286465; 길이=474 6	834
TGME49_chr VIII	557302 3	5577518	+	ID=TGME49_269850; 길이=449 5	835
TGME49_chr V	688702	691280	-	ID=TGME49_212880; 길이=257 8	836
TGME49_chr VIIa	718101	722948	-	ID=TGME49_206700; 길이=484 7	837
TGME49_chr VIIb	107862 3	1080134	+	ID=TGME49_262690; 길이=151 1	838

[0154]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	122484	127476	+	ID=TGME49_229270;길이=499 2	839
TGME49_chr VIII	198445 5	1988743	+	ID=TGME49_232270;길이=428 8	840
TGME49_chr Ib	163556 0	1637014	+	ID=TGME49_321685;길이=145 4	841
TGME49_chr XII	493610 0	4940316	-	ID=TGME49_249890;길이=421 6	842
TGME49_chr XI	542439	545032	-	ID=TGME49_309185;길이=259 3	843
TGME49_chr X	442190 9	4423573	+	ID=TGME49_234505;길이=166 4	844
TGME49_chr XI	617218 1	6176170	-	ID=TGME49_216400;길이=398 9	845
TGME49_chr X	229151 0	2293010	-	ID=TGME49_225350;길이=150 0	846
TGME49_chr V	174954 2	1751790	+	ID=TGME49_286630;길이=224 8	847
TGME49_chr VI	131981 1	1322525	+	ID=TGME49_240570;길이=271 4	848
TGME49_chr VIIb	229491	232296	-	ID=TGME49_264030;길이=280 5	849
TGME49_chr VI	231085 4	2312930	+	ID=TGME49_242810;길이=207 6	850
TGME49_chr X	650267 8	6507667	-	ID=TGME49_214800;길이=498 9	851
TGME49_chr XI	206033 9	2062705	-	ID=TGME49_311400;길이=236 6	852
TGME49_chr VIII	926825	929619	+	ID=TGME49_230650;길이=279 4	853
TGME49_chr XII	105272	106503	-	ID=TGME49_300300;길이=123 1	854
TGME49_chr VIII	453277	455115	-	ID=TGME49_229800;길이=183 8	855
TGME49_chr X	164456 2	1648123	+	ID=TGME49_226420;길이=356 1	856
TGME49_chr II	151743 8	1521865	+	ID=TGME49_297080;길이=442 7	857

[0155]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	404650 9	4047748	-	ID=TGME49_281360;길이=123 9	858
TGME49_chr X	284781 2	2849682	-	ID=TGME49_224740;길이=187 0	859
TGME49_chr IX	240400 1	2406112	+	ID=TGME49_288240;길이=211 1	860
TGME49_chr II	205967 9	2062541	-	ID=TGME49_297830;길이=286 2	861
TGME49_chr VI	148376 6	1486135	+	ID=TGME49_240870;길이=236 9	862
TGME49_chr VIII	570119 2	5703410	-	ID=TGME49_269670;길이=221 8	863
TGME49_chr V	301102 2	3012612	+	ID=TGME49_283720;길이=159 0	864
TGME49_chr V	287381 4	2875242	-	ID=TGME49_283900;길이=142 8	865
TGME49_chr X	267763 8	2679002	-	ID=TGME49_224928;길이=136 4	866
TGME49_chr VI	459221	463664	-	ID=TGME49_239090;길이=444 3	867
TGME49_chr IX	248169 1	2483404	+	ID=TGME49_288380;길이=171 3	868
TGME49_chr XII	633646 6	6338146	-	ID=TGME49_278050;길이=168 0	869
TGME49_chr XI	346172 6	3464489	-	ID=TGME49_313530;길이=276 3	870
TGME49_chr IV	494931	499385	-	ID=TGME49_320105;길이=445 4	871
TGME49_chr VIIb	321678 5	3221009	+	ID=TGME49_258730;길이=422 4	872
TGME49_chr IV	238756 9	2389243	-	ID=TGME49_301330;길이=167 4	873
TGME49_chr XII	458199 2	4584975	+	ID=TGME49_249510;길이=298 3	874
TGME49_chr X	764443	766659	-	ID=TGME49_227870;길이=221 6	875
TGME49_chr XI	527243 4	5274572	+	ID=TGME49_316400;길이=213 8	876

[0156]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	907526	912198	-	ID=TGME49_266910;길이=467 2	877
TGME49_chr VIII	334873 8	3350248	-	ID=TGME49_273620;길이=151 0	878
TGME49_chr XII	497796 6	4980165	-	ID=TGME49_249990;길이=219 9	879
TGME49_chr V	297103 6	2974678	-	ID=TGME49_283790;길이=364 2	880
TGME49_chr XII	619450 1	6196639	+	ID=TGME49_278250;길이=213 8	881
TGME49_chr VIIb	488643 4	4890628	-	ID=TGME49_255350;길이=419 4	882
TGME49_chr VIIb	153746 2	1538674	-	ID=TGME49_261770;길이=121 2	883
TGME49_chr IX	267344 1	2676363	-	ID=TGME49_288680;길이=292 2	884
TGME49_chr X	378794 1	3790472	+	ID=TGME49_223480;길이=253 1	885
TGME49_chr XII	363588 4	3640897	-	ID=TGME49_247940;길이=501 3	886
TGME49_chr VI	349133 7	3495343	+	ID=TGME49_244726;길이=400 6	887
TGME49_chr XII	342590 1	3428625	-	ID=TGME49_247580;길이=272 4	888
TGME49_chr VIIb	166003 9	1663128	+	ID=TGME49_261540;길이=308 9	889
TGME49_chr VI	110931	113077	-	ID=TGME49_238180;길이=214 6	890
TGME49_chr XII	156901 1	1573385	-	ID=TGME49_218362;길이=437 4	891
TGME49_chr VIIb	304883 7	3050490	-	ID=TGME49_258990;길이=165 3	892
TGME49_chr VIIb	301194	305916	+	ID=TGME49_263820;길이=472 2	893
TGME49_chr VIIa	438672 7	4390549	-	ID=TGME49_282120;길이=382 2	894
TGME49_chr IV	205415	209239	+	ID=TGME49_320600;길이=382 4	895

[0157]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	281401	284597	-	ID=TGME49_279315;길이=319 6	896
TGME49_chr VIIb	424794 7	4250288	+	ID=TGME49_257060;길이=234 1	897
TGME49_chr XI	434759 3	4351033	-	ID=TGME49_314850;길이=344 0	898
TGME49_chr X	167129 5	1673894	-	ID=TGME49_226385;길이=259 9	899
TGME49_chr XII	189850 4	1900791	-	ID=TGME49_217540;길이=228 7	900
TGME49_chr VI	162350 1	1626197	+	ID=TGME49_241130;길이=269 6	901
TGME49_chr XI	508311 8	5085552	+	ID=TGME49_315940;길이=243 4	902
TGME49_chr XII	110864 8	1110707	-	ID=TGME49_219150;길이=205 9	903
TGME49_chr XI	369175 4	3696010	-	ID=TGME49_313780;길이=425 6	904
TGME49_chr IX	120105 5	1203450	+	ID=TGME49_266360;길이=239 5	905
TGME49_chr IX	162875 3	1630162	+	ID=TGME49_265290;길이=140 9	906
TGME49_chr IX	580216 6	5805344	+	ID=TGME49_306080;길이=317 8	907
TGME49_chr V	126932 4	1271922	-	ID=TGME49_213730;길이=259 8	908
TGME49_chr VIII	654494 3	6546577	+	ID=TGME49_268320;길이=163 4	909
TGME49_chr VI	256589 9	2570600	+	ID=TGME49_243350;길이=470 1	910
TGME49_chr V	244725	247396	-	ID=TGME49_220250;길이=267 1	911
TGME49_chr X	425358 1	4254822	-	ID=TGME49_234260;길이=124 1	912
TGME49_chr XII	141229	143333	+	ID=TGME49_300230;길이=210 4	913
TGME49_chr X	524875 5	5253245	+	ID=TGME49_236050;길이=449 0	914

[0158]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr II	125597 4	1257956	-	ID=TGME49_222840;길이=198 2	915
TGME49_chr VIII	142126 5	1423169	-	ID=TGME49_231430;길이=190 4	916
TGME49_chr VIIa	789026	794038	-	ID=TGME49_206610;길이=501 2	917
TGME49_chr VI	145469 6	1457473	+	ID=TGME49_240810;길이=277 7	918
TGME49_chr X	443271 9	4434480	+	ID=TGME49_234520;길이=176 1	919
TGME49_chr Ia	999746	1003574	-	ID=TGME49_294610;길이=382 8	920
TGME49_chr VIIa	374254	376921	-	ID=TGME49_280480;길이=266 7	921
TGME49_chr IV	146510	149451	+	ID=TGME49_320670;길이=294 1	922
TGME49_chr IX	295565 0	2958322	-	ID=TGME49_289060;길이=267 2	923
TGME49_chr V	228328 8	2285190	-	ID=TGME49_285700;길이=190 2	924
TGME49_chr VIII	261928 7	2621303	+	ID=TGME49_233390;길이=201 6	925
TGME49_chr XI	224621 8	2248260	-	ID=TGME49_311740;길이=204 2	926
TGME49_chr XII	330442 5	3309462	+	ID=TGME49_247390;길이=503 7	927
TGME49_chr X	682255 9	6826683	-	ID=TGME49_215210;길이=412 4	928
TGME49_chr XI	104859 0	1053342	+	ID=TGME49_310100;길이=475 2	929
TGME49_chr X	142915 3	1433385	+	ID=TGME49_226690;길이=423 2	930
TGME49_chr IX	260277 1	2606731	+	ID=TGME49_288540;길이=396 0	931
TGME49_chr X	76000	78305	-	ID=TGME49_200590;길이=230 5	932
TGME49_chr VI	313147 4	3132802	+	ID=TGME49_244240;길이=132 8	933

[0159]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	274696 2	2750934	-	ID=TGME49_243600;길이=397 2	934
TGME49_chr X	486970 3	4872065	+	ID=TGME49_235440;길이=236 2	935
TGME49_chr Ia	245706	248432	-	ID=TGME49_293310;길이=272 6	936
TGME49_chr VI	18291	19862	-	ID=TGME49_238030;길이=157 1	937
TGME49_chr Ia	102588 3	1028407	+	ID=TGME49_294640;길이=252 4	938
TGME49_chr XII	632904 5	6330752	-	ID=TGME49_278060;길이=170 7	939
TGME49_chr XI	634357 5	6346044	+	ID=TGME49_216200;길이=246 9	940
TGME49_chr X	552801 6	5528444	-	ID=TGME49_236830;길이=428	941
TGME49_chr VIIa	400612 2	4008450	+	ID=TGME49_201140;길이=232 8	942
TGME49_chr XI	744895	746156	+	ID=TGME49_309590;길이=126 1	943
TGME49_chr IV	777767	779444	+	ID=TGME49_319700;길이=167 7	944
TGME49_chr Ia	170499 3	1707763	-	ID=TGME49_295600;길이=277 0	945
TGME49_chr IV	251460	253297	-	ID=TGME49_320580;길이=183 7	946
TGME49_chr VIIb	454334 5	4545276	+	ID=TGME49_256050;길이=193 1	947
TGME49_chr VI	288006 3	2882722	+	ID=TGME49_243920;길이=265 9	948
TGME49_chr V	229700 9	2301830	-	ID=TGME49_285670;길이=482 1	949
TGME49_chr IV	742966	745952	+	ID=TGME49_319850;길이=298 6	950
TGME49_chr II	551419	555255	-	ID=TGME49_221670;길이=383 6	951
TGME49_chr IX	903708	908281	+	ID=TGME49_266900;길이=457 3	952

[0160]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	657189 0	6574505	+	ID=TGME49_277685;길이=261 5	953
TGME49_chr IV	251100 2	2514234	+	ID=TGME49_301470;길이=323 2	954
TGME49_chr X	288188 2	2886012	-	ID=TGME49_224680;길이=413 0	955
TGME49_chr XII	118994 3	1192566	-	ID=TGME49_218955;길이=262 3	956
TGME49_chr XI	163671 5	1638328	+	ID=TGME49_310870;길이=161 3	957
TGME49_chr V	174083 8	1743872	-	ID=TGME49_286650;길이=303 4	958
TGME49_chr IV	203802 8	2039463	-	ID=TGME49_210815;길이=143 5	959
TGME49_chr X	624617 0	6248972	+	ID=TGME49_214320;길이=280 2	960
TGME49_chr VIIb	460354	462837	-	ID=TGME49_263590;길이=248 3	961
TGME49_chr XI	423919 8	4241167	+	ID=TGME49_314715;길이=196 9	962
TGME49_chr X	174788 6	1749867	-	ID=TGME49_226280;길이=198 1	963
TGME49_chr VIII	487295 3	4877607	+	ID=TGME49_270920;길이=465 4	964
TGME49_chr II	420859	424002	-	ID=TGME49_221530;길이=314 3	965
TGME49_chr XI	490263 9	4904888	+	ID=TGME49_315690;길이=224 9	966
TGME49_chr IX	240452 6	2406796	-	ID=TGME49_288230;길이=227 0	967
TGME49_chr XI	500909 3	5010699	-	ID=TGME49_315810;길이=160 6	968
TGME49_chr VIII	680985 8	6812222	-	ID=TGME49_200330;길이=236 4	969
TGME49_chr VI	197391 1	1974670	+	ID=TGME49_242340;길이=759	970
TGME49_chr XII	316928	321044	-	ID=TGME49_299825;길이=411 6	971

[0161]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr II	683949	688778	+	ID=TGME49_221910;길이=482 9	972
TGME49_chr Ib	607119	609291	-	ID=TGME49_208310;길이=217 2	973
TGME49_chr XI	171749 0	1721072	+	ID=TGME49_311000;길이=358 2	974
TGME49_chr XI	288726 2	2889295	-	ID=TGME49_312650;길이=203 3	975
TGME49_chr VIIa	332983	334493	+	ID=TGME49_280522;길이=151 0	976
TGME49_chr X	153192 3	1536680	+	ID=TGME49_226560;길이=475 7	977
TGME49_chr VIII	262605 7	2627682	+	ID=TGME49_233405;길이=162 5	978
TGME49_chr VIIb	117015 2	1173763	-	ID=TGME49_262550;길이=361 1	979
TGME49_chr IV	194144 1	1943945	+	ID=TGME49_211060;길이=250 4	980
TGME49_chr VIII	444752 2	4450597	+	ID=TGME49_271600;길이=307 5	981
TGME49_chr VIII	196522 5	1967627	+	ID=TGME49_232240;길이=240 2	982
TGME49_chr IX	359664 8	3598874	+	ID=TGME49_290040;길이=222 6	983
TGME49_chr VIIb	396833 6	3973027	-	ID=TGME49_257572;길이=469 1	984
TGME49_chr V	187252	190551	-	ID=TGME49_220170;길이=329 9	985
TGME49_chr VIII	127411 4	1276871	+	ID=TGME49_231160;길이=275 7	986
TGME49_chr VIIb	463323 9	4633990	-	ID=TGME49_255910;길이=751	987
TGME49_chr XII	656774 0	6569055	+	ID=TGME49_277690;길이=131 5	988
TGME49_chr II	605002	607207	-	ID=TGME49_221710;길이=220 5	989
TGME49_chr Ib	139120 8	1394231	+	ID=TGME49_209680;길이=302 3	990

[0162]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	468532	470265	+	ID=TGME49_239120; 길이=173 3	991
TGME49_chr X	292163 0	2925549	-	ID=TGME49_224630; 길이=391 9	992
TGME49_chr VI	279900 7	2803879	-	ID=TGME49_243690; 길이=487 2	993
TGME49_chr VI	290492 7	2906963	-	ID=TGME49_243940; 길이=203 6	994
TGME49_chr II	466401	468740	-	ID=TGME49_221585; 길이=233 9	995
TGME49_chr VIII	661628 3	6618113	-	ID=TGME49_268240; 길이=183 0	996
TGME49_chr X	556597 0	5568898	-	ID=TGME49_236890; 길이=292 8	997
TGME49_chr XII	651262	652841	+	ID=TGME49_219770; 길이=157 9	998
TGME49_chr IX	243209 6	2434121	+	ID=TGME49_288280; 길이=202 5	999
TGME49_chr XII	163621 7	1640467	-	ID=TGME49_218270; 길이=425 0	1000
TGME49_chr VIIa	187250 8	1874024	+	ID=TGME49_204330; 길이=151 6	1001
TGME49_chr XII	373730 0	3739417	+	ID=TGME49_248200; 길이=211 7	1002
TGME49_chr XI	385851 0	3860201	+	ID=TGME49_313990; 길이=169 1	1003
TGME49_chr VI	253560 9	2537835	-	ID=TGME49_243302; 길이=222 6	1004
TGME49_chr VIII	218635	220518	+	ID=TGME49_229380; 길이=188 3	1005
TGME49_chr XII	589922 6	5904153	+	ID=TGME49_278750; 길이=492 7	1006
TGME49_chr VIIb	791575	793258	-	ID=TGME49_263120; 길이=168 3	1007
TGME49_chr XII	965702	969227	-	ID=TGME49_219370; 길이=352 5	1008
TGME49_chr VIIb	224792 1	2252571	-	ID=TGME49_260470; 길이=465 0	1009

[0163]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr II	925169	930001	-	ID=TGME49_222160;길이=483 2	1010
TGME49_chr VIII	432812 2	4331040	-	ID=TGME49_271870;길이=291 8	1011
TGME49_chr VIIb	456580 3	4568166	-	ID=TGME49_256020;길이=236 3	1012
TGME49_chr IX	401868	404259	-	ID=TGME49_267730;길이=239 1	1013
TGME49_chr IV	883987	886188	+	ID=TGME49_319580;길이=220 1	1014
TGME49_chr XII	327121 2	3273508	-	ID=TGME49_247330;길이=229 6	1015
TGME49_chr IV	117918 0	1180121	-	ID=TGME49_318632;길이=941	1016
TGME49_chr IX	590474 8	5906644	-	ID=TGME49_306270;길이=189 6	1017
TGME49_chr VIII	288287 8	2885243	+	ID=TGME49_233905;길이=236 5	1018
TGME49_chr Ib	319440	322320	+	ID=TGME49_207830;길이=288 0	1019
TGME49_chr XI	527606 4	5279392	+	ID=TGME49_316410;길이=332 8	1020
TGME49_chr VIIb	432783 5	4329892	-	ID=TGME49_256965;길이=205 7	1021
TGME49_chr VIIa	138366 4	1387009	-	ID=TGME49_205480;길이=334 5	1022
TGME49_chr X	118327 7	1184615	-	ID=TGME49_226970;길이=133 8	1023
TGME49_chr V	301169 6	3013612	-	ID=TGME49_283730;길이=191 6	1024
TGME49_chr X	153192 3	1533938	+	ID=TGME49_226565;길이=201 5	1025
TGME49_chr X	224839 0	2249697	+	ID=TGME49_225420;길이=130 7	1026
TGME49_chr VIII	792105	796468	+	ID=TGME49_230450;길이=436 3	1027
TGME49_chr IX	347147 3	3473649	+	ID=TGME49_289830;길이=217 6	1028

[0164]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	608623 2	6089255	-	ID=TGME49_216560;길이=302 3	1029
TGME49_chr VIII	598005 9	5982851	-	ID=TGME49_269232;길이=279 2	1030
TGME49_chr VIII	202367 0	2028207	+	ID=TGME49_232350;길이=453 7	1031
TGME49_chr XII	364110 4	3645165	+	ID=TGME49_247970;길이=406 1	1032
TGME49_chr VIIb	883251	885953	-	ID=TGME49_262990;길이=270 2	1033
TGME49_chr IV	262664 4	2631162	-	ID=TGME49_237880;길이=451 8	1034
TGME49_chr Ia	111397	113812	+	ID=TGME49_293060;길이=241 5	1035
TGME49_chr VI	428224	431908	-	ID=TGME49_239030;길이=368 4	1036
TGME49_chr VIII	254040 9	2542122	-	ID=TGME49_233245;길이=171 3	1037
TGME49_chr XI	572898 7	5730625	+	ID=TGME49_217000;길이=163 8	1038
TGME49_chr XII	439411 1	4398427	-	ID=TGME49_249240;길이=431 6	1039
TGME49_chr VIIa	397620 4	3977892	-	ID=TGME49_201210;길이=168 8	1040
TGME49_chr Ia	135999	139033	-	ID=TGME49_293170;길이=303 4	1041
TGME49_chr VIIb	244632 2	2450162	-	ID=TGME49_260220;길이=384 0	1042
TGME49_chr XI	400506 5	4007884	+	ID=TGME49_314330;길이=281 9	1043
TGME49_chr IV	172185 8	1725651	+	ID=TGME49_211430;길이=379 3	1044
TGME49_chr VI	144025 6	1442654	+	ID=TGME49_240780;길이=239 8	1045
TGME49_chr VIIb	230943 7	2311494	+	ID=TGME49_260400;길이=205 7	1046
TGME49_chr VIII	105731 4	1061637	+	ID=TGME49_230850;길이=432 3	1047

[0165]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	310459 5	3106681	+	ID=TGME49_258880;길이=208 6	1048
TGME49_chr IX	355389 8	3558050	+	ID=TGME49_289970;길이=415 2	1049
TGME49_chr VIIb	747456	750990	-	ID=TGME49_263180;길이=353 4	1050
TGME49_chr Ib	508499	510809	+	ID=TGME49_208010;길이=231 0	1051
TGME49_chr VIII	340393 9	3407719	-	ID=TGME49_273560;길이=378 0	1052
TGME49_chr VIIb	232825 8	2331030	-	ID=TGME49_260380;길이=277 2	1053
TGME49_chr IX	544756 9	5449517	+	ID=TGME49_305520;길이=194 8	1054
TGME49_chr XII	454089 8	4544602	-	ID=TGME49_249440;길이=370 4	1055
TGME49_chr IX	118066 2	1185700	-	ID=TGME49_266380;길이=503 8	1056
TGME49_chr II	741431	743464	-	ID=TGME49_221990;길이=203 3	1057
TGME49_chr IX	330242 3	3304195	-	ID=TGME49_289550;길이=177 2	1058
TGME49_chr XII	516334 4	5167027	-	ID=TGME49_250740;길이=368 3	1059
TGME49_chr Ib	136487 7	1366149	-	ID=TGME49_209620;길이=127 2	1060
TGME49_chr VIIb	858403	860259	+	ID=TGME49_263020;길이=185 6	1061
TGME49_chr VI	208086 1	2082634	-	ID=TGME49_242580;길이=177 3	1062
TGME49_chr XI	512650 9	5128203	+	ID=TGME49_316100;길이=169 4	1063
TGME49_chr VIIb	214207 2	2145018	+	ID=TGME49_260580;길이=294 6	1064
TGME49_chr XII	268528 3	2687256	+	ID=TGME49_246150;길이=197 3	1065
TGME49_chr VI	110307	112590	+	ID=TGME49_238190;길이=228 3	1066

[0166]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	283747 8	2839433	-	ID=TGME49_233830;길이=195 5	1067
TGME49_chr X	867923	871948	+	ID=TGME49_227615;길이=402 5	1068
TGME49_chr IX	507122 3	5073998	-	ID=TGME49_304880;길이=277 5	1069
TGME49_chr VIII	209089 0	2095794	-	ID=TGME49_232430;길이=490 4	1070
TGME49_chr VIIb	278163 1	2784134	-	ID=TGME49_259550;길이=250 3	1071
TGME49_chr X	193904	195964	+	ID=TGME49_228690;길이=206 0	1072
TGME49_chr Ia	105971 2	1062031	-	ID=TGME49_294670;길이=231 9	1073
TGME49_chr VIIa	389034 4	3893030	+	ID=TGME49_201520;길이=268 6	1074
TGME49_chr IX	521467 6	5217074	+	ID=TGME49_305100;길이=239 8	1075
TGME49_chr VIIa	899877	902361	+	ID=TGME49_206520;길이=248 4	1076
TGME49_chr IX	353934 7	3541778	-	ID=TGME49_289940;길이=243 1	1077
TGME49_chr VIIb	452881 1	4530770	-	ID=TGME49_256080;길이=195 9	1078
TGME49_chr VIII	110877	112644	-	ID=TGME49_229250;길이=176 7	1079
TGME49_chr XI	229676 5	2300817	+	ID=TGME49_311810;길이=405 2	1080
TGME49_chr XI	274295 8	2745345	-	ID=TGME49_312500;길이=238 7	1081
TGME49_chr V	417057	419288	+	ID=TGME49_220500;길이=223 1	1082
TGME49_chr VIIb	205752 5	2060480	+	ID=TGME49_260680;길이=295 5	1083
TGME49_chr Ib	746521	750200	+	ID=TGME49_208530;길이=367 9	1084
TGME49_chr X	547496 8	5478116	-	ID=TGME49_236650;길이=314 8	1085

[0167]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	507493 7	5076733	-	ID=TGME49_235710;길이=179 6	1086
TGME49_chr Ib	128207 7	1283563	+	ID=TGME49_209510;길이=148 6	1087
TGME49_chr Ia	617372	619206	+	ID=TGME49_293870;길이=183 4	1088
TGME49_chr X	524875 5	5250532	+	ID=TGME49_236040;길이=177 7	1089
TGME49_chr XII	528804 6	5290319	-	ID=TGME49_250860;길이=227 3	1090
TGME49_chr IX	272022 5	2724939	+	ID=TGME49_288750;길이=471 4	1091
TGME49_chr IX	544999	547818	+	ID=TGME49_267585;길이=281 9	1092
TGME49_chr VIIa	106802 3	1069996	+	ID=TGME49_206310;길이=197 3	1093
TGME49_chr VI	830758	833127	+	ID=TGME49_239690;길이=236 9	1094
TGME49_chr IX	226505 5	2268965	-	ID=TGME49_287960;길이=391 0	1095
TGME49_chr XI	608718 3	6089255	-	ID=TGME49_216550;길이=207 2	1096
TGME49_chr IV	257825 7	2581065	+	ID=TGME49_237840;길이=280 8	1097
TGME49_chr VIII	991782	995395	-	ID=TGME49_230705;길이=361 3	1098
TGME49_chr II	188418 6	1886034	+	ID=TGME49_297643;길이=184 8	1099
TGME49_chr XI	231205 0	2313267	+	ID=TGME49_311830;길이=121 7	1100
TGME49_chr II	125450 6	1256879	+	ID=TGME49_222850;길이=237 3	1101
TGME49_chr II	766484	768700	+	ID=TGME49_222030;길이=221 6	1102
TGME49_chr IX	196108 8	1961769	+	ID=TGME49_264850;길이=681	1103
TGME49_chr VIII	534426 9	5348104	-	ID=TGME49_270200;길이=383 5	1104

[0168]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	138077 5	1382606	-	ID=TGME49_240660;길이=183 1	1105
TGME49_chr VIIb	180471 6	1807943	+	ID=TGME49_261240;길이=322 7	1106
TGME49_chr X	338228 6	3386675	+	ID=TGME49_224020;길이=438 9	1107
TGME49_chr XI	190834 2	1912400	-	ID=TGME49_311240;길이=405 8	1108
TGME49_chr VIIa	443861 0	4442652	+	ID=TGME49_282200;길이=404 2	1109
TGME49_chr IX	584471 2	5848045	+	ID=TGME49_306230;길이=333 3	1110
TGME49_chr XI	150281 5	1504291	-	ID=TGME49_310650;길이=147 6	1111
TGME49_chr XI	197035 5	1973898	+	ID=TGME49_311320;길이=354 3	1112
TGME49_chr X	230569 5	2308125	+	ID=TGME49_225330;길이=243 0	1113
TGME49_chr VIIb	173656 2	1738490	-	ID=TGME49_261460;길이=192 8	1114
TGME49_chr XI	228884 0	2290926	+	ID=TGME49_311790;길이=208 6	1115
TGME49_chr X	500070 3	5002026	+	ID=TGME49_235635;길이=132 3	1116
TGME49_chr XI	305180 9	3053089	+	ID=TGME49_313025;길이=128 0	1117
TGME49_chr V	122681 9	1229241	-	ID=TGME49_213670;길이=242 2	1118
TGME49_chr VI	184693 0	1848152	+	ID=TGME49_242040;길이=122 2	1119
TGME49_chr XI	512710 1	5129194	-	ID=TGME49_316090;길이=209 3	1120
TGME49_chr VIIa	489530	492510	+	ID=TGME49_280370;길이=298 0	1121
TGME49_chr VIII	273311 8	2736128	-	ID=TGME49_233702;길이=301 0	1122
TGME49_chr XI	639877 1	6401970	-	ID=TGME49_216120;길이=319 9	1123

[0169]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	530082	533588	-	ID=TGME49_309160;길이=350 6	1124
TGME49_chr VIII	428448	432358	-	ID=TGME49_229750;길이=391 0	1125
TGME49_chr II	207783 2	2082637	+	ID=TGME49_297850;길이=480 5	1126
TGME49_chr IV	208847 0	2090595	-	ID=TGME49_210770;길이=212 5	1127
TGME49_chr IV	111280 1	1114995	-	ID=TGME49_318742;길이=219 4	1128
TGME49_chr VIII	269451 2	2696420	+	ID=TGME49_233530;길이=190 8	1129
TGME49_chr Ib	139218 8	1394786	-	ID=TGME49_209650;길이=259 8	1130
TGME49_chr V	469162	470010	+	ID=TGME49_220580;길이=848	1131
TGME49_chr IX	203409 8	2036991	+	ID=TGME49_264770;길이=289 3	1132
TGME49_chr VIII	285596 6	2857966	-	ID=TGME49_233850;길이=200 0	1133
TGME49_chr XI	159535 0	1597733	+	ID=TGME49_310798;길이=238 3	1134
TGME49_chr IX	554150 0	5543417	+	ID=TGME49_305750;길이=191 7	1135
TGME49_chr IX	414252 3	4144608	+	ID=TGME49_291130;길이=208 5	1136
TGME49_chr VIIb	790933	792672	+	ID=TGME49_263110;길이=173 9	1137
TGME49_chr VIIa	221047 7	2211546	-	ID=TGME49_203815;길이=106 9	1138
TGME49_chr VIII	406376 4	4065564	+	ID=TGME49_272340;길이=180 0	1139
TGME49_chr IX	862193	864770	+	ID=TGME49_266970;길이=257 7	1140
TGME49_chr X	600535 0	6009045	-	ID=TGME49_237585;길이=369 5	1141
TGME49_chr IV	812682	816552	-	ID=TGME49_319650;길이=387 0	1142

[0170]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	135102 5	1353144	+	ID=TGME49_318410;길이=211 9	1143
TGME49_chr VIIb	628035	632181	+	ID=TGME49_263323;길이=414 6	1144
TGME49_chr II	464340	467546	+	ID=TGME49_221590;길이=320 6	1145
TGME49_chr VIIa	235318 9	2355787	-	ID=TGME49_203682;길이=259 8	1146
TGME49_chr Ia	136533 1	1367979	+	ID=TGME49_295060;길이=264 8	1147
TGME49_chr XI	308637 9	3090390	+	ID=TGME49_313090;길이=401 1	1148
TGME49_chr II	639786	644118	+	ID=TGME49_221870;길이=433 2	1149
TGME49_chr IV	128354 1	1287463	-	ID=TGME49_318490;길이=392 2	1150
TGME49_chr X	254494 8	2548532	-	ID=TGME49_225070;길이=358 4	1151
TGME49_chr VIIb	541912	545460	-	ID=TGME49_263470;길이=354 8	1152
TGME49_chr IX	359156 0	3593074	-	ID=TGME49_290020;길이=151 4	1153
TGME49_chr X	392816 3	3932517	-	ID=TGME49_212310;길이=435 4	1154
TGME49_chr VIIb	470129 2	4702972	-	ID=TGME49_255720;길이=168 0	1155
TGME49_chr VIII	550659 3	5510411	+	ID=TGME49_269940;길이=381 8	1156
TGME49_chr IV	592700	595047	+	ID=TGME49_320005;길이=234 7	1157
TGME49_chr VIIb	451962 9	4521475	-	ID=TGME49_256100;길이=184 6	1158
TGME49_chr Ia	184853 3	1850781	-	ID=TGME49_295320;길이=224 8	1159
TGME49_chr X	376111 2	3762929	-	ID=TGME49_223530;길이=181 7	1160
TGME49_chr VIII	383925 0	3840966	-	ID=TGME49_272620;길이=171 6	1161

[0171]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	553332 4	5536592	+	ID=TGME49_236850;길이=326 8	1162
TGME49_chr X	523329 1	5235370	-	ID=TGME49_235990;길이=207 9	1163
TGME49_chr Ib	181656 4	1818369	+	ID=TGME49_321430;길이=180 5	1164
TGME49_chr XI	332700 9	3329669	+	ID=TGME49_313380;길이=266 0	1165
TGME49_chr IX	336348 8	3365112	+	ID=TGME49_289650;길이=162 4	1166
TGME49_chr V	287641	288269	-	ID=TGME49_220310;길이=628	1167
TGME49_chr II	207783 2	2079808	+	ID=TGME49_297845;길이=197 6	1168
TGME49_chr VIIb	365773 5	3659476	+	ID=TGME49_258000;길이=174 1	1169
TGME49_chr IX	203901 3	2043206	+	ID=TGME49_264760;길이=419 3	1170
TGME49_chr XII	698884 0	6990981	+	ID=TGME49_276810;길이=214 1	1171
TGME49_chr IX	361236 5	3615024	-	ID=TGME49_290160;길이=265 9	1172
TGME49_chr Ia	125954 5	1263126	-	ID=TGME49_294898;길이=358 1	1173
TGME49_chr XI	616571 5	6166848	+	ID=TGME49_216415;길이=113 3	1174
TGME49_chr IX	351148 9	3512915	-	ID=TGME49_289890;길이=142 6	1175
TGME49_chr IX	174828 3	1752414	+	ID=TGME49_265130;길이=413 1	1176
TGME49_chr IV	101527 8	1019035	+	ID=TGME49_319340;길이=375 7	1177
TGME49_chr VI	905412	908079	-	ID=TGME49_239770;길이=266 7	1178
TGME49_chr XI	570018	574932	-	ID=TGME49_309220;길이=491 4	1179
TGME49_chr VIII	222898 3	2231436	+	ID=TGME49_232690;길이=245 3	1180

[0172]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	375637 5	3758818	+	ID=TGME49_313870;길이=244 3	1181
TGME49_chr XI	168333 0	1684845	-	ID=TGME49_310940;길이=151 5	1182
TGME49_chr Ib	802516	804677	-	ID=TGME49_208580;길이=216 1	1183
TGME49_chr V	307335 0	3075701	-	ID=TGME49_283580;길이=235 1	1184
TGME49_chr IX	243319 9	2434876	-	ID=TGME49_288270;길이=167 7	1185
TGME49_chr VIII	524749 9	5249101	+	ID=TGME49_270360;길이=160 2	1186
TGME49_chr Ia	538347	541224	+	ID=TGME49_293740;길이=287 7	1187
TGME49_chr XI	103440 2	1037980	-	ID=TGME49_310055;길이=357 8	1188
TGME49_chr VIII	427376 5	4277392	+	ID=TGME49_271930;길이=362 7	1189
TGME49_chr X	394221 0	3943072	+	ID=TGME49_212280;길이=862	1190
TGME49_chr XI	642721 3	6429335	-	ID=TGME49_216060;길이=212 2	1191
TGME49_chr VIII	577698 4	5780816	-	ID=TGME49_269470;길이=383 2	1192
TGME49_chr VI	133406 6	1335457	+	ID=TGME49_240600;길이=139 1	1193
TGME49_chr VIIa	423495 9	4237402	+	ID=TGME49_281640;길이=244 3	1194
TGME49_chr V	124054 1	1242474	+	ID=TGME49_213700;길이=193 3	1195
TGME49_chr X	107905 4	1081448	-	ID=TGME49_227140;길이=239 4	1196
TGME49_chr XII	236234 1	2363912	-	ID=TGME49_245540;길이=157 1	1197
TGME49_chr VIIb	473595 0	4738492	-	ID=TGME49_255690;길이=254 2	1198
TGME49_chr VIIb	215535	217628	-	ID=TGME49_264060;길이=209 3	1199

[0173]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	376768 5	3770308	+	ID=TGME49_313880;길이=262 3	1200
TGME49_chr VIIb	382525	387001	-	ID=TGME49_263710;길이=447 6	1201
TGME49_chr VIII	376414 6	3769011	-	ID=TGME49_272730;길이=486 5	1202
TGME49_chr VIII	251824 2	2523170	+	ID=TGME49_233230;길이=492 8	1203
TGME49_chr X	251298 1	2514745	+	ID=TGME49_225105;길이=176 4	1204
TGME49_chr X	174733 7	1749496	+	ID=TGME49_226270;길이=215 9	1205
TGME49_chr XI	255645 0	2561384	+	ID=TGME49_312280;길이=493 4	1206
TGME49_chr XI	150851 1	1511130	+	ID=TGME49_310670;길이=261 9	1207
TGME49_chr X	135707 3	1358633	-	ID=TGME49_226800;길이=156 0	1208
TGME49_chr XII	185601 8	1859951	-	ID=TGME49_217460;길이=393 3	1209
TGME49_chr VI	103211 3	1035230	+	ID=TGME49_240060;길이=311 7	1210
TGME49_chr VIIb	475024 0	4753174	-	ID=TGME49_255660;길이=293 4	1211
TGME49_chr IV	248832 2	2491013	+	ID=TGME49_301450;길이=269 1	1212
TGME49_chr VIIa	239943 7	2401178	+	ID=TGME49_203610;길이=174 1	1213
TGME49_chr IV	717427	720591	-	ID=TGME49_319870;길이=316 4	1214
TGME49_chr IX	633939	636510	+	ID=TGME49_267450;길이=257 1	1215
TGME49_chr II	106427 7	1067130	-	ID=TGME49_222350;길이=285 3	1216
TGME49_chr X	658751 2	6589629	-	ID=TGME49_214910;길이=211 7	1217
TGME49_chr VIIb	110027 3	1103123	+	ID=TGME49_262650;길이=285 0	1218

[0174]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	401969 3	4021700	-	ID=TGME49_212150;길이=200 7	1219
TGME49_chr IV	910057	912578	+	ID=TGME49_319560;길이=252 1	1220
TGME49_chr XI	595462 3	5956672	+	ID=TGME49_216680;길이=204 9	1221
TGME49_chr VIIb	936733	939153	+	ID=TGME49_262900;길이=242 0	1222
TGME49_chr IX	262448 1	2626169	+	ID=TGME49_288580;길이=168 8	1223
TGME49_chr X	611798 5	6120211	+	ID=TGME49_214220;길이=222 6	1224
TGME49_chr IX	467057 5	4671677	-	ID=TGME49_292310;길이=110 2	1225
TGME49_chr VIIa	158670 1	1588039	+	ID=TGME49_205140;길이=133 8	1226
TGME49_chr V	343813	347336	-	ID=TGME49_220380;길이=352 3	1227
TGME49_chr VIIa	282454 3	2828105	-	ID=TGME49_203060;길이=356 2	1228
TGME49_chr VI	284207 2	2843767	-	ID=TGME49_243750;길이=169 5	1229
TGME49_chr XII	590166 4	5905896	-	ID=TGME49_278757;길이=423 2	1230
TGME49_chr IX	864169	866128	-	ID=TGME49_266980;길이=195 9	1231
TGME49_chr V	405382	408887	-	ID=TGME49_220470;길이=350 5	1232
TGME49_chr VIIb	251207 6	2514420	-	ID=TGME49_260140;길이=234 4	1233
TGME49_chr VI	209833 6	2100722	-	ID=TGME49_242600;길이=238 6	1234
TGME49_chr X	150888 4	1511053	-	ID=TGME49_226610;길이=216 9	1235
TGME49_chr VIIa	204366 6	2046086	+	ID=TGME49_204020;길이=242 0	1236
TGME49_chr VIIb	103052 8	1035441	+	ID=TGME49_262760;길이=491 3	1237

[0175]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ia	906891	908355	-	ID=TGME49_294420;길이=146 4	1238
TGME49_chr IX	394909 6	3950443	-	ID=TGME49_290925;길이=134 7	1239
TGME49_chr V	202116 0	2025024	+	ID=TGME49_286060;길이=386 4	1240
TGME49_chr XI	333428 6	3335654	-	ID=TGME49_313385;길이=136 8	1241
TGME49_chr IX	459233 7	4595459	-	ID=TGME49_292170;길이=312 2	1242
TGME49_chr XII	883327	885042	-	ID=TGME49_219530;길이=171 5	1243
TGME49_chr VIIa	646040	650529	+	ID=TGME49_304720;길이=448 9	1244
TGME49_chr XII	258296 8	2583778	+	ID=TGME49_245995;길이=810	1245
TGME49_chr VIIa	149253 4	1497097	+	ID=TGME49_205280;길이=456 3	1246
TGME49_chr VIII	652929 2	6532178	-	ID=TGME49_268340;길이=288 6	1247
TGME49_chr X	177547 3	1776642	-	ID=TGME49_226240;길이=116 9	1248
TGME49_chr X	328288 6	3287547	+	ID=TGME49_224160;길이=466 1	1249
TGME49_chr XI	639792 0	6400037	+	ID=TGME49_216090;길이=211 7	1250
TGME49_chr VI	270652 9	2711143	+	ID=TGME49_243545;길이=461 4	1251
TGME49_chr XI	416696	419057	-	ID=TGME49_308980;길이=236 1	1252
TGME49_chr Ib	134225 7	1346867	+	ID=TGME49_209580;길이=461 0	1253
TGME49_chr X	550975 5	5511547	-	ID=TGME49_236790;길이=179 2	1254
TGME49_chr XI	463158	465197	-	ID=TGME49_309050;길이=203 9	1255
TGME49_chr VI	256977	258317	-	ID=TGME49_238505;길이=134 0	1256

[0176]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	691681 3	6920734	-	ID=TGME49_215343;길이=392 1	1257
TGME49_chr XII	478934 7	4790800	+	ID=TGME49_249770;길이=145 3	1258
TGME49_chr XII	222150 9	2225506	-	ID=TGME49_217910;길이=399 7	1259
TGME49_chr XII	635109	638817	-	ID=TGME49_219810;길이=370 8	1260
TGME49_chr X	996966	1001699	-	ID=TGME49_227360;길이=473 3	1261
TGME49_chr XII	475935 7	4761502	-	ID=TGME49_249720;길이=214 5	1262
TGME49_chr VIII	880481	882435	-	ID=TGME49_230580;길이=195 4	1263
TGME49_chr VIIa	239382 0	2395507	-	ID=TGME49_203630;길이=168 7	1264
TGME49_chr X	396967 3	3972540	-	ID=TGME49_212230;길이=286 7	1265
TGME49_chr VIIa	373071 8	3732764	+	ID=TGME49_201870;길이=204 6	1266
TGME49_chr VIII	100116 9	1003387	+	ID=TGME49_230820;길이=221 8	1267
TGME49_chr IX	460067 4	4601980	-	ID=TGME49_292190;길이=130 6	1268
TGME49_chr IV	131879 3	1321000	-	ID=TGME49_318460;길이=220 7	1269
TGME49_chr XII	500864 5	5010570	-	ID=TGME49_250050;길이=192 5	1270
TGME49_chr VIII	282110 8	2824516	+	ID=TGME49_233820;길이=340 8	1271
TGME49_chr VIIa	945242	947003	+	ID=TGME49_206470;길이=176 1	1272
TGME49_chr VIIa	618512	620275	-	ID=TGME49_304670;길이=176 3	1273
TGME49_chr XI	543108 3	5433154	-	ID=TGME49_316610;길이=207 1	1274
TGME49_chr XI	389491 5	3897284	+	ID=TGME49_314042;길이=236 9	1275

[0177]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	613785	617334	-	ID=TGME49_239885;길이=354 9	1276
TGME49_chr XII	608064 5	6082084	+	ID=TGME49_278470;길이=143 9	1277
TGME49_chr XII	453005 7	4533822	-	ID=TGME49_249425;길이=376 5	1278
TGME49_chr VIIb	498355 2	4986683	-	ID=TGME49_255240;길이=313 1	1279
TGME49_chr IX	616250 9	6166258	+	ID=TGME49_306540;길이=374 9	1280
TGME49_chr VIII	119179 0	1195369	-	ID=TGME49_231000;길이=357 9	1281
TGME49_chr VIIb	253967 1	2543923	-	ID=TGME49_260000;길이=425 2	1282
TGME49_chr VIIb	849810	852648	-	ID=TGME49_263060;길이=283 8	1283
TGME49_chr VIIb	648112	651155	-	ID=TGME49_263300;길이=304 3	1284
TGME49_chr IX	338476 3	3389725	+	ID=TGME49_289710;길이=496 2	1285
TGME49_chr IV	166770 4	1671687	-	ID=TGME49_211610;길이=398 3	1286
TGME49_chr VI	337067 0	3372867	-	ID=TGME49_244570;길이=219 7	1287
TGME49_chr Ia	138453 1	1387176	-	ID=TGME49_295070;길이=264 5	1288
TGME49_chr II	138073 6	1382666	+	ID=TGME49_223045;길이=193 0	1289
TGME49_chr VIIa	405129 3	4053186	-	ID=TGME49_281370;길이=189 3	1290
TGME49_chr X	395598 5	3958323	+	ID=TGME49_212250;길이=233 8	1291
TGME49_chr VI	320087	321893	-	ID=TGME49_238930;길이=180 6	1292
TGME49_chr V	182141 2	1825437	+	ID=TGME49_286450;길이=402 5	1293
TGME49_chr X	455866 8	4561661	-	ID=TGME49_234950;길이=299 3	1294

[0178]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	151283 3	1516330	+	ID=TGME49_265510;길이=349 7	1295
TGME49_chr VIII	679404 5	6796697	+	ID=TGME49_200320;길이=265 2	1296
TGME49_chr X	697826 4	6981039	+	ID=TGME49_215490;길이=277 5	1297
TGME49_chr X	217421 1	2176205	-	ID=TGME49_225540;길이=199 4	1298
TGME49_chr VIII	129822 4	1302758	+	ID=TGME49_231180;길이=453 4	1299
TGME49_chr II	214288 2	2147668	-	ID=TGME49_297960;길이=478 6	1300
TGME49_chr XII	343369 0	3435922	+	ID=TGME49_247600;길이=223 2	1301
TGME49_chr VIIa	231750 1	2320428	-	ID=TGME49_203700;길이=292 7	1302
TGME49_chr XII	667460 7	6677822	-	ID=TGME49_277490;길이=321 5	1303
TGME49_chr XI	423372 1	4237966	-	ID=TGME49_314700;길이=424 5	1304
TGME49_chr IV	425592	427430	-	ID=TGME49_320230;길이=183 8	1305
TGME49_chr VIIa	251486 2	2517330	-	ID=TGME49_203420;길이=246 8	1306
TGME49_chr IX	457946 1	4584034	-	ID=TGME49_292140;길이=457 3	1307
TGME49_chr XII	560933 6	5612206	+	ID=TGME49_251850;길이=287 0	1308
TGME49_chr VIIb	234889 2	2349464	+	ID=TGME49_260330;길이=572	1309
TGME49_chr VI	182904 1	1831040	-	ID=TGME49_242010;길이=199 9	1310
TGME49_chr VIII	229890 8	2301088	+	ID=TGME49_232970;길이=218 0	1311
TGME49_chr VIIb	505158 8	5052399	+	ID=TGME49_255175;길이=811	1312
TGME49_chr X	183501 7	1837256	-	ID=TGME49_226068;길이=223 9	1313

[0179]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	3842477	3844120	-	ID=TGME49_313960; 길이=1643	1314
TGME49_chr VIIb	821627	824086	-	ID=TGME49_263085; 길이=2459	1315
TGME49_chr IV	250795	252483	+	ID=TGME49_320570; 길이=1688	1316
TGME49_chr X	2164468	2166075	-	ID=TGME49_225555; 길이=1607	1317
TGME49_chr X	1105074	1106948	-	ID=TGME49_227070; 길이=1874	1318
TGME49_chr VIIb	1404269	1407193	+	ID=TGME49_262050; 길이=2924	1319
TGME49_chr IX	599004	602300	+	ID=TGME49_267520; 길이=3296	1320
TGME49_chr VIIa	3270410	3274311	-	ID=TGME49_202510; 길이=3901	1321
TGME49_chr VIII	3516693	3521323	+	ID=TGME49_273410; 길이=4630	1322
TGME49_chr V	2626675	2628503	+	ID=TGME49_284670; 길이=1828	1323
TGME49_chr X	7344849	7347942	-	ID=TGME49_207020; 길이=3093	1324
TGME49_chr VIIa	1741358	1745785	+	ID=TGME49_204500; 길이=4427	1325
TGME49_chr XI	4646243	4648666	-	ID=TGME49_315310; 길이=2423	1326
TGME49_chr VIIb	4281282	4283353	+	ID=TGME49_257010; 길이=2071	1327
TGME49_chr Ib	1755720	1757922	+	ID=TGME49_321520; 길이=2202	1328
TGME49_chr X	6940384	6941995	+	ID=TGME49_215400; 길이=1611	1329
TGME49_chr VI	1108072	1112890	-	ID=TGME49_240243; 길이=4818	1330
TGME49_chr XII	4472490	4474867	-	ID=TGME49_249340; 길이=2377	1331
TGME49_chr VIIa	970566	973439	-	ID=TGME49_206450; 길이=2873	1332

[0180]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ib	601001	603218	+	ID=TGME49_208300;길이=221 7	1333
TGME49_chr IX	576283 8	5764549	+	ID=TGME49_306035;길이=171 1	1334
TGME49_chr IX	653845	657554	-	ID=TGME49_267440;길이=370 9	1335
TGME49_chr X	296749 4	2971910	+	ID=TGME49_224570;길이=441 6	1336
TGME49_chr VIII	528692 6	5289744	-	ID=TGME49_270310;길이=281 8	1337
TGME49_chr VIII	187793 0	1881330	+	ID=TGME49_232130;길이=340 0	1338
TGME49_chr XI	852387	855185	-	ID=TGME49_309865;길이=279 8	1339
TGME49_chr XI	626174 1	6265340	-	ID=TGME49_216280;길이=359 9	1340
TGME49_chr X	271211 4	2714287	-	ID=TGME49_224890;길이=217 3	1341
TGME49_chr XII	259270 7	2596028	-	ID=TGME49_246010;길이=332 1	1342
TGME49_chr X	167383 7	1675489	+	ID=TGME49_226380;길이=165 2	1343
TGME49_chr XII	478412 5	4785752	-	ID=TGME49_249750;길이=162 7	1344
TGME49_chr VIIb	137964 9	1382568	+	ID=TGME49_262090;길이=291 9	1345
TGME49_chr VIIb	292075	294154	-	ID=TGME49_263850;길이=207 9	1346
TGME49_chr XII	258296 8	2585062	+	ID=TGME49_246000;길이=209 4	1347
TGME49_chr IX	548089 7	5483034	-	ID=TGME49_305580;길이=213 7	1348
TGME49_chr IX	678959	682427	+	ID=TGME49_267370;길이=346 8	1349
TGME49_chr IX	128334 8	1288325	-	ID=TGME49_266130;길이=497 7	1350
TGME49_chr XI	652819 1	6531898	+	ID=TGME49_215910;길이=370 7	1351

[0181]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	453672 5	4538969	+	ID=TGME49_256060;길이=224 4	1352
TGME49_chr IX	800121	801864	+	ID=TGME49_267050;길이=174 3	1353
TGME49_chr XI	285782 0	2862733	+	ID=TGME49_312635;길이=491 3	1354
TGME49_chr VIIa	217378 0	2176161	-	ID=TGME49_203870;길이=238 1	1355
TGME49_chr V	176137 2	1763556	+	ID=TGME49_286610;길이=218 4	1356
TGME49_chr VIII	265791 2	2660930	+	ID=TGME49_233450;길이=301 8	1357
TGME49_chr VIIa	265617 5	2659506	+	ID=TGME49_203230;길이=333 1	1358
TGME49_chr VIIb	392731 6	3929847	-	ID=TGME49_257670;길이=253 1	1359
TGME49_chr IX	242926 6	2431241	-	ID=TGME49_288265;길이=197 5	1360
TGME49_chr VIII	220746 8	2209626	-	ID=TGME49_232650;길이=215 8	1361
TGME49_chr IV	482747	486460	-	ID=TGME49_320130;길이=371 3	1362
TGME49_chr VIIb	179251 3	1796589	-	ID=TGME49_261300;길이=407 6	1363
TGME49_chr X	608341 0	6086247	+	ID=TGME49_214180;길이=283 7	1364
TGME49_chr X	674800 4	6750095	-	ID=TGME49_215080;길이=209 1	1365
TGME49_chr X	491979 3	4924423	-	ID=TGME49_235500;길이=463 0	1366
TGME49_chr VIIa	336574 5	3369481	-	ID=TGME49_202390;길이=373 6	1367
TGME49_chr VIIa	88266	91194	+	ID=TGME49_280780;길이=292 8	1368
TGME49_chr XII	672550 4	6728703	-	ID=TGME49_277080;길이=319 9	1369
TGME49_chr VIII	569977 8	5702719	+	ID=TGME49_269660;길이=294 1	1370

[0182]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	101470	104091	+	ID=TGME49_320740; 길이=262 1	1371
TGME49_chr XI	431779 9	4319648	-	ID=TGME49_314820; 길이=184 9	1372
TGME49_chr Ib	172739 6	1729180	-	ID=TGME49_321570; 길이=178 4	1373
TGME49_chr XI	384173 5	3843470	+	ID=TGME49_313970; 길이=173 5	1374
TGME49_chr VIIb	328643 1	3288841	-	ID=TGME49_258650; 길이=241 0	1375
TGME49_chr IX	270638 9	2708077	-	ID=TGME49_288710; 길이=168 8	1376
TGME49_chr X	912881	916723	-	ID=TGME49_227570; 길이=384 2	1377
TGME49_chr VIIb	176220 9	1764225	+	ID=TGME49_261410; 길이=201 6	1378
TGME49_chr XI	272324 0	2725414	+	ID=TGME49_312490; 길이=217 4	1379
TGME49_chr IX	932063	933944	-	ID=TGME49_266840; 길이=188 1	1380
TGME49_chr Ia	296552	299464	+	ID=TGME49_293390; 길이=291 2	1381
TGME49_chr VI	312560 5	3127814	-	ID=TGME49_244210; 길이=220 9	1382
TGME49_chr VIII	206793 0	2069608	-	ID=TGME49_232380; 길이=167 8	1383
TGME49_chr XI	656827	661285	+	ID=TGME49_309390; 길이=445 8	1384
TGME49_chr XII	184684 1	1847991	-	ID=TGME49_217450; 길이=115 0	1385
TGME49_chr VIIb	863548	865419	+	ID=TGME49_263000; 길이=187 1	1386
TGME49_chr XI	900050	902305	+	ID=TGME49_309920; 길이=225 5	1387
TGME49_chr VIIb	523777	525912	+	ID=TGME49_263490; 길이=213 5	1388
TGME49_chr IV	452586	457475	-	ID=TGME49_320170; 길이=488 9	1389

[0183]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 탁	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	434515 5	4348378	-	ID=TGME49_291690;길이=322 3	1390
TGME49_chr X	573532 1	5736518	+	ID=TGME49_237140;길이=119 7	1391
TGME49_chr V	971313	973576	-	ID=TGME49_213380;길이=226 3	1392
TGME49_chr X	366801 1	3669970	+	ID=TGME49_223660;길이=195 9	1393
TGME49_chr VIII	295652 9	2961446	-	ID=TGME49_274170;길이=491 7	1394
TGME49_chr Ib	714291	719214	+	ID=TGME49_208470;길이=492 3	1395
TGME49_chr XII	400940 0	4010849	+	ID=TGME49_248580;길이=144 9	1396
TGME49_chr V	254971 2	2552335	-	ID=TGME49_285190;길이=262 3	1397
TGME49_chr II	192728 1	1928097	+	ID=TGME49_297700;길이=816	1398
TGME49_chr VIII	268952 1	2690407	-	ID=TGME49_233510;길이=886	1399
TGME49_chr VIIa	222073 1	2225084	+	ID=TGME49_203800;길이=435 3	1400
TGME49_chr VI	279818 9	2801702	+	ID=TGME49_243700;길이=351 3	1401
TGME49_chr XI	810675	812617	+	ID=TGME49_309790;길이=194 2	1402
TGME49_chr Ia	521377	525024	+	ID=TGME49_293720;길이=364 7	1403
TGME49_chr XII	427582 5	4279900	+	ID=TGME49_248970;길이=407 5	1404
TGME49_chr II	748920	750747	-	ID=TGME49_222000;길이=182 7	1405
TGME49_chr IX	440080 3	4404708	+	ID=TGME49_291920;길이=390 5	1406
TGME49_chr VIII	550725 3	5511071	-	ID=TGME49_269950;길이=381 8	1407
TGME49_chr XII	139843 5	1401335	-	ID=TGME49_218590;길이=290 0	1408

[0184]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	115439 8	1159024	+	ID=TGME49_262568;길이=462 6	1409
TGME49_chr VIIb	283468 4	2838145	-	ID=TGME49_259260;길이=346 1	1410
TGME49_chr VIIb	102039 3	1022780	-	ID=TGME49_262800;길이=238 7	1411
TGME49_chr X	871374	874994	-	ID=TGME49_227620;길이=362 0	1412
TGME49_chr Ia	270952	273178	+	ID=TGME49_293350;길이=222 6	1413
TGME49_chr XI	457952 1	4583971	-	ID=TGME49_315210;길이=445 0	1414
TGME49_chr X	211473 7	2118243	-	ID=TGME49_225710;길이=350 6	1415
TGME49_chr XI	915530	919805	-	ID=TGME49_309930;길이=427 5	1416
TGME49_chr VIII	487465 8	4879348	-	ID=TGME49_270925;길이=469 0	1417
TGME49_chr VIIb	239690 4	2397972	-	ID=TGME49_260280;길이=106 8	1418
TGME49_chr VIII	433993 3	4342675	-	ID=TGME49_271840;길이=274 2	1419
TGME49_chr II	197882 6	1981903	+	ID=TGME49_297760;길이=307 7	1420
TGME49_chr VI	724098	726949	+	ID=TGME49_239510;길이=285 1	1421
TGME49_chr VIII	394955	397268	-	ID=TGME49_229710;길이=231 3	1422
TGME49_chr X	253834 6	2540172	+	ID=TGME49_225080;길이=182 6	1423
TGME49_chr X	395703 3	3959160	-	ID=TGME49_212260;길이=212 7	1424
TGME49_chr VIII	603620 4	6038366	-	ID=TGME49_269160;길이=216 2	1425
TGME49_chr Ia	150704 1	1511154	+	ID=TGME49_295770;길이=411 3	1426
TGME49_chr VIIa	256069	257838	-	ID=TGME49_280660;길이=176 9	1427

[0185]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	876562	878297	-	ID=TGME49_219540;길이=173 5	1428
TGME49_chr VIIa	438632 1	4390549	-	ID=TGME49_282100;길이=422 8	1429
TGME49_chr X	734443 2	7346618	+	ID=TGME49_207040;길이=218 6	1430
TGME49_chr VIII	456050 5	4562544	+	ID=TGME49_271335;길이=203 9	1431
TGME49_chr XI	431686 3	4319362	+	ID=TGME49_314830;길이=249 9	1432
TGME49_chr VIIb	142280 8	1424669	-	ID=TGME49_262030;길이=186 1	1433
TGME49_chr VIII	228521 2	2287451	-	ID=TGME49_232830;길이=223 9	1434
TGME49_chr VIIa	399253 3	3996332	-	ID=TGME49_201170;길이=379 9	1435
TGME49_chr XI	100400 0	1006816	+	ID=TGME49_310010;길이=281 6	1436
TGME49_chr IX	595729 9	5959752	-	ID=TGME49_306310;길이=245 3	1437
TGME49_chr X	734443 2	7345679	+	ID=TGME49_207030;길이=124 7	1438
TGME49_chr VIIb	425360 2	4256192	+	ID=TGME49_257050;길이=259 0	1439
TGME49_chr X	145231 2	1454768	-	ID=TGME49_226670;길이=245 6	1440
TGME49_chr V	469797	472077	-	ID=TGME49_220570;길이=228 0	1441
TGME49_chr IX	209440 8	2096713	+	ID=TGME49_264710;길이=230 5	1442
TGME49_chr VIIa	366260 2	3666008	+	ID=TGME49_202060;길이=340 6	1443
TGME49_chr XII	325384 1	3255658	-	ID=TGME49_247320;길이=181 7	1444
TGME49_chr Ib	547531	550624	-	ID=TGME49_208040;길이=309 3	1445
TGME49_chr IX	213312 8	2135664	+	ID=TGME49_264660;길이=253 6	1446

[0186]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	129245 8	1295329	-	ID=TGME49_266120;길이=287 1	1447
TGME49_chr XI	132898 0	1332607	+	ID=TGME49_310430;길이=362 7	1448
TGME49_chr X	627078 5	6272853	-	ID=TGME49_214370;길이=206 8	1449
TGME49_chr VIIb	251585	254066	-	ID=TGME49_264000;길이=248 1	1450
TGME49_chr VI	161272 6	1614168	+	ID=TGME49_240990;길이=144 2	1451
TGME49_chr IX	153014 2	1532118	-	ID=TGME49_265500;길이=197 6	1452
TGME49_chr IX	623274 9	6234329	-	ID=TGME49_306630;길이=158 0	1453
TGME49_chr XI	475370 1	4755221	+	ID=TGME49_315495;길이=152 0	1454
TGME49_chr VIIa	384433 8	3846794	-	ID=TGME49_201700;길이=245 6	1455
TGME49_chr XII	105843 8	1061957	-	ID=TGME49_219222;길이=351 9	1456
TGME49_chr VIII	363265 4	3634741	+	ID=TGME49_273140;길이=208 7	1457
TGME49_chr VIII	503287 1	5035049	-	ID=TGME49_270740;길이=217 8	1458
TGME49_chr Ia	89272	92865	+	ID=TGME49_293010;길이=359 3	1459
TGME49_chr XII	268641 9	2690798	-	ID=TGME49_246140;길이=437 9	1460
TGME49_chr XII	219708 1	2200494	+	ID=TGME49_217880;길이=341 3	1461
TGME49_chr XI	453678 2	4540443	+	ID=TGME49_315165;길이=366 1	1462
TGME49_chr XII	727484	728939	-	ID=TGME49_219690;길이=145 5	1463
TGME49_chr VIIb	469993 7	4702102	+	ID=TGME49_255715;길이=216 5	1464
TGME49_chr VIIb	457370 0	4576785	+	ID=TGME49_255980;길이=308 5	1465

[0187]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	475047	477267	-	ID=TGME49_263570;길이=222 0	1466
TGME49_chr V	170580 2	1710404	+	ID=TGME49_286720;길이=460 2	1467
TGME49_chr V	232667 7	2329241	-	ID=TGME49_285650;길이=256 4	1468
TGME49_chr Ib	164165 0	1645144	+	ID=TGME49_321660;길이=349 4	1469
TGME49_chr VIII	219884 3	2203273	+	ID=TGME49_232640;길이=443 0	1470
TGME49_chr V	153288 3	1536115	+	ID=TGME49_287180;길이=323 2	1471
TGME49_chr V	190895 0	1912837	-	ID=TGME49_286230;길이=388 7	1472
TGME49_chr XII	441345 7	4417115	+	ID=TGME49_249270;길이=365 8	1473
TGME49_chr IX	589883 2	5900782	-	ID=TGME49_306250;길이=195 0	1474
TGME49_chr VIIb	415476 5	4156893	-	ID=TGME49_257290;길이=212 8	1475
TGME49_chr VIII	126891 4	1270935	+	ID=TGME49_231150;길이=202 1	1476
TGME49_chr VIIb	971154	973119	-	ID=TGME49_262870;길이=196 5	1477
TGME49_chr IV	282678	285486	+	ID=TGME49_320515;길이=280 8	1478
TGME49_chr XII	688077 2	6883692	+	ID=TGME49_276880;길이=292 0	1479
TGME49_chr X	603275 6	6036014	+	ID=TGME49_214110;길이=325 8	1480
TGME49_chr X	406111 5	4063643	+	ID=TGME49_212100;길이=252 8	1481
TGME49_chr V	249899 9	2501500	-	ID=TGME49_285240;길이=250 1	1482
TGME49_chr XII	172414 4	1728800	-	ID=TGME49_218188;길이=465 6	1483
TGME49_chr IX	543718 6	5438779	-	ID=TGME49_305485;길이=159 3	1484

[0188]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	679558 9	6797461	-	ID=TGME49_200310;길이=187 2	1485
TGME49_chr IX	182941 5	1830688	-	ID=TGME49_265030;길이=127 3	1486
TGME49_chr VI	182826 5	1830308	+	ID=TGME49_242020;길이=204 3	1487
TGME49_chr VIII	201646 3	2018840	-	ID=TGME49_232320;길이=237 7	1488
TGME49_chr XI	374085 5	3743951	-	ID=TGME49_313852;길이=309 6	1489
TGME49_chr VIIb	427510 9	4277123	-	ID=TGME49_257030;길이=201 4	1490
TGME49_chr X	676798 1	6769751	-	ID=TGME49_215120;길이=177 0	1491
TGME49_chr VIIa	207575 6	2076930	+	ID=TGME49_203970;길이=117 4	1492
TGME49_chr VIIb	241685 6	2418383	-	ID=TGME49_260260;길이=152 7	1493
TGME49_chr IX	377993 1	3784973	+	ID=TGME49_290630;길이=504 2	1494
TGME49_chr VIIb	581365	584740	+	ID=TGME49_263390;길이=337 5	1495
TGME49_chr XII	446646 6	4468532	-	ID=TGME49_249330;길이=206 6	1496
TGME49_chr II	185898 9	1860788	+	ID=TGME49_297530;길이=179 9	1497
TGME49_chr II	22256	25319	-	ID=TGME49_220840;길이=306 3	1498
TGME49_chr IX	386864 3	3870136	+	ID=TGME49_290730;길이=149 3	1499
TGME49_chr XI	551152	554422	+	ID=TGME49_309200;길이=327 0	1500
TGME49_chr Ib	142227 7	1424478	-	ID=TGME49_209730;길이=220 1	1501
TGME49_chr IX	183090 8	1832938	+	ID=TGME49_265020;길이=203 0	1502
TGME49_chr XII	283946 3	2841372	-	ID=TGME49_246535;길이=190 9	1503

[0189]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	583051 0	5832051	-	ID=TGME49_269413;길이=154 1	1504
TGME49_chr VIIb	316069 0	3162547	+	ID=TGME49_258826;길이=185 7	1505
TGME49_chr XI	430731 3	4309840	+	ID=TGME49_314810;길이=252 7	1506
TGME49_chr VIII	406789	409738	-	ID=TGME49_229730;길이=294 9	1507
TGME49_chr XII	245614 0	2459097	+	ID=TGME49_245670;길이=295 7	1508
TGME49_chr VIIa	261948 7	2621645	-	ID=TGME49_203290;길이=215 8	1509
TGME49_chr V	192428 2	1927117	+	ID=TGME49_286190;길이=283 5	1510
TGME49_chr VI	716743	721319	+	ID=TGME49_239500;길이=457 6	1511
TGME49_chr X	577009 0	5772025	-	ID=TGME49_237180;길이=193 5	1512
TGME49_chr XII	283297 0	2834932	-	ID=TGME49_246520;길이=196 2	1513
TGME49_chr XII	549979 5	5502016	-	ID=TGME49_251620;길이=222 1	1514
TGME49_chr VIII	399607 4	3999088	+	ID=TGME49_272400;길이=301 4	1515
TGME49_chr IX	196156 7	1963588	-	ID=TGME49_264860;길이=202 1	1516
TGME49_chr VIIa	102839 3	1032556	+	ID=TGME49_206380;길이=416 3	1517
TGME49_chr X	300474 1	3008120	-	ID=TGME49_224530;길이=337 9	1518
TGME49_chr II	171095 1	1714500	-	ID=TGME49_297350;길이=354 9	1519
TGME49_chr V	244391	246292	+	ID=TGME49_220260;길이=190 1	1520
TGME49_chr X	444690 2	4449402	-	ID=TGME49_234540;길이=250 0	1521
TGME49_chr VIII	341079 3	3412947	+	ID=TGME49_273540;길이=215 4	1522

[0190]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	368619 0	3687061	+	ID=TGME49_313775;길이=871	1523
TGME49_chr IV	196199 9	1964761	-	ID=TGME49_211030;길이=276 2	1524
TGME49_chr VIIb	421752 7	4220783	+	ID=TGME49_257100;길이=325 6	1525
TGME49_chr IV	235526 1	2356404	-	ID=TGME49_301260;길이=114 3	1526
TGME49_chr VIIb	197865 5	1980752	+	ID=TGME49_261000;길이=209 7	1527
TGME49_chr XII	170743 4	1711430	-	ID=TGME49_218195;길이=399 6	1528
TGME49_chr VI	262670 7	2630269	-	ID=TGME49_243430;길이=356 2	1529
TGME49_chr VIIb	308652 3	3088120	-	ID=TGME49_258930;길이=159 7	1530
TGME49_chr Ib	820471	822527	-	ID=TGME49_208710;길이=205 6	1531
TGME49_chr X	609719 7	6099437	-	ID=TGME49_214190;길이=224 0	1532
TGME49_chr X	574772 4	5750210	-	ID=TGME49_237150;길이=248 6	1533
TGME49_chr Ib	105214 6	1053746	+	ID=TGME49_209120;길이=160 0	1534
TGME49_chr VIIb	821098	823077	+	ID=TGME49_263080;길이=197 9	1535
TGME49_chr XII	127652 1	1280802	-	ID=TGME49_218830;길이=428 1	1536
TGME49_chr XII	131425 4	1315857	-	ID=TGME49_218780;길이=160 3	1537
TGME49_chr VIII	380831 6	3811592	+	ID=TGME49_272660;길이=327 6	1538
TGME49_chr XII	333992 7	3343970	-	ID=TGME49_247440;길이=404 3	1539
TGME49_chr X	669041	669809	-	ID=TGME49_228020;길이=768	1540
TGME49_chr Ia	180142 6	1803846	-	ID=TGME49_295380;길이=242 0	1541

[0191]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	115243 5	1155997	+	ID=TGME49_266400;길이=356 2	1542
TGME49_chr XII	473617 6	4738097	-	ID=TGME49_249685;길이=192 1	1543
TGME49_chr VIII	646264 6	6464783	-	ID=TGME49_268400;길이=213 7	1544
TGME49_chr X	240592 5	2408633	+	ID=TGME49_225200;길이=270 8	1545
TGME49_chr X	425066 7	4254283	+	ID=TGME49_234270;길이=361 6	1546
TGME49_chr IV	258067 6	2583197	-	ID=TGME49_237835;길이=252 1	1547
TGME49_chr X	283771 7	2842141	-	ID=TGME49_224760;길이=442 4	1548
TGME49_chr VIIa	122549 0	1228154	+	ID=TGME49_205658;길이=266 4	1549
TGME49_chr IV	472782	476325	-	ID=TGME49_320150;길이=354 3	1550
TGME49_chr VIII	249532 6	2497228	-	ID=TGME49_233200;길이=190 2	1551
TGME49_chr IX	139824 6	1400896	-	ID=TGME49_265870;길이=265 0	1552
TGME49_chr VIIb	779047	782310	-	ID=TGME49_263135;길이=326 3	1553
TGME49_chr VIIa	249938 7	2501343	+	ID=TGME49_203440;길이=195 6	1554
TGME49_chr XII	317934 3	3181561	+	ID=TGME49_247230;길이=221 8	1555
TGME49_chr VIIb	906498	907438	+	ID=TGME49_262940;길이=940	1556
TGME49_chr X	310608 6	3109088	+	ID=TGME49_224290;길이=300 2	1557
TGME49_chr VIIb	297253 6	2974185	-	ID=TGME49_259100;길이=164 9	1558
TGME49_chr VIII	322273	327193	-	ID=TGME49_229620;길이=492 0	1559
TGME49_chr VI	272641 9	2728299	-	ID=TGME49_243570;길이=188 0	1560

[0192]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ib	176347 6	1764810	-	ID=TGME49_321510;길이=133 4	1561
TGME49_chr VIII	191593 6	1917426	-	ID=TGME49_232170;길이=149 0	1562
TGME49_chr XI	119838 1	1203275	-	ID=TGME49_310260;길이=489 4	1563
TGME49_chr V	116497 0	1166774	-	ID=TGME49_213600;길이=180 4	1564
TGME49_chr XII	112045 9	1123972	-	ID=TGME49_219125;길이=351 3	1565
TGME49_chr XI	308796 0	3092164	-	ID=TGME49_313080;길이=420 4	1566
TGME49_chr XI	197658 5	1979964	+	ID=TGME49_311335;길이=337 9	1567
TGME49_chr XII	505955 4	5061900	-	ID=TGME49_250340;길이=234 6	1568
TGME49_chr IX	708789	710487	+	ID=TGME49_267330;길이=169 8	1569
TGME49_chr VI	287448 3	2878854	+	ID=TGME49_243910;길이=437 1	1570
TGME49_chr X	385749 6	3859431	-	ID=TGME49_223420;길이=193 5	1571
TGME49_chr VIIa	176036	178132	+	ID=TGME49_280690;길이=209 6	1572
TGME49_chr X	563791 9	5640447	+	ID=TGME49_236980;길이=252 8	1573
TGME49_chr VIII	598127 3	5982851	-	ID=TGME49_269225;길이=157 8	1574
TGME49_chr IV	182111 8	1825235	+	ID=TGME49_211330;길이=411 7	1575
TGME49_chr V	254869 9	2551643	+	ID=TGME49_285180;길이=294 4	1576
TGME49_chr VIIb	198929 0	1990938	+	ID=TGME49_260990;길이=164 8	1577
TGME49_chr X	183466 9	1836342	+	ID=TGME49_226060;길이=167 3	1578
TGME49_chr V	817024	819593	+	ID=TGME49_213050;길이=256 9	1579

[0193]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	223431 8	2235909	+	ID=TGME49_232710;길이=159 1	1580
TGME49_chr VIIb	314787 5	3150412	+	ID=TGME49_258832;길이=253 7	1581
TGME49_chr VIIb	474004 3	4742016	-	ID=TGME49_255680;길이=197 3	1582
TGME49_chr VIII	358534 9	3587718	-	ID=TGME49_273340;길이=236 9	1583
TGME49_chr VI	161949 3	1622431	-	ID=TGME49_241000;길이=293 8	1584
TGME49_chr VI	323548 2	3240036	+	ID=TGME49_244400;길이=455 4	1585
TGME49_chr VIII	462431 2	4626375	-	ID=TGME49_271250;길이=206 3	1586
TGME49_chr IV	126040 0	1264074	-	ID=TGME49_318525;길이=367 4	1587
TGME49_chr XII	294621 7	2948125	+	ID=TGME49_246730;길이=190 8	1588
TGME49_chr V	110255 6	1104367	+	ID=TGME49_213490;길이=181 1	1589
TGME49_chr VIIb	106452 8	1067088	-	ID=TGME49_262715;길이=256 0	1590
TGME49_chr IV	564447	565815	-	ID=TGME49_320040;길이=136 8	1591
TGME49_chr V	129591 8	1298121	-	ID=TGME49_213760;길이=220 3	1592
TGME49_chr VIII	185918 1	1860943	-	ID=TGME49_232100;길이=176 2	1593
TGME49_chr XI	585213 7	5854406	+	ID=TGME49_216840;길이=226 9	1594
TGME49_chr X	604718 1	6050358	+	ID=TGME49_214130;길이=317 7	1595
TGME49_chr V	702364	705795	+	ID=TGME49_212937;길이=343 1	1596
TGME49_chr X	644166	645619	-	ID=TGME49_228065;길이=145 3	1597
TGME49_chr Ib	707596	710331	+	ID=TGME49_208440;길이=273 5	1598

[0194]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	425402 5	4256840	+	ID=TGME49_271970; 길이=281 5	1599
TGME49_chr VIIa	175267 7	1754734	-	ID=TGME49_204490; 길이=205 7	1600
TGME49_chr IX	303126 0	3032617	+	ID=TGME49_289160; 길이=135 7	1601
TGME49_chr Ia	161058 9	1612536	-	ID=TGME49_295690; 길이=194 7	1602
TGME49_chr XII	365228 4	3655006	+	ID=TGME49_248100; 길이=272 2	1603
TGME49_chr V	225328 5	2254950	-	ID=TGME49_285760; 길이=166 5	1604
TGME49_chr Ia	644712	646745	-	ID=TGME49_294010; 길이=203 3	1605
TGME49_chr VIIb	263484 2	2637275	-	ID=TGME49_259890; 길이=243 3	1606
TGME49_chr XII	335759 4	3360110	-	ID=TGME49_247460; 길이=251 6	1607
TGME49_chr Ib	458487	461835	-	ID=TGME49_207950; 길이=334 8	1608
TGME49_chr II	309176	312120	-	ID=TGME49_221390; 길이=294 4	1609
TGME49_chr XII	524097 5	5243070	-	ID=TGME49_250810; 길이=209 5	1610
TGME49_chr IX	150106 4	1504713	-	ID=TGME49_265530; 길이=364 9	1611
TGME49_chr Ib	48324	49906	-	ID=TGME49_207420; 길이=158 2	1612
TGME49_chr VIIa	296070 9	2963102	+	ID=TGME49_202880; 길이=239 3	1613
TGME49_chr XII	275930 3	2762582	-	ID=TGME49_246230; 길이=327 9	1614
TGME49_chr VIIa	336429 1	3368281	+	ID=TGME49_202380; 길이=399 0	1615
TGME49_chr VIII	584747 1	5851413	+	ID=TGME49_269380; 길이=394 2	1616
TGME49_chr XI	280391 5	2808538	+	ID=TGME49_312590; 길이=462 3	1617

[0195]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	358727 5	3589602	+	ID=TGME49_313665;길이=232 7	1618
TGME49_chr XII	416832 0	4169758	+	ID=TGME49_248780;길이=143 8	1619
TGME49_chr X	507445 3	5075975	+	ID=TGME49_235720;길이=152 2	1620
TGME49_chr II	212756 2	2129984	+	ID=TGME49_297950;길이=242 2	1621
TGME49_chr VIIb	894167	897847	-	ID=TGME49_262970;길이=368 0	1622
TGME49_chr VIII	242077 8	2422638	+	ID=TGME49_233110;길이=186 0	1623
TGME49_chr XII	543063 4	5433016	-	ID=TGME49_251490;길이=238 2	1624
TGME49_chr X	438371	442269	+	ID=TGME49_228280;길이=389 8	1625
TGME49_chr V	205334 2	2058060	-	ID=TGME49_286020;길이=471 8	1626
TGME49_chr IX	154837 0	1553308	-	ID=TGME49_265450;길이=493 8	1627
TGME49_chr Ib	136166 5	1366149	-	ID=TGME49_209610;길이=448 4	1628
TGME49_chr II	116050 6	1162386	-	ID=TGME49_222440;길이=188 0	1629
TGME49_chr XII	382562 5	3827372	+	ID=TGME49_248370;길이=174 7	1630
TGME49_chr Ia	695084	698240	+	ID=TGME49_294200;길이=315 6	1631
TGME49_chr XI	639121 6	6392903	-	ID=TGME49_216130;길이=168 7	1632
TGME49_chr XI	496472	497645	+	ID=TGME49_309095;길이=117 3	1633
TGME49_chr VI	210503 6	2106954	-	ID=TGME49_242610;길이=191 8	1634
TGME49_chr VIIa	20277	22070	-	ID=TGME49_279550;길이=179 3	1635
TGME49_chr VIII	558816 3	5591148	+	ID=TGME49_269810;길이=298 5	1636

[0196]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr II	1643776	1646520	-	ID=TGME49_297245;길이=2744	1637
TGME49_chr XII	1661314	1663812	-	ID=TGME49_218230;길이=2498	1638
TGME49_chr VIIa	1958747	1961164	-	ID=TGME49_204140;길이=2417	1639
TGME49_chr IV	1317765	1320416	+	ID=TGME49_318450;길이=2651	1640
TGME49_chr X	4551871	4556156	-	ID=TGME49_234930;길이=4285	1641
TGME49_chr V	1361167	1363437	-	ID=TGME49_213830;길이=2270	1642
TGME49_chr V	2135398	2138100	-	ID=TGME49_285940;길이=2702	1643
TGME49_chr VIII	4288270	4290925	+	ID=TGME49_271910;길이=2655	1644
TGME49_chr X	5448896	5450860	+	ID=TGME49_236620;길이=1964	1645
TGME49_chr X	7170482	7175111	-	ID=TGME49_275310;길이=4629	1646
TGME49_chr IX	3092344	3096555	-	ID=TGME49_289218;길이=4211	1647
TGME49_chr IV	866827	869130	+	ID=TGME49_319590;길이=2303	1648
TGME49_chr X	6109656	6111516	-	ID=TGME49_214200;길이=1860	1649
TGME49_chr Ia	716367	719854	-	ID=TGME49_294210;길이=3487	1650
TGME49_chr IX	2520742	2523456	-	ID=TGME49_288420;길이=2714	1651
TGME49_chr IX	3369880	3371358	-	ID=TGME49_289660;길이=1478	1652
TGME49_chr X	456771	458903	+	ID=TGME49_228240;길이=2132	1653
TGME49_chr VIIb	2969500	2972803	+	ID=TGME49_259090;길이=3303	1654
TGME49_chr VIIb	711535	716415	-	ID=TGME49_263210;길이=4880	1655

[0197]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	212253 8	2126263	-	ID=TGME49_232500;길이=372 5	1656
TGME49_chr IV	209693 4	2099104	-	ID=TGME49_210750;길이=217 0	1657
TGME49_chr Ib	863212	866544	+	ID=TGME49_208800;길이=333 2	1658
TGME49_chr VIII	521978 5	5222055	-	ID=TGME49_270520;길이=227 0	1659
TGME49_chr VI	128526 1	1288152	-	ID=TGME49_240450;길이=289 1	1660
TGME49_chr VIIa	303176 3	3033039	-	ID=TGME49_202790;길이=127 6	1661
TGME49_chr XI	323540 7	3237049	-	ID=TGME49_313277;길이=164 2	1662
TGME49_chr XII	446034 9	4461980	-	ID=TGME49_249325;길이=163 1	1663
TGME49_chr VIIb	106209 8	1065932	+	ID=TGME49_262710;길이=383 4	1664
TGME49_chr VIII	215542 8	2158102	+	ID=TGME49_232550;길이=267 4	1665
TGME49_chr IX	325672	328132	+	ID=TGME49_267820;길이=246 0	1666
TGME49_chr XI	515729 9	5158701	+	ID=TGME49_316150;길이=140 2	1667
TGME49_chr VIIb	484234 7	4847324	+	ID=TGME49_255400;길이=497 7	1668
TGME49_chr X	228767 8	2289457	-	ID=TGME49_225360;길이=177 9	1669
TGME49_chr VIIa	381905 8	3822835	+	ID=TGME49_201750;길이=377 7	1670
TGME49_chr X	484393 2	4845765	-	ID=TGME49_235398;길이=183 3	1671
TGME49_chr IV	114500 0	1147010	+	ID=TGME49_318690;길이=201 0	1672
TGME49_chr XII	558864 6	5590856	-	ID=TGME49_251780;길이=221 0	1673
TGME49_chr XI	612911 4	6134065	-	ID=TGME49_216470;길이=495 1	1674

[0198]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	455338	457067	-	ID=TGME49_239083;길이=172 9	1675
TGME49_chr VIII	328988 3	3294737	+	ID=TGME49_273750;길이=485 4	1676
TGME49_chr VIII	368921 9	3691099	+	ID=TGME49_273060;길이=188 0	1677
TGME49_chr X	332658 9	3328196	-	ID=TGME49_224100;길이=160 7	1678
TGME49_chr VIIa	106083 3	1063141	+	ID=TGME49_206320;길이=230 8	1679
TGME49_chr II	130177 6	1305290	+	ID=TGME49_222910;길이=351 4	1680
TGME49_chr II	151226 3	1514584	+	ID=TGME49_297065;길이=232 1	1681
TGME49_chr VIII	303073 3	3033855	+	ID=TGME49_274090;길이=312 2	1682
TGME49_chr II	342210	344003	+	ID=TGME49_221430;길이=179 3	1683
TGME49_chr VI	132068 9	1322846	-	ID=TGME49_240560;길이=215 7	1684
TGME49_chr XI	485179 6	4855798	+	ID=TGME49_315610;길이=400 2	1685
TGME49_chr XII	286621 7	2868700	+	ID=TGME49_246590;길이=248 3	1686
TGME49_chr VIIb	239506 7	2397478	+	ID=TGME49_260270;길이=241 1	1687
TGME49_chr V	766839	769527	+	ID=TGME49_213000;길이=268 8	1688
TGME49_chr XII	192713 6	1929197	-	ID=TGME49_217580;길이=206 1	1689
TGME49_chr XII	659783 6	6600162	-	ID=TGME49_275568;길이=232 6	1690
TGME49_chr IX	533074 0	5332155	+	ID=TGME49_305280;길이=141 5	1691
TGME49_chr X	625914 5	6260711	+	ID=TGME49_214350;길이=156 6	1692
TGME49_chr IX	273024 3	2732515	-	ID=TGME49_288765;길이=227 2	1693

[0199]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	416922 7	4173719	-	ID=TGME49_314515;길이=449 2	1694
TGME49_chr XI	172289 5	1726565	+	ID=TGME49_311020;길이=367 0	1695
TGME49_chr XI	205978 0	2062470	+	ID=TGME49_311410;길이=269 0	1696
TGME49_chr VIIa	420201 1	4206408	+	ID=TGME49_281580;길이=439 7	1697
TGME49_chr VIIa	294635 9	2950755	+	ID=TGME49_202900;길이=439 6	1698
TGME49_chr VIIb	267808 8	2682997	+	ID=TGME49_259830;길이=490 9	1699
TGME49_chr VIIa	899877	903405	+	ID=TGME49_206510;길이=352 8	1700
TGME49_chr XI	399607 7	3999430	-	ID=TGME49_314310;길이=335 3	1701
TGME49_chr XII	535341 1	5355727	+	ID=TGME49_251400;길이=231 6	1702
TGME49_chr XII	217686 8	2180818	+	ID=TGME49_217860;길이=395 0	1703
TGME49_chr VIII	579267 3	5796876	-	ID=TGME49_269450;길이=420 3	1704
TGME49_chr VIII	686350 0	6867930	-	ID=TGME49_200400;길이=443 0	1705
TGME49_chr IX	164201 1	1646868	-	ID=TGME49_265270;길이=485 7	1706
TGME49_chr Ia	451232	453213	+	ID=TGME49_293610;길이=198 1	1707
TGME49_chr VI	144574 1	1449188	+	ID=TGME49_240800;길이=344 7	1708
TGME49_chr VIIb	899808	902193	+	ID=TGME49_262950;길이=238 5	1709
TGME49_chr XII	552655 1	5531499	+	ID=TGME49_251690;길이=494 8	1710
TGME49_chr IV	215487 8	2157331	+	ID=TGME49_210690;길이=245 3	1711
TGME49_chr VIIa	224470 1	2247997	+	ID=TGME49_203770;길이=329 6	1712

[0200]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	177396 9	1777524	-	ID=TGME49_261400;길이=355 5	1713
TGME49_chr IX	208764 4	2089518	-	ID=TGME49_264730;길이=187 4	1714
TGME49_chr X	532609 6	5328125	-	ID=TGME49_236200;길이=202 9	1715
TGME49_chr IX	528018 0	5282539	+	ID=TGME49_305200;길이=235 9	1716
TGME49_chr V	181504 7	1818388	+	ID=TGME49_286480;길이=334 1	1717
TGME49_chr VIIa	624310	629301	+	ID=TGME49_304700;길이=499 1	1718
TGME49_chr II	505138	509495	-	ID=TGME49_221630;길이=435 7	1719
TGME49_chr VI	315301 4	3156401	+	ID=TGME49_244280;길이=338 7	1720
TGME49_chr VIII	399709 7	3999384	-	ID=TGME49_272410;길이=228 7	1721
TGME49_chr XII	620537 6	6207991	+	ID=TGME49_278245;길이=261 5	1722
TGME49_chr VIII	510823 6	5110579	-	ID=TGME49_270650;길이=234 3	1723
TGME49_chr IX	141588 1	1418195	+	ID=TGME49_265840;길이=231 4	1724
TGME49_chr VIIb	386309 7	3864612	-	ID=TGME49_257740;길이=151 5	1725
TGME49_chr VIII	421582 5	4218765	-	ID=TGME49_272020;길이=294 0	1726
TGME49_chr VIIa	162934 2	1632196	-	ID=TGME49_205120;길이=285 4	1727
TGME49_chr VIIa	463960	467129	+	ID=TGME49_280390;길이=316 9	1728
TGME49_chr VIIa	142654 2	1431194	-	ID=TGME49_205390;길이=465 2	1729
TGME49_chr II	201437	204275	-	ID=TGME49_221275;길이=283 8	1730
TGME49_chr XII	243762 7	2439102	-	ID=TGME49_245620;길이=147 5	1731

[0201]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	233216 2	2334662	-	ID=TGME49_260370;길이=250 0	1732
TGME49_chr VIIa	788333	792905	+	ID=TGME49_206600;길이=457 2	1733
TGME49_chr IX	410878 8	4113576	+	ID=TGME49_291090;길이=478 8	1734
TGME49_chr IX	468242 7	4683833	+	ID=TGME49_292325;길이=140 6	1735
TGME49_chr XI	241744 5	2418466	-	ID=TGME49_312075;길이=102 1	1736
TGME49_chr Ia	556012	560537	+	ID=TGME49_293790;길이=452 5	1737
TGME49_chr IX	779646	784608	+	ID=TGME49_267090;길이=496 2	1738
TGME49_chr X	259295 7	2594193	+	ID=TGME49_225005;길이=123 6	1739
TGME49_chr IX	241059 5	2414911	-	ID=TGME49_288245;길이=431 6	1740
TGME49_chr VIIb	260230 3	2605077	+	ID=TGME49_259940;길이=277 4	1741
TGME49_chr X	539587 1	5397679	+	ID=TGME49_236520;길이=180 8	1742
TGME49_chr IV	110727 5	1109514	+	ID=TGME49_318750;길이=223 9	1743
TGME49_chr VI	191582	194227	+	ID=TGME49_238400;길이=264 5	1744
TGME49_chr X	658678 9	6588930	+	ID=TGME49_214920;길이=214 1	1745
TGME49_chr XII	637109 4	6373426	-	ID=TGME49_277990;길이=233 2	1746
TGME49_chr Ia	181250 6	1814521	-	ID=TGME49_295350;길이=201 5	1747
TGME49_chr XII	665698 2	6660694	+	ID=TGME49_277500;길이=371 2	1748
TGME49_chr XII	266364 3	2665815	+	ID=TGME49_246100;길이=217 2	1749
TGME49_chr XI	436997	438672	-	ID=TGME49_309010;길이=167 5	1750

[0202]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	544282 9	5445816	-	ID=TGME49_305498;길이=298 7	1751
TGME49_chr VI	41637	43605	+	ID=TGME49_238060;길이=196 8	1752
TGME49_chr XII	613045	617971	+	ID=TGME49_219828;길이=492 6	1753
TGME49_chr X	202602 0	2028673	-	ID=TGME49_225820;길이=265 3	1754
TGME49_chr IX	369096 4	3692526	+	ID=TGME49_290300;길이=156 2	1755
TGME49_chr IX	652699	654379	+	ID=TGME49_267435;길이=168 0	1756
TGME49_chr V	489825	492876	-	ID=TGME49_220610;길이=305 1	1757
TGME49_chr VIIb	486067	488472	+	ID=TGME49_263540;길이=240 5	1758
TGME49_chr VIII	328373 3	3286012	+	ID=TGME49_273770;길이=227 9	1759
TGME49_chr Ib	978776	983209	+	ID=TGME49_209010;길이=443 3	1760
TGME49_chr VI	177511 9	1776850	-	ID=TGME49_241860;길이=173 1	1761
TGME49_chr Ia	114695 1	1148726	-	ID=TGME49_294790;길이=177 5	1762
TGME49_chr XII	104173 1	1043438	-	ID=TGME49_219250;길이=170 7	1763
TGME49_chr VIII	733619	737486	-	ID=TGME49_230350;길이=386 7	1764
TGME49_chr II	160369 4	1605698	-	ID=TGME49_297190;길이=200 4	1765
TGME49_chr IX	271119 1	2713335	-	ID=TGME49_288720;길이=214 4	1766
TGME49_chr X	119654 3	1199550	+	ID=TGME49_226950;길이=300 7	1767
TGME49_chr IX	539354 4	5395750	+	ID=TGME49_305455;길이=220 6	1768
TGME49_chr XI	149916 1	1503181	+	ID=TGME49_310660;길이=402 0	1769

[0203]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	500825 4	5010201	+	ID=TGME49_315820;길이=194 7	1770
TGME49_chr VI	139036 8	1392791	-	ID=TGME49_240690;길이=242 3	1771
TGME49_chr II	112039 3	1123132	+	ID=TGME49_222410;길이=273 9	1772
TGME49_chr X	739417	741694	-	ID=TGME49_227920;길이=227 7	1773
TGME49_chr VIII	554828 2	5553068	-	ID=TGME49_269910;길이=478 6	1774
TGME49_chr VIII	503704	505886	-	ID=TGME49_229990;길이=218 2	1775
TGME49_chr X	252189 1	2524155	+	ID=TGME49_225102;길이=226 4	1776
TGME49_chr VIIb	246923 2	2470805	+	ID=TGME49_260190;길이=157 3	1777
TGME49_chr IX	381279	384341	+	ID=TGME49_267750;길이=306 2	1778
TGME49_chr XII	260311 8	2605598	+	ID=TGME49_246030;길이=248 0	1779
TGME49_chr II	137385 6	1375582	+	ID=TGME49_223025;길이=172 6	1780
TGME49_chr VIIb	216776 1	2170472	-	ID=TGME49_260550;길이=271 1	1781
TGME49_chr XI	424019 4	4244498	-	ID=TGME49_314710;길이=430 4	1782
TGME49_chr VIIa	293961	296113	-	ID=TGME49_280570;길이=215 2	1783
TGME49_chr IX	132348 7	1325964	-	ID=TGME49_266065;길이=247 7	1784
TGME49_chr VIII	151380 3	1516857	+	ID=TGME49_231640;길이=305 4	1785
TGME49_chr V	342801	346665	+	ID=TGME49_220390;길이=386 4	1786
TGME49_chr VIIa	166310 1	1666170	+	ID=TGME49_205030;길이=306 9	1787
TGME49_chr VI	284797 1	2852954	-	ID=TGME49_243760;길이=498 3	1788

[0204]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	5351150	5353348	+	ID=TGME49_305320;길이=2198	1789
TGME49_chr XII	4131891	4133450	-	ID=TGME49_248730;길이=1559	1790
TGME49_chr XI	133543	134623	+	ID=TGME49_306990;길이=1080	1791
TGME49_chr X	6353248	6354650	-	ID=TGME49_214550;길이=1402	1792
TGME49_chr VIII	6042411	6044655	+	ID=TGME49_269140;길이=2244	1793
TGME49_chr IX	1688833	1690933	-	ID=TGME49_265230;길이=2100	1794
TGME49_chr Ia	306442	309887	+	ID=TGME49_293420;길이=3445	1795
TGME49_chr VIIa	1824928	1827582	+	ID=TGME49_204390;길이=2654	1796
TGME49_chr XII	951031	952710	+	ID=TGME49_219430;길이=1679	1797
TGME49_chr VI	581992	583744	-	ID=TGME49_239350;길이=1752	1798
TGME49_chr X	3441657	3444661	-	ID=TGME49_223940;길이=3004	1799
TGME49_chr VIII	846765	849139	+	ID=TGME49_230520;길이=2374	1800
TGME49_chr XII	3323790	3326774	+	ID=TGME49_247400;길이=2984	1801
TGME49_chr VIIa	2920724	2923694	-	ID=TGME49_202960;길이=2970	1802
TGME49_chr XI	4578541	4582751	+	ID=TGME49_315220;길이=4210	1803
TGME49_chr IX	1528778	1531783	+	ID=TGME49_265470;길이=3005	1804
TGME49_chr XI	1239947	1242270	-	ID=TGME49_310290;길이=2323	1805
TGME49_chr VIIb	222702	224691	-	ID=TGME49_264040;길이=1989	1806
TGME49_chr VIII	405193	409738	-	ID=TGME49_229720;길이=4545	1807

[0205]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	625071	629635	-	ID=TGME49_304680;길이=456 4	1808
TGME49_chr IX	250728 7	2509481	-	ID=TGME49_288400;길이=219 4	1809
TGME49_chr VIIa	326093 7	3263671	-	ID=TGME49_202530;길이=273 4	1810
TGME49_chr IX	227007	229288	+	ID=TGME49_279360;길이=228 1	1811
TGME49_chr X	402165 5	4024338	+	ID=TGME49_212140;길이=268 3	1812
TGME49_chr VIIb	121590 8	1219966	+	ID=TGME49_262460;길이=405 8	1813
TGME49_chr X	745793 7	7460592	-	ID=TGME49_207230;길이=265 5	1814
TGME49_chr VIII	107151 4	1075639	-	ID=TGME49_230870;길이=412 5	1815
TGME49_chr X	502920 2	5030634	-	ID=TGME49_235660;길이=143 2	1816
TGME49_chr VIIb	483829 7	4840986	-	ID=TGME49_255420;길이=268 9	1817
TGME49_chr VIII	574328	576120	-	ID=TGME49_230070;길이=179 2	1818
TGME49_chr VIIa	143452 9	1437210	+	ID=TGME49_205370;길이=268 1	1819
TGME49_chr VIIb	318471 4	3187955	-	ID=TGME49_258790;길이=324 1	1820
TGME49_chr VIIb	452002	453575	+	ID=TGME49_263595;길이=157 3	1821
TGME49_chr II	179917 7	1801013	-	ID=TGME49_297460;길이=183 6	1822
TGME49_chr IX	134801 9	1350404	+	ID=TGME49_266010;길이=238 5	1823
TGME49_chr XI	422982	426252	-	ID=TGME49_308990;길이=327 0	1824
TGME49_chr VIIa	263864 0	2643428	+	ID=TGME49_203250;길이=478 8	1825
TGME49_chr XII	311210 6	3117089	+	ID=TGME49_247030;길이=498 3	1826

[0206]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr V	178611 7	1787739	+	ID=TGME49_286550;길이=162 2	1827
TGME49_chr Ib	163636 9	1639495	-	ID=TGME49_321690;길이=312 6	1828
TGME49_chr XII	474406 2	4745703	-	ID=TGME49_249698;길이=164 1	1829
TGME49_chr XI	104928 8	1054295	-	ID=TGME49_310080;길이=500 7	1830
TGME49_chr XII	299736 4	3001613	+	ID=TGME49_246800;길이=424 9	1831
TGME49_chr VIIa	276480	280573	-	ID=TGME49_280600;길이=409 3	1832
TGME49_chr VIIa	204483 4	2047221	-	ID=TGME49_204040;길이=238 7	1833
TGME49_chr IV	144357 5	1445262	-	ID=TGME49_318290;길이=168 7	1834
TGME49_chr VIIb	135854 3	1363574	-	ID=TGME49_262125;길이=503 1	1835
TGME49_chr XII	188973 9	1893641	-	ID=TGME49_217520;길이=390 2	1836
TGME49_chr VIII	621815 6	6222777	+	ID=TGME49_268890;길이=462 1	1837
TGME49_chr IX	212823	215942	-	ID=TGME49_279390;길이=311 9	1838
TGME49_chr V	307466 8	3075701	-	ID=TGME49_283570;길이=103 3	1839
TGME49_chr VIIa	329088	331013	-	ID=TGME49_280540;길이=192 5	1840
TGME49_chr XII	113585 9	1136707	-	ID=TGME49_219090;길이=848	1841
TGME49_chr XI	562038	563532	-	ID=TGME49_309210;길이=149 4	1842
TGME49_chr XI	507976 3	5082015	+	ID=TGME49_315930;길이=225 2	1843
TGME49_chr XII	423001 0	4231788	+	ID=TGME49_248870;길이=177 8	1844
TGME49_chr VIII	347018	350776	+	ID=TGME49_229640;길이=375 8	1845

[0207]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	336895 8	3370369	+	ID=TGME49_289670;길이=141 1	1846
TGME49_chr VIII	268743 6	2690407	-	ID=TGME49_233500;길이=297 1	1847
TGME49_chr VIIb	611076	613065	-	ID=TGME49_263360;길이=198 9	1848
TGME49_chr VIIb	397000 6	3973027	-	ID=TGME49_257568;길이=302 1	1849
TGME49_chr VIIb	132523 9	1328902	+	ID=TGME49_262160;길이=366 3	1850
TGME49_chr VIII	441311 3	4415505	-	ID=TGME49_271760;길이=239 2	1851
TGME49_chr VIIa	381450 3	3816891	+	ID=TGME49_201760;길이=238 8	1852
TGME49_chr XI	405853 5	4061396	+	ID=TGME49_314400;길이=286 1	1853
TGME49_chr XI	185439 5	1859046	+	ID=TGME49_311210;길이=465 1	1854
TGME49_chr X	463211 0	4634094	+	ID=TGME49_235140;길이=198 4	1855
TGME49_chr IX	581529 6	5819202	+	ID=TGME49_306190;길이=390 6	1856
TGME49_chr VIIb	290895 5	2910810	-	ID=TGME49_259180;길이=185 5	1857
TGME49_chr VIII	242121 2	2423837	-	ID=TGME49_233100;길이=262 5	1858
TGME49_chr XI	431000	433353	-	ID=TGME49_309000;길이=235 3	1859
TGME49_chr XI	227103 0	2275657	+	ID=TGME49_311770;길이=462 7	1860
TGME49_chr VIII	433207 0	4335007	+	ID=TGME49_271850;길이=293 7	1861
TGME49_chr XII	498916 0	4990606	+	ID=TGME49_250020;길이=144 6	1862
TGME49_chr XII	267735 8	2679539	+	ID=TGME49_246130;길이=218 1	1863
TGME49_chr VIIa	305043	307438	+	ID=TGME49_280550;길이=239 5	1864

[0208]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	466818 1	4671233	+	ID=TGME49_315360;길이=305 2	1865
TGME49_chr X	203508 8	2038686	+	ID=TGME49_225790;길이=359 8	1866
TGME49_chr VIIb	325987 2	3262590	-	ID=TGME49_258690;길이=271 8	1867
TGME49_chr XII	491282 9	4914644	-	ID=TGME49_249860;길이=181 5	1868
TGME49_chr VI	244008 6	2442352	-	ID=TGME49_243200;길이=226 6	1869
TGME49_chr VIII	388033 6	3884798	+	ID=TGME49_272560;길이=446 2	1870
TGME49_chr XII	383160 7	3833051	-	ID=TGME49_248390;길이=144 4	1871
TGME49_chr XI	226279 6	2265505	-	ID=TGME49_311760;길이=270 9	1872
TGME49_chr Ia	741460	745719	-	ID=TGME49_294240;길이=425 9	1873
TGME49_chr Ib	178261 7	1787380	-	ID=TGME49_321470;길이=476 3	1874
TGME49_chr VIIa	166993 1	1670876	-	ID=TGME49_205020;길이=945	1875
TGME49_chr VIII	632649 1	6329179	-	ID=TGME49_268770;길이=268 8	1876
TGME49_chr V	166266	168190	-	ID=TGME49_220145;길이=192 4	1877
TGME49_chr IV	576195	580895	-	ID=TGME49_320020;길이=470 0	1878
TGME49_chr VIII	129822 4	1301679	+	ID=TGME49_231175;길이=345 5	1879
TGME49_chr VIIb	496442 4	4968613	-	ID=TGME49_255250;길이=418 9	1880
TGME49_chr IX	709923	711569	-	ID=TGME49_267340;길이=164 6	1881
TGME49_chr X	455693 6	4560782	+	ID=TGME49_234970;길이=384 6	1882
TGME49_chr VIIb	393977	397643	-	ID=TGME49_263690;길이=366 6	1883

[0209]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	542293 1	5424831	-	ID=TGME49_251480;길이=190 0	1884
TGME49_chr IX	914298	915352	+	ID=TGME49_266880;길이=105 4	1885
TGME49_chr V	428812	432815	+	ID=TGME49_220520;길이=400 3	1886
TGME49_chr XI	640495 4	6409920	-	ID=TGME49_216080;길이=496 6	1887
TGME49_chr II	861618	866482	-	ID=TGME49_222080;길이=486 4	1888
TGME49_chr XII	566986 7	5671445	+	ID=TGME49_251930;길이=157 8	1889
TGME49_chr VI	253292 9	2537138	+	ID=TGME49_243310;길이=420 9	1890
TGME49_chr IX	380782 1	3810806	-	ID=TGME49_290640;길이=298 5	1891
TGME49_chr VIIa	901698	904817	-	ID=TGME49_206540;길이=311 9	1892
TGME49_chr IX	184746 3	1852082	+	ID=TGME49_265000;길이=461 9	1893
TGME49_chr VIIa	245453 2	2456953	+	ID=TGME49_203510;길이=242 1	1894
TGME49_chr VIII	360469 8	3606638	+	ID=TGME49_273290;길이=194 0	1895
TGME49_chr VIII	223475 2	2236893	-	ID=TGME49_232700;길이=214 1	1896
TGME49_chr VI	244932 1	2450374	+	ID=TGME49_243220;길이=105 3	1897
TGME49_chr X	693718 4	6938923	+	ID=TGME49_215385;길이=173 9	1898
TGME49_chr IX	680988	684814	-	ID=TGME49_267380;길이=382 6	1899
TGME49_chr VIIa	226102 7	2263156	-	ID=TGME49_203760;길이=212 9	1900
TGME49_chr IX	314527 5	3148375	-	ID=TGME49_289280;길이=310 0	1901
TGME49_chr VIIa	248972 2	2491017	+	ID=TGME49_203470;길이=129 5	1902

[0210]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	176988 5	1774294	-	ID=TGME49_232020;길이=440 9	1903
TGME49_chr VIIa	399353 3	3996332	-	ID=TGME49_201160;길이=279 9	1904
TGME49_chr X	451479 9	4516300	+	ID=TGME49_234660;길이=150 1	1905
TGME49_chr V	860484	863029	-	ID=TGME49_213100;길이=254 5	1906
TGME49_chr VIIb	359128 1	3593195	-	ID=TGME49_258085;길이=191 4	1907
TGME49_chr IV	151486 5	1518877	+	ID=TGME49_318160;길이=401 2	1908
TGME49_chr X	327966 6	3282705	-	ID=TGME49_224180;길이=303 9	1909
TGME49_chr VIII	975775	977748	+	ID=TGME49_230700;길이=197 3	1910
TGME49_chr VIIb	308572 9	3088120	-	ID=TGME49_258940;길이=239 1	1911
TGME49_chr XII	529861	532149	+	ID=TGME49_308050;길이=228 8	1912
TGME49_chr V	239790	243541	-	ID=TGME49_220240;길이=375 1	1913
TGME49_chr II	146151 3	1463416	-	ID=TGME49_223125;길이=190 3	1914
TGME49_chr XI	522211 7	5224159	-	ID=TGME49_316280;길이=204 2	1915
TGME49_chr II	146830 6	1470065	+	ID=TGME49_223140;길이=175 9	1916
TGME49_chr XI	235371 5	2358433	+	ID=TGME49_311890;길이=471 8	1917
TGME49_chr II	158212 3	1586805	+	ID=TGME49_297170;길이=468 2	1918
TGME49_chr IX	199072	203223	+	ID=TGME49_279400;길이=415 1	1919
TGME49_chr IV	284392	286223	-	ID=TGME49_320525;길이=183 1	1920
TGME49_chr IX	484293 4	4844771	-	ID=TGME49_210370;길이=183 7	1921

[0211]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	445216 7	4456567	-	ID=TGME49_314970;길이=440 0	1922
TGME49_chr XI	249977 2	2502355	-	ID=TGME49_312200;길이=258 3	1923
TGME49_chr Ib	890079	892589	-	ID=TGME49_208830;길이=251 0	1924
TGME49_chr VIII	196636 2	1967945	-	ID=TGME49_232230;길이=158 3	1925
TGME49_chr VI	989945	991803	-	ID=TGME49_239880;길이=185 8	1926
TGME49_chr VIIb	351889 5	3521575	+	ID=TGME49_258200;길이=268 0	1927
TGME49_chr V	216186	217667	-	ID=TGME49_220208;길이=148 1	1928
TGME49_chr XII	564027 6	5641811	+	ID=TGME49_251885;길이=153 5	1929
TGME49_chr XII	382653 8	3828410	-	ID=TGME49_248360;길이=187 2	1930
TGME49_chr IX	736629	737403	+	ID=TGME49_267290;길이=774	1931
TGME49_chr V	578793	583050	-	ID=TGME49_212740;길이=425 7	1932
TGME49_chr XII	288673 2	2889046	+	ID=TGME49_246620;길이=231 4	1933
TGME49_chr XII	417636 5	4178211	+	ID=TGME49_248800;길이=184 6	1934
TGME49_chr VIII	506374 7	5066564	-	ID=TGME49_270710;길이=281 7	1935
TGME49_chr V	190733 2	1909721	+	ID=TGME49_286220;길이=238 9	1936
TGME49_chr XI	339747 4	3401749	-	ID=TGME49_313440;길이=427 5	1937
TGME49_chr VIIa	386182 4	3865091	+	ID=TGME49_201670;길이=326 7	1938
TGME49_chr XII	556968 4	5571506	-	ID=TGME49_251760;길이=182 2	1939
TGME49_chr XII	222592 1	2229690	+	ID=TGME49_217920;길이=376 9	1940

[0212]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	330787 2	3310644	+	ID=TGME49_289570; 길이=277 2	1941
TGME49_chr Ia	156682	159073	+	ID=TGME49_293200; 길이=239 1	1942
TGME49_chr XII	388133 2	3885535	-	ID=TGME49_248470; 길이=420 3	1943
TGME49_chr X	418777	421046	-	ID=TGME49_228330; 길이=226 9	1944
TGME49_chr V	227402 5	2276420	-	ID=TGME49_285720; 길이=239 5	1945
TGME49_chr XI	299221 7	2995109	-	ID=TGME49_312940; 길이=289 2	1946
TGME49_chr Ia	390048	391767	-	ID=TGME49_293520; 길이=171 9	1947
TGME49_chr VIII	644570 9	6450718	-	ID=TGME49_268450; 길이=500 9	1948
TGME49_chr VIIa	392439 8	3927902	-	ID=TGME49_201270; 길이=350 4	1949
TGME49_chr IX	261252 6	2615415	+	ID=TGME49_288560; 길이=288 9	1950
TGME49_chr IX	539402 5	5396129	-	ID=TGME49_305450; 길이=210 4	1951
TGME49_chr VI	244932 1	2454332	+	ID=TGME49_243240; 길이=501 1	1952
TGME49_chr X	114167 8	1144996	+	ID=TGME49_227000; 길이=331 8	1953
TGME49_chr VIIa	358063 3	3582769	-	ID=TGME49_202140; 길이=213 6	1954
TGME49_chr VIII	712149	714535	+	ID=TGME49_230340; 길이=238 6	1955
TGME49_chr X	653775	657724	-	ID=TGME49_228050; 길이=394 9	1956
TGME49_chr X	152907 6	1530823	-	ID=TGME49_226580; 길이=174 7	1957
TGME49_chr VIIa	333465 1	3338417	-	ID=TGME49_202430; 길이=376 6	1958
TGME49_chr VIIb	216320 1	2165337	-	ID=TGME49_260570; 길이=213 6	1959

[0213]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	104384 8	1045795	+	ID=TGME49_262740;길이=194 7	1960
TGME49_chr X	131105 3	1316055	+	ID=TGME49_226825;길이=500 2	1961
TGME49_chr VIII	397749 6	3979941	-	ID=TGME49_272430;길이=244 5	1962
TGME49_chr V	178919 2	1791334	+	ID=TGME49_286530;길이=214 2	1963
TGME49_chr VIIb	417392 2	4175290	+	ID=TGME49_257170;길이=136 8	1964
TGME49_chr XI	459139 6	4593178	+	ID=TGME49_315230;길이=178 2	1965
TGME49_chr VIII	249237	251305	-	ID=TGME49_229420;길이=206 8	1966
TGME49_chr V	646486	648649	-	ID=TGME49_212840;길이=216 3	1967
TGME49_chr XI	112033 0	1122240	+	ID=TGME49_310180;길이=191 0	1968
TGME49_chr XI	557532 1	5577263	-	ID=TGME49_316760;길이=194 2	1969
TGME49_chr VIII	287461 3	2878765	-	ID=TGME49_233870;길이=415 2	1970
TGME49_chr XII	551151 6	5512810	+	ID=TGME49_251650;길이=129 4	1971
TGME49_chr IV	162815 7	1629047	+	ID=TGME49_211675;길이=890	1972
TGME49_chr V	142262 9	1425901	-	ID=TGME49_213900;길이=327 2	1973
TGME49_chr VIIa	186501	190276	+	ID=TGME49_280670;길이=377 5	1974
TGME49_chr VIIa	929557	930012	-	ID=TGME49_206500;길이=455	1975
TGME49_chr IX	297127 0	2973519	+	ID=TGME49_289080;길이=224 9	1976
TGME49_chr VIII	393034 0	3931981	-	ID=TGME49_272510;길이=164 1	1977
TGME49_chr XI	181107	183028	-	ID=TGME49_306930;길이=192 1	1978

[0214]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	164966 3	1652849	+	ID=TGME49_265255;길이=318 6	1979
TGME49_chr XII	107392 7	1076130	+	ID=TGME49_219200;길이=220 3	1980
TGME49_chr IV	247103 7	2473860	+	ID=TGME49_301430;길이=282 3	1981
TGME49_chr XII	636486 6	6366334	+	ID=TGME49_278005;길이=146 8	1982
TGME49_chr Ib	842071	845707	-	ID=TGME49_208740;길이=363 6	1983
TGME49_chr VI	790118	795087	+	ID=TGME49_239600;길이=496 9	1984
TGME49_chr X	142429 8	1426804	+	ID=TGME49_226700;길이=250 6	1985
TGME49_chr V	560109	564542	-	ID=TGME49_287490;길이=443 3	1986
TGME49_chr X	248367 0	2486271	+	ID=TGME49_225120;길이=260 1	1987
TGME49_chr VIIa	139372 5	1398244	-	ID=TGME49_205460;길이=451 9	1988
TGME49_chr XII	109259 2	1094200	+	ID=TGME49_219175;길이=160 8	1989
TGME49_chr X	705828	707714	-	ID=TGME49_227960;길이=188 6	1990
TGME49_chr IX	440449 6	4406990	-	ID=TGME49_291910;길이=249 4	1991
TGME49_chr X	699818 5	6999653	-	ID=TGME49_215510;길이=146 8	1992
TGME49_chr X	452551 9	4527356	+	ID=TGME49_234680;길이=183 7	1993
TGME49_chr X	136441 3	1366308	+	ID=TGME49_226780;길이=189 5	1994
TGME49_chr VIIb	143448 2	1435459	-	ID=TGME49_262000;길이=977	1995
TGME49_chr VIII	319832 8	3202978	-	ID=TGME49_273885;길이=465 0	1996
TGME49_chr VIII	589194 6	5894191	+	ID=TGME49_269320;길이=224 5	1997

[0215]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr II	180127 3	1805605	+	ID=TGME49_297470;길이=433 2	1998
TGME49_chr II	158336 6	1587369	-	ID=TGME49_297160;길이=400 3	1999
TGME49_chr XI	101569 0	1017565	-	ID=TGME49_310030;길이=187 5	2000
TGME49_chr VIII	284128	286310	+	ID=TGME49_229470;길이=218 2	2001
TGME49_chr IV	206127	211040	-	ID=TGME49_320610;길이=491 3	2002
TGME49_chr IV	954032	956564	-	ID=TGME49_319510;길이=253 2	2003
TGME49_chr X	110247 7	1104098	-	ID=TGME49_227080;길이=162 1	2004
TGME49_chr IX	366798 1	3670156	-	ID=TGME49_290250;길이=217 5	2005
TGME49_chr VIII	651963 8	6522878	+	ID=TGME49_268360;길이=324 0	2006
TGME49_chr XI	544011 1	5443988	-	ID=TGME49_316620;길이=387 7	2007
TGME49_chr VIIa	217741 6	2179962	+	ID=TGME49_203840;길이=254 6	2008
TGME49_chr VIII	508420 9	5085825	+	ID=TGME49_270680;길이=161 6	2009
TGME49_chr XI	299546 4	2997405	+	ID=TGME49_312960;길이=194 1	2010
TGME49_chr II	162592 3	1628671	+	ID=TGME49_297230;길이=274 8	2011
TGME49_chr XI	161890 0	1619991	+	ID=TGME49_310830;길이=109 1	2012
TGME49_chr XII	675150 4	6754864	-	ID=TGME49_277060;길이=336 0	2013
TGME49_chr XI	616571 5	6168615	+	ID=TGME49_216410;길이=290 0	2014
TGME49_chr V	263664 7	2639120	+	ID=TGME49_284645;길이=247 3	2015
TGME49_chr VIIb	447349 7	4476055	+	ID=TGME49_256770;길이=255 8	2016

[0216]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 탁	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	525383 8	5255754	-	ID=TGME49_270350;길이=191 6	2017
TGME49_chr VI	995195	999093	-	ID=TGME49_239890;길이=389 8	2018
TGME49_chr VI	154674 3	1551741	-	ID=TGME49_240900;길이=499 8	2019
TGME49_chr VIIb	357082 3	3572905	-	ID=TGME49_258110;길이=208 2	2020
TGME49_chr IX	168738 8	1690438	+	ID=TGME49_265220;길이=305 0	2021
TGME49_chr VIII	186192 8	1864368	+	ID=TGME49_232120;길이=244 0	2022
TGME49_chr V	488616	490907	+	ID=TGME49_220620;길이=229 1	2023
TGME49_chr VI	340246 4	3405837	-	ID=TGME49_244620;길이=337 3	2024
TGME49_chr V	469162	471286	+	ID=TGME49_220585;길이=212 4	2025
TGME49_chr X	448104	450711	-	ID=TGME49_228270;길이=260 7	2026
TGME49_chr Ia	840385	841380	-	ID=TGME49_294350;길이=995	2027
TGME49_chr XI	164217 0	1643093	+	ID=TGME49_310875;길이=923	2028
TGME49_chr VIII	499571 9	4997442	+	ID=TGME49_270780;길이=172 3	2029
TGME49_chr VI	927570	932508	-	ID=TGME49_239800;길이=493 8	2030
TGME49_chr VIIa	184331 3	1845988	+	ID=TGME49_204370;길이=267 5	2031
TGME49_chr X	454960 6	4553931	+	ID=TGME49_234940;길이=432 5	2032
TGME49_chr VI	170878 5	1711030	+	ID=TGME49_241610;길이=224 5	2033
TGME49_chr X	493897 2	4940429	-	ID=TGME49_235540;길이=145 7	2034
TGME49_chr VIIb	164856	169420	+	ID=TGME49_264120;길이=456 4	2035

[0217]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	402759 8	4029731	+	ID=TGME49_291000;길이=213 3	2036
TGME49_chr VIIa	141959 9	1421687	+	ID=TGME49_205402;길이=208 8	2037
TGME49_chr XI	436362	437746	+	ID=TGME49_309020;길이=138 4	2038
TGME49_chr XI	517629 9	5179174	+	ID=TGME49_316190;길이=287 5	2039
TGME49_chr VIIb	271212 0	2714104	-	ID=TGME49_259690;길이=198 4	2040
TGME49_chr Ib	145031 4	1450964	+	ID=TGME49_209780;길이=650	2041
TGME49_chr XII	593935 9	5941323	-	ID=TGME49_278680;길이=196 4	2042
TGME49_chr XII	602054	603985	-	ID=TGME49_219850;길이=193 1	2043
TGME49_chr IX	443187 8	4435031	+	ID=TGME49_291960;길이=315 3	2044
TGME49_chr V	216750 0	2172395	-	ID=TGME49_285860;길이=489 5	2045
TGME49_chr IX	604975 2	6053318	+	ID=TGME49_306400;길이=356 6	2046
TGME49_chr VIIb	166256 8	1663864	-	ID=TGME49_261550;길이=129 6	2047
TGME49_chr X	280719 7	2808264	+	ID=TGME49_224820;길이=106 7	2048
TGME49_chr IX	194182 0	1943728	-	ID=TGME49_264875;길이=190 8	2049
TGME49_chr VI	41637	46647	+	ID=TGME49_238070;길이=501 0	2050
TGME49_chr XI	642083 5	6425390	-	ID=TGME49_216070;길이=455 5	2051
TGME49_chr IX	469404	472283	+	ID=TGME49_267670;길이=287 9	2052
TGME49_chr X	600717 6	6009045	-	ID=TGME49_237595;길이=186 9	2053
TGME49_chr XI	560847 2	5610173	-	ID=TGME49_316900;길이=170 1	2054

[0218]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	617199 5	6176026	+	ID=TGME49_214250;길이=403 1	2055
TGME49_chr IX	278634 8	2787500	-	ID=TGME49_288870;길이=115 2	2056
TGME49_chr IX	407134 0	4075503	-	ID=TGME49_291020;길이=416 3	2057
TGME49_chr XI	362611	365152	-	ID=TGME49_308920;길이=254 1	2058
TGME49_chr XII	603810 2	6039598	-	ID=TGME49_278540;길이=149 6	2059
TGME49_chr Ia	138386 6	1386224	+	ID=TGME49_295080;길이=235 8	2060
TGME49_chr XI	125521 0	1257092	+	ID=TGME49_310320;길이=188 2	2061
TGME49_chr X	580093 0	5803170	-	ID=TGME49_237230;길이=224 0	2062
TGME49_chr IX	372593 4	3727613	+	ID=TGME49_290460;길이=167 9	2063
TGME49_chr VI	831846	833871	-	ID=TGME49_239680;길이=202 5	2064
TGME49_chr X	184156	186759	-	ID=TGME49_228730;길이=260 3	2065
TGME49_chr IX	608936	612060	-	ID=TGME49_267510;길이=312 4	2066
TGME49_chr VIII	260404 2	2605811	+	ID=TGME49_233350;길이=176 9	2067
TGME49_chr VI	337029 2	3371967	+	ID=TGME49_244580;길이=167 5	2068
TGME49_chr VIIb	431302 8	4313787	-	ID=TGME49_256975;길이=759	2069
TGME49_chr XI	577542 7	5777232	-	ID=TGME49_216960;길이=180 5	2070
TGME49_chr VIIb	210373 7	2106170	-	ID=TGME49_260640;길이=243 3	2071
TGME49_chr X	179560 4	1797542	+	ID=TGME49_226100;길이=193 8	2072
TGME49_chr X	418101	419981	+	ID=TGME49_228320;길이=188 0	2073

[0219]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	134061 6	1343000	+	ID=TGME49_310440;길이=238 4	2074
TGME49_chr IX	335530 8	3357831	+	ID=TGME49_289630;길이=252 3	2075
TGME49_chr VIII	219258 3	2194733	+	ID=TGME49_232620;길이=215 0	2076
TGME49_chr VIIb	463656 1	4638383	-	ID=TGME49_255900;길이=182 2	2077
TGME49_chr VIII	558816 3	5590158	+	ID=TGME49_269820;길이=199 5	2078
TGME49_chr VI	324750 6	3250212	-	ID=TGME49_244408;길이=270 6	2079
TGME49_chr VIIa	205149 6	2056236	-	ID=TGME49_204010;길이=474 0	2080
TGME49_chr VIII	491985	494558	+	ID=TGME49_229980;길이=257 3	2081
TGME49_chr VIIa	205653 6	2058106	+	ID=TGME49_203985;길이=157 0	2082
TGME49_chr VIIa	140276	144404	+	ID=TGME49_280725;길이=412 8	2083
TGME49_chr VIII	225069 8	2252771	-	ID=TGME49_232750;길이=207 3	2084
TGME49_chr VIII	588704 7	5889397	-	ID=TGME49_269340;길이=235 0	2085
TGME49_chr XI	105280 3	1054295	-	ID=TGME49_310090;길이=149 2	2086
TGME49_chr VI	127977 2	1281594	+	ID=TGME49_240440;길이=182 2	2087
TGME49_chr VIIb	756456	758017	-	ID=TGME49_263160;길이=156 1	2088
TGME49_chr II	181199 3	1815135	+	ID=TGME49_297480;길이=314 2	2089
TGME49_chr VIIa	990948	995424	-	ID=TGME49_206430;길이=447 6	2090
TGME49_chr V	298611 3	2990861	-	ID=TGME49_283770;길이=474 8	2091
TGME49_chr XII	850493	852277	-	ID=TGME49_219560;길이=178 4	2092

[0220]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	134416 2	1349005	-	ID=TGME49_318430;길이=484 3	2093
TGME49_chr VIIb	105633 3	1059103	-	ID=TGME49_262730;길이=277 0	2094
TGME49_chr VIII	466171 3	4663360	-	ID=TGME49_271170;길이=164 7	2095
TGME49_chr XI	594276 8	5945248	+	ID=TGME49_216720;길이=248 0	2096
TGME49_chr XI	177952 0	1783053	+	ID=TGME49_311075;길이=353 3	2097
TGME49_chr Ib	182066 4	1822422	+	ID=TGME49_321420;길이=175 8	2098
TGME49_chr X	194415 3	1948496	+	ID=TGME49_225900;길이=434 3	2099
TGME49_chr VIIa	120133 5	1202972	+	ID=TGME49_205710;길이=163 7	2100
TGME49_chr XI	487233 4	4874729	-	ID=TGME49_315640;길이=239 5	2101
TGME49_chr VIII	155463 3	1557549	+	ID=TGME49_231815;길이=291 6	2102
TGME49_chr XI	305180 9	3056712	+	ID=TGME49_313030;길이=490 3	2103
TGME49_chr X	284025 0	2842141	-	ID=TGME49_224750;길이=189 1	2104
TGME49_chr IX	241922 1	2423061	+	ID=TGME49_288260;길이=384 0	2105
TGME49_chr II	443749	446045	-	ID=TGME49_221560;길이=229 6	2106
TGME49_chr VIIb	196919 2	1973085	-	ID=TGME49_261018;길이=389 3	2107
TGME49_chr X	297138 9	2973789	-	ID=TGME49_224575;길이=240 0	2108
TGME49_chr IX	509919	513149	-	ID=TGME49_267642;길이=323 0	2109
TGME49_chr XI	578743 2	5789807	-	ID=TGME49_216930;길이=237 5	2110
TGME49_chr IX	446902 8	4471277	-	ID=TGME49_292000;길이=224 9	2111

[0221]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	427623 7	4279338	-	ID=TGME49_291360;길이=310 1	2112
TGME49_chr VIIb	234217 7	2343737	-	ID=TGME49_260360;길이=156 0	2113
TGME49_chr XI	128744 5	1292319	+	ID=TGME49_310360;길이=487 4	2114
TGME49_chr XII	507069 2	5074348	-	ID=TGME49_250360;길이=365 6	2115
TGME49_chr VIIb	156955 9	1572751	+	ID=TGME49_261710;길이=319 2	2116
TGME49_chr X	258337 3	2586162	-	ID=TGME49_225020;길이=278 9	2117
TGME49_chr VIII	138633 9	1390571	-	ID=TGME49_231370;길이=423 2	2118
TGME49_chr IX	334174 9	3343589	-	ID=TGME49_289600;길이=184 0	2119
TGME49_chr IX	485250 0	4855230	+	ID=TGME49_210345;길이=273 0	2120
TGME49_chr VIII	199923 2	2003285	-	ID=TGME49_232300;길이=405 3	2121
TGME49_chr X	121791 8	1218840	+	ID=TGME49_226930;길이=922	2122
TGME49_chr IX	393414	395802	+	ID=TGME49_267740;길이=238 8	2123
TGME49_chr VIII	223983 1	2241664	-	ID=TGME49_232720;길이=183 3	2124
TGME49_chr X	177808 2	1780845	+	ID=TGME49_226220;길이=276 3	2125
TGME49_chr VIIb	432518 0	4329892	-	ID=TGME49_256970;길이=471 2	2126
TGME49_chr IV	185525	187612	+	ID=TGME49_320630;길이=208 7	2127
TGME49_chr XII	501645 0	5018497	+	ID=TGME49_250090;길이=204 7	2128
TGME49_chr IX	597155 2	5972595	+	ID=TGME49_306334;길이=104 3	2129
TGME49_chr IV	165490 4	1658845	-	ID=TGME49_211640;길이=394 1	2130

[0222]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	169110 2	1693242	+	ID=TGME49_211470;길이=214 0	2131
TGME49_chr VIII	144072 1	1442757	+	ID=TGME49_231460;길이=203 6	2132
TGME49_chr XI	217306 6	2177892	-	ID=TGME49_311640;길이=482 6	2133
TGME49_chr X	523272 0	5234701	+	ID=TGME49_236000;길이=198 1	2134
TGME49_chr XI	236132 5	2365388	+	ID=TGME49_311905;길이=406 3	2135
TGME49_chr VIII	248247 9	2486633	-	ID=TGME49_233180;길이=415 4	2136
TGME49_chr XII	205121	208744	-	ID=TGME49_300120;길이=362 3	2137
TGME49_chr XII	529337 8	5296947	-	ID=TGME49_250870;길이=356 9	2138
TGME49_chr IX	458277 3	4584034	-	ID=TGME49_292150;길이=126 1	2139
TGME49_chr VIIb	211865 7	2123522	-	ID=TGME49_260620;길이=486 5	2140
TGME49_chr XII	363282 9	3637477	+	ID=TGME49_247950;길이=464 8	2141
TGME49_chr VIII	341650 8	3419960	+	ID=TGME49_273520;길이=345 2	2142
TGME49_chr X	700708 5	7010674	-	ID=TGME49_215540;길이=358 9	2143
TGME49_chr X	261083 6	2612776	-	ID=TGME49_224990;길이=194 0	2144
TGME49_chr XII	286679	290951	+	ID=TGME49_300000;길이=427 2	2145
TGME49_chr XI	106758 1	1069045	-	ID=TGME49_310122;길이=146 4	2146
TGME49_chr VIIa	252372 4	2528425	-	ID=TGME49_203390;길이=470 1	2147
TGME49_chr VIII	636858 4	6372245	+	ID=TGME49_268670;길이=366 1	2148
TGME49_chr IX	237917 1	2383345	+	ID=TGME49_288210;길이=417 4	2149

[0223]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	624706 0	6249835	-	ID=TGME49_214310;길이=277 5	2150
TGME49_chr X	441072 4	4415344	-	ID=TGME49_234470;길이=462 0	2151
TGME49_chr VIII	483790	485820	+	ID=TGME49_229950;길이=203 0	2152
TGME49_chr VIIa	120794 0	1212921	+	ID=TGME49_205690;길이=498 1	2153
TGME49_chr IV	548750	550949	+	ID=TGME49_320050;길이=219 9	2154
TGME49_chr XI	333571 9	3337418	+	ID=TGME49_313390;길이=169 9	2155
TGME49_chr X	449972 9	4504428	+	ID=TGME49_234625;길이=469 9	2156
TGME49_chr IX	130617 1	1308162	-	ID=TGME49_266100;길이=199 1	2157
TGME49_chr X	498737 3	4988579	+	ID=TGME49_235620;길이=120 6	2158
TGME49_chr II	204915 3	2053496	-	ID=TGME49_297820;길이=434 3	2159
TGME49_chr Ib	100539 2	1010351	-	ID=TGME49_209040;길이=495 9	2160
TGME49_chr IV	141691 0	1419099	+	ID=TGME49_318320;길이=218 9	2161
TGME49_chr V	182371 3	1827597	-	ID=TGME49_286460;길이=388 4	2162
TGME49_chr XII	650588 8	6507354	-	ID=TGME49_277800;길이=146 6	2163
TGME49_chr XII	388967 1	3891930	-	ID=TGME49_248490;길이=225 9	2164
TGME49_chr VIIa	151611 3	1517866	-	ID=TGME49_205250;길이=175 3	2165
TGME49_chr VIIa	414725 7	4149471	-	ID=TGME49_281480;길이=221 4	2166
TGME49_chr VIII	266858 7	2671322	+	ID=TGME49_233480;길이=273 5	2167
TGME49_chr IX	560831 5	5609770	+	ID=TGME49_305830;길이=145 5	2168

[0224]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	546061 5	5465206	-	ID=TGME49_236630;길이=459 1	2169
TGME49_chr Ib	446581	448900	-	ID=TGME49_207930;길이=231 9	2170
TGME49_chr VI	295820 4	2962910	+	ID=TGME49_244020;길이=470 6	2171
TGME49_chr XI	255363 5	2555730	-	ID=TGME49_312260;길이=209 5	2172
TGME49_chr VIII	535366 9	5357579	+	ID=TGME49_270170;길이=391 0	2173
TGME49_chr XII	224079	225774	+	ID=TGME49_300090;길이=169 5	2174
TGME49_chr VIIb	461492 8	4619845	-	ID=TGME49_255960;길이=491 7	2175
TGME49_chr VIII	147327 1	1475198	-	ID=TGME49_231480;길이=192 7	2176
TGME49_chr VIIa	270767 5	2711017	+	ID=TGME49_203170;길이=334 2	2177
TGME49_chr X	432539 4	4328594	+	ID=TGME49_234375;길이=320 0	2178
TGME49_chr VIIb	201826	206450	+	ID=TGME49_264075;길이=462 4	2179
TGME49_chr XI	398770 4	3989680	-	ID=TGME49_314280;길이=197 6	2180
TGME49_chr IV	243110 7	2432795	+	ID=TGME49_301390;길이=168 8	2181
TGME49_chr VIIb	155404 7	1557249	-	ID=TGME49_261740;길이=320 2	2182
TGME49_chr XI	607789 8	6080164	+	ID=TGME49_216570;길이=226 6	2183
TGME49_chr IX	590787 7	5909447	-	ID=TGME49_306280;길이=157 0	2184
TGME49_chr IX	129127 4	1293712	+	ID=TGME49_266110;길이=243 8	2185
TGME49_chr Ib	3431	5000	+	ID=TGME49_207360;길이=156 9	2186
TGME49_chr IV	749326	751746	+	ID=TGME49_319740;길이=242 0	2187

[0225]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	157448 4	1575737	+	ID=TGME49_261700;길이=125 3	2188
TGME49_chr VI	133892 1	1343149	+	ID=TGME49_240630;길이=422 8	2189
TGME49_chr XII	553953 4	5541403	-	ID=TGME49_251720;길이=186 9	2190
TGME49_chr VIIb	489662 3	4898784	+	ID=TGME49_255330;길이=216 1	2191
TGME49_chr XII	473381 7	4737060	+	ID=TGME49_249690;길이=324 3	2192
TGME49_chr II	138387 1	1385210	+	ID=TGME49_223050;길이=133 9	2193
TGME49_chr XI	461734 6	4620622	+	ID=TGME49_315280;길이=327 6	2194
TGME49_chr XI	187012 5	1871822	+	ID=TGME49_311220;길이=169 7	2195
TGME49_chr XII	384324 5	3845735	+	ID=TGME49_248425;길이=249 0	2196
TGME49_chr XII	538950 6	5393276	+	ID=TGME49_251450;길이=377 0	2197
TGME49_chr VIII	598049 5	5982851	-	ID=TGME49_269228;길이=235 6	2198
TGME49_chr IV	147971 8	1482540	-	ID=TGME49_318220;길이=282 2	2199
TGME49_chr VIIa	391075 2	3912895	-	ID=TGME49_201390;길이=214 3	2200
TGME49_chr VI	286019 9	2862974	-	ID=TGME49_243790;길이=277 5	2201
TGME49_chr VIIa	217851 3	2180276	-	ID=TGME49_203860;길이=176 3	2202
TGME49_chr II	134193 1	1344535	+	ID=TGME49_222970;길이=260 4	2203
TGME49_chr XII	434870 0	4350687	-	ID=TGME49_249160;길이=198 7	2204
TGME49_chr V	181725 2	1819572	-	ID=TGME49_286485;길이=232 0	2205
TGME49_chr IX	409656 8	4099371	+	ID=TGME49_291070;길이=280 3	2206

[0226]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr V	145637 7	1459175	-	ID=TGME49_213940;길이=279 8	2207
TGME49_chr Ia	112826 8	1130676	-	ID=TGME49_294760;길이=240 8	2208
TGME49_chr XII	112149	115996	+	ID=TGME49_300270;길이=384 7	2209
TGME49_chr Ia	114118 2	1145699	-	ID=TGME49_294780;길이=451 7	2210
TGME49_chr Ia	684768	686694	-	ID=TGME49_294180;길이=192 6	2211
TGME49_chr XII	198253 3	1984559	-	ID=TGME49_217665;길이=202 6	2212
TGME49_chr VIIb	136836	141095	-	ID=TGME49_264150;길이=425 9	2213
TGME49_chr IX	364488 9	3646816	-	ID=TGME49_290200;길이=192 7	2214
TGME49_chr XI	341684 4	3420688	+	ID=TGME49_313475;길이=384 4	2215
TGME49_chr XII	555831 1	5563031	+	ID=TGME49_251750;길이=472 0	2216
TGME49_chr VIII	359112 6	3594224	-	ID=TGME49_273330;길이=309 8	2217
TGME49_chr XI	190716 5	1911891	+	ID=TGME49_311250;길이=472 6	2218
TGME49_chr Ib	606581	608427	+	ID=TGME49_208320;길이=184 6	2219
TGME49_chr IV	317723	320840	+	ID=TGME49_320470;길이=311 7	2220
TGME49_chr Ia	123136 6	1233810	+	ID=TGME49_294870;길이=244 4	2221
TGME49_chr V	799204	803341	+	ID=TGME49_213030;길이=413 7	2222
TGME49_chr XII	414126 7	4145015	-	ID=TGME49_248740;길이=374 8	2223
TGME49_chr VIII	683103 2	6832955	-	ID=TGME49_200370;길이=192 3	2224
TGME49_chr VIII	581418 1	5817773	+	ID=TGME49_269417;길이=359 2	2225

[0227]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ia	288432	290836	+	ID=TGME49_293380;길이=240 4	2226
TGME49_chr X	375771	377308	+	ID=TGME49_228360;길이=153 7	2227
TGME49_chr VIIa	281707 5	2820018	+	ID=TGME49_203070;길이=294 3	2228
TGME49_chr IX	264242 6	2644741	+	ID=TGME49_288630;길이=231 5	2229
TGME49_chr VIIa	377832 4	3780703	-	ID=TGME49_201810;길이=237 9	2230
TGME49_chr XI	213696 8	2138370	-	ID=TGME49_311500;길이=140 2	2231
TGME49_chr X	674660 4	6749287	+	ID=TGME49_215090;길이=268 3	2232
TGME49_chr VIIa	428379	432545	-	ID=TGME49_280420;길이=416 6	2233
TGME49_chr VI	318713 9	3188303	+	ID=TGME49_244320;길이=116 4	2234
TGME49_chr VI	146360 1	1465416	-	ID=TGME49_240830;길이=181 5	2235
TGME49_chr X	627386 0	6275989	+	ID=TGME49_214400;길이=212 9	2236
TGME49_chr VI	222030 9	2222591	+	ID=TGME49_242740;길이=228 2	2237
TGME49_chr Ib	135187 2	1355146	+	ID=TGME49_209590;길이=327 4	2238
TGME49_chr VIII	294473	299452	+	ID=TGME49_229490;길이=497 9	2239
TGME49_chr IV	199645 3	1998125	+	ID=TGME49_210970;길이=167 2	2240
TGME49_chr VIII	260800 7	2611227	+	ID=TGME49_233370;길이=322 0	2241
TGME49_chr VIIa	379539 3	3798765	+	ID=TGME49_201775;길이=337 2	2242
TGME49_chr Ia	129382 6	1295850	+	ID=TGME49_294970;길이=202 4	2243
TGME49_chr IX	453575 0	4537308	-	ID=TGME49_292070;길이=155 8	2244

[0228]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	227995 2	2283671	-	ID=TGME49_203740;길이=371 9	2245
TGME49_chr VIIa	485370	487434	+	ID=TGME49_280380;길이=206 4	2246
TGME49_chr XI	109558 0	1099919	+	ID=TGME49_310160;길이=433 9	2247
TGME49_chr VIIb	216676 2	2169888	+	ID=TGME49_260540;길이=312 6	2248
TGME49_chr X	549238 1	5494853	+	ID=TGME49_236780;길이=247 2	2249
TGME49_chr VIIa	525141	528720	-	ID=TGME49_304490;길이=357 9	2250
TGME49_chr XII	125146 2	1253195	+	ID=TGME49_218840;길이=173 3	2251
TGME49_chr VIIb	104456 0	1046178	-	ID=TGME49_262750;길이=161 8	2252
TGME49_chr XII	494142 6	4942964	+	ID=TGME49_249920;길이=153 8	2253
TGME49_chr VIIb	199587 9	1997531	-	ID=TGME49_260870;길이=165 2	2254
TGME49_chr XI	429925 8	4301184	-	ID=TGME49_314780;길이=192 6	2255
TGME49_chr II	176990 5	1774752	-	ID=TGME49_297420;길이=484 7	2256
TGME49_chr Ib	132004 0	1321949	-	ID=TGME49_209540;길이=190 9	2257
TGME49_chr IX	617711 7	6181474	-	ID=TGME49_306550;길이=435 7	2258
TGME49_chr V	172509 2	1727430	+	ID=TGME49_286680;길이=233 8	2259
TGME49_chr VI	811913	814755	+	ID=TGME49_239630;길이=284 2	2260
TGME49_chr IX	387628 2	3878405	+	ID=TGME49_290840;길이=212 3	2261
TGME49_chr II	169302 9	1695406	-	ID=TGME49_297330;길이=237 7	2262
TGME49_chr Ib	121402 2	1218129	+	ID=TGME49_209440;길이=410 7	2263

[0229]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	157430 3	1578976	+	ID=TGME49_231840;길이=467 3	2264
TGME49_chr VIIb	491424 3	4916993	+	ID=TGME49_255300;길이=275 0	2265
TGME49_chr XI	174501 4	1749860	-	ID=TGME49_311030;길이=484 6	2266
TGME49_chr VIII	413189 6	4134904	-	ID=TGME49_272230;길이=300 8	2267
TGME49_chr XI	186373	190635	+	ID=TGME49_306910;길이=426 2	2268
TGME49_chr VIII	496945 9	4972682	+	ID=TGME49_270820;길이=322 3	2269
TGME49_chr II	252286	255240	-	ID=TGME49_221320;길이=295 4	2270
TGME49_chr XII	466530 7	4667213	+	ID=TGME49_249590;길이=190 6	2271
TGME49_chr XII	183074	185954	+	ID=TGME49_300140;길이=288 0	2272
TGME49_chr X	210764 2	2109483	-	ID=TGME49_225730;길이=184 1	2273
TGME49_chr VIII	508420 9	5087859	+	ID=TGME49_270670;길이=365 0	2274
TGME49_chr VI	314133 8	3146169	-	ID=TGME49_244250;길이=483 1	2275
TGME49_chr IX	164172 8	1646063	+	ID=TGME49_265260;길이=433 5	2276
TGME49_chr Ib	162508 7	1627665	-	ID=TGME49_321700;길이=257 8	2277
TGME49_chr II	170859 5	1711391	+	ID=TGME49_297360;길이=279 6	2278
TGME49_chr XII	256157 0	2563897	+	ID=TGME49_245770;길이=232 7	2279
TGME49_chr XI	366208 3	3664424	-	ID=TGME49_313750;길이=234 1	2280
TGME49_chr IX	267897 6	2683389	+	ID=TGME49_288700;길이=441 3	2281
TGME49_chr VIIa	245253 3	2454348	-	ID=TGME49_203520;길이=181 5	2282

[0230]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	371670	372973	-	ID=TGME49_229660;길이=130 3	2283
TGME49_chr VIII	133833 3	1339664	-	ID=TGME49_231215;길이=133 1	2284
TGME49_chr XI	239343 5	2396761	+	ID=TGME49_312050;길이=332 6	2285
TGME49_chr VIIb	483404 4	4836547	-	ID=TGME49_255430;길이=250 3	2286
TGME49_chr Ib	454627	456429	-	ID=TGME49_207940;길이=180 2	2287
TGME49_chr XII	236457 5	2368999	+	ID=TGME49_245560;길이=442 4	2288
TGME49_chr IV	290608	295448	+	ID=TGME49_320500;길이=484 0	2289
TGME49_chr X	264779 2	2650609	+	ID=TGME49_224940;길이=281 7	2290
TGME49_chr II	595002	596475	-	ID=TGME49_221720;길이=147 3	2291
TGME49_chr V	6880	10388	-	ID=TGME49_296121;길이=350 8	2292
TGME49_chr X	493856 3	4939819	+	ID=TGME49_235550;길이=125 6	2293
TGME49_chr II	24693	25319	-	ID=TGME49_220850;길이=626	2294
TGME49_chr XII	656819 0	6570515	-	ID=TGME49_277700;길이=232 5	2295
TGME49_chr IV	205860 3	2061707	+	ID=TGME49_210787;길이=310 4	2296
TGME49_chr X	445107 9	4454735	-	ID=TGME49_234550;길이=365 6	2297
TGME49_chr X	155871	160694	-	ID=TGME49_228760;길이=482 3	2298
TGME49_chr X	704198 1	7044359	-	ID=TGME49_215590;길이=237 8	2299
TGME49_chr VIIb	197916 6	1981300	-	ID=TGME49_261010;길이=213 4	2300
TGME49_chr VIIa	266318	267937	+	ID=TGME49_280605;길이=161 9	2301

[0231]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	285557 3	2856668	+	ID=TGME49_233860;길이=109 5	2302
TGME49_chr Ib	609246	614107	+	ID=TGME49_208340;길이=486 1	2303
TGME49_chr X	638413 4	6388240	-	ID=TGME49_214580;길이=410 6	2304
TGME49_chr VI	280442	282228	+	ID=TGME49_238880;길이=178 6	2305
TGME49_chr IX	184894 2	1852708	-	ID=TGME49_265005;길이=376 6	2306
TGME49_chr X	541898 1	5422356	-	ID=TGME49_236550;길이=337 5	2307
TGME49_chr Ia	127468 1	1276904	+	ID=TGME49_294930;길이=222 3	2308
TGME49_chr Ia	665674	667870	-	ID=TGME49_294050;길이=219 6	2309
TGME49_chr VIIb	276184 4	2763517	+	ID=TGME49_259580;길이=167 3	2310
TGME49_chr IV	159649 7	1598239	+	ID=TGME49_211695;길이=174 2	2311
TGME49_chr VIII	233225 8	2334583	-	ID=TGME49_233000;길이=232 5	2312
TGME49_chr VIIb	345118 8	3453211	-	ID=TGME49_258370;길이=202 3	2313
TGME49_chr IX	525787 5	5259734	+	ID=TGME49_305160;길이=185 9	2314
TGME49_chr VIII	539273 3	5393889	-	ID=TGME49_270130;길이=115 6	2315
TGME49_chr XI	568855 1	5689284	-	ID=TGME49_217178;길이=733	2316
TGME49_chr Ia	115005 1	1152041	-	ID=TGME49_294800;길이=199 0	2317
TGME49_chr VIIa	691948	694230	-	ID=TGME49_304755;길이=228 2	2318
TGME49_chr X	419670 7	4198737	+	ID=TGME49_234220;길이=203 0	2319
TGME49_chr VI	709612	711661	-	ID=TGME49_239480;길이=204 9	2320

[0232]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	264566 8	2648078	-	ID=TGME49_246070;길이=241 0	2321
TGME49_chr VIIb	381484	385908	+	ID=TGME49_263700;길이=442 4	2322
TGME49_chr XI	382280 5	3823979	+	ID=TGME49_313940;길이=117 4	2323
TGME49_chr VIII	549297 3	5494998	-	ID=TGME49_269970;길이=202 5	2324
TGME49_chr II	195536 4	1959181	-	ID=TGME49_297725;길이=381 7	2325
TGME49_chr VIIa	440245 9	4404312	+	ID=TGME49_282150;길이=185 3	2326
TGME49_chr X	372363 4	3724688	-	ID=TGME49_223590;길이=105 4	2327
TGME49_chr X	302344 2	3025405	-	ID=TGME49_224510;길이=196 3	2328
TGME49_chr VIII	195667 4	1958845	-	ID=TGME49_232210;길이=217 1	2329
TGME49_chr IX	217788 1	2182679	+	ID=TGME49_264600;길이=479 8	2330
TGME49_chr VI	322813 4	3231037	-	ID=TGME49_244380;길이=290 3	2331
TGME49_chr XII	161554	164207	+	ID=TGME49_300190;길이=265 3	2332
TGME49_chr V	238695 5	2388910	-	ID=TGME49_285490;길이=195 5	2333
TGME49_chr XI	592380 6	5928393	-	ID=TGME49_216750;길이=458 7	2334
TGME49_chr VIII	521860 4	5220893	+	ID=TGME49_270510;길이=228 9	2335
TGME49_chr XII	448136	451773	-	ID=TGME49_307850;길이=363 7	2336
TGME49_chr XI	329830	333208	+	ID=TGME49_308890;길이=337 8	2337
TGME49_chr VIIb	498222 3	4984936	+	ID=TGME49_255230;길이=271 3	2338
TGME49_chr VI	133892 1	1340659	+	ID=TGME49_240620;길이=173 8	2339

[0233]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	2710672	2712535	-	ID=TGME49_203175; 길이=1863	2340
TGME49_chr Ia	783634	786312	+	ID=TGME49_294300; 길이=2678	2341
TGME49_chr VIIa	2207067	2211546	-	ID=TGME49_203820; 길이=4479	2342
TGME49_chr VIIb	1410124	1411940	+	ID=TGME49_262040; 길이=1816	2343
TGME49_chr V	1762123	1764217	-	ID=TGME49_286620; 길이=2094	2344
TGME49_chr XI	2444171	2445480	-	ID=TGME49_312120; 길이=1309	2345
TGME49_chr IX	2304200	2309017	+	ID=TGME49_288030; 길이=4817	2346
TGME49_chr XII	3107046	3108961	+	ID=TGME49_247020; 길이=1915	2347
TGME49_chr XII	1088408	1090747	-	ID=TGME49_219190; 길이=2339	2348
TGME49_chr VIII	5243101	5244559	-	ID=TGME49_270380; 길이=1458	2349
TGME49_chr IX	3661389	3662897	+	ID=TGME49_290240; 길이=1508	2350
TGME49_chr Ib	1465240	1466759	-	ID=TGME49_209810; 길이=1519	2351
TGME49_chr VIIb	4093997	4097159	+	ID=TGME49_257360; 길이=3162	2352
TGME49_chr IX	2730019	2732515	-	ID=TGME49_288760; 길이=2496	2353
TGME49_chr XI	1804715	1808023	+	ID=TGME49_311100; 길이=3308	2354
TGME49_chr X	4252113	4254822	-	ID=TGME49_234250; 길이=2709	2355
TGME49_chr XI	3602353	3604400	-	ID=TGME49_313677; 길이=2047	2356
TGME49_chr VIII	2912818	2914466	+	ID=TGME49_233940; 길이=1648	2357
TGME49_chr X	7000639	7004503	+	ID=TGME49_215530; 길이=3864	2358

[0234]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	228976 8	2291993	-	ID=TGME49_232940;길이=222 5	2359
TGME49_chr X	525819 8	5260065	-	ID=TGME49_236060;길이=186 7	2360
TGME49_chr VIII	188448 5	1889437	+	ID=TGME49_232150;길이=495 2	2361
TGME49_chr XII	188297 6	1885676	+	ID=TGME49_217510;길이=270 0	2362
TGME49_chr X	104990 5	1054351	-	ID=TGME49_227280;길이=444 6	2363
TGME49_chr Ia	124626 3	1247746	-	ID=TGME49_294880;길이=148 3	2364
TGME49_chr XII	589219 8	5894986	-	ID=TGME49_278770;길이=278 8	2365
TGME49_chr V	160407	162730	-	ID=TGME49_220132;길이=232 3	2366
TGME49_chr X	375707 6	3761771	+	ID=TGME49_223520;길이=469 5	2367
TGME49_chr VIII	380916 6	3812131	-	ID=TGME49_272670;길이=296 5	2368
TGME49_chr VI	281631 4	2820874	-	ID=TGME49_243720;길이=456 0	2369
TGME49_chr X	186691 9	1870597	+	ID=TGME49_226010;길이=367 8	2370
TGME49_chr Ia	165590 6	1660726	+	ID=TGME49_295640;길이=482 0	2371
TGME49_chr XII	249704 5	2499685	+	ID=TGME49_245730;길이=264 0	2372
TGME49_chr Ib	136890 7	1370576	+	ID=TGME49_209640;길이=166 9	2373
TGME49_chr VIIa	105516 3	1058273	-	ID=TGME49_206340;길이=311 0	2374
TGME49_chr X	210696 8	2108843	+	ID=TGME49_225720;길이=187 5	2375
TGME49_chr VIIa	647552	651135	-	ID=TGME49_304710;길이=358 3	2376
TGME49_chr VIIb	243397 7	2435254	+	ID=TGME49_260230;길이=127 7	2377

[0235]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	509374 9	5096679	+	ID=TGME49_270660;길이=293 0	2378
TGME49_chr IX	471251 2	4716695	+	ID=TGME49_292375;길이=418 3	2379
TGME49_chr IX	382464 8	3829311	+	ID=TGME49_290670;길이=466 3	2380
TGME49_chr VIIa	293718 4	2941974	+	ID=TGME49_202930;길이=479 0	2381
TGME49_chr Ib	264375	266961	+	ID=TGME49_207760;길이=258 6	2382
TGME49_chr X	106409 5	1066354	+	ID=TGME49_227150;길이=225 9	2383
TGME49_chr VIIa	223865 1	2240842	+	ID=TGME49_203780;길이=219 1	2384
TGME49_chr XII	551151 6	5514022	+	ID=TGME49_251660;길이=250 6	2385
TGME49_chr IX	272952 3	2732515	-	ID=TGME49_288755;길이=299 2	2386
TGME49_chr XI	652363 1	6524512	-	ID=TGME49_215930;길이=881	2387
TGME49_chr VIIa	147705 4	1478405	+	ID=TGME49_205310;길이=135 1	2388
TGME49_chr Ia	129989 6	1301681	+	ID=TGME49_294980;길이=178 5	2389
TGME49_chr XII	547882 6	5481198	+	ID=TGME49_251600;길이=237 2	2390
TGME49_chr IX	195627	197977	+	ID=TGME49_279410;길이=235 0	2391
TGME49_chr IX	258525 5	2587746	-	ID=TGME49_288500;길이=249 1	2392
TGME49_chr X	551024	553273	+	ID=TGME49_228130;길이=224 9	2393
TGME49_chr VIII	124629 9	1247749	-	ID=TGME49_231110;길이=145 0	2394
TGME49_chr IX	607677 2	6079949	+	ID=TGME49_306440;길이=317 7	2395
TGME49_chr XI	112403	113739	+	ID=TGME49_307030;길이=133 6	2396

[0236]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	148672 4	1489206	-	ID=TGME49_205300;길이=248 2	2397
TGME49_chr IX	390172 3	3904302	+	ID=TGME49_290870;길이=257 9	2398
TGME49_chr IX	300087 1	3002525	-	ID=TGME49_289110;길이=165 4	2399
TGME49_chr XII	645740 3	6459638	-	ID=TGME49_277880;길이=223 5	2400
TGME49_chr XI	138311 3	1385121	-	ID=TGME49_310490;길이=200 8	2401
TGME49_chr XII	358677 5	3589201	+	ID=TGME49_247790;길이=242 6	2402
TGME49_chr VI	251547 9	2520512	-	ID=TGME49_243290;길이=503 3	2403
TGME49_chr V	219744 0	2199492	+	ID=TGME49_285825;길이=205 2	2404
TGME49_chr VIIb	263966 5	2642073	-	ID=TGME49_259880;길이=240 8	2405
TGME49_chr IV	431416	433165	-	ID=TGME49_320220;길이=174 9	2406
TGME49_chr X	520247 5	5203919	+	ID=TGME49_235960;길이=144 4	2407
TGME49_chr Ia	171675 8	1718720	-	ID=TGME49_295590;길이=196 2	2408
TGME49_chr XI	515548 6	5157169	-	ID=TGME49_316140;길이=168 3	2409
TGME49_chr IX	315670 5	3158620	+	ID=TGME49_289300;길이=191 5	2410
TGME49_chr XI	143303 1	1437316	-	ID=TGME49_310530;길이=428 5	2411
TGME49_chr XII	686030 2	6862811	+	ID=TGME49_276900;길이=250 9	2412
TGME49_chr XI	497621 9	4980235	+	ID=TGME49_315780;길이=401 6	2413
TGME49_chr V	234089 0	2344008	+	ID=TGME49_285530;길이=311 8	2414
TGME49_chr IX	153988 8	1543369	-	ID=TGME49_265460;길이=348 1	2415

[0237]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	447801	449204	+	ID=TGME49_228250;길이=140 3	2416
TGME49_chr VI	314005 4	3144151	+	ID=TGME49_244260;길이=409 7	2417
TGME49_chr VIII	158400 8	1588110	+	ID=TGME49_231850;길이=410 2	2418
TGME49_chr XII	286200 4	2863907	-	ID=TGME49_246570;길이=190 3	2419
TGME49_chr XI	266441 5	2666362	+	ID=TGME49_312410;길이=194 7	2420
TGME49_chr VIIb	421947 8	4221342	-	ID=TGME49_257110;길이=186 4	2421
TGME49_chr VIIa	771238	775785	+	ID=TGME49_206620;길이=454 7	2422
TGME49_chr II	198867 1	1990219	+	ID=TGME49_297780;길이=154 8	2423
TGME49_chr IX	220586 0	2206820	+	ID=TGME49_264468;길이=960	2424
TGME49_chr VIIb	357578 6	3577531	-	ID=TGME49_258100;길이=174 5	2425
TGME49_chr IV	232473 2	2325789	-	ID=TGME49_301218;길이=105 7	2426
TGME49_chr XII	303307 6	3037430	+	ID=TGME49_246960;길이=435 4	2427
TGME49_chr XI	636074 3	6365335	-	ID=TGME49_216180;길이=459 2	2428
TGME49_chr VIIa	436474 3	4368384	-	ID=TGME49_282055;길이=364 1	2429
TGME49_chr VIII	426557 5	4269776	+	ID=TGME49_271950;길이=420 1	2430
TGME49_chr IX	327730	328648	-	ID=TGME49_267830;길이=918	2431
TGME49_chr II	138188 1	1383797	-	ID=TGME49_223040;길이=191 6	2432
TGME49_chr VIIb	318912 8	3193873	-	ID=TGME49_258780;길이=474 5	2433
TGME49_chr X	660251 9	6604937	+	ID=TGME49_214940;길이=241 8	2434

[0238]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	622111 1	6222788	+	ID=TGME49_278220;길이=167 7	2435
TGME49_chr IX	239457 6	2396348	+	ID=TGME49_288220;길이=177 2	2436
TGME49_chr XI	169684 9	1700575	-	ID=TGME49_310960;길이=372 6	2437
TGME49_chr X	178817 2	1791138	+	ID=TGME49_226110;길이=296 6	2438
TGME49_chr XI	244228 2	2445480	-	ID=TGME49_312110;길이=319 8	2439
TGME49_chr IX	219922	222865	+	ID=TGME49_279370;길이=294 3	2440
TGME49_chr XI	487335 8	4874729	-	ID=TGME49_315650;길이=137 1	2441
TGME49_chr X	744639 8	7448098	-	ID=TGME49_207200;길이=170 0	2442
TGME49_chr V	224509 7	2246666	-	ID=TGME49_285780;길이=156 9	2443
TGME49_chr VIIa	515933	519026	+	ID=TGME49_304480;길이=309 3	2444
TGME49_chr Ib	174008 0	1742565	+	ID=TGME49_321540;길이=248 5	2445
TGME49_chr XI	425793 3	4259598	+	ID=TGME49_314740;길이=166 5	2446
TGME49_chr Ib	761021	764259	+	ID=TGME49_208540;길이=323 8	2447
TGME49_chr VI	345096 6	3453208	-	ID=TGME49_244680;길이=224 2	2448
TGME49_chr XI	475504 2	4759341	-	ID=TGME49_315490;길이=429 9	2449
TGME49_chr X	737277 3	7375242	-	ID=TGME49_207070;길이=246 9	2450
TGME49_chr XI	158713 9	1588848	-	ID=TGME49_310770;길이=170 9	2451
TGME49_chr VIII	943428	945265	-	ID=TGME49_230660;길이=183 7	2452
TGME49_chr X	552123	553994	-	ID=TGME49_228145;길이=187 1	2453

[0239]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	345971 4	3462359	-	ID=TGME49_289790;길이=264 5	2454
TGME49_chr VIIa	333906 6	3342796	+	ID=TGME49_202410;길이=373 0	2455
TGME49_chr XI	649150 4	6494435	+	ID=TGME49_215980;길이=293 1	2456
TGME49_chr XII	258371 2	2585703	-	ID=TGME49_245990;길이=199 1	2457
TGME49_chr VI	263743 9	2640089	-	ID=TGME49_243440;길이=265 0	2458
TGME49_chr V	238613 0	2388506	+	ID=TGME49_285480;길이=237 6	2459
TGME49_chr XII	301562 0	3017791	-	ID=TGME49_246910;길이=217 1	2460
TGME49_chr VIII	430270 0	4305790	-	ID=TGME49_271888;길이=309 0	2461
TGME49_chr VIIa	186625 1	1869833	-	ID=TGME49_204350;길이=358 2	2462
TGME49_chr X	557001 3	5572759	-	ID=TGME49_236910;길이=274 6	2463
TGME49_chr VIII	317957 8	3181888	+	ID=TGME49_273905;길이=231 0	2464
TGME49_chr X	622031 4	6222244	-	ID=TGME49_214295;길이=193 0	2465
TGME49_chr IX	232316 4	2325191	-	ID=TGME49_288040;길이=202 7	2466
TGME49_chr X	560387 7	5606138	-	ID=TGME49_236950;길이=226 1	2467
TGME49_chr VI	302787 4	3028418	+	ID=TGME49_244105;길이=544	2468
TGME49_chr VIIb	289433 7	2897600	-	ID=TGME49_259200;길이=326 3	2469
TGME49_chr VIII	558816 3	5592490	+	ID=TGME49_269800;길이=432 7	2470
TGME49_chr X	211429 8	2117359	+	ID=TGME49_225690;길이=306 1	2471
TGME49_chr XII	480677 7	4808523	+	ID=TGME49_249810;길이=174 6	2472

[0240]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	199072	199671	+	ID=TGME49_279405;길이=599	2473
TGME49_chr X	276832 6	2773227	-	ID=TGME49_224860;길이=490 1	2474
TGME49_chr Ia	148738 8	1491082	-	ID=TGME49_295920;길이=369 4	2475
TGME49_chr X	222675 5	2227625	-	ID=TGME49_225460;길이=870	2476
TGME49_chr VIIa	420357 4	4207561	-	ID=TGME49_281575;길이=398 7	2477
TGME49_chr IX	514360 8	5146410	+	ID=TGME49_304990;길이=280 2	2478
TGME49_chr II	700644	704009	+	ID=TGME49_221930;길이=336 5	2479
TGME49_chr VIII	488775 3	4889510	+	ID=TGME49_270900;길이=175 7	2480
TGME49_chr VIIb	238808	241001	-	ID=TGME49_264010;길이=219 3	2481
TGME49_chr X	649445 8	6497510	-	ID=TGME49_214780;길이=305 2	2482
TGME49_chr X	394502 5	3947454	+	ID=TGME49_212275;길이=242 9	2483
TGME49_chr XI	784810	787257	+	ID=TGME49_309752;길이=244 7	2484
TGME49_chr VIIb	654090	658976	+	ID=TGME49_263280;길이=488 6	2485
TGME49_chr VI	111653 3	1119178	+	ID=TGME49_240255;길이=264 5	2486
TGME49_chr VIII	323292 0	3235018	-	ID=TGME49_273840;길이=209 8	2487
TGME49_chr X	449972 9	4502574	+	ID=TGME49_234622;길이=284 5	2488
TGME49_chr V	143972 1	1442480	-	ID=TGME49_213920;길이=275 9	2489
TGME49_chr VIIb	340936 6	3413789	+	ID=TGME49_258450;길이=442 3	2490
TGME49_chr VIIb	142475 4	1426396	+	ID=TGME49_262010;길이=164 2	2491

[0241]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	371574	373882	+	ID=TGME49_267760;길이=230 8	2492
TGME49_chr VIII	558432 8	5586338	+	ID=TGME49_269830;길이=201 0	2493
TGME49_chr VI	465237	466979	+	ID=TGME49_239110;길이=174 2	2494
TGME49_chr X	266989 4	2671902	-	ID=TGME49_224932;길이=200 8	2495
TGME49_chr VIIa	442220 1	4425705	-	ID=TGME49_282170;길이=350 4	2496
TGME49_chr XI	611994	614956	-	ID=TGME49_309280;길이=296 2	2497
TGME49_chr Ib	717976	721681	-	ID=TGME49_208460;길이=370 5	2498
TGME49_chr XII	142348 5	1426090	-	ID=TGME49_218570;길이=260 5	2499
TGME49_chr XII	230042	234619	-	ID=TGME49_300080;길이=457 7	2500
TGME49_chr XII	245764 7	2459970	-	ID=TGME49_245660;길이=232 3	2501
TGME49_chr VIII	676155 2	6766520	-	ID=TGME49_200250;길이=496 8	2502
TGME49_chr XII	228799 9	2289797	-	ID=TGME49_245460;길이=179 8	2503
TGME49_chr XII	376732 5	3771010	+	ID=TGME49_248270;길이=368 5	2504
TGME49_chr VIIb	426706 2	4268545	+	ID=TGME49_257040;길이=148 3	2505
TGME49_chr XI	573974 7	5741353	+	ID=TGME49_216980;길이=160 6	2506
TGME49_chr VIIa	356600 6	3567436	+	ID=TGME49_202160;길이=143 0	2507
TGME49_chr VIII	321618	326501	+	ID=TGME49_229630;길이=488 3	2508
TGME49_chr XI	451846 1	4520837	-	ID=TGME49_315140;길이=237 6	2509
TGME49_chr X	594950 4	5953689	+	ID=TGME49_237530;길이=418 5	2510

[0242]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	378040 6	3782419	+	ID=TGME49_223490;길이=201 3	2511
TGME49_chr II	115623 1	1160734	+	ID=TGME49_222660;길이=450 3	2512
TGME49_chr VI	285174 8	2852954	-	ID=TGME49_243770;길이=120 6	2513
TGME49_chr VI	539374	541507	+	ID=TGME49_239310;길이=213 3	2514
TGME49_chr XII	299776 4	3002544	-	ID=TGME49_246780;길이=478 0	2515
TGME49_chr XII	849594	852277	-	ID=TGME49_219570;길이=268 3	2516
TGME49_chr X	224072 0	2242446	+	ID=TGME49_225435;길이=172 6	2517
TGME49_chr VIII	200550 4	2007905	-	ID=TGME49_232310;길이=240 1	2518
TGME49_chr VIIb	82870	85185	-	ID=TGME49_264210;길이=231 5	2519
TGME49_chr II	267810	272793	+	ID=TGME49_221340;길이=498 3	2520
TGME49_chr V	246881 0	2471121	+	ID=TGME49_285268;길이=231 1	2521
TGME49_chr IX	244529 6	2446946	-	ID=TGME49_288320;길이=165 0	2522
TGME49_chr VIIa	133327	135436	-	ID=TGME49_280740;길이=210 9	2523
TGME49_chr Ib	864047	867064	-	ID=TGME49_208790;길이=301 7	2524
TGME49_chr X	676467 4	6769143	+	ID=TGME49_215130;길이=446 9	2525
TGME49_chr X	230633 0	2309400	-	ID=TGME49_225340;길이=307 0	2526
TGME49_chr VIII	330001 3	3302035	-	ID=TGME49_273740;길이=202 2	2527
TGME49_chr IX	210221 3	2103786	+	ID=TGME49_264700;길이=157 3	2528
TGME49_chr XI	288223	289585	-	ID=TGME49_308820;길이=136 2	2529

[0243]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	719188 5	7195726	-	ID=TGME49_275340; 길이=384 1	2530
TGME49_chr IX	348767 2	3492693	-	ID=TGME49_289850; 길이=502 1	2531
TGME49_chr X	702812 4	7032199	-	ID=TGME49_215570; 길이=407 5	2532
TGME49_chr VIIa	218671 6	2190767	+	ID=TGME49_203830; 길이=405 1	2533
TGME49_chr VIII	425163 9	4253470	-	ID=TGME49_271980; 길이=183 1	2534
TGME49_chr Ib	164306 9	1646070	-	ID=TGME49_321680; 길이=300 1	2535
TGME49_chr IX	560245 0	5604206	+	ID=TGME49_305820; 길이=175 6	2536
TGME49_chr VIII	299196 8	2993305	-	ID=TGME49_274140; 길이=133 7	2537
TGME49_chr VIII	529929 7	5301755	-	ID=TGME49_270273; 길이=245 8	2538
TGME49_chr X	215024 5	2152288	-	ID=TGME49_225570; 길이=204 3	2539
TGME49_chr VI	394289	399092	-	ID=TGME49_239010; 길이=480 3	2540
TGME49_chr V	187562 0	1880133	-	ID=TGME49_286270; 길이=451 3	2541
TGME49_chr XI	136638 1	1368421	-	ID=TGME49_310455; 길이=204 0	2542
TGME49_chr XII	411371 0	4117497	+	ID=TGME49_248720; 길이=378 7	2543
TGME49_chr XII	265367 6	2656148	-	ID=TGME49_246080; 길이=247 2	2544
TGME49_chr V	134947 9	1353386	-	ID=TGME49_213810; 길이=390 7	2545
TGME49_chr VIIa	229051 6	2292314	+	ID=TGME49_203720; 길이=179 8	2546
TGME49_chr IV	110162 7	1104332	-	ID=TGME49_318770; 길이=270 5	2547
TGME49_chr VIIb	428872	432171	+	ID=TGME49_263610; 길이=329 9	2548

[0244]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	609434 3	6098588	-	ID=TGME49_306450; 길이=424 5	2549
TGME49_chr VIIa	945669	947912	-	ID=TGME49_206480; 길이=224 3	2550
TGME49_chr VI	106138 9	1062893	+	ID=TGME49_240200; 길이=150 4	2551
TGME49_chr X	527649 3	5278337	-	ID=TGME49_236080; 길이=184 4	2552
TGME49_chr IX	440080 3	4405615	+	ID=TGME49_291930; 길이=481 2	2553
TGME49_chr IV	183045 8	1834833	+	ID=TGME49_211310; 길이=437 5	2554
TGME49_chr IV	800777	803054	+	ID=TGME49_319658; 길이=227 7	2555
TGME49_chr II	355915	357775	-	ID=TGME49_221440; 길이=186 0	2556
TGME49_chr XI	185770 6	1859770	-	ID=TGME49_311200; 길이=206 4	2557
TGME49_chr IV	173575	175464	+	ID=TGME49_320640; 길이=188 9	2558
TGME49_chr IX	498112 0	4983371	-	ID=TGME49_307575; 길이=225 1	2559
TGME49_chr II	151451 5	1516458	-	ID=TGME49_297060; 길이=194 3	2560
TGME49_chr VIIa	375536 8	3756835	+	ID=TGME49_201830; 길이=146 7	2561
TGME49_chr VI	148470 1	1486911	-	ID=TGME49_240860; 길이=221 0	2562
TGME49_chr XI	451688	453382	-	ID=TGME49_309030; 길이=169 4	2563
TGME49_chr VIIb	655477	659865	-	ID=TGME49_263290; 길이=438 8	2564
TGME49_chr X	309061	310991	+	ID=TGME49_228440; 길이=193 0	2565
TGME49_chr VIIa	436328 4	4367705	+	ID=TGME49_282070; 길이=442 1	2566
TGME49_chr X	339917 7	3401893	-	ID=TGME49_224000; 길이=271 6	2567

[0245]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	311090 2	3114645	-	ID=TGME49_289240;길이=374 3	2568
TGME49_chr X	714920 9	7152824	+	ID=TGME49_215775;길이=361 5	2569
TGME49_chr IV	566220	568593	+	ID=TGME49_320030;길이=237 3	2570
TGME49_chr VIII	436027 3	4363025	-	ID=TGME49_271800;길이=275 2	2571
TGME49_chr XII	214979 3	2150458	-	ID=TGME49_217810;길이=665	2572
TGME49_chr X	167741 2	1680531	+	ID=TGME49_226370;길이=311 9	2573
TGME49_chr IX	200953 7	2012433	-	ID=TGME49_264805;길이=289 6	2574
TGME49_chr XII	898597	901257	+	ID=TGME49_219500;길이=266 0	2575
TGME49_chr VIII	506870 4	5071169	-	ID=TGME49_270700;길이=246 5	2576
TGME49_chr VIIa	202767 1	2030677	+	ID=TGME49_204050;길이=300 6	2577
TGME49_chr VIII	164942 6	1651273	-	ID=TGME49_231920;길이=184 7	2578
TGME49_chr XII	500812 0	5009885	+	ID=TGME49_250060;길이=176 5	2579
TGME49_chr VIII	388039	391218	-	ID=TGME49_229690;길이=317 9	2580
TGME49_chr IX	245238 6	2456727	+	ID=TGME49_288340;길이=434 1	2581
TGME49_chr VIII	382189 5	3824021	-	ID=TGME49_272645;길이=212 6	2582
TGME49_chr XI	139023 1	1391395	+	ID=TGME49_310515;길이=116 4	2583
TGME49_chr XI	115147 8	1152895	-	ID=TGME49_310200;길이=141 7	2584
TGME49_chr VI	345004 2	3452022	+	ID=TGME49_244690;길이=198 0	2585
TGME49_chr VI	8252	9653	+	ID=TGME49_238010;길이=140 1	2586

[0246]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	105445 3	1057137	+	ID=TGME49_206330;길이=268 4	2587
TGME49_chr VIIb	398583 2	3987219	+	ID=TGME49_257540;길이=138 7	2588
TGME49_chr IX	797312	799366	-	ID=TGME49_267070;길이=205 4	2589
TGME49_chr VIIa	311326 9	3117191	+	ID=TGME49_202670;길이=392 2	2590
TGME49_chr IX	110892 2	1111021	-	ID=TGME49_266480;길이=209 9	2591
TGME49_chr VIII	600755 7	6009244	-	ID=TGME49_269190;길이=168 7	2592
TGME49_chr II	188862 3	1893021	-	ID=TGME49_297647;길이=439 8	2593
TGME49_chr V	871531	873751	-	ID=TGME49_213240;길이=222 0	2594
TGME49_chr VIII	63466	67252	+	ID=TGME49_229170;길이=378 6	2595
TGME49_chr V	177782 2	1780056	+	ID=TGME49_286570;길이=223 4	2596
TGME49_chr X	222510 0	2226843	+	ID=TGME49_225450;길이=174 3	2597
TGME49_chr VIII	561740	564177	-	ID=TGME49_230030;길이=243 7	2598
TGME49_chr X	193899 3	1940952	+	ID=TGME49_225910;길이=195 9	2599
TGME49_chr Ib	471344	476049	+	ID=TGME49_207965;길이=470 5	2600
TGME49_chr IX	497891 6	4982404	+	ID=TGME49_307580;길이=348 8	2601
TGME49_chr VIIa	160728	162946	-	ID=TGME49_280710;길이=221 8	2602
TGME49_chr VIIa	275203	280157	+	ID=TGME49_280590;길이=495 4	2603
TGME49_chr VIIb	858403	859587	+	ID=TGME49_263030;길이=118 4	2604
TGME49_chr VIII	660043 8	6602216	+	ID=TGME49_268250;길이=177 8	2605

[0247]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	439589 4	4398590	+	ID=TGME49_282140; 길이=269 6	2606
TGME49_chr Ia	192097	195881	+	ID=TGME49_293250; 길이=378 4	2607
TGME49_chr V	225290 0	2254312	+	ID=TGME49_285750; 길이=141 2	2608
TGME49_chr XI	131716 0	1319239	+	ID=TGME49_310400; 길이=207 9	2609
TGME49_chr VIII	166471 8	1667016	+	ID=TGME49_231950; 길이=229 8	2610
TGME49_chr IX	289972 9	2901760	-	ID=TGME49_288990; 길이=203 1	2611
TGME49_chr X	697253 9	6973901	+	ID=TGME49_215470; 길이=136 2	2612
TGME49_chr IX	439677 6	4400328	-	ID=TGME49_291890; 길이=355 2	2613
TGME49_chr IX	772170	775776	-	ID=TGME49_267120; 길이=360 6	2614
TGME49_chr XI	111045 5	1114100	+	ID=TGME49_310173; 길이=364 5	2615
TGME49_chr XII	571105 1	5713503	-	ID=TGME49_278990; 길이=245 2	2616
TGME49_chr IV	111855 9	1122425	-	ID=TGME49_318730; 길이=386 6	2617
TGME49_chr VIIa	125919 2	1261805	-	ID=TGME49_205625; 길이=261 3	2618
TGME49_chr X	694154 3	6942949	-	ID=TGME49_215390; 길이=140 6	2619
TGME49_chr X	438564 4	4390371	+	ID=TGME49_234440; 길이=472 7	2620
TGME49_chr X	452551 9	4528145	+	ID=TGME49_234690; 길이=262 6	2621
TGME49_chr XI	391709 0	3919270	-	ID=TGME49_314090; 길이=218 0	2622
TGME49_chr XI	637074 0	6375773	+	ID=TGME49_216155; 길이=503 3	2623
TGME49_chr V	192567 3	1927982	-	ID=TGME49_286200; 길이=230 9	2624

[0248]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	638184 1	6386433	+	ID=TGME49_277950;길이=459 2	2625
TGME49_chr X	804068	805942	+	ID=TGME49_227810;길이=187 4	2626
TGME49_chr VIIb	466846 0	4670573	+	ID=TGME49_255870;길이=211 3	2627
TGME49_chr VIII	229222 3	2295223	+	ID=TGME49_232960;길이=300 0	2628
TGME49_chr VIII	531086 0	5313259	-	ID=TGME49_270250;길이=239 9	2629
TGME49_chr XII	802072	803527	+	ID=TGME49_219630;길이=145 5	2630
TGME49_chr VIII	454670 0	4548626	+	ID=TGME49_271360;길이=192 6	2631
TGME49_chr XI	599056	600665	+	ID=TGME49_309265;길이=160 9	2632
TGME49_chr VIII	392454 9	3926856	-	ID=TGME49_272530;길이=230 7	2633
TGME49_chr XI	125576 6	1257660	-	ID=TGME49_310310;길이=189 4	2634
TGME49_chr VIIb	276283 2	2764576	-	ID=TGME49_259590;길이=174 4	2635
TGME49_chr X	245605 6	2459220	-	ID=TGME49_225140;길이=316 4	2636
TGME49_chr VIII	577592 1	5778051	+	ID=TGME49_269460;길이=213 0	2637
TGME49_chr VI	301653 2	3018964	-	ID=TGME49_244090;길이=243 2	2638
TGME49_chr VIIa	167784 1	1681517	+	ID=TGME49_205000;길이=367 6	2639
TGME49_chr XI	358235 1	3585505	-	ID=TGME49_313650;길이=315 4	2640
TGME49_chr II	127110 9	1273811	-	ID=TGME49_222860;길이=270 2	2641
TGME49_chr XII	577408	579217	-	ID=TGME49_308096;길이=180 9	2642
TGME49_chr XII	317551 4	3177639	-	ID=TGME49_247195;길이=212 5	2643

[0249]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	257184 0	2574320	-	ID=TGME49_203330;길이=248 0	2644
TGME49_chr VIIa	252324 0	2527928	+	ID=TGME49_203380;길이=468 8	2645
TGME49_chr IV	194144 1	1942608	+	ID=TGME49_211080;길이=116 7	2646
TGME49_chr XII	608943 4	6093280	-	ID=TGME49_278460;길이=384 6	2647
TGME49_chr XII	608105 8	6083036	-	ID=TGME49_278490;길이=197 8	2648
TGME49_chr XII	294113 7	2943790	+	ID=TGME49_246720;길이=265 3	2649
TGME49_chr VI	319629 3	3199662	-	ID=TGME49_244335;길이=336 9	2650
TGME49_chr VIIb	103157 1	1036168	-	ID=TGME49_262780;길이=459 7	2651
TGME49_chr VI	130318 1	1305102	-	ID=TGME49_240510;길이=192 1	2652
TGME49_chr IV	202165 8	2023438	-	ID=TGME49_210840;길이=178 0	2653
TGME49_chr VIII	322642 2	3228068	-	ID=TGME49_273850;길이=164 6	2654
TGME49_chr VIIb	310147 2	3103925	-	ID=TGME49_258900;길이=245 3	2655
TGME49_chr XI	116083 5	1164143	+	ID=TGME49_310220;길이=330 8	2656
TGME49_chr XI	551152	552779	+	ID=TGME49_309195;길이=162 7	2657
TGME49_chr XI	283782 1	2840040	-	ID=TGME49_312622;길이=221 9	2658
TGME49_chr II	138704 1	1390571	+	ID=TGME49_223060;길이=353 0	2659
TGME49_chr IV	194144 1	1943297	+	ID=TGME49_211070;길이=185 6	2660
TGME49_chr XI	785847	788515	-	ID=TGME49_309740;길이=266 8	2661
TGME49_chr X	305224 3	3054585	-	ID=TGME49_224470;길이=234 2	2662

[0250]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	427765 9	4279338	-	ID=TGME49_291370;길이=167 9	2663
TGME49_chr XI	826261	828335	-	ID=TGME49_309800;길이=207 4	2664
TGME49_chr XII	684026 2	6842703	+	ID=TGME49_276930;길이=244 1	2665
TGME49_chr IV	346077	348428	-	ID=TGME49_320450;길이=235 1	2666
TGME49_chr XII	164998 8	1651365	-	ID=TGME49_218250;길이=137 7	2667
TGME49_chr XII	515101 0	5152773	+	ID=TGME49_250730;길이=176 3	2668
TGME49_chr X	400247 0	4005528	+	ID=TGME49_212160;길이=305 8	2669
TGME49_chr VIIb	212693 2	2129789	+	ID=TGME49_260600;길이=285 7	2670
TGME49_chr XI	440680 5	4410963	-	ID=TGME49_314910;길이=415 8	2671
TGME49_chr VIII	625755 6	6259358	+	ID=TGME49_268835;길이=180 2	2672
TGME49_chr XII	187538 1	1876656	+	ID=TGME49_217490;길이=127 5	2673
TGME49_chr IX	385675 6	3857919	-	ID=TGME49_290710;길이=116 3	2674
TGME49_chr VIII	470060	474349	+	ID=TGME49_229930;길이=428 9	2675
TGME49_chr XI	402592 0	4030724	+	ID=TGME49_314358;길이=480 4	2676
TGME49_chr Ib	460087	461835	-	ID=TGME49_207955;길이=174 8	2677
TGME49_chr VIIa	249073 1	2493062	-	ID=TGME49_203480;길이=233 1	2678
TGME49_chr II	562040	565277	+	ID=TGME49_221685;길이=323 7	2679
TGME49_chr V	246215 1	2465375	-	ID=TGME49_285290;길이=322 4	2680
TGME49_chr V	645279	647282	+	ID=TGME49_212850;길이=200 3	2681

[0251]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	533141 4	5333301	+	ID=TGME49_270210; 길이=188 7	2682
TGME49_chr VIIb	912343	914333	-	ID=TGME49_262935; 길이=199 0	2683
TGME49_chr VIIa	412687 1	4128947	+	ID=TGME49_281450; 길이=207 6	2684
TGME49_chr VI	215890 9	2160846	+	ID=TGME49_242650; 길이=193 7	2685
TGME49_chr VIIb	412989 4	4131374	-	ID=TGME49_257330; 길이=148 0	2686
TGME49_chr XII	155500 9	1560065	-	ID=TGME49_218380; 길이=505 6	2687
TGME49_chr XII	379805 8	3802342	-	ID=TGME49_248300; 길이=428 4	2688
TGME49_chr X	277365 7	2776323	+	ID=TGME49_224850; 길이=266 6	2689
TGME49_chr XII	859876	861462	-	ID=TGME49_219550; 길이=158 6	2690
TGME49_chr VIIb	313382 0	3137682	+	ID=TGME49_258840; 길이=386 2	2691
TGME49_chr IX	456077 8	4562922	+	ID=TGME49_292120; 길이=214 4	2692
TGME49_chr IX	131779 9	1319959	+	ID=TGME49_266070; 길이=216 0	2693
TGME49_chr VIIa	58368	61406	-	ID=TGME49_280810; 길이=303 8	2694
TGME49_chr VIII	636518 9	6366539	-	ID=TGME49_268690; 길이=135 0	2695
TGME49_chr XI	605897 8	6060618	-	ID=TGME49_216600; 길이=164 0	2696
TGME49_chr VI	133479 9	1336826	-	ID=TGME49_240590; 길이=202 7	2697
TGME49_chr V	197348 9	1975650	-	ID=TGME49_286130; 길이=216 1	2698
TGME49_chr VIIb	110119 3	1106043	-	ID=TGME49_262655; 길이=485 0	2699
TGME49_chr II	403605	405254	+	ID=TGME49_221510; 길이=164 9	2700

[0252]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	173532 2	1737748	-	ID=TGME49_211420;길이=242 6	2701
TGME49_chr VIII	465098 5	4654271	+	ID=TGME49_271182;길이=328 6	2702
TGME49_chr VIIb	921322	925018	-	ID=TGME49_262930;길이=369 6	2703
TGME49_chr VI	231179 7	2313889	-	ID=TGME49_242800;길이=209 2	2704
TGME49_chr IX	482013 1	4821972	+	ID=TGME49_210390;길이=184 1	2705
TGME49_chr II	162667 5	1629738	-	ID=TGME49_297220;길이=306 3	2706
TGME49_chr XII	344546 0	3450482	+	ID=TGME49_247630;길이=502 2	2707
TGME49_chr X	480009 8	4801840	-	ID=TGME49_235350;길이=174 2	2708
TGME49_chr VIII	651925	653885	-	ID=TGME49_230160;길이=196 0	2709
TGME49_chr VIII	667493 3	6676585	+	ID=TGME49_268035;길이=165 2	2710
TGME49_chr XI	26464	30284	-	ID=TGME49_307260;길이=382 0	2711
TGME49_chr VI	311517 0	3117323	-	ID=TGME49_244200;길이=215 3	2712
TGME49_chr XII	899075	901898	-	ID=TGME49_219510;길이=282 3	2713
TGME49_chr X	716937 1	7172828	+	ID=TGME49_275320;길이=345 7	2714
TGME49_chr XII	295344 2	2955259	+	ID=TGME49_246740;길이=181 7	2715
TGME49_chr Ia	144546 8	1449325	+	ID=TGME49_295990;길이=385 7	2716
TGME49_chr VIIb	461405 5	4617990	+	ID=TGME49_255940;길이=393 5	2717
TGME49_chr Ib	147167 3	1474994	-	ID=TGME49_209820;길이=332 1	2718
TGME49_chr VI	918303	921331	+	ID=TGME49_239795;길이=302 8	2719

[0253]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	134373 9	1346394	+	ID=TGME49_205540; 길이=265 5	2720
TGME49_chr XI	325915 3	3260521	-	ID=TGME49_313305; 길이=136 8	2721
TGME49_chr IX	546161 9	5466485	+	ID=TGME49_305560; 길이=486 6	2722
TGME49_chr V	299743 7	2999458	+	ID=TGME49_283740; 길이=202 1	2723
TGME49_chr IX	490373 6	4907468	+	ID=TGME49_210270; 길이=373 2	2724
TGME49_chr VIIa	332321 7	3327698	-	ID=TGME49_202450; 길이=448 1	2725
TGME49_chr X	530604 5	5306976	+	ID=TGME49_236153; 길이=931	2726
TGME49_chr IV	116682 5	1168908	+	ID=TGME49_318650; 길이=208 3	2727
TGME49_chr VIIb	982149	984168	-	ID=TGME49_262840; 길이=201 9	2728
TGME49_chr IX	543533 4	5438062	+	ID=TGME49_305490; 길이=272 8	2729
TGME49_chr XI	298915 2	2990445	-	ID=TGME49_312930; 길이=129 3	2730
TGME49_chr IX	363241 8	3634414	-	ID=TGME49_290180; 길이=199 6	2731
TGME49_chr VIIa	184398 2	1846698	-	ID=TGME49_204380; 길이=271 6	2732
TGME49_chr VIII	188718 6	1890535	-	ID=TGME49_232140; 길이=334 9	2733
TGME49_chr IV	823132	825847	-	ID=TGME49_319630; 길이=271 5	2734
TGME49_chr VI	263672 9	2639733	+	ID=TGME49_243450; 길이=300 4	2735
TGME49_chr X	385673 1	3858953	+	ID=TGME49_223410; 길이=222 2	2736
TGME49_chr XII	467842 1	4682858	-	ID=TGME49_249600; 길이=443 7	2737
TGME49_chr XI	450992 2	4511567	-	ID=TGME49_315130; 길이=164 5	2738

[0254]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ia	1153066	1154657	+	ID=TGME49_294812; 길이=1591	2739
TGME49_chr IX	706165	708319	-	ID=TGME49_267350; 길이=2154	2740
TGME49_chr XII	4392567	4397271	+	ID=TGME49_249250; 길이=4704	2741
TGME49_chr VIII	3620478	3622646	+	ID=TGME49_273200; 길이=2168	2742
TGME49_chr IX	3048775	3052445	-	ID=TGME49_289180; 길이=3670	2743
TGME49_chr X	5786435	5789375	+	ID=TGME49_237220; 길이=2940	2744
TGME49_chr X	3448596	3453595	+	ID=TGME49_223920; 길이=4999	2745
TGME49_chr VI	1618811	1622040	+	ID=TGME49_241010; 길이=3229	2746
TGME49_chr XII	2808694	2813152	-	ID=TGME49_246500; 길이=4458	2747
TGME49_chr IX	952354	954209	-	ID=TGME49_266820; 길이=1855	2748
TGME49_chr X	152090	154165	-	ID=TGME49_228770; 길이=2075	2749
TGME49_chr XII	3243448	3245120	+	ID=TGME49_247305; 길이=1672	2750
TGME49_chr X	1028684	1030566	-	ID=TGME49_227320; 길이=1882	2751
TGME49_chr VI	453972	456175	+	ID=TGME49_239087; 길이=2203	2752
TGME49_chr VIII	370373	371876	+	ID=TGME49_229670; 길이=1503	2753
TGME49_chr XII	2205095	2207381	-	ID=TGME49_217890; 길이=2286	2754
TGME49_chr VIII	1171719	1176344	+	ID=TGME49_230990; 길이=4625	2755
TGME49_chr X	6719697	6721912	-	ID=TGME49_215040; 길이=2215	2756
TGME49_chr XII	3623594	3625340	-	ID=TGME49_247920; 길이=1746	2757

[0255]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	592120 8	5925102	-	ID=TGME49_306290;길이=389 4	2758
TGME49_chr VIIb	945683	947561	+	ID=TGME49_262890;길이=187 8	2759
TGME49_chr VIII	379335 1	3798091	-	ID=TGME49_272695;길이=474 0	2760
TGME49_chr VIIb	283563	284791	-	ID=TGME49_263870;길이=122 8	2761
TGME49_chr XI	289867 5	2900997	+	ID=TGME49_312680;길이=232 2	2762
TGME49_chr XI	426949 3	4271271	+	ID=TGME49_314760;길이=177 8	2763
TGME49_chr IV	743496	746016	-	ID=TGME49_319860;길이=252 0	2764
TGME49_chr XII	594475 2	5946781	-	ID=TGME49_278670;길이=202 9	2765
TGME49_chr VIIb	329609	331237	+	ID=TGME49_263760;길이=162 8	2766
TGME49_chr VIIb	361269 6	3614760	-	ID=TGME49_258070;길이=206 4	2767
TGME49_chr II	446960	451815	+	ID=TGME49_221580;길이=485 5	2768
TGME49_chr XII	514200 0	5143982	+	ID=TGME49_250710;길이=198 2	2769
TGME49_chr VIIa	348808	351228	-	ID=TGME49_280500;길이=242 0	2770
TGME49_chr XII	162631 5	1628343	+	ID=TGME49_218280;길이=202 8	2771
TGME49_chr VIII	498217 0	4987009	-	ID=TGME49_270810;길이=483 9	2772
TGME49_chr XI	521198 6	5213771	-	ID=TGME49_316250;길이=178 5	2773
TGME49_chr VIIa	141959 9	1424205	+	ID=TGME49_205398;길이=460 6	2774
TGME49_chr XII	736337	738273	+	ID=TGME49_219678;길이=193 6	2775
TGME49_chr XII	196947 2	1971512	-	ID=TGME49_217640;길이=204 0	2776

[0256]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	215885 7	2163020	-	ID=TGME49_225560;길이=416 3	2777
TGME49_chr V	152708 4	1529358	-	ID=TGME49_287210;길이=227 4	2778
TGME49_chr XII	298568 1	2987023	-	ID=TGME49_246763;길이=134 2	2779
TGME49_chr IV	118846 0	1192145	+	ID=TGME49_318610;길이=368 5	2780
TGME49_chr VIIb	311862 3	3122518	-	ID=TGME49_258870;길이=389 5	2781
TGME49_chr VIII	433889 5	4340907	+	ID=TGME49_271830;길이=201 2	2782
TGME49_chr XI	120398	121691	+	ID=TGME49_307015;길이=129 3	2783
TGME49_chr VIIb	465223 0	4655422	+	ID=TGME49_255880;길이=319 2	2784
TGME49_chr VIII	222975 3	2232098	-	ID=TGME49_232680;길이=234 5	2785
TGME49_chr XII	320194 6	3205868	-	ID=TGME49_247250;길이=392 2	2786
TGME49_chr VIII	199532 5	1996498	+	ID=TGME49_232290;길이=117 3	2787
TGME49_chr XII	234949 5	2351982	+	ID=TGME49_245530;길이=248 7	2788
TGME49_chr VIII	529682 0	5298844	-	ID=TGME49_270277;길이=202 4	2789
TGME49_chr XII	647409 1	6476198	-	ID=TGME49_277860;길이=210 7	2790
TGME49_chr XI	133178 5	1333925	-	ID=TGME49_310420;길이=214 0	2791
TGME49_chr X	660659 9	6611152	+	ID=TGME49_214950;길이=455 3	2792
TGME49_chr Ib	183802 4	1840558	+	ID=TGME49_321400;길이=253 4	2793
TGME49_chr X	186767 5	1871933	-	ID=TGME49_226020;길이=425 8	2794
TGME49_chr VIII	681217 0	6815991	+	ID=TGME49_200350;길이=382 1	2795

[0257]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	479739 5	4799343	-	ID=TGME49_249780; 길이=194 8	2796
TGME49_chr VIII	510689 4	5110114	+	ID=TGME49_270640; 길이=322 0	2797
TGME49_chr XI	185692 9	1859770	-	ID=TGME49_311190; 길이=284 1	2798
TGME49_chr VIIa	342913 0	3430859	-	ID=TGME49_202320; 길이=172 9	2799
TGME49_chr VIIb	181366	185076	+	ID=TGME49_264100; 길이=371 0	2800
TGME49_chr VIIb	364658 2	3648630	-	ID=TGME49_258020; 길이=204 8	2801
TGME49_chr V	279844 8	2800018	+	ID=TGME49_284160; 길이=157 0	2802
TGME49_chr XII	543018 1	5431564	+	ID=TGME49_251500; 길이=138 3	2803
TGME49_chr Ia	684229	685834	+	ID=TGME49_294190; 길이=160 5	2804
TGME49_chr X	451479 9	4517679	+	ID=TGME49_234670; 길이=288 0	2805
TGME49_chr Ib	19922	22201	-	ID=TGME49_207380; 길이=227 9	2806
TGME49_chr XII	283785 2	2840190	+	ID=TGME49_246540; 길이=233 8	2807
TGME49_chr VIIa	325989 6	3262598	+	ID=TGME49_202520; 길이=270 2	2808
TGME49_chr XI	266552 5	2666765	-	ID=TGME49_312400; 길이=124 0	2809
TGME49_chr II	355180	357222	+	ID=TGME49_221450; 길이=204 2	2810
TGME49_chr X	243323 0	2435647	+	ID=TGME49_225190; 길이=241 7	2811
TGME49_chr VIII	57748	60111	-	ID=TGME49_229150; 길이=236 3	2812
TGME49_chr VIIb	488564 3	4888514	+	ID=TGME49_255340; 길이=287 1	2813
TGME49_chr V	725744	726888	+	ID=TGME49_212955; 길이=114 4	2814

[0258]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	158074 4	1581416	-	ID=TGME49_240940;길이=672	2815
TGME49_chr VIII	928298	930205	-	ID=TGME49_230640;길이=190 7	2816
TGME49_chr XII	283274 2	2834747	+	ID=TGME49_246530;길이=200 5	2817
TGME49_chr VIII	56761	59366	+	ID=TGME49_229160;길이=260 5	2818
TGME49_chr IX	366672 9	3669016	+	ID=TGME49_290260;길이=228 7	2819
TGME49_chr VIII	637409 4	6376344	-	ID=TGME49_268660;길이=225 0	2820
TGME49_chr IV	169211 0	1694217	-	ID=TGME49_211480;길이=210 7	2821
TGME49_chr VIIb	227297 4	2275367	-	ID=TGME49_260440;길이=239 3	2822
TGME49_chr VIII	488029 8	4882600	+	ID=TGME49_270910;길이=230 2	2823
TGME49_chr XII	985332	987309	+	ID=TGME49_219300;길이=197 7	2824
TGME49_chr X	543004 1	5431958	+	ID=TGME49_236570;길이=191 7	2825
TGME49_chr VIIa	184782 3	1850467	+	ID=TGME49_204360;길이=264 4	2826
TGME49_chr XII	374368 0	3747903	+	ID=TGME49_248225;길이=422 3	2827
TGME49_chr X	378378 1	3785405	+	ID=TGME49_223485;길이=162 4	2828
TGME49_chr XI	427024 3	4271815	-	ID=TGME49_314750;길이=157 2	2829
TGME49_chr X	107854 3	1080826	+	ID=TGME49_227115;길이=228 3	2830
TGME49_chr XII	465961 9	4662247	-	ID=TGME49_249575;길이=262 8	2831
TGME49_chr VIIb	202396 4	2026656	-	ID=TGME49_260825;길이=269 2	2832
TGME49_chr IX	463941 8	4641832	+	ID=TGME49_292245;길이=241 4	2833

[0259]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	579808 6	5801508	+	ID=TGME49_269430;길이=342 2	2834
TGME49_chr X	508089 2	5083213	-	ID=TGME49_235730;길이=232 1	2835
TGME49_chr IX	283315	284597	-	ID=TGME49_279310;길이=128 2	2836
TGME49_chr XII	919752	924441	-	ID=TGME49_219485;길이=468 9	2837
TGME49_chr IX	254492 1	2548040	+	ID=TGME49_288450;길이=311 9	2838
TGME49_chr XI	534332 3	5345659	-	ID=TGME49_316480;길이=233 6	2839
TGME49_chr VI	207532	210236	+	ID=TGME49_238410;길이=270 4	2840
TGME49_chr XI	216523	218588	+	ID=TGME49_306880;길이=206 5	2841
TGME49_chr XI	513332	516847	+	ID=TGME49_309130;길이=351 5	2842
TGME49_chr IX	535194 5	5353735	-	ID=TGME49_305310;길이=179 0	2843
TGME49_chr IX	126094 0	1263377	+	ID=TGME49_266260;길이=243 7	2844
TGME49_chr VIII	677308 5	6775554	+	ID=TGME49_200290;길이=246 9	2845
TGME49_chr II	185931 3	1862244	-	ID=TGME49_297520;길이=293 1	2846
TGME49_chr VIIb	422173 7	4224344	+	ID=TGME49_257090;길이=260 7	2847
TGME49_chr VIII	207469 4	2076558	-	ID=TGME49_232400;길이=186 4	2848
TGME49_chr X	518456 5	5187267	-	ID=TGME49_235920;길이=270 2	2849
TGME49_chr VIIb	386221 2	3863945	+	ID=TGME49_257730;길이=173 3	2850
TGME49_chr IX	393562 3	3938663	+	ID=TGME49_290920;길이=304 0	2851
TGME49_chr Ib	609246	611891	+	ID=TGME49_208330;길이=264 5	2852

[0260]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	556909 4	5572139	+	ID=TGME49_236920;길이=304 5	2853
TGME49_chr VIIb	455122 7	4555100	-	ID=TGME49_256040;길이=387 3	2854
TGME49_chr X	753755	755679	-	ID=TGME49_227890;길이=192 4	2855
TGME49_chr VI	686164	689115	-	ID=TGME49_239475;길이=295 1	2856
TGME49_chr XI	394134 0	3945803	+	ID=TGME49_314240;길이=446 3	2857
TGME49_chr VIIb	317583 2	3180410	-	ID=TGME49_258810;길이=457 8	2858
TGME49_chr VIII	408176 9	4082967	+	ID=TGME49_272300;길이=119 8	2859
TGME49_chr VIIb	153505 7	1538674	-	ID=TGME49_261780;길이=361 7	2860
TGME49_chr XI	334541 2	3347300	-	ID=TGME49_313400;길이=188 8	2861
TGME49_chr VIII	223907 8	2241114	+	ID=TGME49_232730;길이=203 6	2862
TGME49_chr X	398543 0	3987663	+	ID=TGME49_212190;길이=223 3	2863
TGME49_chr XII	626186 1	6263784	+	ID=TGME49_278160;길이=192 3	2864
TGME49_chr X	113413 3	1136564	+	ID=TGME49_227015;길이=243 1	2865
TGME49_chr IX	492738 0	4929331	-	ID=TGME49_210255;길이=195 1	2866
TGME49_chr VIII	494173	497365	-	ID=TGME49_229970;길이=319 2	2867
TGME49_chr XI	460367 4	4605166	-	ID=TGME49_315250;길이=149 2	2868
TGME49_chr VIIa	385701	390631	-	ID=TGME49_280465;길이=493 0	2869
TGME49_chr XI	518667 4	5188422	+	ID=TGME49_316210;길이=174 8	2870
TGME49_chr VIII	272113 8	2725943	-	ID=TGME49_233610;길이=480 5	2871

[0261]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	307645 0	3078386	-	ID=TGME49_224340;길이=193 6	2872
TGME49_chr VIII	107071 4	1074839	+	ID=TGME49_230880;길이=412 5	2873
TGME49_chr XI	612081 0	6122479	+	ID=TGME49_216480;길이=166 9	2874
TGME49_chr XI	126835 0	1270276	-	ID=TGME49_310330;길이=192 6	2875
TGME49_chr VIII	374985 6	3752478	+	ID=TGME49_272740;길이=262 2	2876
TGME49_chr X	147998 8	1481931	+	ID=TGME49_226620;길이=194 3	2877
TGME49_chr XI	588699 2	5889236	+	ID=TGME49_216780;길이=224 4	2878
TGME49_chr X	952154	954291	-	ID=TGME49_227420;길이=213 7	2879
TGME49_chr VIIa	102891 1	1033633	-	ID=TGME49_206390;길이=472 2	2880
TGME49_chr X	447427 7	4477145	-	ID=TGME49_234570;길이=286 8	2881
TGME49_chr VIII	140470 1	1406518	+	ID=TGME49_231410;길이=181 7	2882
TGME49_chr V	374249	377042	-	ID=TGME49_220430;길이=279 3	2883
TGME49_chr X	336095 8	3364401	-	ID=TGME49_224060;길이=344 3	2884
TGME49_chr XII	345449 0	3456588	+	ID=TGME49_247648;길이=209 8	2885
TGME49_chr VI	249854 9	2500123	+	ID=TGME49_243280;길이=157 4	2886
TGME49_chr XI	244023 0	2444604	+	ID=TGME49_312130;길이=437 4	2887
TGME49_chr IX	652699	656532	+	ID=TGME49_267430;길이=383 3	2888
TGME49_chr VIII	551685 8	5520480	+	ID=TGME49_269930;길이=362 2	2889
TGME49_chr XII	513069 0	5133986	+	ID=TGME49_250700;길이=329 6	2890

[0262]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	694315 9	6945000	+	ID=TGME49_215410;길이=184 1	2891
TGME49_chr IV	208699 8	2089481	+	ID=TGME49_210760;길이=248 3	2892
TGME49_chr IX	532300 5	5326221	+	ID=TGME49_305270;길이=321 6	2893
TGME49_chr VIII	623527 6	6239397	+	ID=TGME49_268870;길이=412 1	2894
TGME49_chr VIII	657188 4	6573723	-	ID=TGME49_268290;길이=183 9	2895
TGME49_chr X	706425 9	7067143	+	ID=TGME49_215650;길이=288 4	2896
TGME49_chr VIIb	736866	738425	-	ID=TGME49_263190;길이=155 9	2897
TGME49_chr X	331808 0	3319616	-	ID=TGME49_224120;길이=153 6	2898
TGME49_chr IV	111356 8	1114995	-	ID=TGME49_318738;길이=142 7	2899
TGME49_chr X	341797 1	3419580	+	ID=TGME49_223970;길이=160 9	2900
TGME49_chr II	164314 0	1646065	+	ID=TGME49_297270;길이=292 5	2901
TGME49_chr IX	224195 0	2246458	+	ID=TGME49_264430;길이=450 8	2902
TGME49_chr II	892236	894195	+	ID=TGME49_222130;길이=195 9	2903
TGME49_chr II	775384	778953	+	ID=TGME49_222040;길이=356 9	2904
TGME49_chr VIII	623600 0	6240061	-	ID=TGME49_268880;길이=406 1	2905
TGME49_chr XI	148751 6	1489916	+	ID=TGME49_310630;길이=240 0	2906
TGME49_chr XI	448029 7	4482368	+	ID=TGME49_315120;길이=207 1	2907
TGME49_chr V	651209	653981	+	ID=TGME49_212860;길이=277 2	2908
TGME49_chr XII	563461 5	5636719	-	ID=TGME49_251860;길이=210 4	2909

[0263]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	582670 9	5829287	-	ID=TGME49_306195;길이=257 8	2910
TGME49_chr VIIb	402561 1	4030642	+	ID=TGME49_257470;길이=503 1	2911
TGME49_chr Ib	726992	728777	-	ID=TGME49_208490;길이=178 5	2912
TGME49_chr VIIb	363982 3	3643240	-	ID=TGME49_258030;길이=341 7	2913
TGME49_chr X	183654	185507	+	ID=TGME49_228720;길이=185 3	2914
TGME49_chr X	110441 8	1106139	+	ID=TGME49_227060;길이=172 1	2915
TGME49_chr VIII	265034	267090	-	ID=TGME49_229450;길이=205 6	2916
TGME49_chr XII	268528 3	2688777	+	ID=TGME49_246160;길이=349 4	2917
TGME49_chr XII	149346 9	1496095	-	ID=TGME49_218500;길이=262 6	2918
TGME49_chr X	293471	295200	+	ID=TGME49_228470;길이=172 9	2919
TGME49_chr Ia	114868 1	1150982	+	ID=TGME49_294805;길이=230 1	2920
TGME49_chr XII	514938 8	5150805	-	ID=TGME49_250720;길이=141 7	2921
TGME49_chr IV	246530 2	2467886	+	ID=TGME49_301420;길이=258 4	2922
TGME49_chr VI	902188	906938	+	ID=TGME49_239780;길이=475 0	2923
TGME49_chr VIIb	511337	515116	+	ID=TGME49_263505;길이=377 9	2924
TGME49_chr Ia	50386	52683	-	ID=TGME49_292960;길이=229 7	2925
TGME49_chr Ib	141039 8	1412319	-	ID=TGME49_209710;길이=192 1	2926
TGME49_chr II	60741	63309	-	ID=TGME49_220910;길이=256 8	2927
TGME49_chr XI	250297 0	2504148	+	ID=TGME49_312210;길이=117 8	2928

[0264]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	979074	983263	-	ID=TGME49_266760;길이=418 9	2929
TGME49_chr VIII	580027 7	5801876	-	ID=TGME49_269438;길이=159 9	2930
TGME49_chr XI	643499 2	6437143	-	ID=TGME49_216053;길이=215 1	2931
TGME49_chr XII	128101 7	1283487	+	ID=TGME49_218810;길이=247 0	2932
TGME49_chr X	663241 9	6636375	+	ID=TGME49_214970;길이=395 6	2933
TGME49_chr II	222418 2	2225712	+	ID=TGME49_298050;길이=153 0	2934
TGME49_chr XII	125252 0	1254167	-	ID=TGME49_218850;길이=164 7	2935
TGME49_chr XI	201833	203587	+	ID=TGME49_306900;길이=175 4	2936
TGME49_chr II	193775 1	1940101	+	ID=TGME49_297720;길이=235 0	2937
TGME49_chr XI	164349 4	1645015	-	ID=TGME49_310880;길이=152 1	2938
TGME49_chr Ia	162600 0	1628841	-	ID=TGME49_295662;길이=284 1	2939
TGME49_chr Ib	643892	647186	-	ID=TGME49_208380;길이=329 4	2940
TGME49_chr X	649593 9	6497510	-	ID=TGME49_214783;길이=157 1	2941
TGME49_chr X	332429 1	3327072	+	ID=TGME49_224090;길이=278 1	2942
TGME49_chr II	101066 6	1012466	-	ID=TGME49_222280;길이=180 0	2943
TGME49_chr IV	237763 8	2379502	+	ID=TGME49_301300;길이=186 4	2944
TGME49_chr IV	953527	955274	+	ID=TGME49_319500;길이=174 7	2945
TGME49_chr X	676741 5	6769751	-	ID=TGME49_215110;길이=233 6	2946
TGME49_chr VIIb	202927 8	2031836	-	ID=TGME49_260820;길이=255 8	2947

[0265]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	254786	256497	-	ID=TGME49_279340; 길이=171 1	2948
TGME49_chr XII	175694 1	1759557	+	ID=TGME49_217340; 길이=261 6	2949
TGME49_chr XI	412126 8	4122993	+	ID=TGME49_314480; 길이=172 5	2950
TGME49_chr IX	384719 8	3850189	+	ID=TGME49_290700; 길이=299 1	2951
TGME49_chr IX	519976 6	5203644	+	ID=TGME49_305050; 길이=387 8	2952
TGME49_chr VIIa	969639	972289	+	ID=TGME49_206440; 길이=265 0	2953
TGME49_chr Ib	140290	142474	+	ID=TGME49_207590; 길이=218 4	2954
TGME49_chr Ib	110916 4	1113311	-	ID=TGME49_209190; 길이=414 7	2955
TGME49_chr X	237416 5	2376239	+	ID=TGME49_225250; 길이=207 4	2956
TGME49_chr VI	234504 4	2347093	+	ID=TGME49_242840; 길이=204 9	2957
TGME49_chr IX	161378 3	1618496	+	ID=TGME49_265320; 길이=471 3	2958
TGME49_chr XI	399440 5	3998830	+	ID=TGME49_314320; 길이=442 5	2959
TGME49_chr V	168635 8	1689982	-	ID=TGME49_286760; 길이=362 4	2960
TGME49_chr XI	290748 2	2911745	-	ID=TGME49_312690; 길이=426 3	2961
TGME49_chr VI	883138	887371	+	ID=TGME49_239748; 길이=423 3	2962
TGME49_chr X	218330 0	2187485	+	ID=TGME49_225520; 길이=418 5	2963
TGME49_chr XI	557472 3	5577030	+	ID=TGME49_316770; 길이=230 7	2964
TGME49_chr II	531485	533086	+	ID=TGME49_221665; 길이=160 1	2965
TGME49_chr IX	351021 8	3512191	+	ID=TGME49_289900; 길이=197 3	2966

[0266]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	621494 5	6217062	+	ID=TGME49_214290;길이=211 7	2967
TGME49_chr VIIb	298361 8	2984755	-	ID=TGME49_259080;길이=113 7	2968
TGME49_chr VIIb	157650	161052	-	ID=TGME49_264140;길이=340 2	2969
TGME49_chr XII	353508	355474	-	ID=TGME49_299780;길이=196 6	2970
TGME49_chr X	319333 6	3197198	+	ID=TGME49_224235;길이=386 2	2971
TGME49_chr XII	351854	354229	+	ID=TGME49_299670;길이=237 5	2972
TGME49_chr VIIb	469174 2	4696076	+	ID=TGME49_255730;길이=433 4	2973
TGME49_chr VIII	231475 0	2316635	-	ID=TGME49_232980;길이=188 5	2974
TGME49_chr Ib	105374 7	1054786	-	ID=TGME49_209112;길이=103 9	2975
TGME49_chr VI	127108 8	1275407	-	ID=TGME49_240410;길이=431 9	2976
TGME49_chr IX	191375 0	1916033	-	ID=TGME49_264900;길이=228 3	2977
TGME49_chr X	691619	694702	+	ID=TGME49_227980;길이=308 3	2978
TGME49_chr VIII	562904 8	5630894	+	ID=TGME49_269740;길이=184 6	2979
TGME49_chr VIIb	341028 9	3414291	-	ID=TGME49_258458;길이=400 2	2980
TGME49_chr VIII	643003 0	6432264	-	ID=TGME49_268570;길이=223 4	2981
TGME49_chr IV	122113 2	1223825	-	ID=TGME49_318570;길이=269 3	2982
TGME49_chr VIII	213715 6	2141623	-	ID=TGME49_232520;길이=446 7	2983
TGME49_chr Ib	928521	933382	-	ID=TGME49_208970;길이=486 1	2984
TGME49_chr VIIa	89778	91426	-	ID=TGME49_280790;길이=164 8	2985

[0267]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	280024 0	2802305	+	ID=TGME49_288910;길이=206 5	2986
TGME49_chr V	584166	587344	-	ID=TGME49_212760;길이=317 8	2987
TGME49_chr VIII	560227 3	5604583	+	ID=TGME49_269770;길이=231 0	2988
TGME49_chr X	442874 9	4429928	+	ID=TGME49_234507;길이=117 9	2989
TGME49_chr XII	119838 2	1200277	-	ID=TGME49_218950;길이=189 5	2990
TGME49_chr X	274179	278462	-	ID=TGME49_228620;길이=428 3	2991
TGME49_chr IV	117776 0	1179793	+	ID=TGME49_318620;길이=203 3	2992
TGME49_chr Ia	547592	550266	+	ID=TGME49_293770;길이=267 4	2993
TGME49_chr XI	651808 5	6519956	-	ID=TGME49_215940;길이=187 1	2994
TGME49_chr VI	140023 6	1402037	+	ID=TGME49_240710;길이=180 1	2995
TGME49_chr XII	370584 1	3707649	-	ID=TGME49_248150;길이=180 8	2996
TGME49_chr X	686896 5	6872314	-	ID=TGME49_215260;길이=334 9	2997
TGME49_chr IX	498008 5	4983371	-	ID=TGME49_307570;길이=328 6	2998
TGME49_chr IX	624176 2	6243674	-	ID=TGME49_306650;길이=191 2	2999
TGME49_chr X	701460 9	7017444	+	ID=TGME49_215560;길이=283 5	3000
TGME49_chr XI	368686 0	3689632	-	ID=TGME49_313770;길이=277 2	3001
TGME49_chr IX	263222 0	2636771	-	ID=TGME49_288600;길이=455 1	3002
TGME49_chr II	83969	86643	+	ID=TGME49_220950;길이=267 4	3003
TGME49_chr VIIb	448383 2	4488559	+	ID=TGME49_256700;길이=472 7	3004

[0268]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	920403	922803	+	ID=TGME49_262920; 길이=240 0	3005
TGME49_chr IX	372686 3	3728579	-	ID=TGME49_290340; 길이=171 6	3006
TGME49_chr IV	226551 3	2268004	-	ID=TGME49_301000; 길이=249 1	3007
TGME49_chr VIII	461744 2	4619870	-	ID=TGME49_271270; 길이=242 8	3008
TGME49_chr VIII	491618 4	4918619	-	ID=TGME49_270880; 길이=243 5	3009
TGME49_chr XI	541082	545032	-	ID=TGME49_309180; 길이=395 0	3010
TGME49_chr VI	142117 0	1423356	-	ID=TGME49_240730; 길이=218 6	3011
TGME49_chr X	531123 5	5312787	+	ID=TGME49_236190; 길이=155 2	3012
TGME49_chr VIIa	193409 0	1936122	-	ID=TGME49_204270; 길이=203 2	3013
TGME49_chr X	368992 1	3692588	+	ID=TGME49_223620; 길이=266 7	3014
TGME49_chr IV	666975	669700	-	ID=TGME49_319920; 길이=272 5	3015
TGME49_chr VIII	270231 7	2704841	+	ID=TGME49_233540; 길이=252 4	3016
TGME49_chr XII	423031 4	4232511	-	ID=TGME49_248860; 길이=219 7	3017
TGME49_chr XI	267568 5	2678516	+	ID=TGME49_312430; 길이=283 1	3018
TGME49_chr XII	424232 7	4243685	-	ID=TGME49_248880; 길이=135 8	3019
TGME49_chr VIIa	347864 9	3480506	-	ID=TGME49_202255; 길이=185 7	3020
TGME49_chr XII	157841	160945	-	ID=TGME49_300220; 길이=310 4	3021
TGME49_chr IX	185890 8	1862051	+	ID=TGME49_264990; 길이=314 3	3022
TGME49_chr IV	112677 4	1128732	-	ID=TGME49_318720; 길이=195 8	3023

[0269]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	342230	347024	-	ID=TGME49_263750;길이=479 4	3024
TGME49_chr VIIa	343171 6	3434599	+	ID=TGME49_202300;길이=288 3	3025
TGME49_chr IX	336402 9	3366093	-	ID=TGME49_289640;길이=206 4	3026
TGME49_chr IV	184611 8	1847509	+	ID=TGME49_211300;길이=139 1	3027
TGME49_chr VI	193932 1	1941969	+	ID=TGME49_242290;길이=264 8	3028
TGME49_chr Ib	183802 4	1841751	+	ID=TGME49_321390;길이=372 7	3029
TGME49_chr XII	302544 3	3028262	-	ID=TGME49_246930;길이=281 9	3030
TGME49_chr Ib	982520	984651	-	ID=TGME49_209005;길이=213 1	3031
TGME49_chr IX	544001 4	5444552	+	ID=TGME49_305510;길이=453 8	3032
TGME49_chr Ib	178563 4	1787380	-	ID=TGME49_321460;길이=174 6	3033
TGME49_chr IX	126952 9	1271869	-	ID=TGME49_266150;길이=234 0	3034
TGME49_chr IV	136530	141115	+	ID=TGME49_320680;길이=458 5	3035
TGME49_chr II	212914 7	2131563	-	ID=TGME49_297940;길이=241 6	3036
TGME49_chr X	531170 6	5313875	-	ID=TGME49_236160;길이=216 9	3037
TGME49_chr IX	117514 2	1176935	-	ID=TGME49_266390;길이=179 3	3038
TGME49_chr XII	327042 8	3272692	+	ID=TGME49_247340;길이=226 4	3039
TGME49_chr VIIa	438652 3	4390549	-	ID=TGME49_282110;길이=402 6	3040
TGME49_chr XI	571254 2	5714427	+	ID=TGME49_217020;길이=188 5	3041
TGME49_chr Ib	508930	511554	-	ID=TGME49_207990;길이=262 4	3042

[0270]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	509090	514052	+	ID=TGME49_320090;길이=496 2	3043
TGME49_chr XII	232359 6	2325670	-	ID=TGME49_245500;길이=207 4	3044
TGME49_chr II	183879 3	1840776	-	ID=TGME49_297500;길이=198 3	3045
TGME49_chr Ia	184807 6	1849826	+	ID=TGME49_295310;길이=175 0	3046
TGME49_chr VIIa	118366	123372	+	ID=TGME49_280750;길이=500 6	3047
TGME49_chr IV	232361 9	2324963	+	ID=TGME49_301222;길이=134 4	3048
TGME49_chr VIIb	252580 3	2527506	+	ID=TGME49_260010;길이=170 3	3049
TGME49_chr VIII	260478 9	2607085	-	ID=TGME49_233340;길이=229 6	3050
TGME49_chr VIIb	629441	632828	-	ID=TGME49_263327;길이=338 7	3051
TGME49_chr VI	718257	722058	-	ID=TGME49_239490;길이=380 1	3052
TGME49_chr VIII	121917 1	1224214	-	ID=TGME49_231060;길이=504 3	3053
TGME49_chr X	736648 5	7369133	-	ID=TGME49_207060;길이=264 8	3054
TGME49_chr IX	326465	328648	-	ID=TGME49_267840;길이=218 3	3055
TGME49_chr VIIb	340084 1	3404561	+	ID=TGME49_258470;길이=372 0	3056
TGME49_chr VIII	367401 4	3677250	+	ID=TGME49_273075;길이=323 6	3057
TGME49_chr VIIa	212133 9	2125267	-	ID=TGME49_203940;길이=392 8	3058
TGME49_chr XII	219708 1	2199723	+	ID=TGME49_217875;길이=264 2	3059
TGME49_chr XI	569487	571481	+	ID=TGME49_309230;길이=199 4	3060
TGME49_chr X	660185	662395	-	ID=TGME49_228040;길이=221 0	3061

[0271]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	229408 9	2295780	-	ID=TGME49_232955;길이=169 1	3062
TGME49_chr XII	547668 5	5478806	-	ID=TGME49_251590;길이=212 1	3063
TGME49_chr Ib	633161	636374	+	ID=TGME49_208370;길이=321 3	3064
TGME49_chr XII	626259 2	6264233	-	ID=TGME49_278170;길이=164 1	3065
TGME49_chr XII	625932 7	6260911	-	ID=TGME49_278180;길이=158 4	3066
TGME49_chr VIIb	284829 9	2850481	+	ID=TGME49_259230;길이=218 2	3067
TGME49_chr IV	176800 3	1771226	+	ID=TGME49_211385;길이=322 3	3068
TGME49_chr VIII	172065 5	1723473	-	ID=TGME49_231994;길이=281 8	3069
TGME49_chr IX	408007 8	4082079	+	ID=TGME49_291040;길이=200 1	3070
TGME49_chr VI	131741 4	1319297	-	ID=TGME49_240540;길이=188 3	3071
TGME49_chr V	165286 5	1654841	+	ID=TGME49_286810;길이=197 6	3072
TGME49_chr VIIb	325161 9	3253665	-	ID=TGME49_258700;길이=204 6	3073
TGME49_chr VIIb	137035 4	1372539	+	ID=TGME49_262110;길이=218 5	3074
TGME49_chr VIIb	144950 9	1451279	+	ID=TGME49_261970;길이=177 0	3075
TGME49_chr XI	781501	783875	-	ID=TGME49_309730;길이=237 4	3076
TGME49_chr VIIb	164934 6	1654154	-	ID=TGME49_261580;길이=480 8	3077
TGME49_chr VIII	181487	183193	-	ID=TGME49_229340;길이=170 6	3078
TGME49_chr X	291164 9	2913447	-	ID=TGME49_224650;길이=179 8	3079
TGME49_chr Ib	306500	307968	+	ID=TGME49_207810;길이=146 8	3080

[0272]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	951504	953111	-	ID=TGME49_219440;길이=160 7	3081
TGME49_chr X	692138 4	6924980	+	ID=TGME49_215360;길이=359 6	3082
TGME49_chr Ia	387758	391767	-	ID=TGME49_293510;길이=400 9	3083
TGME49_chr VIIb	272936 4	2731606	+	ID=TGME49_259650;길이=224 2	3084
TGME49_chr X	592859	595829	-	ID=TGME49_228100;길이=297 0	3085
TGME49_chr X	702993 9	7032199	-	ID=TGME49_215580;길이=226 0	3086
TGME49_chr Ib	119160 1	1193002	-	ID=TGME49_209290;길이=140 1	3087
TGME49_chr X	302726 8	3029865	-	ID=TGME49_224500;길이=259 7	3088
TGME49_chr XII	689773 2	6900123	+	ID=TGME49_276830;길이=239 1	3089
TGME49_chr XII	680980 2	6813303	+	ID=TGME49_276980;길이=350 1	3090
TGME49_chr V	185135 0	1853522	-	ID=TGME49_286410;길이=217 2	3091
TGME49_chr XI	494616 4	4950718	+	ID=TGME49_315760;길이=455 4	3092
TGME49_chr IV	199645 3	2000862	+	ID=TGME49_210960;길이=440 9	3093
TGME49_chr X	708747 4	7089312	+	ID=TGME49_215690;길이=183 8	3094
TGME49_chr XI	228963 7	2291430	-	ID=TGME49_311780;길이=179 3	3095
TGME49_chr VIII	262734 1	2629242	-	ID=TGME49_233400;길이=190 1	3096
TGME49_chr X	683642 9	6838321	+	ID=TGME49_215250;길이=189 2	3097
TGME49_chr X	540048 1	5403238	+	ID=TGME49_236530;길이=275 7	3098
TGME49_chr V	293862 7	2941078	+	ID=TGME49_283820;길이=245 1	3099

[0273]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	181056 3	1815332	+	ID=TGME49_204400;길이=476 9	3100
TGME49_chr XII	574770 6	5751318	+	ID=TGME49_278930;길이=361 2	3101
TGME49_chr XII	616826 5	6171686	-	ID=TGME49_278290;길이=342 1	3102
TGME49_chr V	134446 0	1347471	-	ID=TGME49_213800;길이=301 1	3103
TGME49_chr II	41471	44914	-	ID=TGME49_220890;길이=344 3	3104
TGME49_chr Ib	709441	711471	-	ID=TGME49_208430;길이=203 0	3105
TGME49_chr XII	563313 1	5634774	+	ID=TGME49_251870;길이=164 3	3106
TGME49_chr VIIa	136419 9	1366359	+	ID=TGME49_205500;길이=216 0	3107
TGME49_chr VIIb	220452 7	2206884	+	ID=TGME49_260490;길이=235 7	3108
TGME49_chr X	437403 2	4376202	-	ID=TGME49_234420;길이=217 0	3109
TGME49_chr VIII	500876 0	5011510	-	ID=TGME49_270770;길이=275 0	3110
TGME49_chr V	123722 6	1239000	+	ID=TGME49_213690;길이=177 4	3111
TGME49_chr V	955818	959487	-	ID=TGME49_213360;길이=366 9	3112
TGME49_chr VIII	220681 8	2209210	+	ID=TGME49_232655;길이=239 2	3113
TGME49_chr X	363568 0	3638226	-	ID=TGME49_223725;길이=254 6	3114
TGME49_chr VI	173458 1	1739230	-	ID=TGME49_241830;길이=464 9	3115
TGME49_chr IV	183247 6	1835918	-	ID=TGME49_211320;길이=344 2	3116
TGME49_chr X	119702 6	1200743	-	ID=TGME49_226960;길이=371 7	3117
TGME49_chr VIII	560329 8	5605973	-	ID=TGME49_269775;길이=267 5	3118

[0274]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	358769 3	3590070	-	ID=TGME49_258090;길이=237 7	3119
TGME49_chr X	630533 7	6307575	-	ID=TGME49_214470;길이=223 8	3120
TGME49_chr X	238950 0	2393945	-	ID=TGME49_225230;길이=444 5	3121
TGME49_chr X	968991	973953	+	ID=TGME49_227380;길이=496 2	3122
TGME49_chr II	119430 0	1198358	+	ID=TGME49_222700;길이=405 8	3123
TGME49_chr XII	559432 6	5596456	-	ID=TGME49_251800;길이=213 0	3124
TGME49_chr V	270021 4	2702822	-	ID=TGME49_284590;길이=260 8	3125
TGME49_chr VIII	638591 9	6387483	+	ID=TGME49_268630;길이=156 4	3126
TGME49_chr VIIa	254215 9	2544885	-	ID=TGME49_203370;길이=272 6	3127
TGME49_chr IX	495497 4	4957346	-	ID=TGME49_210230;길이=237 2	3128
TGME49_chr Ia	101131 2	1015928	-	ID=TGME49_294620;길이=461 6	3129
TGME49_chr VIII	331933 3	3323273	-	ID=TGME49_273690;길이=394 0	3130
TGME49_chr Ia	108975 5	1093766	-	ID=TGME49_294710;길이=401 1	3131
TGME49_chr II	683949	685295	+	ID=TGME49_221905;길이=134 6	3132
TGME49_chr X	534422 4	5344882	-	ID=TGME49_236230;길이=658	3133
TGME49_chr VIII	613714 1	6141591	-	ID=TGME49_269015;길이=445 0	3134
TGME49_chr VIII	385503 6	3855734	+	ID=TGME49_272593;길이=698	3135
TGME49_chr VI	249899 0	2500814	-	ID=TGME49_243265;길이=182 4	3136
TGME49_chr VI	138391 6	1388756	-	ID=TGME49_240680;길이=484 0	3137

[0275]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	182675 1	1828019	-	ID=TGME49_226072;길이=126 8	3138
TGME49_chr XII	426360 5	4265733	-	ID=TGME49_248940;길이=212 8	3139
TGME49_chr X	483370 4	4835258	-	ID=TGME49_235390;길이=155 4	3140
TGME49_chr IX	549273 4	5495529	+	ID=TGME49_305600;길이=279 5	3141
TGME49_chr IV	159720 7	1599157	-	ID=TGME49_211700;길이=195 0	3142
TGME49_chr VIIb	220039 4	2201672	-	ID=TGME49_260510;길이=127 8	3143
TGME49_chr X	649193 9	6496460	+	ID=TGME49_214790;길이=452 1	3144
TGME49_chr XII	929521	931802	+	ID=TGME49_219450;길이=228 1	3145
TGME49_chr XII	147419 7	1475820	-	ID=TGME49_218540;길이=162 3	3146
TGME49_chr X	240686 1	2409830	-	ID=TGME49_225220;길이=296 9	3147
TGME49_chr X	165816 6	1660752	-	ID=TGME49_226410;길이=258 6	3148
TGME49_chr IV	211770 2	2122018	-	ID=TGME49_210730;길이=431 6	3149
TGME49_chr VI	232235 9	2326694	-	ID=TGME49_242820;길이=433 5	3150
TGME49_chr X	672039 0	6721912	-	ID=TGME49_215050;길이=152 2	3151
TGME49_chr XII	333033 6	3332740	-	ID=TGME49_247410;길이=240 4	3152
TGME49_chr X	479982 8	4801328	+	ID=TGME49_235360;길이=150 0	3153
TGME49_chr X	108020 6	1081448	-	ID=TGME49_227130;길이=124 2	3154
TGME49_chr XII	152903 4	1531895	-	ID=TGME49_218420;길이=286 1	3155
TGME49_chr XI	476195 6	4764431	+	ID=TGME49_315510;길이=247 5	3156

[0276]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	450638 2	4509664	+	ID=TGME49_249390;길이=328 2	3157
TGME49_chr X	153901 8	1541043	+	ID=TGME49_226550;길이=202 5	3158
TGME49_chr X	676709	678567	+	ID=TGME49_228000;길이=185 8	3159
TGME49_chr XII	604041 0	6044218	+	ID=TGME49_278518;길이=380 8	3160
TGME49_chr VIIa	205346 7	2056236	-	ID=TGME49_204000;길이=276 9	3161
TGME49_chr IX	674942	676609	-	ID=TGME49_267400;길이=166 7	3162
TGME49_chr V	117425 1	1179266	+	ID=TGME49_213620;길이=501 5	3163
TGME49_chr Ib	107448 6	1077281	-	ID=TGME49_209140;길이=279 5	3164
TGME49_chr XI	347581 6	3477674	-	ID=TGME49_313560;길이=185 8	3165
TGME49_chr XI	293500	294822	+	ID=TGME49_308840;길이=132 2	3166
TGME49_chr XI	255757 1	2561791	-	ID=TGME49_312270;길이=422 0	3167
TGME49_chr VIII	453196 0	4533762	+	ID=TGME49_271375;길이=180 2	3168
TGME49_chr XI	387515 3	3877145	-	ID=TGME49_314000;길이=199 2	3169
TGME49_chr VIIb	214816	216778	+	ID=TGME49_264050;길이=196 2	3170
TGME49_chr XII	348881 0	3491174	+	ID=TGME49_247690;길이=236 4	3171
TGME49_chr XI	156674	158998	-	ID=TGME49_306960;길이=232 4	3172
TGME49_chr VI	129514 7	1297637	-	ID=TGME49_240490;길이=249 0	3173
TGME49_chr XI	534295 4	5345109	+	ID=TGME49_316490;길이=215 5	3174
TGME49_chr VIIb	359026 5	3592441	+	ID=TGME49_258080;길이=217 6	3175

[0277]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	159020 7	1593920	-	ID=TGME49_310780;길이=371 3	3176
TGME49_chr X	524080 8	5243220	-	ID=TGME49_236010;길이=241 2	3177
TGME49_chr IX	209510 4	2097103	-	ID=TGME49_264720;길이=199 9	3178
TGME49_chr XI	234307 1	2344870	-	ID=TGME49_311870;길이=179 9	3179
TGME49_chr VIII	626852 9	6273255	+	ID=TGME49_268820;길이=472 6	3180
TGME49_chr X	500444 8	5006565	+	ID=TGME49_235640;길이=211 7	3181
TGME49_chr XI	137383 1	1375397	+	ID=TGME49_310470;길이=156 6	3182
TGME49_chr IX	525787 5	5261530	+	ID=TGME49_305170;길이=365 5	3183
TGME49_chr XII	189710 6	1899724	+	ID=TGME49_217550;길이=261 8	3184
TGME49_chr XII	603670 0	6038574	+	ID=TGME49_278530;길이=187 4	3185
TGME49_chr VIIa	379301 3	3794469	-	ID=TGME49_201785;길이=145 6	3186
TGME49_chr VIIa	402542 2	4029337	+	ID=TGME49_201120;길이=391 5	3187
TGME49_chr V	581559	583050	-	ID=TGME49_212750;길이=149 1	3188
TGME49_chr XII	599215 6	5994337	+	ID=TGME49_278620;길이=218 1	3189
TGME49_chr VI	554234	557286	+	ID=TGME49_239340;길이=305 2	3190
TGME49_chr XI	647286 9	6475497	+	ID=TGME49_216000;길이=262 8	3191
TGME49_chr IX	363778 3	3640204	-	ID=TGME49_290190;길이=242 1	3192
TGME49_chr VI	266936 9	2670449	+	ID=TGME49_243490;길이=108 0	3193
TGME49_chr XII	382058 0	3822334	+	ID=TGME49_248350;길이=175 4	3194

[0278]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr V	695402	700329	-	ID=TGME49_212900;길이=492 7	3195
TGME49_chr XI	396071 5	3962825	+	ID=TGME49_314250;길이=211 0	3196
TGME49_chr VIIb	361919 0	3621196	+	ID=TGME49_258050;길이=200 6	3197
TGME49_chr IX	249313 3	2494671	-	ID=TGME49_288390;길이=153 8	3198
TGME49_chr X	369146 3	3693211	-	ID=TGME49_223630;길이=174 8	3199
TGME49_chr X	240774 6	2409830	-	ID=TGME49_225210;길이=208 4	3200
TGME49_chr VIIa	117193 5	1174196	-	ID=TGME49_205760;길이=226 1	3201
TGME49_chr X	566188 1	5663299	-	ID=TGME49_237000;길이=141 8	3202
TGME49_chr X	651560 4	6517875	+	ID=TGME49_214830;길이=227 1	3203
TGME49_chr II	364035	366572	+	ID=TGME49_221460;길이=253 7	3204
TGME49_chr VIII	318145 1	3182748	-	ID=TGME49_273915;길이=129 7	3205
TGME49_chr XI	299096 9	2994121	+	ID=TGME49_312950;길이=315 2	3206
TGME49_chr XI	380755 5	3811116	+	ID=TGME49_313930;길이=356 1	3207
TGME49_chr VIIb	395152 2	3953639	+	ID=TGME49_257595;길이=211 7	3208
TGME49_chr X	432539 4	4329853	+	ID=TGME49_234380;길이=445 9	3209
TGME49_chr VIII	638681 0	6388130	-	ID=TGME49_268640;길이=132 0	3210
TGME49_chr VIIa	107686 3	1079600	+	ID=TGME49_206290;길이=273 7	3211
TGME49_chr IX	126168 7	1263721	-	ID=TGME49_266270;길이=203 4	3212
TGME49_chr V	160175	161766	+	ID=TGME49_220140;길이=159 1	3213

[0279]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	5945676	5948163	+	ID=TGME49_269280;길이=2487	3214
TGME49_chr XI	3960715	3965719	+	ID=TGME49_314260;길이=5004	3215
TGME49_chr XII	2765307	2768904	+	ID=TGME49_246340;길이=3597	3216
TGME49_chr VI	2079734	2081710	+	ID=TGME49_242590;길이=1976	3217
TGME49_chr IV	2078838	2080697	+	ID=TGME49_210778;길이=1859	3218
TGME49_chr VIIa	717178	721171	+	ID=TGME49_206695;길이=3993	3219
TGME49_chr XII	440948	443883	-	ID=TGME49_307840;길이=2935	3220
TGME49_chr XI	3698435	3702023	+	ID=TGME49_313810;길이=3588	3221
TGME49_chr VIII	3942775	3945251	-	ID=TGME49_272490;길이=2476	3222
TGME49_chr VIIa	609399	611880	-	ID=TGME49_304650;길이=2481	3223
TGME49_chr VIII	759334	761144	-	ID=TGME49_230410;길이=1810	3224
TGME49_chr X	6801459	6804369	+	ID=TGME49_215180;길이=2910	3225
TGME49_chr XI	2039625	2043830	+	ID=TGME49_311390;길이=4205	3226
TGME49_chr XII	4548008	4550577	-	ID=TGME49_249450;길이=2569	3227
TGME49_chr XII	3071741	3075581	+	ID=TGME49_246990;길이=3840	3228
TGME49_chr VIII	555529	558130	-	ID=TGME49_230020;길이=2601	3229
TGME49_chr IX	2625217	2629487	-	ID=TGME49_288570;길이=4270	3230
TGME49_chr VIII	4338895	4341797	+	ID=TGME49_271820;길이=2902	3231
TGME49_chr XI	5023123	5027594	-	ID=TGME49_315845;길이=4471	3232

[0280]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	389491 5	3895467	+	ID=TGME49_314038;길이=552	3233
TGME49_chr X	592274	594953	+	ID=TGME49_228080;길이=267 9	3234
TGME49_chr VIIa	790922	794038	-	ID=TGME49_206605;길이=311 6	3235
TGME49_chr X	12618	17436	-	ID=TGME49_200700;길이=481 8	3236
TGME49_chr II	113565	116395	+	ID=TGME49_221190;길이=283 0	3237
TGME49_chr XI	160362 0	1606558	+	ID=TGME49_310810;길이=293 8	3238
TGME49_chr XII	572854 0	5730511	-	ID=TGME49_278960;길이=197 1	3239
TGME49_chr VIII	211326 5	2117768	-	ID=TGME49_232450;길이=450 3	3240
TGME49_chr VI	269301 0	2694809	-	ID=TGME49_243510;길이=179 9	3241
TGME49_chr XII	213354 7	2135173	-	ID=TGME49_217790;길이=162 6	3242
TGME49_chr X	439688	443866	-	ID=TGME49_228290;길이=417 8	3243
TGME49_chr XI	838551	840380	-	ID=TGME49_309840;길이=182 9	3244
TGME49_chr VI	910173	911950	+	ID=TGME49_239790;길이=177 7	3245
TGME49_chr XI	586103 5	5863057	-	ID=TGME49_216830;길이=202 2	3246
TGME49_chr VIII	208515 2	2087343	-	ID=TGME49_232420;길이=219 1	3247
TGME49_chr XI	645712 0	6462057	+	ID=TGME49_216020;길이=493 7	3248
TGME49_chr XI	483761 6	4841215	+	ID=TGME49_315600;길이=359 9	3249
TGME49_chr VIIb	696220	698492	+	ID=TGME49_263220;길이=227 2	3250
TGME49_chr XI	525301 1	5255174	-	ID=TGME49_316350;길이=216 3	3251

[0281]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	620376 0	6205467	+	ID=TGME49_216370;길이=170 7	3252
TGME49_chr VIII	558474 5	5587000	-	ID=TGME49_269840;길이=225 5	3253
TGME49_chr VIIa	546593	549758	+	ID=TGME49_304630;길이=316 5	3254
TGME49_chr Ib	156371 6	1566724	+	ID=TGME49_209945;길이=300 8	3255
TGME49_chr VI	16939	19862	-	ID=TGME49_238020;길이=292 3	3256
TGME49_chr VIII	444495 0	4446452	-	ID=TGME49_271625;길이=150 2	3257
TGME49_chr VIIa	427699 8	4281215	-	ID=TGME49_281920;길이=421 7	3258
TGME49_chr Ia	512763	514787	-	ID=TGME49_293690;길이=202 4	3259
TGME49_chr XII	54016	56494	-	ID=TGME49_300360;길이=247 8	3260
TGME49_chr VIII	523811 9	5240134	-	ID=TGME49_270450;길이=201 5	3261
TGME49_chr X	366009 6	3662573	+	ID=TGME49_223672;길이=247 7	3262
TGME49_chr IV	113783 0	1140106	+	ID=TGME49_318700;길이=227 6	3263
TGME49_chr VIII	528585 9	5288814	+	ID=TGME49_270300;길이=295 5	3264
TGME49_chr VI	546954	551539	+	ID=TGME49_239330;길이=458 5	3265
TGME49_chr VI	94162	97062	-	ID=TGME49_238165;길이=290 0	3266
TGME49_chr XII	567518 7	5677936	+	ID=TGME49_251940;길이=274 9	3267
TGME49_chr VIII	656009 3	6561570	-	ID=TGME49_268300;길이=147 7	3268
TGME49_chr XII	599298 2	5995016	-	ID=TGME49_278630;길이=203 4	3269
TGME49_chr XI	220397 5	2206339	-	ID=TGME49_311680;길이=236 4	3270

[0282]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	285503 6	2857439	-	ID=TGME49_246555;길이=240 3	3271
TGME49_chr VIII	571335 8	5716949	+	ID=TGME49_269650;길이=359 1	3272
TGME49_chr VIIb	106316 8	1067088	-	ID=TGME49_262720;길이=392 0	3273
TGME49_chr X	460357 4	4605486	-	ID=TGME49_235010;길이=191 2	3274
TGME49_chr II	107656 8	1079158	+	ID=TGME49_222370;길이=259 0	3275
TGME49_chr VIII	367389	369573	-	ID=TGME49_229650;길이=218 4	3276
TGME49_chr XII	309988 6	3101996	+	ID=TGME49_247010;길이=211 0	3277
TGME49_chr VIIb	112704 8	1129656	+	ID=TGME49_262610;길이=260 8	3278
TGME49_chr VIII	323235 8	3234398	+	ID=TGME49_273830;길이=204 0	3279
TGME49_chr VIII	392361 1	3925862	+	ID=TGME49_272520;길이=225 1	3280
TGME49_chr IV	278199	282008	-	ID=TGME49_320540;길이=380 9	3281
TGME49_chr X	493321	495081	-	ID=TGME49_228210;길이=176 0	3282
TGME49_chr VIII	176852 8	1773014	+	ID=TGME49_232030;길이=448 6	3283
TGME49_chr VIII	527215 6	5276079	-	ID=TGME49_270330;길이=392 3	3284
TGME49_chr VIII	618311 8	6185406	-	ID=TGME49_268960;길이=228 8	3285
TGME49_chr IV	758992	760757	-	ID=TGME49_319730;길이=176 5	3286
TGME49_chr IV	948350	951893	-	ID=TGME49_319520;길이=354 3	3287
TGME49_chr IX	243886 6	2442135	+	ID=TGME49_288300;길이=326 9	3288
TGME49_chr VIIb	464046 3	4643361	-	ID=TGME49_255895;길이=289 8	3289

[0283]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	520651 0	5208863	+	ID=TGME49_235970;길이=235 3	3290
TGME49_chr VIIb	457066 1	4571741	-	ID=TGME49_256010;길이=108 0	3291
TGME49_chr X	162798 1	1632602	-	ID=TGME49_226450;길이=462 1	3292
TGME49_chr XI	615166	617797	+	ID=TGME49_309300;길이=263 1	3293
TGME49_chr VIII	331882 8	3322791	+	ID=TGME49_273670;길이=396 3	3294
TGME49_chr VIIb	856438	857983	-	ID=TGME49_263050;길이=154 5	3295
TGME49_chr IX	400505 2	4007328	-	ID=TGME49_290970;길이=227 6	3296
TGME49_chr XI	264504 5	2647433	+	ID=TGME49_312380;길이=238 8	3297
TGME49_chr Ib	927952	932691	+	ID=TGME49_208980;길이=473 9	3298
TGME49_chr X	151579 8	1517465	+	ID=TGME49_226590;길이=166 7	3299
TGME49_chr X	128574 3	1290308	-	ID=TGME49_226860;길이=456 5	3300
TGME49_chr VIII	616738 3	6169354	-	ID=TGME49_268985;길이=197 1	3301
TGME49_chr X	302548 5	3029064	+	ID=TGME49_224490;길이=357 9	3302
TGME49_chr IV	204762 7	2048983	-	ID=TGME49_210800;길이=135 6	3303
TGME49_chr IX	998733	1003398	+	ID=TGME49_266710;길이=466 5	3304
TGME49_chr X	439619 4	4397204	+	ID=TGME49_234450;길이=101 0	3305
TGME49_chr II	111277 7	1115543	-	ID=TGME49_222390;길이=276 6	3306
TGME49_chr IV	812222	814651	+	ID=TGME49_319640;길이=242 9	3307
TGME49_chr V	146017 0	1461527	+	ID=TGME49_213960;길이=135 7	3308

[0284]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ia	182514	184547	-	ID=TGME49_293230;길이=203 3	3309
TGME49_chr VIIb	227154 7	2274550	+	ID=TGME49_260430;길이=300 3	3310
TGME49_chr II	924486	928859	+	ID=TGME49_222170;길이=437 3	3311
TGME49_chr X	187466 3	1877819	-	ID=TGME49_226000;길이=315 6	3312
TGME49_chr IX	328901 2	3292661	+	ID=TGME49_289540;길이=364 9	3313
TGME49_chr XI	492369 9	4926214	+	ID=TGME49_315720;길이=251 5	3314
TGME49_chr XII	263335 8	2636013	-	ID=TGME49_246050;길이=265 5	3315
TGME49_chr VIIb	344264 3	3444853	-	ID=TGME49_258390;길이=221 0	3316
TGME49_chr Ib	147111 4	1474353	+	ID=TGME49_209830;길이=323 9	3317
TGME49_chr XII	652905 8	6534063	-	ID=TGME49_277770;길이=500 5	3318
TGME49_chr V	423922	426714	+	ID=TGME49_220510;길이=279 2	3319
TGME49_chr VIIb	174639 1	1751219	-	ID=TGME49_261450;길이=482 8	3320
TGME49_chr IV	163269 3	1634603	-	ID=TGME49_211670;길이=191 0	3321
TGME49_chr VIII	396351 1	3965457	+	ID=TGME49_272440;길이=194 6	3322
TGME49_chr IX	566623 6	5668173	+	ID=TGME49_305920;길이=193 7	3323
TGME49_chr XII	590265 5	5905896	-	ID=TGME49_278753;길이=324 1	3324
TGME49_chr XI	157411 6	1575491	+	ID=TGME49_310760;길이=137 5	3325
TGME49_chr VI	169290 9	1695468	+	ID=TGME49_241300;길이=255 9	3326
TGME49_chr Ib	601374	605206	-	ID=TGME49_208200;길이=383 2	3327

[0285]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	552084 8	5523439	+	ID=TGME49_316730;길이=259 1	3328
TGME49_chr XII	312717 2	3130041	-	ID=TGME49_247040;길이=286 9	3329
TGME49_chr Ib	139983 8	1402434	+	ID=TGME49_209690;길이=259 6	3330
TGME49_chr X	577995 1	5782510	-	ID=TGME49_237200;길이=255 9	3331
TGME49_chr XII	572423 7	5726426	-	ID=TGME49_278965;길이=218 9	3332
TGME49_chr XI	346637 4	3470440	+	ID=TGME49_313550;길이=406 6	3333
TGME49_chr VIIb	474972 2	4752553	+	ID=TGME49_255650;길이=283 1	3334
TGME49_chr IX	561149 0	5613721	+	ID=TGME49_305840;길이=223 1	3335
TGME49_chr IX	429130 4	4293908	-	ID=TGME49_291600;길이=260 4	3336
TGME49_chr XI	345384 9	3456185	+	ID=TGME49_313520;길이=233 6	3337
TGME49_chr XII	474994 2	4752741	+	ID=TGME49_249710;길이=279 9	3338
TGME49_chr Ia	178276 1	1785919	+	ID=TGME49_295390;길이=315 8	3339
TGME49_chr XI	732325	734891	+	ID=TGME49_309580;길이=256 6	3340
TGME49_chr X	649629 4	6497510	-	ID=TGME49_214787;길이=121 6	3341
TGME49_chr X	365554 0	3656902	-	ID=TGME49_223690;길이=136 2	3342
TGME49_chr VIIb	583138	585745	-	ID=TGME49_263400;길이=260 7	3343
TGME49_chr XI	175012	177263	-	ID=TGME49_306940;길이=225 1	3344
TGME49_chr X	625350 3	6255193	-	ID=TGME49_214330;길이=169 0	3345
TGME49_chr VIII	217454 6	2176594	-	ID=TGME49_232580;길이=204 8	3346

[0286]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	584058 7	5844665	+	ID=TGME49_216860;길이=407 8	3347
TGME49_chr Ib	154351 9	1546904	+	ID=TGME49_209910;길이=338 5	3348
TGME49_chr X	376923 6	3773701	+	ID=TGME49_223500;길이=446 5	3349
TGME49_chr VI	158597 3	1590736	-	ID=TGME49_240960;길이=476 3	3350
TGME49_chr V	609849	613843	+	ID=TGME49_212810;길이=399 4	3351
TGME49_chr II	131554 6	1319755	+	ID=TGME49_222940;길이=420 9	3352
TGME49_chr XI	293246 9	2934408	+	ID=TGME49_312830;길이=193 9	3353
TGME49_chr XII	519850 2	5201968	-	ID=TGME49_250770;길이=346 6	3354
TGME49_chr VIII	344477 8	3446250	+	ID=TGME49_273490;길이=147 2	3355
TGME49_chr V	139903 4	1402700	-	ID=TGME49_213870;길이=366 6	3356
TGME49_chr XII	225696 8	2259255	-	ID=TGME49_245432;길이=228 7	3357
TGME49_chr Ia	142394 9	1426873	-	ID=TGME49_296015;길이=292 4	3358
TGME49_chr VIIb	437934 7	4381247	-	ID=TGME49_256900;길이=190 0	3359
TGME49_chr IX	319382 4	3196200	+	ID=TGME49_289330;길이=237 6	3360
TGME49_chr XII	246387 5	2465663	+	ID=TGME49_245680;길이=178 8	3361
TGME49_chr XI	308195	311017	-	ID=TGME49_308860;길이=282 2	3362
TGME49_chr XI	607872 3	6081550	-	ID=TGME49_216580;길이=282 7	3363
TGME49_chr VIII	609952	611492	-	ID=TGME49_230110;길이=154 0	3364
TGME49_chr XI	378842	382347	+	ID=TGME49_308950;길이=350 5	3365

[0287]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	549935 6	5500559	+	ID=TGME49_251630;길이=120 3	3366
TGME49_chr VI	364142 0	3643484	+	ID=TGME49_292610;길이=206 4	3367
TGME49_chr II	146874 6	1470751	-	ID=TGME49_223130;길이=200 5	3368
TGME49_chr V	139777 0	1400442	+	ID=TGME49_213880;길이=267 2	3369
TGME49_chr XI	104119 2	1043750	-	ID=TGME49_310070;길이=255 8	3370
TGME49_chr Ia	837889	840906	+	ID=TGME49_294360;길이=301 7	3371
TGME49_chr V	217373 8	2175720	-	ID=TGME49_285850;길이=198 2	3372
TGME49_chr X	641401 4	6416110	-	ID=TGME49_214600;길이=209 6	3373
TGME49_chr VIII	625286 0	6255582	-	ID=TGME49_268850;길이=272 2	3374
TGME49_chr X	171380 7	1716377	-	ID=TGME49_226330;길이=257 0	3375
TGME49_chr X	620636 3	6211100	-	ID=TGME49_214270;길이=473 7	3376
TGME49_chr XII	557956 2	5582287	-	ID=TGME49_251770;길이=272 5	3377
TGME49_chr IV	206525 3	2067243	-	ID=TGME49_210783;길이=199 0	3378
TGME49_chr VIIb	400859 6	4011217	+	ID=TGME49_257500;길이=262 1	3379
TGME49_chr II	154534 8	1549822	+	ID=TGME49_297120;길이=447 4	3380
TGME49_chr XII	367637 2	3680205	-	ID=TGME49_248120;길이=383 3	3381
TGME49_chr VIIa	133138 4	1334559	+	ID=TGME49_205558;길이=317 5	3382
TGME49_chr IX	259647 1	2598483	+	ID=TGME49_288530;길이=201 2	3383
TGME49_chr XI	210377 0	2107867	-	ID=TGME49_311470;길이=409 7	3384

[0288]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	191160 1	1912822	+	ID=TGME49_217570;길이=122 1	3385
TGME49_chr VIII	321636 8	3219488	+	ID=TGME49_273860;길이=312 0	3386
TGME49_chr VIII	461647 0	4619161	+	ID=TGME49_271260;길이=269 1	3387
TGME49_chr IX	620311 9	6204949	-	ID=TGME49_306590;길이=183 0	3388
TGME49_chr X	865963	867849	-	ID=TGME49_227640;길이=188 6	3389
TGME49_chr IX	301656 5	3020010	+	ID=TGME49_289130;길이=344 5	3390
TGME49_chr Ib	498140	499444	-	ID=TGME49_207980;길이=130 4	3391
TGME49_chr X	567474 2	5676571	-	ID=TGME49_237015;길이=182 9	3392
TGME49_chr X	164534 6	1649764	-	ID=TGME49_226430;길이=441 8	3393
TGME49_chr VI	318164 0	3183599	-	ID=TGME49_244300;길이=195 9	3394
TGME49_chr IV	132847	135011	-	ID=TGME49_320700;길이=216 4	3395
TGME49_chr IX	453406 8	4536660	+	ID=TGME49_292080;길이=259 2	3396
TGME49_chr IX	263117 6	2636201	+	ID=TGME49_288610;길이=502 5	3397
TGME49_chr VIII	330994 9	3314650	-	ID=TGME49_273720;길이=470 1	3398
TGME49_chr XI	637331 2	6376490	-	ID=TGME49_216160;길이=317 8	3399
TGME49_chr VI	284727 9	2852109	+	ID=TGME49_243780;길이=483 0	3400
TGME49_chr X	693787 6	6940165	-	ID=TGME49_215380;길이=228 9	3401
TGME49_chr IX	272200 0	2725631	-	ID=TGME49_288740;길이=363 1	3402
TGME49_chr XI	579207 2	5794118	+	ID=TGME49_216910;길이=204 6	3403

[0289]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	138521 1	1389924	+	ID=TGME49_231380;길이=471 3	3404
TGME49_chr XI	398651 5	3988412	+	ID=TGME49_314295;길이=189 7	3405
TGME49_chr XII	200389 8	2008672	-	ID=TGME49_217680;길이=477 4	3406
TGME49_chr IX	530467	532341	-	ID=TGME49_267600;길이=187 4	3407
TGME49_chr XI	460604 1	4607359	+	ID=TGME49_315260;길이=131 8	3408
TGME49_chr VIII	357686 3	3580229	+	ID=TGME49_273350;길이=336 6	3409
TGME49_chr II	233786	235666	-	ID=TGME49_221310;길이=188 0	3410
TGME49_chr XII	428701 0	4288915	+	ID=TGME49_248990;길이=190 5	3411
TGME49_chr II	695953	698239	-	ID=TGME49_221818;길이=228 6	3412
TGME49_chr X	698314 9	6985034	+	ID=TGME49_215500;길이=188 5	3413
TGME49_chr V	799775	804114	-	ID=TGME49_213020;길이=433 9	3414
TGME49_chr VIIb	506139 8	5064594	+	ID=TGME49_255160;길이=319 6	3415
TGME49_chr VI	341788 2	3420561	+	ID=TGME49_244645;길이=267 9	3416
TGME49_chr XII	307306 4	3076076	-	ID=TGME49_246982;길이=301 2	3417
TGME49_chr VIIa	150026 9	1505002	+	ID=TGME49_205265;길이=473 3	3418
TGME49_chr VIII	211244 8	2114445	+	ID=TGME49_232475;길이=199 7	3419
TGME49_chr XII	118776 9	1192566	-	ID=TGME49_218960;길이=479 7	3420
TGME49_chr VI	180004 5	1804730	-	ID=TGME49_241880;길이=468 5	3421
TGME49_chr IX	550593 7	5508990	-	ID=TGME49_305610;길이=305 3	3422

[0290]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	253436	258317	-	ID=TGME49_238500;길이=4881	3423
TGME49_chr VIIb	3933802	3935262	-	ID=TGME49_257650;길이=1460	3424
TGME49_chr VIII	6330739	6334570	-	ID=TGME49_268760;길이=3831	3425
TGME49_chr VIII	793083	797090	-	ID=TGME49_230440;길이=4007	3426
TGME49_chr VIIa	186501	187589	+	ID=TGME49_280680;길이=1088	3427
TGME49_chr XII	6705701	6707565	-	ID=TGME49_277220;길이=1864	3428
TGME49_chr II	2003854	2005661	-	ID=TGME49_297790;길이=1807	3429
TGME49_chr VI	2742265	2744014	-	ID=TGME49_243590;길이=1749	3430
TGME49_chr X	7067044	7071859	-	ID=TGME49_215640;길이=4815	3431
TGME49_chr VIIa	1741358	1742899	+	ID=TGME49_204505;길이=1541	3432
TGME49_chr XI	1843155	1846445	+	ID=TGME49_311180;길이=3290	3433
TGME49_chr VI	948026	952595	-	ID=TGME49_239820;길이=4569	3434
TGME49_chr XII	1834934	1837076	-	ID=TGME49_217430;길이=2142	3435
TGME49_chr XI	3142479	3147503	+	ID=TGME49_313160;길이=5024	3436
TGME49_chr X	7130359	7132487	+	ID=TGME49_215730;길이=2128	3437
TGME49_chr VIII	2286666	2287451	-	ID=TGME49_232840;길이=785	3438
TGME49_chr XI	1636892	1638984	-	ID=TGME49_310860;길이=2092	3439
TGME49_chr VIIa	4276229	4277993	+	ID=TGME49_281930;길이=1764	3440
TGME49_chr VIII	6329519	6334023	+	ID=TGME49_268750;길이=4504	3441

[0291]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	528450	531729	-	ID=TGME49_239290;길이=327 9	3442
TGME49_chr VIIa	135506 7	1359343	-	ID=TGME49_205530;길이=427 6	3443
TGME49_chr XI	587790 7	5880229	-	ID=TGME49_216800;길이=232 2	3444
TGME49_chr VIIb	267966 3	2683799	-	ID=TGME49_259835;길이=413 6	3445
TGME49_chr IX	559844 2	5601226	-	ID=TGME49_305800;길이=278 4	3446
TGME49_chr Ia	676197	678509	-	ID=TGME49_294100;길이=231 2	3447
TGME49_chr XII	480745 2	4810501	-	ID=TGME49_249800;길이=304 9	3448
TGME49_chr XI	295233 4	2953239	-	ID=TGME49_312850;길이=905	3449
TGME49_chr VI	85967	88465	+	ID=TGME49_238150;길이=249 8	3450
TGME49_chr VI	177487 0	1776217	+	ID=TGME49_241870;길이=134 7	3451
TGME49_chr X	244382 0	2445343	+	ID=TGME49_225160;길이=152 3	3452
TGME49_chr V	225686 5	2258465	+	ID=TGME49_285740;길이=160 0	3453
TGME49_chr VIIa	305508 7	3057294	-	ID=TGME49_202760;길이=220 7	3454
TGME49_chr XI	521599 9	5218760	+	ID=TGME49_316270;길이=276 1	3455
TGME49_chr IV	164128 9	1644518	-	ID=TGME49_211650;길이=322 9	3456
TGME49_chr X	572012 6	5723099	+	ID=TGME49_237110;길이=297 3	3457
TGME49_chr XII	274845 8	2750074	+	ID=TGME49_246210;길이=161 6	3458
TGME49_chr VIII	532289 9	5326644	+	ID=TGME49_270220;길이=374 5	3459
TGME49_chr XII	889364	891927	-	ID=TGME49_219520;길이=256 3	3460

[0292]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VI	137994 1	1381383	+	ID=TGME49_240670;길이=144 2	3461
TGME49_chr XI	137383 1	1378479	+	ID=TGME49_310480;길이=464 8	3462
TGME49_chr XII	120818 9	1212694	-	ID=TGME49_218930;길이=450 5	3463
TGME49_chr XII	361644 4	3617866	-	ID=TGME49_247850;길이=142 2	3464
TGME49_chr V	148594 8	1487275	+	ID=TGME49_287270;길이=132 7	3465
TGME49_chr V	132180 0	1325747	-	ID=TGME49_213780;길이=394 7	3466
TGME49_chr IV	121684 0	1218366	-	ID=TGME49_318580;길이=152 6	3467
TGME49_chr VIIa	396964 2	3972217	-	ID=TGME49_201220;길이=257 5	3468
TGME49_chr X	493096 0	4934578	-	ID=TGME49_235515;길이=361 8	3469
TGME49_chr X	184851 4	1851776	+	ID=TGME49_226040;길이=326 2	3470
TGME49_chr Ia	120166 4	1204376	-	ID=TGME49_294830;길이=271 2	3471
TGME49_chr VIII	421000 0	4212465	-	ID=TGME49_272030;길이=246 5	3472
TGME49_chr XII	511743	514831	-	ID=TGME49_308020;길이=308 8	3473
TGME49_chr VIIb	260854 8	2610923	+	ID=TGME49_259920;길이=237 5	3474
TGME49_chr X	529061 1	5294071	-	ID=TGME49_236120;길이=346 0	3475
TGME49_chr VIIa	384934 4	3854159	+	ID=TGME49_201680;길이=481 5	3476
TGME49_chr VIII	655751 7	6561570	-	ID=TGME49_268310;길이=405 3	3477
TGME49_chr X	580692 6	5808940	-	ID=TGME49_237240;길이=201 4	3478
TGME49_chr X	922178	924766	+	ID=TGME49_227450;길이=258 8	3479

[0293]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	265901 8	2661986	-	ID=TGME49_288650;길이=296 8	3480
TGME49_chr VI	275901 9	2762419	-	ID=TGME49_243620;길이=340 0	3481
TGME49_chr X	647478 4	6479194	+	ID=TGME49_214760;길이=441 0	3482
TGME49_chr VIIb	167016 3	1672456	-	ID=TGME49_261530;길이=229 3	3483
TGME49_chr XI	580156 5	5802917	-	ID=TGME49_216900;길이=135 2	3484
TGME49_chr X	697992 7	6981500	-	ID=TGME49_215480;길이=157 3	3485
TGME49_chr XII	407848 5	4082874	+	ID=TGME49_248677;길이=438 9	3486
TGME49_chr X	153327 7	1537059	-	ID=TGME49_226570;길이=378 2	3487
TGME49_chr IX	167065 8	1673385	+	ID=TGME49_265240;길이=272 7	3488
TGME49_chr X	535113 0	5352320	+	ID=TGME49_236250;길이=119 0	3489
TGME49_chr XII	302852	304279	-	ID=TGME49_299980;길이=142 7	3490
TGME49_chr Ib	140395 3	1405251	+	ID=TGME49_209700;길이=129 8	3491
TGME49_chr X	300370 5	3007325	+	ID=TGME49_224520;길이=362 0	3492
TGME49_chr IV	194285	196070	+	ID=TGME49_320620;길이=178 5	3493
TGME49_chr VIII	518932 3	5191091	-	ID=TGME49_270570;길이=176 8	3494
TGME49_chr X	971149	975816	-	ID=TGME49_227390;길이=466 7	3495
TGME49_chr V	114538 6	1146565	+	ID=TGME49_213560;길이=117 9	3496
TGME49_chr XII	566119 0	5663297	-	ID=TGME49_251910;길이=210 7	3497
TGME49_chr Ib	168598 9	1690920	-	ID=TGME49_321630;길이=493 1	3498

[0294]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ia	662350	666276	+	ID=TGME49_294060;길이=392 6	3499
TGME49_chr XI	334749 9	3350293	+	ID=TGME49_313410;길이=279 4	3500
TGME49_chr XI	611336	614210	+	ID=TGME49_309290;길이=287 4	3501
TGME49_chr IX	438590 9	4387593	-	ID=TGME49_291860;길이=168 4	3502
TGME49_chr XII	267117 6	2675189	-	ID=TGME49_246110;길이=401 3	3503
TGME49_chr XII	565309	566062	-	ID=TGME49_308075;길이=753	3504
TGME49_chr XII	472715 5	4729832	-	ID=TGME49_249670;길이=267 7	3505
TGME49_chr VI	447757	449748	-	ID=TGME49_239070;길이=199 1	3506
TGME49_chr II	287426	290540	-	ID=TGME49_221360;길이=311 4	3507
TGME49_chr VIIb	187335 0	1876420	+	ID=TGME49_261070;길이=307 0	3508
TGME49_chr VIII	401155 0	4016029	-	ID=TGME49_272390;길이=447 9	3509
TGME49_chr VIII	261052 2	2615562	-	ID=TGME49_233360;길이=504 0	3510
TGME49_chr VIII	543706 5	5439034	-	ID=TGME49_270070;길이=196 9	3511
TGME49_chr VI	75690	77850	-	ID=TGME49_238130;길이=216 0	3512
TGME49_chr VIIa	153090 3	1532616	-	ID=TGME49_205230;길이=171 3	3513
TGME49_chr VIIb	275460 2	2756634	-	ID=TGME49_259610;길이=203 2	3514
TGME49_chr XI	115807 9	1160818	-	ID=TGME49_310210;길이=273 9	3515
TGME49_chr VIII	530520	533240	-	ID=TGME49_230000;길이=272 0	3516
TGME49_chr IX	552856 9	5530025	+	ID=TGME49_305635;길이=145 6	3517

[0295]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	163337 5	1637998	+	ID=TGME49_218260;길이=462 3	3518
TGME49_chr VIII	353033 8	3532583	-	ID=TGME49_273400;길이=224 5	3519
TGME49_chr XI	220048 0	2202879	-	ID=TGME49_311670;길이=239 9	3520
TGME49_chr IX	430572 6	4310108	-	ID=TGME49_291630;길이=438 2	3521
TGME49_chr Ia	126614 5	1267436	-	ID=TGME49_294902;길이=129 1	3522
TGME49_chr Ib	209955	214235	+	ID=TGME49_207690;길이=428 0	3523
TGME49_chr XII	285884 7	2863310	+	ID=TGME49_246580;길이=446 3	3524
TGME49_chr XII	823067	826469	+	ID=TGME49_219610;길이=340 2	3525
TGME49_chr VIIa	383349 3	3834672	+	ID=TGME49_201710;길이=117 9	3526
TGME49_chr VIIb	329606 0	3297939	+	ID=TGME49_258625;길이=187 9	3527
TGME49_chr VI	867209	869418	-	ID=TGME49_239710;길이=220 9	3528
TGME49_chr VIIa	127542 3	1276455	-	ID=TGME49_205615;길이=103 2	3529
TGME49_chr XII	470870 2	4710344	-	ID=TGME49_249630;길이=164 2	3530
TGME49_chr X	417174 8	4175262	-	ID=TGME49_234165;길이=351 4	3531
TGME49_chr XII	120499	122563	+	ID=TGME49_300260;길이=206 4	3532
TGME49_chr VI	498397	501660	-	ID=TGME49_239260;길이=326 3	3533
TGME49_chr VIII	493816	497365	-	ID=TGME49_229960;길이=354 9	3534
TGME49_chr VIIa	361628 0	3620711	-	ID=TGME49_202090;길이=443 1	3535
TGME49_chr X	697368 4	6974864	-	ID=TGME49_215460;길이=118 0	3536

[0296]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	672589 0	6729429	-	ID=TGME49_215060;길이=353 9	3537
TGME49_chr XI	276280 5	2765415	-	ID=TGME49_312520;길이=261 0	3538
TGME49_chr VIIa	989384	994150	+	ID=TGME49_206415;길이=476 6	3539
TGME49_chr Ib	103305 7	1035956	-	ID=TGME49_209080;길이=289 9	3540
TGME49_chr VIIb	363934	367739	+	ID=TGME49_263720;길이=380 5	3541
TGME49_chr IX	367932 9	3681333	+	ID=TGME49_290290;길이=200 4	3542
TGME49_chr XI	132724 1	1328715	-	ID=TGME49_310410;길이=147 4	3543
TGME49_chr Ib	162965	165017	+	ID=TGME49_207630;길이=205 2	3544
TGME49_chr VIII	341163 0	3413948	-	ID=TGME49_273550;길이=231 8	3545
TGME49_chr IX	423761 3	4239542	-	ID=TGME49_291310;길이=192 9	3546
TGME49_chr V	271127 7	2713061	+	ID=TGME49_284560;길이=178 4	3547
TGME49_chr VI	66661	71093	-	ID=TGME49_238100;길이=443 2	3548
TGME49_chr Ib	110818 1	1112225	+	ID=TGME49_209200;길이=404 4	3549
TGME49_chr X	112501 8	1129103	+	ID=TGME49_227030;길이=408 5	3550
TGME49_chr XII	147672 0	1480771	+	ID=TGME49_218510;길이=405 1	3551
TGME49_chr VIII	302829 4	3030583	-	ID=TGME49_274110;길이=228 9	3552
TGME49_chr IX	727730	732199	-	ID=TGME49_267312;길이=446 9	3553
TGME49_chr VI	172377 5	1727714	+	ID=TGME49_241820;길이=393 9	3554
TGME49_chr VIII	560930	562293	+	ID=TGME49_230040;길이=136 3	3555

[0297]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr II	141962 6	1421332	+	ID=TGME49_223070;길이=170 6	3556
TGME49_chr XI	281672 5	2818748	+	ID=TGME49_312600;길이=202 3	3557
TGME49_chr X	708587 3	7087326	-	ID=TGME49_215680;길이=145 3	3558
TGME49_chr IV	116295 8	1165755	-	ID=TGME49_318675;길이=279 7	3559
TGME49_chr IV	193260 8	1935398	-	ID=TGME49_211150;길이=279 0	3560
TGME49_chr XII	302417 6	3027111	+	ID=TGME49_246940;길이=293 5	3561
TGME49_chr VIIb	171839 4	1720099	+	ID=TGME49_261475;길이=170 5	3562
TGME49_chr VIII	518858 9	5190591	+	ID=TGME49_270560;길이=200 2	3563
TGME49_chr X	692247 4	6926889	-	ID=TGME49_215350;길이=441 5	3564
TGME49_chr IX	211463 3	2116655	+	ID=TGME49_264670;길이=202 2	3565
TGME49_chr IX	530262 0	5305770	+	ID=TGME49_305240;길이=315 0	3566
TGME49_chr XI	372226 5	3724229	+	ID=TGME49_313840;길이=196 4	3567
TGME49_chr X	367939 6	3681487	+	ID=TGME49_223650;길이=209 1	3568
TGME49_chr XI	161225 5	1614074	+	ID=TGME49_310820;길이=181 9	3569
TGME49_chr XI	430366 3	4305739	-	ID=TGME49_314790;길이=207 6	3570
TGME49_chr VIIa	303796 0	3042664	-	ID=TGME49_202780;길이=470 4	3571
TGME49_chr VIII	535366 9	5354773	+	ID=TGME49_270180;길이=110 4	3572
TGME49_chr XI	518667 4	5188879	+	ID=TGME49_316220;길이=220 5	3573
TGME49_chr XII	649143 0	6491855	-	ID=TGME49_277830;길이=425	3574

[0298]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	117836 0	1180121	-	ID=TGME49_318640;길이=176 1	3575
TGME49_chr Ib	139120 8	1393087	+	ID=TGME49_209670;길이=187 9	3576
TGME49_chr Ib	801471	804370	+	ID=TGME49_208590;길이=289 9	3577
TGME49_chr VIII	415461	417463	-	ID=TGME49_229740;길이=200 2	3578
TGME49_chr II	127498 6	1276921	+	ID=TGME49_222880;길이=193 5	3579
TGME49_chr X	246664 0	2469050	+	ID=TGME49_225125;길이=241 0	3580
TGME49_chr VIIb	327759 6	3280720	-	ID=TGME49_258660;길이=312 4	3581
TGME49_chr VIIb	139578 5	1399179	-	ID=TGME49_262070;길이=339 4	3582
TGME49_chr XII	659704 7	6599362	+	ID=TGME49_277560;길이=231 5	3583
TGME49_chr X	721585 3	7217846	-	ID=TGME49_275380;길이=199 3	3584
TGME49_chr X	676616 6	6769751	-	ID=TGME49_215100;길이=358 5	3585
TGME49_chr X	538683 4	5389094	-	ID=TGME49_236400;길이=226 0	3586
TGME49_chr II	153154 4	1535065	-	ID=TGME49_297100;길이=352 1	3587
TGME49_chr XI	207309 1	2077650	-	ID=TGME49_311440;길이=455 9	3588
TGME49_chr VIIa	321612 4	3218042	-	ID=TGME49_202572;길이=191 8	3589
TGME49_chr Ia	138804 1	1391447	+	ID=TGME49_295090;길이=340 6	3590
TGME49_chr X	896541	897868	-	ID=TGME49_227600;길이=132 7	3591
TGME49_chr XII	622202 1	6223691	-	ID=TGME49_278230;길이=167 0	3592
TGME49_chr IX	582599 7	5828317	+	ID=TGME49_306210;길이=232 0	3593

[0299]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	328288 6	3284073	+	ID=TGME49_224170; 길이=118 7	3594
TGME49_chr VIII	377418	380433	-	ID=TGME49_229680; 길이=301 5	3595
TGME49_chr V	310419 1	3107086	+	ID=TGME49_283510; 길이=289 5	3596
TGME49_chr V	220200 9	2203415	-	ID=TGME49_285820; 길이=140 6	3597
TGME49_chr IV	197043 0	1971908	-	ID=TGME49_211015; 길이=147 8	3598
TGME49_chr VI	105291 9	1057698	+	ID=TGME49_240090; 길이=477 9	3599
TGME49_chr VI	133053 3	1332686	-	ID=TGME49_240580; 길이=215 3	3600
TGME49_chr X	529636 0	5298183	+	ID=TGME49_236140; 길이=182 3	3601
TGME49_chr VIIa	157585 1	1578088	+	ID=TGME49_205150; 길이=223 7	3602
TGME49_chr VIIb	366899 5	3670754	+	ID=TGME49_257990; 길이=175 9	3603
TGME49_chr Ib	27811	29823	+	ID=TGME49_207400; 길이=201 2	3604
TGME49_chr VIII	367401 4	3678518	+	ID=TGME49_273070; 길이=450 4	3605
TGME49_chr IV	202072 8	2022776	+	ID=TGME49_210830; 길이=204 8	3606
TGME49_chr Ia	501242	504308	+	ID=TGME49_293680; 길이=306 6	3607
TGME49_chr VIII	418829 4	4190240	+	ID=TGME49_272040; 길이=194 6	3608
TGME49_chr VIIb	159327 4	1595045	+	ID=TGME49_261670; 길이=177 1	3609
TGME49_chr VI	234504 4	2347765	+	ID=TGME49_242845; 길이=272 1	3610
TGME49_chr VIIb	892798	896825	+	ID=TGME49_262960; 길이=402 7	3611
TGME49_chr VIIb	457653 5	4578100	-	ID=TGME49_255990; 길이=156 5	3612

[0300]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIb	3564269	3567431	-	ID=TGME49_258120;길이=3162	3613
TGME49_chr V	841156	844040	-	ID=TGME49_213067;길이=2884	3614
TGME49_chr VIIb	400077	401984	-	ID=TGME49_263680;길이=1907	3615
TGME49_chr VIII	5651257	5654273	-	ID=TGME49_269720;길이=3016	3616
TGME49_chr XI	5824519	5825439	-	ID=TGME49_216875;길이=920	3617
TGME49_chr Ia	289525	291377	-	ID=TGME49_293370;길이=1852	3618
TGME49_chr VIIb	340984	345618	+	ID=TGME49_263740;길이=4634	3619
TGME49_chr VI	3334624	3336932	-	ID=TGME49_244515;길이=2308	3620
TGME49_chr VIII	6462178	6464044	+	ID=TGME49_268390;길이=1866	3621
TGME49_chr II	1825535	1830439	-	ID=TGME49_297495;길이=4904	3622
TGME49_chr VI	151812	155358	+	ID=TGME49_238250;길이=3546	3623
TGME49_chr X	4153234	4155867	+	ID=TGME49_211870;길이=2633	3624
TGME49_chr VIIa	3118368	3121954	-	ID=TGME49_202660;길이=3586	3625
TGME49_chr XII	3689537	3692256	-	ID=TGME49_248140;길이=2719	3626
TGME49_chr XI	3279967	3283134	-	ID=TGME49_313330;길이=3167	3627
TGME49_chr VIII	3960669	3963072	-	ID=TGME49_272460;길이=2403	3628
TGME49_chr X	5463469	5465206	-	ID=TGME49_236635;길이=1737	3629
TGME49_chr V	1402650	1404500	+	ID=TGME49_213890;길이=1850	3630
TGME49_chr X	4153234	4155275	+	ID=TGME49_211880;길이=2041	3631

[0301]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	126699 3	1269615	+	ID=TGME49_226880; 길이=262 2	3632
TGME49_chr IX	152877 8	1530786	+	ID=TGME49_265480; 길이=200 8	3633
TGME49_chr IX	174584 5	1747343	-	ID=TGME49_265150; 길이=149 8	3634
TGME49_chr VI	884386	888183	-	ID=TGME49_239740; 길이=379 7	3635
TGME49_chr XI	531719 4	5320938	+	ID=TGME49_316460; 길이=374 4	3636
TGME49_chr VIIb	776365	780112	+	ID=TGME49_263130; 길이=374 7	3637
TGME49_chr XI	644282 5	6444555	-	ID=TGME49_216050; 길이=173 0	3638
TGME49_chr X	231852 5	2320515	+	ID=TGME49_225310; 길이=199 0	3639
TGME49_chr VIII	429630 4	4298540	-	ID=TGME49_271892; 길이=223 6	3640
TGME49_chr VIII	361143 8	3613139	+	ID=TGME49_273280; 길이=170 1	3641
TGME49_chr V	217283 0	2174806	+	ID=TGME49_285840; 길이=197 6	3642
TGME49_chr Ia	271448	273727	-	ID=TGME49_293340; 길이=227 9	3643
TGME49_chr VIIb	266046 3	2662578	+	ID=TGME49_259850; 길이=211 5	3644
TGME49_chr VIIb	292475 5	2925875	-	ID=TGME49_259168; 길이=112 0	3645
TGME49_chr XII	609433 5	6096858	+	ID=TGME49_278440; 길이=252 3	3646
TGME49_chr IX	514613 0	5146913	-	ID=TGME49_304980; 길이=783	3647
TGME49_chr XI	360068 8	3604400	-	ID=TGME49_313673; 길이=371 2	3648
TGME49_chr VIIb	180220 6	1804702	-	ID=TGME49_261260; 길이=249 6	3649
TGME49_chr XI	611665 9	6118655	-	ID=TGME49_216500; 길이=199 6	3650

[0302]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	185497 1	1859523	+	ID=TGME49_217470;길이=455 2	3651
TGME49_chr X	293996	296317	-	ID=TGME49_228490;길이=232 1	3652
TGME49_chr IX	531834 5	5320794	+	ID=TGME49_305260;길이=244 9	3653
TGME49_chr VI	239901 9	2400763	+	ID=TGME49_242900;길이=174 4	3654
TGME49_chr VIIa	164247 4	1645461	-	ID=TGME49_205080;길이=298 7	3655
TGME49_chr VIII	612397 1	6127883	-	ID=TGME49_269035;길이=391 2	3656
TGME49_chr V	254318 4	2545309	-	ID=TGME49_285200;길이=212 5	3657
TGME49_chr XII	449269 7	4496623	+	ID=TGME49_249365;길이=392 6	3658
TGME49_chr VI	303372	308255	+	ID=TGME49_238915;길이=488 3	3659
TGME49_chr II	179710	182938	+	ID=TGME49_221260;길이=322 8	3660
TGME49_chr XII	429488 8	4296930	-	ID=TGME49_249000;길이=204 2	3661
TGME49_chr IX	350524 5	3508638	-	ID=TGME49_289880;길이=339 3	3662
TGME49_chr VIIb	286929 9	2871159	+	ID=TGME49_259210;길이=186 0	3663
TGME49_chr VIIa	377764 8	3779712	+	ID=TGME49_201800;길이=206 4	3664
TGME49_chr XI	307207 4	3074339	-	ID=TGME49_313055;길이=226 5	3665
TGME49_chr VIIa	415722 0	4159151	-	ID=TGME49_281500;길이=193 1	3666
TGME49_chr VIIb	57559	61364	-	ID=TGME49_264225;길이=380 5	3667
TGME49_chr XI	187673 5	1880862	+	ID=TGME49_311230;길이=412 7	3668
TGME49_chr VIIb	444059 7	4442145	+	ID=TGME49_256810;길이=154 8	3669

[0303]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	307230 9	3074641	+	ID=TGME49_202730;길이=233 2	3670
TGME49_chr VIII	295302	299523	-	ID=TGME49_229480;길이=422 1	3671
TGME49_chr XI	370084 2	3703550	-	ID=TGME49_313800;길이=270 8	3672
TGME49_chr Ib	783599	787408	-	ID=TGME49_208560;길이=380 9	3673
TGME49_chr VIII	633795 4	6339540	+	ID=TGME49_268730;길이=158 6	3674
TGME49_chr XI	263004 5	2632405	+	ID=TGME49_312360;길이=236 0	3675
TGME49_chr IX	123527 7	1239596	-	ID=TGME49_266300;길이=431 9	3676
TGME49_chr IX	894353	898324	+	ID=TGME49_266920;길이=397 1	3677
TGME49_chr VIII	415896 4	4160790	+	ID=TGME49_272180;길이=182 6	3678
TGME49_chr X	244382 0	2448305	+	ID=TGME49_225150;길이=448 5	3679
TGME49_chr Ia	236822	238568	+	ID=TGME49_293290;길이=174 6	3680
TGME49_chr IX	582599 7	5827653	+	ID=TGME49_306200;길이=165 6	3681
TGME49_chr IX	235479 6	2356195	-	ID=TGME49_288050;길이=139 9	3682
TGME49_chr VIII	312835 3	3129861	-	ID=TGME49_273995;길이=150 8	3683
TGME49_chr VIIb	282534	283983	+	ID=TGME49_263860;길이=144 9	3684
TGME49_chr V	128544 9	1287602	-	ID=TGME49_213748;길이=215 3	3685
TGME49_chr IX	412707 8	4130241	+	ID=TGME49_291120;길이=316 3	3686
TGME49_chr VIII	274726 3	2749263	+	ID=TGME49_233720;길이=200 0	3687
TGME49_chr XII	341463 9	3417680	-	ID=TGME49_247550;길이=304 1	3688

[0304]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	601034 4	6014213	+	ID=TGME49_214080;길이=386 9	3689
TGME49_chr XI	763150	767129	+	ID=TGME49_309720;길이=397 9	3690
TGME49_chr VI	118877	121839	+	ID=TGME49_238200;길이=296 2	3691
TGME49_chr XI	829867	831550	-	ID=TGME49_309810;길이=168 3	3692
TGME49_chr VI	236022 8	2365079	-	ID=TGME49_242860;길이=485 1	3693
TGME49_chr X	397854 5	3981345	+	ID=TGME49_212200;길이=280 0	3694
TGME49_chr XII	685241 9	6855685	-	ID=TGME49_276920;길이=326 6	3695
TGME49_chr VIIb	494394 3	4948498	+	ID=TGME49_255260;길이=455 5	3696
TGME49_chr XII	470757 7	4709680	+	ID=TGME49_249650;길이=210 3	3697
TGME49_chr VIIb	470997 2	4711447	-	ID=TGME49_255710;길이=147 5	3698
TGME49_chr IX	208344 0	2086073	-	ID=TGME49_264740;길이=263 3	3699
TGME49_chr V	285090 6	2853929	-	ID=TGME49_284040;길이=302 3	3700
TGME49_chr X	595151 3	5954484	-	ID=TGME49_237520;길이=297 1	3701
TGME49_chr VIII	511389 9	5115543	+	ID=TGME49_270630;길이=164 4	3702
TGME49_chr Ib	781751	786180	+	ID=TGME49_208570;길이=442 9	3703
TGME49_chr X	237739 5	2379215	+	ID=TGME49_225240;길이=182 0	3704
TGME49_chr X	313455 6	3137082	+	ID=TGME49_224275;길이=252 6	3705
TGME49_chr V	100583 6	1007767	+	ID=TGME49_213410;길이=193 1	3706
TGME49_chr XI	346904 8	3470899	-	ID=TGME49_313540;길이=185 1	3707

[0305]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIII	104947 3	1053414	-	ID=TGME49_230830;길이=394 1	3708
TGME49_chr VI	330076 9	3304052	-	ID=TGME49_244470;길이=328 3	3709
TGME49_chr XI	793193	797745	-	ID=TGME49_309760;길이=455 2	3710
TGME49_chr XII	736911	739042	-	ID=TGME49_219682;길이=213 1	3711
TGME49_chr V	176429 2	1768196	+	ID=TGME49_286595;길이=390 4	3712
TGME49_chr VI	267854 4	2680887	+	ID=TGME49_243500;길이=234 3	3713
TGME49_chr VI	294441 4	2946280	+	ID=TGME49_244000;길이=186 6	3714
TGME49_chr VI	325328 7	3255288	+	ID=TGME49_244430;길이=200 1	3715
TGME49_chr X	620559 5	6210365	+	ID=TGME49_214280;길이=477 0	3716
TGME49_chr IX	403728 6	4041660	-	ID=TGME49_291005;길이=437 4	3717
TGME49_chr IX	458528 4	4586943	-	ID=TGME49_292160;길이=165 9	3718
TGME49_chr Ia	108836 1	1093316	+	ID=TGME49_294720;길이=495 5	3719
TGME49_chr VIII	280589 8	2808434	+	ID=TGME49_233810;길이=253 6	3720
TGME49_chr V	860119	861470	+	ID=TGME49_213115;길이=135 1	3721
TGME49_chr Ia	156022 1	1563486	+	ID=TGME49_295720;길이=326 5	3722
TGME49_chr IV	266713 6	2669610	+	ID=TGME49_317720;길이=247 4	3723
TGME49_chr VI	165534 1	1658987	+	ID=TGME49_241155;길이=364 6	3724
TGME49_chr VIIb	430148	433668	-	ID=TGME49_263630;길이=352 0	3725
TGME49_chr IX	467769 7	4679657	-	ID=TGME49_292300;길이=196 0	3726

[0306]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr X	353173 1	3534835	+	ID=TGME49_223845;길이=310 4	3727
TGME49_chr X	655214 4	6552859	+	ID=TGME49_214860;길이=715	3728
TGME49_chr VIII	192863 5	1933235	+	ID=TGME49_232190;길이=460 0	3729
TGME49_chr VIIb	496384 8	4965565	+	ID=TGME49_255245;길이=171 7	3730
TGME49_chr XI	227226 7	2276540	-	ID=TGME49_311765;길이=427 3	3731
TGME49_chr XI	320638 6	3210859	-	ID=TGME49_313235;길이=447 3	3732
TGME49_chr VIII	114915 9	1152853	+	ID=TGME49_230970;길이=369 4	3733
TGME49_chr II	447679	452475	-	ID=TGME49_221570;길이=479 6	3734
TGME49_chr XII	386080	388449	-	ID=TGME49_307760;길이=236 9	3735
TGME49_chr VIII	676375	678638	+	ID=TGME49_230200;길이=226 3	3736
TGME49_chr XII	318052 7	3182528	-	ID=TGME49_247220;길이=200 1	3737
TGME49_chr VIII	594567 6	5950322	+	ID=TGME49_269270;길이=464 6	3738
TGME49_chr VIII	451670	454022	+	ID=TGME49_229900;길이=235 2	3739
TGME49_chr XII	263270 3	2633950	+	ID=TGME49_246060;길이=124 7	3740
TGME49_chr XI	293014 7	2932129	-	ID=TGME49_312820;길이=198 2	3741
TGME49_chr IX	459067 8	4593804	+	ID=TGME49_292180;길이=312 6	3742
TGME49_chr V	265078 4	2654467	-	ID=TGME49_284630;길이=368 3	3743
TGME49_chr X	202414 8	2027899	+	ID=TGME49_225810;길이=375 1	3744
TGME49_chr VIIa	422618 4	4229009	+	ID=TGME49_281630;길이=282 5	3745

[0307]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	496061 8	4964965	-	ID=TGME49_249960;길이=434 7	3746
TGME49_chr XII	113463 5	1136707	-	ID=TGME49_219100;길이=207 2	3747
TGME49_chr VIII	684588	686890	-	ID=TGME49_230205;길이=230 2	3748
TGME49_chr IV	120944 1	1210630	-	ID=TGME49_318590;길이=118 9	3749
TGME49_chr VI	269244 9	2693266	+	ID=TGME49_243520;길이=817	3750
TGME49_chr V	183828 2	1841112	-	ID=TGME49_286420;길이=283 0	3751
TGME49_chr VIII	920039	922135	-	ID=TGME49_230610;길이=209 6	3752
TGME49_chr X	269803 3	2701877	-	ID=TGME49_224905;길이=384 4	3753
TGME49_chr XI	211457 5	2119619	+	ID=TGME49_311485;길이=504 4	3754
TGME49_chr XII	140128 5	1403127	+	ID=TGME49_218580;길이=184 2	3755
TGME49_chr VIIb	487413 8	4879043	-	ID=TGME49_255370;길이=490 5	3756
TGME49_chr VIII	433411 0	4336235	-	ID=TGME49_271860;길이=212 5	3757
TGME49_chr VIII	195586 5	1958248	+	ID=TGME49_232220;길이=238 3	3758
TGME49_chr VIIa	405823 1	4061062	+	ID=TGME49_281400;길이=283 1	3759
TGME49_chr XII	560574 8	5608371	-	ID=TGME49_251830;길이=262 3	3760
TGME49_chr X	714518 9	7146960	+	ID=TGME49_215750;길이=177 1	3761
TGME49_chr IX	530427 1	5305970	-	ID=TGME49_305230;길이=169 9	3762
TGME49_chr Ib	170989 5	1713439	+	ID=TGME49_321600;길이=354 4	3763
TGME49_chr XII	566781 9	5669852	-	ID=TGME49_251920;길이=203 3	3764

[0308]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	103294 5	1037980	-	ID=TGME49_310050;길이=503 5	3765
TGME49_chr XI	510653 7	5108324	-	ID=TGME49_315958;길이=178 7	3766
TGME49_chr VIIb	111776 6	1121043	-	ID=TGME49_262630;길이=327 7	3767
TGME49_chr Ib	772266	774883	+	ID=TGME49_208550;길이=261 7	3768
TGME49_chr Ib	627070	629071	-	ID=TGME49_208350;길이=200 1	3769
TGME49_chr X	631966 0	6321243	+	ID=TGME49_214500;길이=158 3	3770
TGME49_chr VIIb	219263 9	2196472	-	ID=TGME49_260520;길이=383 3	3771
TGME49_chr VI	898593	901403	-	ID=TGME49_239755;길이=281 0	3772
TGME49_chr XI	416864 2	4173147	+	ID=TGME49_314530;길이=450 5	3773
TGME49_chr Ia	111718	114297	-	ID=TGME49_293050;길이=257 9	3774
TGME49_chr XII	278369 1	2785982	-	ID=TGME49_246450;길이=229 1	3775
TGME49_chr XI	128813 3	1292845	-	ID=TGME49_310350;길이=471 2	3776
TGME49_chr XII	162730	165254	-	ID=TGME49_300200;길이=252 4	3777
TGME49_chr IX	357596 0	3579143	-	ID=TGME49_290000;길이=318 3	3778
TGME49_chr XII	335648 5	3359532	+	ID=TGME49_247470;길이=304 7	3779
TGME49_chr VIII	211244 8	2113740	+	ID=TGME49_232460;길이=129 2	3780
TGME49_chr VIIa	352033 1	3522747	-	ID=TGME49_202210;길이=241 6	3781
TGME49_chr VIIb	180750 7	1811746	-	ID=TGME49_261250;길이=423 9	3782
TGME49_chr VIIb	132648 6	1331064	-	ID=TGME49_262170;길이=457 8	3783

[0309]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	474298 2	4745450	+	ID=TGME49_249702;길이=246 8	3784
TGME49_chr V	269976 7	2701801	+	ID=TGME49_284580;길이=203 4	3785
TGME49_chr XI	271680 5	2718646	+	ID=TGME49_312480;길이=184 1	3786
TGME49_chr IX	772823	775776	-	ID=TGME49_267110;길이=295 3	3787
TGME49_chr VI	168355 1	1687309	+	ID=TGME49_241240;길이=375 8	3788
TGME49_chr IV	170886 2	1710770	+	ID=TGME49_211440;길이=190 8	3789
TGME49_chr VIIb	234889 2	2350447	+	ID=TGME49_260325;길이=155 5	3790
TGME49_chr X	101235 9	1015635	+	ID=TGME49_227335;길이=327 6	3791
TGME49_chr X	660326 0	6606386	-	ID=TGME49_214930;길이=312 6	3792
TGME49_chr VIII	434978	437027	+	ID=TGME49_229780;길이=204 9	3793
TGME49_chr VIII	153636 1	1538858	-	ID=TGME49_231780;길이=249 7	3794
TGME49_chr VI	890233	892412	+	ID=TGME49_239752;길이=217 9	3795
TGME49_chr X	775064	778810	+	ID=TGME49_227840;길이=374 6	3796
TGME49_chr VIII	512857 6	5133324	-	ID=TGME49_270620;길이=474 8	3797
TGME49_chr V	169635 2	1699779	+	ID=TGME49_286740;길이=342 7	3798
TGME49_chr IX	457016 7	4571563	-	ID=TGME49_292130;길이=139 6	3799
TGME49_chr Ib	150699 7	1508664	-	ID=TGME49_209870;길이=166 7	3800
TGME49_chr XI	588868 2	5890417	-	ID=TGME49_216785;길이=173 5	3801
TGME49_chr XI	216523	219848	+	ID=TGME49_306870;길이=332 5	3802

[0310]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	374595 1	3750483	-	ID=TGME49_201850;길이=453 2	3803
TGME49_chr XII	591184 6	5916676	-	ID=TGME49_278740;길이=483 0	3804
TGME49_chr VIIb	302542 3	3026890	-	ID=TGME49_259020;길이=146 7	3805
TGME49_chr XI	147565 4	1480111	-	ID=TGME49_310610;길이=445 7	3806
TGME49_chr XII	576082 1	5764702	+	ID=TGME49_278910;길이=388 1	3807
TGME49_chr IX	516306 3	5165571	-	ID=TGME49_305010;길이=250 8	3808
TGME49_chr Ia	808274	811964	+	ID=TGME49_294340;길이=369 0	3809
TGME49_chr XII	425609	430368	-	ID=TGME49_307810;길이=475 9	3810
TGME49_chr IX	189607	191648	-	ID=TGME49_279430;길이=204 1	3811
TGME49_chr XII	669940 6	6704060	-	ID=TGME49_277240;길이=465 4	3812
TGME49_chr X	386211 6	3866423	+	ID=TGME49_223390;길이=430 7	3813
TGME49_chr Ib	163682	165355	-	ID=TGME49_207620;길이=167 3	3814
TGME49_chr VIIb	628606	632828	-	ID=TGME49_263330;길이=422 2	3815
TGME49_chr VIII	427667 6	4280983	-	ID=TGME49_271935;길이=430 7	3816
TGME49_chr V	115182 6	1153503	+	ID=TGME49_213580;길이=167 7	3817
TGME49_chr IX	359734 4	3600415	-	ID=TGME49_290030;길이=307 1	3818
TGME49_chr VIIa	120794 0	1209729	+	ID=TGME49_205700;길이=178 9	3819
TGME49_chr XII	171609 1	1718180	-	ID=TGME49_218192;길이=208 9	3820
TGME49_chr VI	107220 8	1074913	+	ID=TGME49_240220;길이=270 5	3821

[0311]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	334489 8	3346813	+	ID=TGME49_289615;길이=191 5	3822
TGME49_chr XII	193234	197614	-	ID=TGME49_300130;길이=438 0	3823
TGME49_chr IX	567874 2	5680658	-	ID=TGME49_305930;길이=191 6	3824
TGME49_chr Ia	511367	514250	+	ID=TGME49_293700;길이=288 3	3825
TGME49_chr XI	323464 4	3236534	+	ID=TGME49_313280;길이=189 0	3826
TGME49_chr Ia	134288 5	1345816	-	ID=TGME49_295035;길이=293 1	3827
TGME49_chr IX	476754	479709	+	ID=TGME49_267660;길이=295 5	3828
TGME49_chr XII	545486 0	5457281	-	ID=TGME49_251550;길이=242 1	3829
TGME49_chr X	655214 4	6556896	+	ID=TGME49_214870;길이=475 2	3830
TGME49_chr VIIa	318034 8	3184059	+	ID=TGME49_202590;길이=371 1	3831
TGME49_chr IX	528088 3	5283665	-	ID=TGME49_305190;길이=278 2	3832
TGME49_chr X	370180 7	3706821	-	ID=TGME49_223610;길이=501 4	3833
TGME49_chr VIII	474291 8	4744434	-	ID=TGME49_271070;길이=151 6	3834
TGME49_chr X	632925 7	6330831	-	ID=TGME49_214510;길이=157 4	3835
TGME49_chr VIIb	413527 7	4137872	+	ID=TGME49_257300;길이=259 5	3836
TGME49_chr VIIb	329660 4	3298791	-	ID=TGME49_258630;길이=218 7	3837
TGME49_chr VIII	259757 9	2599382	-	ID=TGME49_233330;길이=180 3	3838
TGME49_chr X	551024	552313	+	ID=TGME49_228140;길이=128 9	3839
TGME49_chr IX	461473 3	4617149	+	ID=TGME49_292220;길이=241 6	3840

[0312]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IV	110065	114937	+	ID=TGME49_320720;길이=487 2	3841
TGME49_chr IX	338310 2	3384808	-	ID=TGME49_289690;길이=170 6	3842
TGME49_chr XI	316684 9	3168996	+	ID=TGME49_313200;길이=214 7	3843
TGME49_chr VIII	165829 3	1660173	+	ID=TGME49_231940;길이=188 0	3844
TGME49_chr XI	749160	751293	+	ID=TGME49_309600;길이=213 3	3845
TGME49_chr X	534057 1	5342425	-	ID=TGME49_236220;길이=185 4	3846
TGME49_chr IX	410988 1	4114158	-	ID=TGME49_291080;길이=427 7	3847
TGME49_chr VIIb	579048	580735	-	ID=TGME49_263410;길이=168 7	3848
TGME49_chr Ib	135475 8	1356812	-	ID=TGME49_209585;길이=205 4	3849
TGME49_chr II	114763	116965	-	ID=TGME49_221180;길이=220 2	3850
TGME49_chr X	745735 2	7459980	+	ID=TGME49_207240;길이=262 8	3851
TGME49_chr XI	362216 5	3624128	+	ID=TGME49_313700;길이=196 3	3852
TGME49_chr XI	459491 1	4596494	+	ID=TGME49_315240;길이=158 3	3853
TGME49_chr VIIa	366787 0	3670309	-	ID=TGME49_202050;길이=243 9	3854
TGME49_chr VIII	375097 7	3753691	-	ID=TGME49_272760;길이=271 4	3855
TGME49_chr V	273192 8	2734972	-	ID=TGME49_284540;길이=304 4	3856
TGME49_chr IX	531295 5	5315417	+	ID=TGME49_305250;길이=246 2	3857
TGME49_chr VIII	124218 4	1246962	+	ID=TGME49_231120;길이=477 8	3858
TGME49_chr II	127056 1	1272652	+	ID=TGME49_222870;길이=209 1	3859

[0313]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr Ia	139458 1	1398592	+	ID=TGME49_295100;길이=401 1	3860
TGME49_chr II	695109	697038	+	ID=TGME49_221922;길이=192 9	3861
TGME49_chr IV	231725	234333	+	ID=TGME49_320588;길이=260 8	3862
TGME49_chr XII	473177	474441	+	ID=TGME49_307980;길이=126 4	3863
TGME49_chr VIIb	384933 7	3852143	+	ID=TGME49_257755;길이=280 6	3864
TGME49_chr VIIa	166462 8	1666761	-	ID=TGME49_205040;길이=213 3	3865
TGME49_chr VIIb	368595 0	3689788	+	ID=TGME49_257970;길이=383 8	3866
TGME49_chr X	192152 4	1925824	+	ID=TGME49_225930;길이=430 0	3867
TGME49_chr X	730268 3	7304952	-	ID=TGME49_275480;길이=226 9	3868
TGME49_chr IX	271022 0	2712817	+	ID=TGME49_288730;길이=259 7	3869
TGME49_chr VIIb	355191 6	3554846	-	ID=TGME49_258150;길이=293 0	3870
TGME49_chr XII	339540 4	3397801	-	ID=TGME49_247530;길이=239 7	3871
TGME49_chr XII	203631 8	2041237	-	ID=TGME49_217710;길이=491 9	3872
TGME49_chr VIII	660108 5	6602909	-	ID=TGME49_268260;길이=182 4	3873
TGME49_chr VIIb	247751 1	2479458	-	ID=TGME49_260180;길이=194 7	3874
TGME49_chr XII	847627	848796	+	ID=TGME49_219580;길이=116 9	3875
TGME49_chr XI	524532 9	5247973	+	ID=TGME49_316340;길이=264 4	3876
TGME49_chr VIII	159595 2	1597448	-	ID=TGME49_231865;길이=149 6	3877
TGME49_chr X	488239 9	4885373	-	ID=TGME49_235460;길이=297 4	3878

[0314]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	151040 0	1513768	+	ID=TGME49_218470;길이=336 8	3879
TGME49_chr XII	127537 7	1278904	+	ID=TGME49_218820;길이=352 7	3880
TGME49_chr IX	432186 9	4323613	-	ID=TGME49_291670;길이=174 4	3881
TGME49_chr IX	160060 3	1603702	+	ID=TGME49_265370;길이=309 9	3882
TGME49_chr XII	216621 5	2167918	-	ID=TGME49_217830;길이=170 3	3883
TGME49_chr IV	169429 2	1697186	+	ID=TGME49_211460;길이=289 4	3884
TGME49_chr X	688460 4	6886087	+	ID=TGME49_215300;길이=148 3	3885
TGME49_chr XI	403064 4	4031150	-	ID=TGME49_314350;길이=506	3886
TGME49_chr XI	571368 5	5715292	-	ID=TGME49_217030;길이=160 7	3887
TGME49_chr VIIa	318754 8	3190806	+	ID=TGME49_202580;길이=325 8	3888
TGME49_chr IX	147951 6	1483804	+	ID=TGME49_265650;길이=428 8	3889
TGME49_chr XII	110804 2	1109700	+	ID=TGME49_219140;길이=165 8	3890
TGME49_chr Ia	144640	149293	-	ID=TGME49_293180;길이=465 3	3891
TGME49_chr VIIa	340277 1	3404549	+	ID=TGME49_202350;길이=177 8	3892
TGME49_chr V	110712 1	1109027	+	ID=TGME49_213500;길이=190 6	3893
TGME49_chr V	165286 5	1655496	+	ID=TGME49_286800;길이=263 1	3894
TGME49_chr X	673203 5	6733904	-	ID=TGME49_215070;길이=186 9	3895
TGME49_chr VIII	333194 3	3336912	+	ID=TGME49_273650;길이=496 9	3896
TGME49_chr XII	675720 4	6757912	-	ID=TGME49_277055;길이=708	3897

[0315]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XI	408674 5	4089078	-	ID=TGME49_314415;길이=233 3	3898
TGME49_chr VIIb	228036	231382	+	ID=TGME49_264020;길이=334 6	3899
TGME49_chr VIIa	422742 7	4230194	-	ID=TGME49_281620;길이=276 7	3900
TGME49_chr V	187480 7	1879170	+	ID=TGME49_286260;길이=436 3	3901
TGME49_chr VI	302787 4	3029432	+	ID=TGME49_244110;길이=155 8	3902
TGME49_chr IV	170960 1	1711557	-	ID=TGME49_211450;길이=195 6	3903
TGME49_chr XII	222086 1	2225036	+	ID=TGME49_217915;길이=417 5	3904
TGME49_chr XI	828620	830503	+	ID=TGME49_309820;길이=188 3	3905
TGME49_chr VIII	519253 9	5195213	+	ID=TGME49_270550;길이=267 4	3906
TGME49_chr X	692762 9	6929143	+	ID=TGME49_215370;길이=151 4	3907
TGME49_chr XI	522438 4	5226744	+	ID=TGME49_316300;길이=236 0	3908
TGME49_chr VI	295920 3	2963259	-	ID=TGME49_244010;길이=405 6	3909
TGME49_chr XI	577465 2	5776514	+	ID=TGME49_216950;길이=186 2	3910
TGME49_chr Ia	180441 1	1808455	+	ID=TGME49_295360;길이=404 4	3911
TGME49_chr VI	102118 8	1023814	+	ID=TGME49_240050;길이=262 6	3912
TGME49_chr Ia	184672	186967	+	ID=TGME49_293240;길이=229 5	3913
TGME49_chr VIIb	157855 3	1580579	-	ID=TGME49_261690;길이=202 6	3914
TGME49_chr XI	155785 1	1562530	+	ID=TGME49_310740;길이=467 9	3915
TGME49_chr X	331481 5	3319616	-	ID=TGME49_224130;길이=480 1	3916

[0316]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	456365 7	4568429	+	ID=TGME49_249480;길이=477 2	3917
TGME49_chr Ib	103246 6	1034841	+	ID=TGME49_209090;길이=237 5	3918
TGME49_chr VI	253415 5	2537835	-	ID=TGME49_243298;길이=368 0	3919
TGME49_chr X	359751 1	3600273	+	ID=TGME49_223770;길이=276 2	3920
TGME49_chr XII	267820 6	2682410	-	ID=TGME49_246120;길이=420 4	3921
TGME49_chr IX	481857 8	4819481	-	ID=TGME49_210400;길이=903	3922
TGME49_chr XI	231652 3	2321340	-	ID=TGME49_311840;길이=481 7	3923
TGME49_chr IV	242008 3	2421297	-	ID=TGME49_301370;길이=121 4	3924
TGME49_chr IV	182218 2	1826088	-	ID=TGME49_211340;길이=390 6	3925
TGME49_chr XII	376447 5	3766489	+	ID=TGME49_248260;길이=201 4	3926
TGME49_chr VIII	120766 9	1210044	-	ID=TGME49_231030;길이=237 5	3927
TGME49_chr X	686854 9	6871573	+	ID=TGME49_215280;길이=302 4	3928
TGME49_chr VIIb	164372 9	1645825	+	ID=TGME49_261590;길이=209 6	3929
TGME49_chr XI	162485 2	1625815	-	ID=TGME49_310840;길이=963	3930
TGME49_chr XII	269284	271834	-	ID=TGME49_300030;길이=255 0	3931
TGME49_chr IX	391432 3	3919217	+	ID=TGME49_290890;길이=489 4	3932
TGME49_chr VIII	349883 5	3500944	-	ID=TGME49_273460;길이=210 9	3933
TGME49_chr XI	326747 4	3271294	+	ID=TGME49_313322;길이=382 0	3934
TGME49_chr X	113530 3	1139273	-	ID=TGME49_227020;길이=397 0	3935

[0317]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	200044 0	2005367	-	ID=TGME49_204100;길이=492 7	3936
TGME49_chr X	213674 5	2141573	-	ID=TGME49_225590;길이=482 8	3937
TGME49_chr Ia	497577	499864	+	ID=TGME49_293670;길이=228 7	3938
TGME49_chr IX	273046 5	2732515	-	ID=TGME49_288770;길이=205 0	3939
TGME49_chr XI	609564 5	6097770	+	ID=TGME49_216510;길이=212 5	3940
TGME49_chr VIII	611063 7	6114023	-	ID=TGME49_269050;길이=338 6	3941
TGME49_chr V	229630 5	2301022	+	ID=TGME49_285660;길이=471 7	3942
TGME49_chr Ib	159348 1	1595867	+	ID=TGME49_209970;길이=238 6	3943
TGME49_chr VIIb	917523	919993	-	ID=TGME49_262933;길이=247 0	3944
TGME49_chr VIIa	356709 4	3568251	-	ID=TGME49_202170;길이=115 7	3945
TGME49_chr VI	130226 2	1303984	+	ID=TGME49_240520;길이=172 2	3946
TGME49_chr XI	637644 5	6376951	+	ID=TGME49_216150;길이=506	3947
TGME49_chr IV	138751 2	1390320	-	ID=TGME49_318370;길이=280 8	3948
TGME49_chr VIII	124868 4	1250326	+	ID=TGME49_231125;길이=164 2	3949
TGME49_chr IX	180540 0	1807228	-	ID=TGME49_265080;길이=182 8	3950
TGME49_chr IX	367751 9	3678219	+	ID=TGME49_290280;길이=700	3951
TGME49_chr II	102044 9	1025166	-	ID=TGME49_222300;길이=471 7	3952
TGME49_chr X	912303	916274	+	ID=TGME49_227560;길이=397 1	3953
TGME49_chr XI	569910 2	5701538	+	ID=TGME49_217050;길이=243 6	3954

[0318]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 탁	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr IX	211482	214977	+	ID=TGME49_279380; 길이=3495	3955
TGME49_chr VIII	5960219	5963166	-	ID=TGME49_269260; 길이=2947	3956
TGME49_chr XII	1341036	1345114	-	ID=TGME49_218740; 길이=4078	3957
TGME49_chr X	5989380	5991089	-	ID=TGME49_237560; 길이=1709	3958
TGME49_chr IV	481795	483580	+	ID=TGME49_320120; 길이=1785	3959
TGME49_chr VIII	3598010	3600888	-	ID=TGME49_273320; 길이=2878	3960
TGME49_chr IX	3065937	3068225	-	ID=TGME49_289190; 길이=2288	3961
TGME49_chr X	1873929	1876445	+	ID=TGME49_225990; 길이=2516	3962
TGME49_chr XII	3889205	3891343	+	ID=TGME49_248500; 길이=2138	3963
TGME49_chr XII	3445460	3446440	+	ID=TGME49_247620; 길이=980	3964
TGME49_chr X	713964	716364	+	ID=TGME49_227948; 길이=2400	3965
TGME49_chr X	7423562	7425356	+	ID=TGME49_207170; 길이=1794	3966
TGME49_chr V	1716156	1718652	-	ID=TGME49_286710; 길이=2496	3967
TGME49_chr V	1238094	1240156	-	ID=TGME49_213680; 길이=2062	3968
TGME49_chr Ib	1132036	1134997	+	ID=TGME49_209230; 길이=2961	3969
TGME49_chr X	5892850	5895594	-	ID=TGME49_237460; 길이=2744	3970
TGME49_chr IX	1635792	1638798	-	ID=TGME49_265280; 길이=3006	3971
TGME49_chr II	2193632	2198046	+	ID=TGME49_298020; 길이=4414	3972
TGME49_chr VIIb	4584305	4588201	+	ID=TGME49_255970; 길이=3896	3973

[0319]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	441386 9	4418183	-	ID=TGME49_249260;길이=431 4	3974
TGME49_chr XII	137529 5	1377205	-	ID=TGME49_218610;길이=191 0	3975
TGME49_chr II	215973 5	2161907	-	ID=TGME49_297990;길이=217 2	3976
TGME49_chr VI	339001 2	3392557	-	ID=TGME49_244600;길이=254 5	3977
TGME49_chr IX	237967 5	2384376	-	ID=TGME49_288190;길이=470 1	3978
TGME49_chr IX	572125 3	5723275	+	ID=TGME49_306010;길이=202 2	3979
TGME49_chr XI	158899 5	1592976	+	ID=TGME49_310790;길이=398 1	3980
TGME49_chr II	152694 2	1530423	-	ID=TGME49_297090;길이=348 1	3981
TGME49_chr IV	212060	214189	+	ID=TGME49_320592;길이=212 9	3982
TGME49_chr IX	302614	305702	-	ID=TGME49_267875;길이=308 8	3983
TGME49_chr X	696419 1	6968709	-	ID=TGME49_215440;길이=451 8	3984
TGME49_chr XI	313837 2	3140384	-	ID=TGME49_313140;길이=201 2	3985
TGME49_chr VIIb	305794	307179	-	ID=TGME49_263830;길이=138 5	3986
TGME49_chr XII	249631	253074	-	ID=TGME49_300048;길이=344 3	3987
TGME49_chr VIIb	465347 9	4655650	-	ID=TGME49_255890;길이=217 1	3988
TGME49_chr VIIb	187335 0	1875365	+	ID=TGME49_261075;길이=201 5	3989
TGME49_chr X	530604 5	5308393	+	ID=TGME49_236158;길이=234 8	3990
TGME49_chr Ia	780454	781800	+	ID=TGME49_294285;길이=134 6	3991
TGME49_chr VIIa	294635 9	2947823	+	ID=TGME49_202910;길이=146 4	3992

[0320]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr XII	385736 7	3862038	-	ID=TGME49_248445;길이=467 1	3993
TGME49_chr Ib	145031 4	1452140	+	ID=TGME49_209790;길이=182 6	3994
TGME49_chr XII	208265 8	2086018	+	ID=TGME49_217740;길이=336 0	3995
TGME49_chr VI	302835 3	3030855	-	ID=TGME49_244100;길이=250 2	3996
TGME49_chr XI	297074 4	2973324	+	ID=TGME49_312905;길이=258 0	3997
TGME49_chr Ib	121014 3	1211342	-	ID=TGME49_209420;길이=119 9	3998
TGME49_chr VIII	225120	227610	+	ID=TGME49_229390;길이=249 0	3999
TGME49_chr VIII	235486 0	2357994	-	ID=TGME49_233030;길이=313 4	4000
TGME49_chr VIII	325941 8	3261475	+	ID=TGME49_273790;길이=205 7	4001
TGME49_chr X	175227 2	1756039	+	ID=TGME49_226260;길이=376 7	4002
TGME49_chr XI	592322 8	5926772	+	ID=TGME49_216740;길이=354 4	4003
TGME49_chr VIIb	413170 2	4133633	+	ID=TGME49_257310;길이=193 1	4004
TGME49_chr VIIa	116948 5	1173218	+	ID=TGME49_205750;길이=373 3	4005
TGME49_chr VIIb	255202	259201	-	ID=TGME49_263990;길이=399 9	4006
TGME49_chr IV	123051 0	1233030	-	ID=TGME49_318560;길이=252 0	4007
TGME49_chr VIIb	161871 7	1621489	-	ID=TGME49_261650;길이=277 2	4008
TGME49_chr V	315111 1	3154171	+	ID=TGME49_283450;길이=306 0	4009
TGME49_chr VIII	574599 3	5747995	+	ID=TGME49_269600;길이=200 2	4010
TGME49_chr VIIb	171966 7	1720796	-	ID=TGME49_261480;길이=112 9	4011

[0321]

염색체	염색체 상 시작 위치	염색체 상 끝 위치	가 닥	유전자명(ID)의 내인성 프로모터, 및 프로모터 서열의 길이	서열번호 :
TGME49_chr VIIa	489530	490382	+	ID=TGME49_280375;길이=852	4012
TGME49_chr VIII	314167 5	3145631	-	ID=TGME49_273970;길이=395 6	4013
TGME49_chr XI	551687 3	5518970	+	ID=TGME49_316710;길이=209 7	4014
TGME49_chr Ia	150832 3	1512231	-	ID=TGME49_295850;길이=390 8	4015
TGME49_chr X	433872 1	4343260	-	ID=TGME49_234400;길이=453 9	4016
TGME49_chr X	309061	312804	+	ID=TGME49_228430;길이=374 3	4017
TGME49_chr Ib	8721	12586	-	ID=TGME49_207365;길이=386 5	4018
TGME49_chr X	625195 0	6254576	+	ID=TGME49_214340;길이=262 6	4019
TGME49_chr VIII	739200	742279	-	ID=TGME49_230380;길이=307 9	4020
TGME49_chr X	157027 8	1574363	+	ID=TGME49_226500;길이=408 5	4021
TGME49_chr X	681974	683378	+	ID=TGME49_227990;길이=140 4	4022
TGME49_chr XI	646760 4	6468954	+	ID=TGME49_216010;길이=135 0	4023
TGME49_chr VIIa	393362 7	3938631	+	ID=TGME49_201250;길이=500 4	4024
TGME49_chr VIIa	300757 4	3010494	-	ID=TGME49_202830;길이=292 0	4025
TGME49_chr X	325680 0	3258378	-	ID=TGME49_224200;길이=157 8	4026
TGME49_chr XI	463918 3	4641514	-	ID=TGME49_315300;길이=233 1	4027
TGME49_chr VI	194745 6	1949773	+	ID=TGME49_242300;길이=231 7	4028
TGME49_chr XII	472634 2	4728931	+	ID=TGME49_249680;길이=258 9	4029
TGME49_chr VIIb	248861 7	2490012	-	ID=TGME49_260170;길이=139 5	4030

[0322]

[0323]

표 1. 본 발명의 일부 구현예의 구조물과 함께 사용될 수 있는 내인성 프로모터의 비-제한적인 예시를 제공한다. 예상되는 프로모터 서열은 유전자 주변 히스톤 마크 테이터를 기반으로 얻었다.

[0324]

표 2는 본 발명의 일부 구현예의 핵산 구조물로 클로닝될 수 있는 적합한 전신발현 및 유도 프로모터를 열거한 것이다.

[0325] [표 2] 전신발현 및 유도 프로모터

프로모터명	유형	프로모터 서열번호:
5RT70	전신발현 프로모터	4031
DHFR	전신발현 프로모터	4032
MIC2	전신발현 프로모터	4033
MIC8	전신발현 프로모터	4034
SAG1	전신발현 프로모터	4035
TetO7SAG1	유도 프로모터	4036
TetO7SAG4	유도 프로모터	4037
TUB1	전신발현 프로모터	4038
TUB8	전신발현 프로모터	4039

[0326]

[0327] 기술한 바와 같이, 이중 폴리뉴클레오티드는 톡소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함한다.

[0328] 본원에서 사용된 구 "톡소플라즈마 분비 단백질(*Toxoplasma secreted protein*)"은 톡소플라즈마에 의해 시험관 내 감염될 때 숙주세포로 분비되기 위하여 충분한 톡소플라즈마 폴리펩티드의 적어도 하나의 기능적 단편(아미노산 서열)을 말한다.

[0329] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질 또는 그의 기능적 단편은 톡소플라즈마에 의해 생체내 감염될 때 숙주세포로 분비될 수 있다.

[0330] 본 발명의 일부 구현예에 따르면, 제1 핵산 서열은 톡소플라즈마 분비 단백질의 기능적 단편을 코딩한다.

[0331] 본 발명의 일부 구현예에 따르면, 제1 핵산 서열은 톡소플라즈마 분비 단백질의 전장 개방형 해독 프레임(ORF)을 코딩한다.

[0332] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질은 톡소플라즈마의 곤봉체로부터 분비된다.

[0333] 본 발명의 일부 구현예에 따르면, 곤봉체로부터 분비되는 톡소플라즈마 분비 단백질은 톡소필린 및/또는 ROP1을 포함한다.

[0334] 본 발명의 일부 구현예에 따르면, 곤봉체로부터 분비되는 톡소플라즈마 분비 단백질은 서열번호 344 내지 465로 구성된 군에서 선택된 아미노산 서열을 포함한다.

[0335] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질은 비-곤봉체 단백질이다.

[0336] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질은 미세간상체 단백질 및 밀집 과립 단백질로 구성된 군에서 선택된다.

[0337] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질은 톡소플라즈마의 밀집 과립으로부터 분비된다.

[0338] 본 발명의 일부 구현예에 따르면, 밀집 과립으로부터 분비된 톡소플라즈마 분비 단백질은 GRA16 및/또는 GRA24를 포함한다.

[0339] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질은 톡소플라즈마의 미세간상체로부터 분비된다.

[0340] 본 발명의 일부 구현예에 따르면, 미세간상체로부터 분비된 단백질은 서열번호 280 내지 322로 구성된 군에서 선택된 아미노산 서열을 포함한다.

[0341] 본 발명의 일부 구현예에 따르면, 밀집 과립으로부터 분비된 단백질은 서열번호 234 내지 279로 구성된 군에서 선택된 아미노산 서열을 포함한다.

[0342] 본 발명의 일부 구현예에 따르면, 톡소플라즈마 분비 단백질은 톡소플라즈마 곤디 대식세포 이동 저해 인자(TgMIF)를 포함한다.

[0343] 하기 표 3은 단백질이 위치하거나 위치할 것으로 예상되는 세포 기관에 따라 정리된, 본 발명의 일부 구현예의 핵산 구조물로 클로닝될 수 있는 톡소플라즈마-분비 단백질을 열거한 것이다.

[0344] [표3] 톡소플라즈마 단백질

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_289620	cathepsin CPC1 (CPC1)	<i>T. gondii</i> ME49	밀집 과립	1	234

[0345]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_276130	cathepsin CPC2 (CPC2)	<i>T. gondii</i> ME49	밀집 과립	2	235
TGME49_268900	dense granular protein GRA10 (GRA10)	<i>T. gondii</i> ME49	밀집 과립	3	236
TGME49_297880	dense granule protein DG32	<i>T. gondii</i> ME49	밀집 과립	4	237
TGME49_270250	dense granule protein GRA1 (GRA1)	<i>T. gondii</i> ME49	밀집 과립	5	238
TGME49_212410	dense granule protein GRA11	<i>T. gondii</i> ME49	밀집 과립	6	239
TGME49_237800	dense granule protein GRA11	<i>T. gondii</i> ME49	밀집 과립	7	240
TGME49_275850	dense granule protein GRA12 (GRA12)	<i>T. gondii</i> ME49	밀집 과립	8	241
TGME49_288650	dense granule protein GRA12 (GRA12)	<i>T. gondii</i> ME49	밀집 과립	9	242
TGME49_239740	dense granule protein GRA14 (GRA14)	<i>T. gondii</i> ME49	밀집 과립	10	243
TGME49_275470	dense granule protein GRA15 (GRA15)	<i>T. gondii</i> ME49	밀집 과립	11	244
TGME49_227620	dense granule protein GRA2 (GRA2)	<i>T. gondii</i> ME49	밀집 과립	12	245
TGME49_227280	dense granule protein GRA3 (GRA3)	<i>T. gondii</i> ME49	밀집 과립	13	246
TGME49_310780	dense granule protein GRA4 (GRA4)	<i>T. gondii</i> ME49	밀집 과립	14	247
TGME49_286450	dense granule protein GRA5 (GRA5)	<i>T. gondii</i> ME49	밀집 과립	15	248
TGME49_275440	dense granule protein GRA6 (GRA6)	<i>T. gondii</i> ME49	밀집 과립	16	249
TGME49_203310	dense granule protein GRA7 (GRA7)	<i>T. gondii</i> ME49	밀집 과립	17	250

[0346]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번 호	Polyp. 서열 번호
TGME49_254720	dense granule protein GRA8 (GRA8)	<i>T. gondii</i> ME49	밀집과립	18	251
TGME49_251540	dense granule protein GRA9 (GRA9)	<i>T. gondii</i> ME49	밀집과립	19	252
TGME49_222170	dense-granule antigen DG32	<i>T. gondii</i> ME49	밀집과립	20	253
TGME49_208830	GRA16	<i>T. gondii</i> ME49	밀집과립	21	254
TGME49_200010	GRA20	<i>T. gondii</i> ME49	밀집과립	22	255
TGME49_241610	GRA21	<i>T. gondii</i> ME49	밀집과립	23	256
TGME49_230180	GRA24	<i>T. gondii</i> ME49	밀집과립	24	257
TGME49_290700	GRA25	<i>T. gondii</i> ME49	밀집과립	25	258
TGME49_231960	GRA28	<i>T. gondii</i> ME49	밀집과립	26	259
TGME49_269690	GRA29	<i>T. gondii</i> ME49	밀집과립	27	260
TGME49_232000	GRA30	<i>T. gondii</i> ME49	밀집과립	28	261
TGME49_220240	GRA31	<i>T. gondii</i> ME49	밀집과립	29	262
TGME49_212300	GRA32	<i>T. gondii</i> ME49	밀집과립	30	263
TGME49_247440	GRA33	<i>T. gondii</i> ME49	밀집과립	31	264
TGME49_226380	GRA35	<i>T. gondii</i> ME49	밀집과립	32	265
TGME49_213067	GRA36	<i>T. gondii</i> ME49	밀집과립	33	266

[0347]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번 호	Polyp. 서열 번호
TGME49_236890	GRA37	<i>T. gondii</i> ME49	밀집 과립	34	267
TGME49_312420	GRA38	<i>T. gondii</i> ME49	밀집 과립	35	268
TGME49_289380	GRA39	<i>T. gondii</i> ME49	밀집 과립	36	269
TGME49_219810	GRA40	<i>T. gondii</i> ME49	밀집 과립	37	270
TGME49_200360	hypothetical protein	<i>T. gondii</i> ME49	밀집 과립	38	271
TGME49_203290	hypothetical protein	<i>T. gondii</i> ME49	밀집 과립	39	272
TGME49_310790	hypothetical protein	<i>T. gondii</i> ME49	밀집 과립	40	273
TGME49_277240	NTPase I	<i>T. gondii</i> ME49	밀집 과립	41	274
TGME49_277270	NTPase II	<i>T. gondii</i> ME49	밀집 과립	42	275
TGME49_217430	protease inhibitor PI1 (PI1)	<i>T. gondii</i> ME49	밀집 과립	43	276
TGME49_208450	protease inhibitor PI2 (PI2)	<i>T. gondii</i> ME49	밀집 과립	44	277
TGGT1_411330	putative dense granule protein GRA11	<i>T. gondii</i> GT1	밀집 과립	45	278
TGME49_275860	putative dense granule protein GRA12	<i>T. gondii</i> VEG	밀집 과립	46	279
TGME49_261710	ankyrin repeat-containing protein	<i>T. gondii</i> ME49	미세간상 체	47	280
TGME49_300130	apical membrane antigen 1 domain- containing protein	<i>T. gondii</i> ME49	미세간상 체	48	281
TGME49_255260	apical membrane antigen AMA1	<i>T. gondii</i> ME49	미세간상 체	49	282

[0348]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_293770	chitinase-like protein CLP1 (CLP1)	<i>T. gondii</i> ME49	미세간상체	50	283
TGME49_204340	GRA34	<i>T. gondii</i> ME49	미세간상체	51	284
TGME49_221480	hypothetical protein	<i>T. gondii</i> ME49	미세간상체	52	285
TGME49_289100	MIC18	<i>T. gondii</i> ME49	미세간상체	53	286
TGME49_294790	MIC19	<i>T. gondii</i> ME49	미세간상체	54	287
TGME49_214940	MIC2-associated protein M2AP	<i>T. gondii</i> ME49	미세간상체	55	288
TGME49_283540	MIC20	<i>T. gondii</i> ME49	미세간상체	56	289
TGME49_291890	microneme protein MIC1 (MIC1)	<i>T. gondii</i> ME49	미세간상체	57	290
TGME49_250710	microneme protein MIC10 (MIC10)	<i>T. gondii</i> ME49	미세간상체	58	291
TGME49_204530	microneme protein MIC11 (MIC11)	<i>T. gondii</i> ME49	미세간상체	59	292
TGME49_267680	microneme protein MIC12 (MIC12)	<i>T. gondii</i> ME49	미세간상체	60	293
TGME49_260190	microneme protein MIC13 (MIC13)	<i>T. gondii</i> ME49	미세간상체	61	294
TGME49_218310	microneme protein MIC14 (MIC14)	<i>T. gondii</i> ME49	미세간상체	62	295
TGME49_247195	microneme protein MIC15 (MIC15)	<i>T. gondii</i> ME49	미세간상체	63	296
TGME49_289630	microneme protein MIC16 (MIC16)	<i>T. gondii</i> ME49	미세간상체	64	297
TGME49_200250	microneme protein MIC17A (MIC17A)	<i>T. gondii</i> ME49	미세간상체	65	298

[0349]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_200240	microneme protein MIC17B (MIC17B)	<i>T. gondii</i> ME49	미세간상체	66	299
TGME49_200230	microneme protein MIC17C (MIC17C)	<i>T. gondii</i> ME49	미세간상체	67	300
TGME49_201780	microneme protein MIC2 (MIC2)	<i>T. gondii</i> ME49	미세간상체	68	301
TGME49_319560	microneme protein MIC3 (MIC3)	<i>T. gondii</i> ME49	미세간상체	69	302
TGME49_208030	microneme protein MIC4 (MIC4)	<i>T. gondii</i> ME49	미세간상체	70	303
TGME49_277080	microneme protein MIC5 (MIC5)	<i>T. gondii</i> ME49	미세간상체	71	304
TGME49_218520	microneme protein MIC6 (MIC6)	<i>T. gondii</i> ME49	미세간상체	72	305
TGME49_261780	microneme protein MIC7 (MIC7)	<i>T. gondii</i> ME49	미세간상체	73	306
TGME49_245490	microneme protein MIC8 (MIC8)	<i>T. gondii</i> ME49	미세간상체	74	307
TGME49_245485	microneme protein MIC9 (MIC9)	<i>T. gondii</i> ME49	미세간상체	75	308
TGME49_208730	microneme protein, putative	<i>T. gondii</i> ME49	미세간상체	76	309
TGME49_208740	microneme protein, putative	<i>T. gondii</i> ME49	미세간상체	77	310
TGME49_254430	microneme protein, putative	<i>T. gondii</i> ME49	미세간상체	78	311
TGME49_275798	microneme protein, putative	<i>T. gondii</i> ME49	미세간상체	79	312
TGME49_244180	microneme-like protein	<i>T. gondii</i> ME49	미세간상체	80	313
TGME49_286740	microneme-like protein	<i>T. gondii</i> ME49	미세간상체	81	314

[0350]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_200270	PAN/Apple domain-containing protein	<i>T. gondii</i> ME49	미세간상체	82	315
TGME49_286150	PAN/Apple domain-containing protein	<i>T. gondii</i> ME49	미세간상체	83	316
TGME49_204130	perforin-like protein PLP1 (PLP1)	<i>T. gondii</i> ME49	미세간상체	84	317
TGVEG_4_39620	putative microneme protein	<i>T. gondii</i> VEG	미세간상체	85	318
TGME49_200290	rhomboid protease ROM1 (ROM1)	<i>T. gondii</i> ME49	미세간상체	86	319
TGME49_293900	sporozoite protein with an altered thrombospondin repeat SPATR	<i>T. gondii</i> ME49	미세간상체	87	320
TGME49_204050	subtilisin SUB1 (SUB1)	<i>T. gondii</i> ME49	미세간상체	88	321
TGME49_206510	toxolysin TLN4 (TLN4)	<i>T. gondii</i> ME49	미세간상체	89	322
TGME49_209030	actin ACT1 (ACT1)	<i>T. gondii</i> ME49	기타	90	323
TGME49_214290	DJ-1 family protein	<i>T. gondii</i> ME49	기타	91	324
TGME49_268850	enolase 2	<i>T. gondii</i> ME49	기타	92	325
TGME49_236040	fructose-1,6-bisphosphate aldolase	<i>T. gondii</i> ME49	기타	93	326
TGME49_289690	glyceraldehyde-3-phosphate dehydrogenase GAPDH1 (GAPDH1)	<i>T. gondii</i> ME49	기타	94	327
TGME49_290040	macrophage migration inhibitory factor, putative	<i>T. gondii</i> ME49	기타	95	328
TGME49_211680	protein disulfide isomerase	<i>T. gondii</i> ME49	기타	96	329
TGME49_273610	Secretory phospholipase A2	<i>T. gondii</i> ME49	기타	97	330
TGME49_273620	Secretory phospholipase A2	<i>T. gondii</i> GT1	기타	98	331
TGME49_271570	Toxoplasma gondii family D protein	<i>T. gondii</i> ME49	기타	99	332
TGME49_205470	translation elongation factor 2 family protein, putative	<i>T. gondii</i> ME49	기타	100	333

[0351]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번 호	Polyp. 서열 번호
TGME49_288360	tryptophanyl-tRNA synthetase (TrpRS2)	<i>T. gondii</i> ME49	기타	101	334
TGME49_208590	vacuolar ATP synthase subunit 54kD, putative	<i>T. gondii</i> ME49	기타	102	335
TGME49_256970	vacuolar ATP synthase subunit A, putative	<i>T. gondii</i> ME49	기타	103	336
TGME49_219800	vacuolar ATP synthase subunit b, putative	<i>T. gondii</i> ME49	기타	104	337
TGME49_315620	vacuolar ATP synthase subunit C, putative	<i>T. gondii</i> ME49	기타	105	338
TGME49_259010	vacuolar ATP synthase subunit d, putative	<i>T. gondii</i> ME49	기타	106	339
TGME49_305290	vacuolar atp synthase subunit e, putative	<i>T. gondii</i> ME49	기타	107	340
TGME49_310960	vacuolar atp synthase subunit f, putative	<i>T. gondii</i> ME49	기타	108	341
TGME49_246560	vacuolar ATP synthase subunit g, putative	<i>T. gondii</i> ME49	기타	109	342
TGME49_212310	vacuolar ATP synthetase	<i>T. gondii</i> ME49	기타	110	343
TGME49_314250	bradyzoite rhoptry protein BRP1 (BRP1)	<i>T. gondii</i> ME49	곤봉체	111	344
TGME49_209985	cAMP-dependent protein kinase	<i>T. gondii</i> ME49	곤봉체	112	345
TGME49_249670	cathepsin B	<i>T. gondii</i> ME49	곤봉체	113	346
TGME49_252200	cell cycle regulator with zn-finger domain-containing protein	<i>T. gondii</i> ME49	곤봉체	114	347
TGME49_210095	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	115	348
TGME49_296015	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	116	349
TGME49_297070	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	117	350
TGME49_311320	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	118	351
TGME49_321700	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	119	352
TGME49_321710	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	120	353
TGME49_322120	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	121	354
TGME49_323320	hypothetical protein	<i>T. gondii</i> ME49	곤봉체	122	355
TGGT1_410610	hypothetical protein	<i>T. gondii</i> GT1	곤봉체	123	356
TGME49_242118	myosin-light-chain kinase	<i>T. gondii</i> ME49	곤봉체	124	357

[0352]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_322000	myosin-light-chain kinase	<i>T. gondii</i> ME49	곤봉체	125	358
TGME49_322010	myosin-light-chain kinase	<i>T. gondii</i> ME49	곤봉체	126	359
TGME49_322100	myosin-light-chain kinase	<i>T. gondii</i> ME49	곤봉체	127	360
TGME49_323300	myosin-light-chain kinase	<i>T. gondii</i> ME49	곤봉체	128	361
TGME49_252500	polo kinase	<i>T. gondii</i> ME49	곤봉체	129	362
TGME49_258225	Predicted rhoptry protein kinase (ROPK)	<i>T. gondii</i> GT1	곤봉체	130	363
TGME49_234950	protein kinase (incomplete catalytic triad)	<i>T. gondii</i> ME49	곤봉체	131	364
TGME49_274170	protein kinase (incomplete catalytic triad)	<i>T. gondii</i> ME49	곤봉체	132	365
TGME49_281675	protein kinase, putative	<i>T. gondii</i> ME49	곤봉체	133	366
TGME49_270320	protein phosphatase 2C domain-containing protein	<i>T. gondii</i> ME49	곤봉체	134	367
TGME49_282055	protein phosphatase PP2C-hn (PP2CHN)	<i>T. gondii</i> ME49	곤봉체	135	368
TGVEG_2_81675A	putative protein kinase	<i>T. gondii</i> VEG	곤봉체	136	369
TGVEG_2_81675B	putative protein kinase	<i>T. gondii</i> VEG	곤봉체	137	370
TGME49_289680	Ras-related protein Rab11	<i>T. gondii</i> ME49	곤봉체	138	371
TGGT1_4_11350	rhoptry kinase family (incomplete catalytic triad) protein	<i>T. gondii</i> GT1	곤봉체	139	372
TGGT1_4_09600	rhoptry kinase family protein	<i>T. gondii</i> GT1	곤봉체	140	373
TGGT1_4_11360	rhoptry kinase family protein	<i>T. gondii</i> GT1	곤봉체	141	374
TGVEG_4_40850	rhoptry kinase family protein	<i>T. gondii</i> VEG	곤봉체	142	375
TGVEG_4_40860	rhoptry kinase family protein	<i>T. gondii</i> VEG	곤봉체	143	376
TGVEG_4_42710	rhoptry kinase family protein	<i>T. gondii</i> VEG	곤봉체	144	377
TGME49_308093	rhoptry kinase family protein (incomplete catalytic triad)	<i>T. gondii</i> ME49	곤봉체	145	378
TGME49_308096	rhoptry kinase family protein (incomplete catalytic triad)	<i>T. gondii</i> ME49	곤봉체	146	379
TGME49_227810	rhoptry kinase family protein ROP11 (incomplete catalytic triad) (ROP11)	<i>T. gondii</i> ME49	곤봉체	147	380

[0353]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번 호	Polyp. 서열 번호
TGME49_242240	rhoptry kinase family protein ROP19A (ROP19A)	<i>T. gondii</i> ME49	곤봉체	148	381
TGME49_242250	rhoptry kinase family protein ROP19B (ROP19B)	<i>T. gondii</i> ME49	곤봉체	149	382
TGME49_258230	rhoptry kinase family protein ROP20 (ROP20)	<i>T. gondii</i> ME49	곤봉체	150	383
TGME49_263220	rhoptry kinase family protein ROP21 (ROP21)	<i>T. gondii</i> ME49	곤봉체	151	384
TGME49_207700	rhoptry kinase family protein ROP22 (incomplete catalytic triad) (ROP22)	<i>T. gondii</i> ME49	곤봉체	152	385
TGME49_239600	rhoptry kinase family protein ROP23 (incomplete catalytic triad) (ROP23)	<i>T. gondii</i> ME49	곤봉체	153	386
TGME49_252360	rhoptry kinase family protein ROP24 (incomplete catalytic triad) (ROP24)	<i>T. gondii</i> ME49	곤봉체	154	387
TGME49_202780	rhoptry kinase family protein ROP25 (ROP25)	<i>T. gondii</i> ME49	곤봉체	155	388
TGME49_211260	rhoptry kinase family protein ROP26 (incomplete catalytic triad) (ROP26)	<i>T. gondii</i> ME49	곤봉체	156	389
TGME49_313330	rhoptry kinase family protein ROP27 (ROP27)	<i>T. gondii</i> ME49	곤봉체	157	390
TGME49_258370	rhoptry kinase family protein ROP28 (ROP28)	<i>T. gondii</i> ME49	곤봉체	158	391
TGME49_242230	rhoptry kinase family protein ROP29 (ROP29)	<i>T. gondii</i> ME49	곤봉체	159	392
TGME49_227010	rhoptry kinase family protein ROP30 (ROP30)	<i>T. gondii</i> ME49	곤봉체	160	393
TGME49_258800	rhoptry kinase family protein ROP31 (ROP31)	<i>T. gondii</i> ME49	곤봉체	161	394
TGME49_270920	rhoptry kinase family protein ROP32 (ROP32)	<i>T. gondii</i> ME49	곤봉체	162	395
TGME49_201130	rhoptry kinase family protein ROP33 (ROP33)	<i>T. gondii</i> ME49	곤봉체	163	396
TGME49_240090	rhoptry kinase family protein ROP34, putative	<i>T. gondii</i> ME49	곤봉체	164	397
TGME49_304740	rhoptry kinase family protein ROP35 (ROP35)	<i>T. gondii</i> ME49	곤봉체	165	398
TGME49_207610	rhoptry kinase family protein ROP36 (incomplete catalytic triad) (ROP36)	<i>T. gondii</i> ME49	곤봉체	166	399
TGME49_294560	rhoptry kinase family protein ROP37 (incomplete catalytic triad) (ROP37)	<i>T. gondii</i> ME49	곤봉체	167	400
TGME49_242110	rhoptry kinase family protein ROP38 (ROP38)	<i>T. gondii</i> ME49	곤봉체	168	401

[0354]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번 호	Polyp. 서열 번호
TGME49_262050	rhoptry kinase family protein ROP39 (ROP39)	<i>T. gondii</i> ME49	곤봉체	169	402
TGME49_291960	rhoptry kinase family protein ROP40 (incomplete catalytic triad) (ROP40)	<i>T. gondii</i> ME49	곤봉체	170	403
TGME49_266100	rhoptry kinase family protein ROP41 (ROP41)	<i>T. gondii</i> ME49	곤봉체	171	404
TGME49_230470	rhoptry kinase family protein ROP46, putative	<i>T. gondii</i> ME49	곤봉체	172	405
TGME49_249470	Rhoptry kinase family protein, truncated (incomplete catalytic triad)	<i>T. gondii</i> ME49	곤봉체	173	406
TGME49_253330	Rhoptry kinase family protein, truncated (incomplete catalytic triad)	<i>T. gondii</i> ME49	곤봉체	174	407
TGVEG_3_22130	rhoptry kinase family ROP19B	<i>T. gondii</i> VEG	곤봉체	175	408
TGVEG_2_69885A	rhoptry metalloprotease toxolysin TLN1	<i>T. gondii</i> VEG	곤봉체	176	409
TGVEG_2_69885B	rhoptry metalloprotease toxolysin TLN1	<i>T. gondii</i> VEG	곤봉체	177	410
TGME49_269885	rhoptry metalloprotease toxolysin TLN1 (TLN1)	<i>T. gondii</i> ME49	곤봉체	178	411
TGVEG_3_10010A	rhoptry neck protein RON1	<i>T. gondii</i> VEG	곤봉체	179	412
TGVEG_3_10010B	rhoptry neck protein RON1	<i>T. gondii</i> VEG	곤봉체	180	413
TGME49_310010	rhoptry neck protein RON1 (RON1)	<i>T. gondii</i> ME49	곤봉체	181	414
TGME49_261750	rhoptry neck protein RON10 (RON10)	<i>T. gondii</i> ME49	곤봉체	182	415
TGME49_300100	rhoptry neck protein RON2 (RON2)	<i>T. gondii</i> ME49	곤봉체	183	416
TGME49_223920	rhoptry neck protein RON3 (RON3)	<i>T. gondii</i> ME49	곤봉체	184	417
TGME49_229010	rhoptry neck protein RON4 (RON4)	<i>T. gondii</i> ME49	곤봉체	185	418
TGME49_311470	rhoptry neck protein RON5 (RON5)	<i>T. gondii</i> ME49	곤봉체	186	419
TGVEG_2_97960A	rhoptry neck protein RON6	<i>T. gondii</i> VEG	곤봉체	187	420
TGVEG_2_97960B	rhoptry neck protein RON6	<i>T. gondii</i> VEG	곤봉체	188	421
TGME49_297960	rhoptry neck protein RON6 (RON6)	<i>T. gondii</i> ME49	곤봉체	189	422
TGME49_306060	rhoptry neck protein RON8 (RON8)	<i>T. gondii</i> ME49	곤봉체	190	423

[0355]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번 호	Polyp. 서열 번호
TGVEG_3 08810A	rhoptry neck protein RON9	<i>T. gondii</i> VEG	곤봉체	191	424
TGVEG_3 08810B	rhoptry neck protein RON9	<i>T. gondii</i> VEG	곤봉체	192	425
TGME49_3 308810	rhoptry neck protein RON9 (RON9)	<i>T. gondii</i> ME49	곤봉체	193	426
TGME49_3 265120	rhoptry neck protein, putative	<i>T. gondii</i> ME49	곤봉체	194	427
TGME49_3 327200	rhoptry neck protein, putative	<i>T. gondii</i> ME49	곤봉체	195	428
TGME49_3 309590	rhoptry protein ROP1 (ROP1)	<i>T. gondii</i> ME49	곤봉체	196	429
TGME49_3 315490	rhoptry protein ROP10 (ROP10)	<i>T. gondii</i> ME49	곤봉체	197	430
TGME49_3 203990	rhoptry protein ROP12 (ROP12)	<i>T. gondii</i> ME49	곤봉체	198	431
TGME49_3 312270	rhoptry protein ROP13 (ROP13)	<i>T. gondii</i> ME49	곤봉체	199	432
TGME49_3 315220	rhoptry protein ROP14 (ROP14)	<i>T. gondii</i> ME49	곤봉체	200	433
TGME49_3 211290	rhoptry protein ROP15 (ROP15)	<i>T. gondii</i> ME49	곤봉체	201	434
TGME49_3 262730	rhoptry protein ROP16 (ROP16)	<i>T. gondii</i> ME49	곤봉체	202	435
TGME49_3 258580	rhoptry protein ROP17 (ROP17)	<i>T. gondii</i> ME49	곤봉체	203	436
TGME49_3 205250	rhoptry protein ROP18 (ROP18)	<i>T. gondii</i> ME49	곤봉체	204	437
TGME49_3 215785	rhoptry protein ROP2A (ROP2A)	<i>T. gondii</i> ME49	곤봉체	205	438
TGME49_3 295125	rhoptry protein ROP4 (ROP4)	<i>T. gondii</i> ME49	곤봉체	206	439
TGGT1_4 11430	rhoptry protein ROP5	<i>T. gondii</i> GT1	곤봉체	207	440
TGVEG_4 42220	rhoptry protein ROP5	<i>T. gondii</i> VEG	곤봉체	208	441
TGME49_3 308090	rhoptry protein ROP5 (ROP5)	<i>T. gondii</i> ME49	곤봉체	209	442
TGME49_3 258660	rhoptry protein ROP6 (ROP6)	<i>T. gondii</i> ME49	곤봉체	210	443
TGGT1_3 65080	rhoptry protein ROP7	<i>T. gondii</i> GT1	곤봉체	211	444
TGME49_3 295110	rhoptry protein ROP7 (ROP7)	<i>T. gondii</i> ME49	곤봉체	212	445
TGVEG_3 63030	rhoptry protein ROP8	<i>T. gondii</i> VEG	곤봉체	213	446
TGME49_3 215775	rhoptry protein ROP8 (ROP8)	<i>T. gondii</i> ME49	곤봉체	214	447

[0356]

유전자 ID	유전자 산물 설명	생물체	소기관	Polyn. 서열번호	Polyp. 서열번호
TGME49_243730	rhoptry protein ROP9 (ROP9)	<i>T. gondii</i> ME49	곤봉체	215	448
TGME49_295105	rhoptry protein, putative	<i>T. gondii</i> ME49	곤봉체	216	449
TGME49_315210	rhoptry protein, putative	<i>T. gondii</i> ME49	곤봉체	217	450
TGME49_315940	rhoptry protein, putative	<i>T. gondii</i> ME49	곤봉체	218	451
TGME49_230350	RON11	<i>T. gondii</i> ME49	곤봉체	219	452
TGME49_232020	RON12	<i>T. gondii</i> ME49	곤봉체	220	453
TGME49_294400	RON2L1	<i>T. gondii</i> ME49	곤봉체	221	454
TGME49_296020	ROP2L11	<i>T. gondii</i> VEG	곤봉체	222	455
TGME49_296000	ROP2L12	<i>T. gondii</i> ME49	곤봉체	223	456
TGME49_242100	ROP38	<i>T. gondii</i> ME49	곤봉체	224	457
TGME49_261740	ROP47	<i>T. gondii</i> ME49	곤봉체	225	458
TGME49_218270	ROP48	<i>T. gondii</i> ME49	곤봉체	226	459
TGME49_308075	ROP5	<i>T. gondii</i> VEG	곤봉체	227	460
TGME49_241000	ROP51	<i>T. gondii</i> ME49	곤봉체	228	461
TGME49_210370	ROP54	<i>T. gondii</i> ME49	곤봉체	229	462
TGME49_300290	SNARE domain-containing protein	<i>T. gondii</i> ME49	곤봉체	230	463
TGME49_299060	sodium/hydrogen exchanger NHE2	<i>T. gondii</i> ME49	곤봉체	231	464
TGME49_314500	subtilisin SUB2 (SUB2)	<i>T. gondii</i> ME49	곤봉체	232	465
TGME49_214080	toxofilin	<i>T. gondii</i> ME49	곤봉체	233	466

[0357]

[0358]

표 3. "polyn." = 폴리뉴클레오티드; "polyp" = 폴리펩티드.

[0359]

본 발명의 일부 구현예에 따르면, 이종 폴리뉴클레오티드는 독소플라즈마 비번역 부위(UTR) 핵산 서열을 추가로 포함한다.

[0360]

본 발명의 일부 구현예에 따르면, 독소플라즈마 비번역 부위(UTR) 핵산 서열은 이종 폴리뉴클레오티드(예를 들어, 약학적 폴리펩티드와 프레임 내 융합된 독소플라즈마 분비 단백질을 코딩하는 것)의 개방형 해독 프레임의 상류 및/또는 하류이다.

[0361]

본 발명의 일부 구현예에 따르면, 독소플라즈마 5'-비번역 부위(5'-UTR)는 독소플라즈마 분비 단백질 개방형 해독 프레임의 상류에 위치한다.

[0362]

본 발명의 일부 구현예에 따르면, 독소플라즈마 3'-비번역 부위(3'-UTR)는 약학적 폴리펩티드와 프레임 내 융합된 독소플라즈마 분비 단백질을 코딩하는 개방형 해독 프레임의 하류에 위치한다.

[0363]

본 발명의 일부 구현예에 따르면, 독소플라즈마 3'-비번역 부위(3'-UTR) 핵산 서열은 GRA2 3'-UTR, GRA16 3'-UTR, GRA24 3'-UTR, SAG1 3'-UTR 또는 DHFR 3'-UTR이다.

[0364]

본 발명의 일부 구현예에 따르면, 독소플라즈마 5'-비번역 부위(5'-UTR) 핵산 서열은 GRA2 5'-UTR, GRA16 5'-UTR, GRA24 5'-UTR, SAG1 5'-UTR 또는 DHFR 5'-UTR이다.

[0365]

본 발명의 일부 구현예에 따르면, 독소플라즈마 비번역 부위(UTR) 핵산 서열은 독소필린 3'-UTR이다.

[0366]

기술한 바와 같이, 이종 폴리뉴클레오티드는 독소플라즈마 분비 단백질의 하류 프레임 내 융합된 약학적 폴리펩

티드를 코딩하는 제2 핵산 서열을 포함한다.

- [0367] 본원에서 사용된 구 "약학적 폴리펩티드"는 치료 효과, 예를 들어, 이를 필요로 하는 개체의 세포에 도입될 때, 병리를 치료할 수 있는, 폴리펩티드를 말한다.
- [0368] 특정 질환에 대해서, 약학적 폴리펩티드는 개체 내 특정한 기관, 조직, 세포, 세포 구획 또는 세포 위치에 도달할 때 효과적일 수 있다는 점을 알아야 한다. 예를 들어, 신경질환 치료에 있어서, 약학적 조성물은 바람직하게는 신경계, 예를 들어, 뉴런, 교세포(glia) 또는 다른 세포를 표적화한다. 추가적으로 또는 대안적으로, 특정한 질환에 있어서, 약학적 폴리펩티드는 약학적 조성물의 표적이 세포 핵 내에 위치한(배치된) 경우, 세포 핵과 같은, 특정한 세포 위치에 도달하여야 한다. 예를 들어, MECP2의 경우, 활성 단백질은 핵 내 DNA에 결합하고 유전자 발현을 조절한다.
- [0369] 본 발명의 일부 구현예에 따르면, 핵산 구조물은 독소플라즈마 분비 단백질로부터 약학적 폴리펩티드를 분리할 수 있는, 적어도 하나의 프레임 내 절단 부위를 추가로 포함한다.
- [0370] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 병리를 치료할 수 있는 내인성 단백질에 상응하는 야생형 아미노산 서열을 포함한다.
- [0371] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 병리를 치료할 수 있는 항체를 포함한다.
- [0372] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 병리를 치료할 수 있는 항원을 포함한다.
- [0373] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 병리를 치료할 수 있는 독소를 포함한다.
- [0374] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 효소, 구조 폴리펩티드, 운동성 폴리펩티드, 조절 폴리펩티드, 저장 폴리펩티드, 신호/리간드 폴리펩티드, 수용체 폴리펩티드, 감각 폴리펩티드, 항체, 단백질 채널 및/또는 수송 폴리펩티드를 포함한다.
- [0375] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 갈락토세레브로시다제(GALC)이다.
- [0376] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 갈락토세레브로시다제(GALC) 이소폼 1, 이소폼 2, 이소폼 3, 이소폼 4 또는 이소폼 5이다.
- [0377] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 메틸-CpG 결합 단백질 2(MECP2)이다.
- [0378] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 메틸-CpG 결합 단백질 2(MECP2) 이소폼 1 또는 이소폼 2이다.
- [0379] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 신경아세포 유래 신경영양 인자(GDNF)이다.
- [0380] 본 발명의 일부 구현예에 따르면, 약학적 폴리펩티드는 신경아세포 유래 신경영양 인자(GDNF) 이소폼 1, 이소폼 2, 이소폼 3, 이소폼 4 또는 이소폼 5이다.
- [0381] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 아스파르트아실라제(Aspartoacylase, ASPA)이다.
- [0382] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 생존 운동 신경원 단백질(Survival Motor Neuron Protein, SMN1)이다.
- [0383] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 생존 운동 신경원 단백질 SMN, 이소폼 SMN-델타5, 이소폼 SMN-델타7 또는 이소폼 SMN-델타57이다.
- [0384] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 파킨(Parkin, PARK2)이다.
- [0385] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 파킨(PARK2) 이소폼 1, 이소폼 2, 이소폼 3, 이소폼 4, 이소폼 5, 이소폼 6, 이소폼 7 또는 이소폼 8이다.
- [0386] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 전사 인자 EB(Transcription Factor EB, TFEB)이다.
- [0387] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 전사 인자 EB(TFEB) 이소폼 1 또는 이소폼 2이다.
- [0388] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 TALEN(TALE 뉴클레아제)이다.
- [0389] 본 발명의 일부 구현예에 따르면, 상기 약학적 폴리펩티드는 TALE TF(TALE 전사 인자)이다.

[0390] 본원에서 하기 표 4는 본 발명의 일부 구현예의 특소플라즈마에 의해 개체로 분비될 수 있는 예시적 치료용 단백질질을 열거한 것이다.

[표4] 전형적 의약 단백질

유전자 명/기호	폴리펩티드 젠뱅크(GenBank) 수탁번호	서열번호:	폴리뉴클레오티드 젠뱅크(GenBank) 수탁번호 (코딩 서열)	서열번호:
TFEB	NP_001258874.1	4610	NM_001271945.1	4600
TFEB	NP_001161299.2	4618	NM_001167827.2	4619
TFEB	NP_001258873.1	4620	NM_001271944.1	4621
TFEB	NP_009093.1	4622	NM_007162.2	4623
TFEB	NP_001258872.1	4624	NM_001271943.1	4625
HGSNAT	NP_689632	4301	NM_152419	4040
MEF2C	NP_001124477	4302	NM_001131005	4041
MEF2C	NP_002388	4303	NM_002397	4042
NRTN	NP_004549	4304	NM_004558	4043
PGF	NP_002623	4305	NM_002632	4044
RPE65	NP_000320	4306	NM_000329	4045
GDNF	NP_000505	4307	NM_000514	4046
GDNF	NP_954701	4308	NM_199231	4047
CNGB3	NP_061971	4309	NM_019098	4048
BDNF	NP_001137277	4310	NM_001143816	4049
BDNF	NP_001137279	4311	NM_001143814	4050
BDNF	NP_001137288	4312	NM_001143813	4051
BDNF	NP_001137278	4313	NM_001143812	4052
BDNF	NP_733931	4314	NM_001143806	4053
BDNF	NP_733930	4315	NM_001143811	4054
BDNF	NP_733929	4316	NM_001709	4055
BDNF	NP_733927	4317	NM_001143805	4056
BDNF	NP_733928	4318	NM_001143810	4057
BDNF	NP_001700	4319	NM_170735	4058
BDNF	NP_001137281	4320	NM_170734	4059
BDNF	NP_001137282	4321	NM_170733	4060
BDNF	NP_001137280	4322	NM_170732	4061
BDNF	NP_001137285	4323	NM_170731	4062
BDNF	NP_001137286	4324	NM_001143809	4063
BDNF	NP_001137283	4325	NM_001143807	4064
BDNF	NP_001137284	4326	NM_001143808	4065
APP	NP_001129601	4327	NM_000484	4066
APP	NP_958817	4328	NM_201414	4067
APP	NP_958816	4329	NM_001136131	4068
APP	NP_001129602	4330	NM_201413	4069
APP	NP_001129488	4331	NM_001136130	4070
APP	NP_000475	4332	NM_001136016	4071
APP	NP_001129603	4333	NM_001136129	4072
ASPA	NP_000040	4334	NM_001128085	4073
ASPA	NP_001121557	4335	NM_000049	4074
S1PR1	NP_001391	4336	NM_001400	4075
IDS	NP_001160022	4337	NM_001166550	4076

[0392]

유전자 명/기호	폴리펩티드 젠뱅크(GenBank) 수탁번호	서열번호:	폴리뉴클레오티드 젠뱅크(GenBank) 수탁번호 (코딩 서열)	서열번호:
IDS	NP_006114	4338	NM_006123	4077
IDS	NP_000193	4339	NM_000202	4078
HTRA2	NP_659540	4340	NM_013247	4079
HTRA2	NP_037379	4341	NM_145074	4080
CDNF	NP_001025125	4342	NM_001029954	4081
DNAJC5	NP_079495	4343	NM_025219	4082
IDUA	NP_000194	4344	NM_000203	4083
SPON1	NP_006099	4345	NM_006108	4084
NMNAT2	NP_733820	4346	NM_015039	4085
NMNAT2	NP_055854	4347	NM_170706	4086
FMR1	NP_002015	4348	NM_002024	4087
MECP2	NP_004983	4349	NM_001110792	4088
MECP2	NP_001104262	4350	NM_004992	4089
GNS	NP_002067	4351	NM_002076	4090
VEGFB	NP_003368	4352	NM_003377	4091
HIF1A	NP_851397	4353	NM_181054	4092
HIF1A	NP_001521	4354	NM_001530	4093
SERPINF1	NP_002606	4355	NM_002615	4094
VEGFA	NP_001165093	4356	NM_001025369	4095
VEGFA	NP_001165094	4357	NM_001025366	4096
VEGFA	NP_001020540	4358	NM_001025367	4097
VEGFA	NP_001020541	4359	NM_001025368	4098
VEGFA	NP_003367	4360	NM_003376	4099
VEGFA	NP_001165101	4361	NM_001171627	4100
VEGFA	NP_001020537	4362	NM_001171626	4101
VEGFA	NP_001165100	4363	NM_001171629	4102
VEGFA	NP_001020539	4364	NM_001171628	4103
VEGFA	NP_001020538	4365	NM_001171624	4104
VEGFA	NP_001028928	4366	NM_001171630	4105
VEGFA	NP_001165098	4367	NM_001171625	4106
VEGFA	NP_001165097	4368	NM_001171622	4107
VEGFA	NP_001165096	4369	NM_001171623	4108
VEGFA	NP_001165095	4370	NM_001033756	4109
VEGFA	NP_001165099	4371	NM_001025370	4110
STC1	NP_003146	4372	NM_003155	4111
NGB	NP_067080	4373	NM_021257	4112
NFE2L2	NP_001138884	4374	NM_006164	4113
NFE2L2	NP_006155	4375	NM_001145412	4114
NFE2L2	NP_001138885	4376	NM_001145413	4115
MAPK7	NP_620603	4377	NM_002749	4116
MAPK7	NP_620602	4378	NM_139034	4117
MAPK7	NP_620601	4379	NM_139033	4118
MAPK7	NP_002740	4380	NM_139032	4119
NMNAT1	NP_073624	4381	NM_022787	4120
NGF	NP_002497	4382	NM_002506	4121

[0393]

유전자 명/기호	폴리펩티드 젠뱅크(GenBank) 수탁번호	서열번호:	폴리뉴클레오티드 젠뱅크(GenBank) 수탁번호 (코딩 서열)	서열번호:
NAGLU	NP_000254	4383	NM_000263	4122
CLU	NP_001822	4384	NM_001831	4123
MME	NP_009218	4385	NM_000902	4124
MME	NP_009219	4386	NM_007289	4125
MME	NP_000893	4387	NM_007287	4126
MME	NP_009220	4388	NM_007288	4127
CTSA	NP_001121167	4389	NM_001167594	4128
CTSA	NP_000299	4390	NM_000308	4129
CTSA	NP_001161066	4391	NM_001127695	4130
PPT1	NP_000301	4392	NM_000310	4131
PPT1	NP_001136076	4393	NM_001142604	4132
TIMP2	NP_003246	4394	NM_003255	4133
MANF	NP_006001	4395	NM_006010	4134
TIMP1	NP_003245	4396	NM_003254	4135
GAD2	NP_000809	4397	NM_001134366	4136
GAD2	NP_001127838	4398	NM_000818	4137
GALC	NP_000144	4399	NM_000153	4138
GAD1	NP_000808	4400	NM_013445	4139
GAD1	NP_038473	4401	NM_000817	4140
NTF3	NP_002518	4402	NM_002527	4141
NTF3	NP_001096124	4403	NM_001102654	4142
GUSB	NP_000172	4404	NM_000181	4143
HGF	NP_001010932	4405	NM_001010933	4144
HGF	NP_001010931	4406	NM_001010932	4145
HGF	NP_001010934	4407	NM_001010931	4146
HGF	NP_000592	4408	NM_000601	4147
HGF	NP_001010933	4409	NM_001010934	4148
SERPINI1	NP_005016	4410	NM_005025	4149
SERPINI1	NP_001116224	4411	NM_001122752	4150
RGS2	NP_002914	4412	NM_002923	4151
NPY	NP_000896	4413	NM_000905	4152
UCP2	NP_003346	4414	NM_003355	4153
SST	NP_001039	4415	NM_001048	4154
SGSH	NP_000190	4416	NM_000199	4155
CYP2J2	NP_000766	4417	NM_000775	4156
GM2A	NP_000396	4418	NM_000405	4157
GM2A	NP_001161079	4419	NM_001167607	4158
HEXA	NP_000511	4420	NM_000520	4159
UCHL1	NP_004172	4421	NM_004181	4160
HEXB	NP_000512	4422	NM_000521	4161
PINK1	NP_115785	4423	NM_032409	4162
PRDX3	NP_006784	4424	NM_006793	4163
PRDX1	NP_859048	4425	NM_002574	4164
PRDX1	NP_859047	4426	NM_181696	4165
PRDX1	NP_002565	4427	NM_181697	4166

[0394]

유전자 명/기호	폴리펩티드 젠뱅크(GenBank) 수탁번호	서열번호:	폴리뉴클레오티드 젠뱅크(GenBank) 수탁번호 (코딩 서열)	서열번호:
GLB1	NP_001129074	4428	NM_001135602	4167
GLB1	NP_001073279	4429	NM_000404	4168
GLB1	NP_000395	4430	NM_001079811	4169
TPP1	NP_000382	4431	NM_000391	4170
ANG	NP_001136	4432	NM_001097577	4171
ANG	NP_001091046	4433	NM_001145	4172
HMOX1	NP_002124	4434	NM_002133	4173
NRG1	NP_039258	4435	NM_001160001	4174
NRG1	NP_001153479	4436	NM_001159995	4175
NRG1	NP_001153476	4437	NM_001160007	4176
NRG1	NP_001153477	4438	NM_001160008	4177
NRG1	NP_039254	4439	NM_001159996	4178
NRG1	NP_039256	4440	NM_001159999	4179
NRG1	NP_001153467	4441	NM_001160002	4180
NRG1	NP_001153468	4442	NM_001160004	4181
NRG1	NP_039250	4443	NM_004495	4182
NRG1	NP_001153471	4444	NM_001160005	4183
NRG1	NP_001153480	4445	NM_013964	4184
NRG1	NP_039251	4446	NM_013960	4185
NRG1	NP_039252	4447	NM_013962	4186
NRG1	NP_039253	4448	NM_013959	4187
NRG1	NP_001153474	4449	NM_013958	4188
NRG1	NP_004486	4450	NM_013957	4189
NRG1	NP_001153473	4451	NM_013956	4190
NFIL3	NP_005375	4452	NM_005384	4191
MAN2B1	NP_000519	4453	NM_000528	4192
DHCR24	NP_055577	4454	NM_014762	4193
DDC	NP_001076440	4455	NM_001082971	4194
DDC	NP_000781	4456	NM_000790	4195
TP53	NP_001119588	4457	NM_001126113	4196
TP53	NP_001119589	4458	NM_001126112	4197
TP53	NP_001119585	4459	NM_000546	4198
TP53	NP_001119584	4460	NM_001126116	4199
TP53	NP_001119587	4461	NM_001126117	4200
TP53	NP_001119586	4462	NM_001126114	4201
TP53	NP_000537	4463	NM_001126115	4202
ADNP	NP_056154	4464	NM_181442	4203
ADNP	NP_852107	4465	NM_015339	4204
GAN	NP_071324	4466	NM_022041	4205
GAL	NP_057057	4467	NM_015973	4206
SMN1	NP_000335	4468	NM_022874	4207
SMN1	NP_075015	4469	NM_017411	4208
SMN1	NP_075014	4470	NM_000344	4209
SMN1	NP_059107	4471	NM_022876	4210
SMN1	NP_075013	4510	NM_022875	4211

[0395]

유전자 명/기호	폴리펩티드 젠뱅크(GenBank) 수탁번호	서열번호:	폴리뉴클레오티드 젠뱅크(GenBank) 수탁번호 (코딩 서열)	서열번호:
SMN1	NP_075012	4511	NM_022877	4212
PROC	NP_000303	4512	NM_000312	4213
TRAP1	NP_057376	4513	NM_016292	4214
IL18BP	NP_001138527	4514	NM_173042	4215
IL18BP	NP_001138529	4515	NM_001145057	4216
IL18BP	NP_766630	4516	NM_001145055	4217
IL18BP	NP_001034749	4517	NM_001039660	4218
IL18BP	NP_001034748	4518	NM_001039659	4219
PRDX6	NP_004896	4519	NM_004905	4220
TXN	NP_003320	4520	NM_003329	4221
GAA	NP_000143	4521	NM_000152	4222
GAA	NP_001073271	4522	NM_001079803	4223
GAA	NP_001073272	4523	NM_001079804	4224
GHRL	NP_001128416	4524	NM_001134945	4225
GHRL	NP_001128417	4525	NM_001134944	4226
GHRL	NP_001128413	4526	NM_001134946	4227
GHRL	NP_057446	4527	NM_016362	4228
GHRL	NP_001128418	4528	NM_001134941	4229
CSF3	NP_757373	4529	NM_000759	4230
CSF3	NP_757374	4530	NM_172220	4231
CSF3	NP_000750	4531	NM_172219	4232
UBE3A	NP_000453	4532	NM_130838	4233
UBE3A	NP_570854	4533	NM_130839	4234
UBE3A	NP_570853	4534	NM_000462	4235
ABCD1	NP_000024	4535	NM_000033	4236
NDP	NP_000257	4536	NM_000266	4237
TH	NP_954986	4537	NM_199292	4238
TH	NP_954987	4538	NM_199293	4239
TH	NP_000351	4539	NM_000360	4240
GCH1	NP_000152	4540	NM_000161	4241
GCH1	NP_001019241	4541	NM_001024070	4242
GCH1	NP_001019242	4542	NM_001024071	4243
GCH1	NP_001019195	4543	NM_001024024	4244
BCL2	NP_000648	4544	NM_000633	4245
BCL2	NP_000624	4545	NM_000657	4246
ENO2	NP_001966	4546	NM_001975	4247
EPO	NP_000790	4547	NM_000799	4248
GBA	NP_001005741	4548	NM_001005742	4249
GBA	NP_001165283	4549	NM_001005741	4250
GBA	NP_001005742	4550	NM_001171811	4251
GBA	NP_001165282	4551	NM_001171812	4252
GBA	NP_000148	4552	NM_000157	4253
AGA	NP_000018	4553	NM_000027	4254
AGA	NP_001165459	4554	NM_001171988	4255
UPF1	NP_002902	4555	NM_002911	4256

[0396]

유전자 명/기호	폴리펩티드 젠뱅크(GenBank) 수탁번호	서열번호:	폴리뉴클레오티드 젠뱅크(GenBank) 수탁번호 (코딩 서열)	서열번호:
PSAP	NP_001035931	4556	NM_001042465	4257
PSAP	NP_002769	4557	NM_001042466	4258
PSAP	NP_001035930	4558	NM_002778	4259
ANXA1	NP_000691	4559	NM_000700	4260
IGF1	NP_001104753	4560	NM_001111284	4261
IGF1	NP_001104754	4561	NM_001111283	4262
IGF1	NP_000609	4562	NM_000618	4263
IGF2	NP_001035835	4563	NM_001007139	4264
IGF2	NP_000603	4564	NM_000612	4265
IGF2	NP_001007140	4565	NM_000207	4266
IGF2	NP_001121070	4566	NM_001127598	4267
IGF2	NP_000198	4567	NM_001042376	4268
PARK2	NP_054642	4568	NM_013988	4269
PARK2	NP_054643	4569	NM_013987	4270
PARK2	NP_004553	4570	NM_004562	4271
FUCA1	NP_000138	4571	NM_000147	4272
SIRT1	NP_001135970	4572	NM_012238	4273
SIRT1	NP_036370	4573	NM_001142498	4274
PARK7	NP_001116849	4574	NM_007262	4275
PARK7	NP_009193	4575	NM_001123377	4276
ANXA2	NP_004030	4576	NM_004039	4277
ANXA2	NP_001002857	4577	NM_001136015	4278
ANXA2	NP_001002858	4578	NM_001002858	4279
ANXA2	NP_001129487	4579	NM_001002857	4280
GCG	NP_002045	4580	NM_002054	4281
LEP	NP_000221	4581	NM_000230	4282
SH3BP5	NP_004835	4582	NM_001018009	4283
SH3BP5	NP_001018009	4583	NM_004844	4284
CNTF	NP_000605	4584	NM_053023	4285
CNTF	NP_444251	4585	NM_000614	4286
GLA	NP_000160	4586	NM_000169	4287
KCNN3	NP_740752	4587	NM_170782	4288
KCNN3	NP_002240	4588	NM_002249	4289
ARSA	NP_001078896	4589	NM_000487	4290
ARSA	NP_001078897	4590	NM_001085428	4291
ARSA	NP_000478	4591	NM_001085426	4292
ARSA	NP_001078894	4592	NM_001085427	4293
ARSA	NP_001078895	4593	NM_001085425	4294
SUMF1	NP_001158147	4594	NM_001164674	4295
SUMF1	NP_001158146	4595	NM_001164675	4296
SUMF1	NP_877437	4596	NM_182760	4297
CRH	NP_000747	4597	NM_000756	4298
SMPD1	NP_000534	4598	NM_000543	4299
SMPD1	NP_001007594	4599	NM_001007593	4300

[0397]

[0398]

본원에 기재된 임의의 서열(예를 들어, 독소플라즈마 분비 단백질 및/또는 치료용 폴리펩티드)은 표적 세포(예를 들어, 독소플라즈마) 내 발현을 위해 코돈 최적화될 수 있다는 것을 알아야 한다. 이러한 서열 변형의 예는 이에 제한되는 것은 아니나, 관심 표적 세포 중에서 전형적으로 발견되는 것에 보다 근접하게 접그하도록 변화된 G/C 함량, 및 일반적으로 코돈 최적화로 불리는, 표적 세포 중에서 이례적으로 발견된 코돈의 제거를 포함한다.

[0399]

구 "코돈 최적화"는 관심 표적 세포 내 코돈 사용량에 접근하는 이의 구조 유전자 또는 단편 내 사용을 위한 적절한 DNA 뉴클레오티드의 선택을 말한다. 그러므로, 최적화된 유전자 또는 핵산 서열은 표적 세포에서 통계학적으로-바람직한 또는 통계학적으로-선호되는 코돈을 사용하기 위하여, 자연 또는 자연적으로 발생된 유전자의 뉴클레오티드 서열이 변형된 유전자를 말한다. 뉴클레오티드 서열은 전형적으로 DNA 수준에서 검사되고, 표적 세포 중에서의 발현을 위해 최적화된 코딩 영역은 임의의 적합한 과정을 이용하여 확인된다. 이러한 방법에서, 코돈 사용량의 표준 편차, 코돈 사용량 바이어스의 측정은 고도로 발현된 표적 세포 유전자와 관련된 자연 유전자

의 각 코돈의 사용량의 제곱 비례 편차를 찾아내어, 평균 제곱 편차를 계산함으로써 계산될 수 있다. 사용된 식: $1 \text{ SDCU} = n = 1/N \left[\left(X_n - Y_n \right) / Y_n \right]^2 / N$, 여기서, X_n 은 고도로 발현된 표적 세포 유전자 내 코돈 n 의 사용량의 빈도를 말하고, 여기서 Y_n 은 관심 유전자 내 코돈 n 의 사용량의 빈도를 말하며, N 은 관심 유전자 내 코돈의 총수를 말한다.

[0400] 특별한 표적 세포 유형에 대한 바람직한 코돈 사용량에 일치하는 핵산 서열을 최적화하는 하나의 방법은 세계적인 DNA 서열 데이터베이스: 2000년 상황,으로부터 표로 만들어진 코돈 사용량을 통한 코돈 사용량 데이터베이스 (Codon Usage Database)에서 온라인상 제공되는 것과 같은 코돈 최적화 테이블의, 추가의 통계학적 계산의 수행 없이, 직접적인 사용에 근거한 것이다. Y Nakamura, T Gojobori, T Ikemura - Nucleic acids research, 2000 - Oxford Univ Press. 코돈 사용량 데이터베이스는 젠뱅크(Genbank)에 존재하는 데이터를 근거로 통계학적으로 결정된 각 코돈 사용량 표와 함께, 다수의 상이한 종에 대한 코돈 사용량 표를 포함한다.

[0401] 특별한 종(예를 들어, 톱소플라즈마 곤디) 내 각 아미노산에 대한 가장 바람직한 또는 가장 선호하는 코돈을 확인하기 위하여 상기 표를 사용하여, 목적단백질을 코딩하는 자연적으로 발생한 뉴클레오티드 서열을 특별한 표적 세포 종에 대하여 코돈 최적화할 수 있다. 이는 특별한 종 계통에서 통계적으로 낮은 발생빈도를 갖는 코돈을, 통계적으로 더 선호되는 아미노산과 관련된 상응하는 코돈으로 대체함으로써 이루어진다. 그러나, 하나 이상의 덜 선호되는 코돈은 존재하는 제한 부위를 제거하기 위하여, 잠재적으로 유용한 접합부(신호 펩티드 또는 종결 카세트를 추가하는 5' 및 3' 말단, 적절한 전장 서열을 생성하는 것과 함께 세그먼트를 절단하고 붙이는데 사용되는 내부 부위)에서 새로운 것들을 만들기 위하여, 또는 mRNA 안정성 또는 발현에 부정적인 영향을 미칠 수 있는 뉴클레오티드 서열을 제거하기 위하여, 선택될 수 있다.

[0402] 자연적으로 발생한 코딩 뉴클레오티드 서열은 이미, 임의의 변형 전에, 특별한 표적 세포 종 내 통계적으로-선호되는 코돈에 상응하는 다수의 코돈을 포함한다. 그러므로, 자연적 뉴클레오티드 서열의 코돈 최적화는 자연적 뉴클레오티드 서열 내 어떠한 코돈이 특별한 표적 세포와 관련하여 통계적으로-선호되지 않는지를 결정하고, 코돈 최적화된 유도체를 생성하기 위하여 특별한 표적 세포의 코돈 사용량 표에 부합되게 이들 코돈을 변형하는 것을 포함한다. 변형된 뉴클레오티드 서열에 의해 코딩된 단백질이 상응하는 자연적으로 발생하거나 자연적 유전자에 의해 코딩된 단백질 보다 더 높은 수준에서 생성된다면, 변형된 뉴클레오티드 서열은 표적 세포 코돈 사용량에 대하여 완전히 또는 부분적으로 최적화될 수 있다. 추가적으로 또는 대체적으로, 코돈 최적화된/사용량 서열은 상응하는 자연적으로 발생하거나 자연적 유전자에 의해 코딩된 단백질 보다 더 잘 접힌다. 추가적으로 또는 대체적으로, 코돈 최적화된/사용량 서열은 상응하는 자연적으로 발생하거나 자연적 유전자 보다 표적 세포 기관에 더 잘 표적화된다. 추가적으로 또는 대체적으로, 코돈 최적화된/사용량 서열은 상응하는 자연적으로 발생하거나 또는 자연적 유전자에 의해 코딩된 단백질 보다 덜 분해된다.

[0403] 예를 들어, 하기 표 5의 톱소플라즈마 코돈 사용량이 사용될 수 있다.

[0404] [표 5]

트리플렛	아미노산(한글자 코드)	분획	빈도: 1000 당
UUU	F	0.35	13.3
UUC	F	0.65	25
UUA	L	0.03	2.6
UUG	L	0.17	14.5
CUU	L	0.17	15
CUC	L	0.31	27.1
CUA	L	0.04	3.8

[0405]

트리플렛	아미노산 (한글자 코드)	분획	빈도: 1000 당
CUG	L	0.28	24
AUU	I	0.38	12.2
AUC	I	0.53	17.4
AUA	I	0.09	2.9
AUG	M	1	18.3
GUU	V	0.22	14.7
GUC	V	0.38	25.4
GUA	V	0.08	5.7
GUG	V	0.32	21.4
UCU	S	0.23	20.3
UCC	S	0.17	15.2
UCA	S	0.09	8.1
UCG	S	0.22	19
CCU	P	0.27	15.4
CCC	P	0.24	13.6
CCA	P	0.18	10.4
CCG	P	0.3	17.3
ACU	T	0.22	12.3
ACC	T	0.24	13
ACA	T	0.24	13.2
ACG	T	0.3	16.4
GCU	A	0.21	20.5
GCC	A	0.24	22.6
GCA	A	0.22	20.8
GCG	A	0.33	31.5
UAU	Y	0.26	5.1
UAC	Y	0.74	14.5
UAA	*	0.34	0.6
UAG	*	0.23	0.4
CAU	H	0.37	7.9
CAC	H	0.63	13.4
CAA	Q	0.36	13.7
CAG	Q	0.64	24.5
AAU	N	0.35	10.1
AAC	N	0.65	18.9
AAA	K	0.38	18.4
AAG	K	0.62	29.8

[0406]

트리플렛	아미노산 (한글자 코드)	분획	빈도: 1000 당
GAU	D	0.32	16.3
GAC	D	0.68	34.3
GAA	E	0.45	32.7
GAG	E	0.55	40.6
UGU	C	0.37	7.2
UGC	C	0.63	12.4
UGA	*	0.43	0.8
UGG	W	1	10.8
CGU	R	0.12	8.2
CGC	R	0.25	17.5
CGA	R	0.18	12.7
CGG	R	0.14	10.1
AGU	S	0.11	9.3
AGC	S	0.18	16.1
AGA	R	0.18	12.8
AGG	R	0.12	8.7
GGU	G	0.18	14.6
GGC	G	0.36	28.5
GGA	G	0.27	21.4
GGG	G	0.18	14.6

[0407]

[0408]

본 발명의 일부 구현예에 따르면, 이중 폴리뉴클레오티드는 선택 마커를 코딩하는 핵산 서열을 추가로 포함한다.

[0409]

본 발명의 일부 구현예에 따르면, 선택 마커는 클로람페니콜 아세틸전달효소(CAT), DHFR-TS, BLE, HXGPRT, UPRT, TK, CD, 형광 단백질(GFP, YFP, RFP, mCherry 또는 그 외와 같은) 또는 그 외와 같은) 또는 에피토프 태그(HA, Myc, Ty-1, FLAG 또는 그 외와 같은)를 포함한다.

[0410]

본 발명의 일부 구현예에 따르면, 선택 마커는 HXGPRT를 포함한다.

[0411]

HXGPRT 활성이 결핍된 톡소플라스마 급분열소체는 6-티오잔틴(6-TX)의 존재 시 선택될 수 있는 반면, HXGPRT 활성을 발현시키는 균주는 마이코페놀릭산(MPA) 및/또는 잔틴에서 선택될 수 있다(Pfefferkorn and Borotz, 1994, Pfefferkorn E. R., Borotz S. (1994) Exp. Parasitol. 79, 374-382).

[0412]

본 발명의 일부 구현예에 따르면, 선택 마커는 클로람페니콜 아세틸전달효소(CAT) (클로람페니콜을 사용하는 양성 선택용), DHFR-TS(피리메타민을 이용한 양성 선택용), HXGPRT(마이코페놀릭산+잔틴을 이용한 양성 선택 또는 6-티오잔틴을 사용한 음성 선택용), UPRT(5'-플루오-2'-데옥시유리딘을 사용한 음성 선택용), TK(간시클로비르를 이용한 양성 선택용), CD(5-플루오로시토신을 이용한 양성 선택용), 형광 단백질(GFP, YFP, RFP, mCherry 또는 그 외와 같은) 또는 에피토프 태그(HA, Myc, Ty-1, FLAG 또는 그 외와 같은)를 포함한다.

[0413]

본 발명의 일부 구현예에 따르면, 핵산 구조물은 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열을 추가로 포함한다.

[0414]

본 발명의 일부 구현예에 따르면, 유도성 자기-파괴 요소는 치료용 카세트와 동일한 프레임 내에 있다.

[0415]

본 발명의 일부 구현예에 따르면, 유도성 자기-파괴 요소는 상이한 조절 요소에 의해 조절된, 별개의 해독 프레임 내에 있다. 예를 들어, 치료용 카세트는 잠복기 프로모터에 의해 유도될 수 있는 반면, 자기-파괴 카세트는 약물-유도 프로모터에 의해 유도될 것이다.

[0416]

본 발명의 일부 구현예에 따르면, 유도성 자기-파괴 요소는 약물에 반응하여 활성이다.

[0417]

본 발명의 일부 구현예에 따르면, 약물은 항생제를 포함한다.

[0418]

본 발명의 일부 구현예에 따르면, 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열은 약학적 폴리펩티드를 코

당하는 제2 핵산 서열 상류에 융합된 프레임 내 독소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 동일한 핵산 구조물 내에 포함된다.

[0419] 본 발명의 일부 구현예에 따르면, 유도성 자기-파괴 요소를 코딩하는 제3 핵산 서열은 약학적 폴리펩티드를 코딩하는 제2 핵산 서열 상류에 융합된 프레임 내 독소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물과 별개의 핵산 구조물 내에 포함된다.

[0420] 본 발명의 일부 구현예에 따르면, 독소플라즈마 비번역 부위(UTR) 핵산 서열은 선택 마커 및/또는 자기-파괴 요소의 개방형 해독 프레임의 상류 및/또는 하류이다.

[0421] 본 발명의 일부 구현예의 일 측면에 따르면, 적어도 2개의 핵산 구조물을 포함하는 핵산 구조물 시스템으로서, 상기 적어도 2개의 핵산 구조물의 제1 핵산 구조물은 본 발명의 일부 구현예의 핵산 구조물이고, 상기 적어도 2개의 핵산 구조물의 제2 핵산 구조물은 선택 마커를 코딩하는 폴리뉴클레오티드를 포함한다.

[0422] 전형적인 클로닝 벡터는 또한 전사 및 번역 개시 서열, 전사 및 번역 종결체 및 아데닐산중합반응 신호를 포함한다.

[0423] 하기는 본 발명의 일부 구현예의 핵산 구조물을 생성하기 위한 백본으로 사용될 수 있는 독소플라즈마 핵산 구조물의 비-제한적인 리스트이다: pGRA, pUPRT, pROP1, pTUB1, pTUB8, pLIC, pTOX0, pMIC2, pHX, pCAT, pDHFR, pBlueScript, pTetO7SAG1, pTetO7SAG4, pSAG1, pSAG4, pHTU, pTKO, pLoxP-DHFR, pminCAT/HXGPRT+, pminCAT/HXGPRT-, pDHFR-TSc3/M3, pDHFR-TSc3/M2M3, pminiHXGPRT, 및 pUC19. 이들 벡터는 비영리 플라스미드 저장소 "애드진(addgene)"; NIH AIDS Reagent Program; Agilent Technologies; NEB; Thermo Fisher Scientific; Sigma Aldrich; GenScript; 및 MoBiTec GmbH과 같은, 다양한 출처로부터 얻을 수 있다.

[0424] 본원에서 하기 표 6은 비-제한적인 예시적 벡터 및 카탈로그 번호를 제공한다.

[0425] [표 6] 벡터 백본

구조물명	제조사	카탈로그 번호
pLIC	Addgene	27989
pCAT	Addgene	59018
pTetO7SAG1	Addgene	59017
pSAG1	Addgene	54467
pUPRT	Addgene	58528
pLoxP-DHFR	Addgene	70147
pminCAT/HXGPRT+	NIH AIDS Reagent Program	2850
pminCAT/HXGPRT-	NIH AIDS Reagent Program	2851
pDHFR-TSc3/M3	NIH AIDS Reagent Program	2853
pDHFR-TSc3/M2M3	NIH AIDS Reagent Program	2854
pminiHXGPRT	NIH AIDS Reagent Program	2855
pBlueScript	Agilent Technologies	200252, 200251, 212205, 212206, 212207, 212208, 212240, 212250

[0426]

구조물명	제조사	카탈로그 번호
pUC19	Addgene; NEB; Thermo Fisher Scientific; Sigma Aldrich; MoBiTec GmbH	50005; N3041; SD0061; D3404; V33202

[0427]

[0428] 본 발명의 일부 구현예의 일 측면에 따르면, 본 발명의 일부 구현예의 핵산 구조물 또는 본 발명의 일부 구현예의 핵산 구조물 시스템으로 형질전환된 독소플라즈마가 제공된다.

[0429] 본원에서 사용된 용어 "독소플라즈마"는 세포내, 기생충 원생동물 독소플라즈마 곤디를 말한다.

[0430] 본 발명의 일부 구현예의 구조물 및 방법에 사용될 수 있는 독소플라즈마 곤디 균주의 비-제한적인 예는 다음을

포함한다:

- [0431] (i) 유형 I- 제한되는 것은 아니나, GT1, RH, ENT, VEL, TgCatCo1 및 CAST를 포함.
- [0432] (ii) 유형 II- 제한되는 것은 아니나, ME49, Beverly, PDS, PLK, PTG, DEG, PIH, TgNmBr1 및 PRU를 포함.
- [0433] (iii) 유형 III- 제한되는 것은 아니나, VEG, C56, CTG, CEP, TgGoatUS4 및 STRL를 포함.
- [0434] (iv) 유형 IV- 제한되는 것은 아니나, TgCTPrC3, TgBbUS1, TgRabbitBr1 및 TgPigUS15를 포함.
- [0435] 본 발명의 일부 구현예에 따르면, 독소플라즈마는 약독화되지 않는다.
- [0436] 종래 기술에서와 같이, 용어 "약독화된(attenuated)"은 비-유전적으로 변형된 자연(야생형) T. 곤디와 비교할 때 약화되고/거나 덜 활발한 T. 곤디 균주를 말한다. 대개, T. 곤디의 약독화된 변이체는 면역 반응을 자극하고 면역력을 생성할 수 있으나, 병을 유발하지는 않는다. 약독화는 제한되는 것은 아니나, γ -조사 또는 피리미딘 영양요구체 생성을 포함하는 종래 방법들에 의해 이루어질 수 있다.
- [0437] 약독화된 독소플라즈마의 비-제한적인 예는 US 20120045477 A1 및 US 8673289 B2에 설명되어 있고, 이는 본원에 참고로서 완전히 원용된다.
- [0438] T. 곤디 복제가 감염의 급성 단계에서 신체에 전파하고 원위 조직에 도달하기 위한 능력, 감염된 세포 내 지속되는 능력 및 숙주 내 만성 낭포를 형성하는 능력에 있어서 필수적이라는 것을 알아야 한다.
- [0439] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 약독화된 독소플라즈마의 증식 속도와 비교하여 더 높은 증식 속도로 특징지어진다.
- [0440] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 영양 요구체가 아니다.
- [0441] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 피리미딘의 데-노보(de-novo) 생합성에 적합한 기능적 내인성 경로를 포함한다.
- [0442] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 느린분열소체 단계로 분화할 수 있다.
- [0443] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 RNA 합성 및/또는 DNA 복제할 수 있다.
- [0444] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 RNA 합성할 수 있다.
- [0445] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 RNA 복제할 수 있다.
- [0446] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 독소플라즈마는 내인성 기능적 카르바모일 인산 합성효소 II (CPSII) 효소(US8673289에 설명된 것과 같음), 예를 들어, 서열번호 4612 내지 4617 중 임의로 제공되는 것을 포함한다.
- [0447] 본 발명의 일부 구현예의 구조물 및 독소플라즈마는 개체 내로, 예를 들어, 새체의 특정한 조직 또는 세포 유형으로, 목적단백질을 전달하는데 사용될 수 있다.
- [0448] 본 발명의 일부 구현예의 일 측면에 따르면, 개체의 목적조직(tissue-of-interest)에 목적단백질을 투여하는 방법으로서, 상기 방법은 본 발명의 일부 구현예의 독소플라즈마, 또는 본 발명의 일부 구현예의 약학적 조성물을 투여하여, 개체의 목적조직에 목적단백질을 투여하는 것을 포함한다.
- [0449] 목적조직의 예는, 이에 제한되는 것은 아니나, 중추신경계, 근육, 안구 부분, 혈액, 림프절, 지라, 백혈구, 소화계 및 점막 고유관을 포함한다.
- [0450] 독소플라즈마는 혈뇌를 가로지를 수 있기 때문에, 이를 필요로 하는 개체의 중추신경계에 목적단백질을 전달할 수 있다는 것을 알아야 한다.
- [0451] 본 발명의 일부 구현예의 일 측면에 따르면, 개체의 중추신경계에 목적단백질을 투여하는 방법으로서, 상기 방법은 본 발명의 일부 구현예의 독소플라즈마 또는 본 발명의 일부 구현예의 약학적 조성물을 개체에 투여하여, 목적단백질을 개체의 중추신경계에 투여하는 것을 포함한다.
- [0452] 따라서, 본 발명의 일부 구현예의 독소플라즈마는 새체를 치료할 수 있는 목적단백질(예를 들어, 치료용 폴리펩

티드)를 전달하여, 이를 필요로 하는 개체를 치료하는데 사용될 수 있다.

- [0453] 본 발명의 일부 구현예의 일 측면에 따르면, 본 발명의 일부 구현예의 독소플라즈마 또는 본 발명의 일부 구현예의 약학적 조성물을 개체의 중추신경계 내 약학적 폴리펩티드의 투여에 의해 치료가능한 병리로 진단된 개체에 투여하여, 이를 필요로 하는 개체를 치료하는 것을 포함하는, 이를 필요로 하는 개체를 치료하는 방법이 제공된다.
- [0454] 본 발명의 일부 구현예의 일 측면에 따르면, 약학적 폴리펩티드를 코딩하는 제2 핵산 서열의 상류에 융합된 프레임 내 독소플라즈마 분비 단백질을 코딩하는 제1 핵산 서열을 포함하는 이중 폴리뉴클레오티드를 포함하는 핵산 구조물을 포함하는 독소플라즈마를 개체에 투여하여, 이를 필요로 하는 개체를 치료하는 것을 포함하는 것으로서, 상기 이중 폴리뉴클레오티드는 독소플라즈마에서 상기 이중 폴리뉴클레오티드의 전사를 유도하기 위한 프로모터에 작동가능하게 연결되며, 개체는 개체의 중추신경계에 약학적 폴리펩티드를 투여하여 치료가능한 병리로 진단된, 이를 필요로 하는 개체를 치료하는 방법이 제공된다.
- [0455] 용어 "치료(treating)"는 병리(질병, 장애 또는 상태)의 발달을 억제, 예방또는 저지하고/하거나 병리의 감소, 차도 또는 퇴보를 유발하는 것을 말한다. 당업자는 다양한 방법론 및 분석을 병리의 발달을 평가하기 위해 사용할 수 있고, 마찬가지로, 다양한 방법론 및 분석을 병리의 감소, 차도 또는 퇴보를 평가하기 위해 사용할 수 있음을 이해할 수 있다.
- [0456] 본원에서 사용된, 용어 "예방(preventing)"은 질병의 위험에 있으나, 아직 질병에 걸린 것으로 진단받지 않은 개체에서의 질병, 질환 또는 상태를 발생으로부터 유지시키는 것을 말한다.
- [0457] 본원에서 사용된, 용어 "개체(subject)"는 포유류, 바람직하게는 병리를 겪고 있는 임의의 나이의 인간을 포함한다. 바람직하게는, 이 용어는 병리를 발달시킬 위험에 있는 개인을 포함한다.
- [0458] 본 발명의 일부 구현예에 따르면, 개체는 개체의 중추신경계 내 결핍된 내인성 단백질에 의해 특징지어진 병리로 진단된다.
- [0459] 본 발명의 일부 구현예에 따르면, 결핍된 내인성 단백질은 내인성 단백질의 야생형 아미노산 서열과 비교하여, 내인성 단백질의 적어도 하나의 아미노산의 결실, 삽입 및/또는 치환을 포함한다.
- [0460] 본 발명의 일부 구현예에 따르면, 결핍된 내인성 단백질은 병리가 없는 건강한 개체 내 내인성 단백질의 수준과 비교하여, 감소된 수준의 내인성 단백질을 포함한다.
- [0461] 본 발명의 일부 구현예에 따르면, 결핍된 내인성 단백질은 병리로 진단된 개체에서 내인성 단백질이 없다.
- [0462] 본 발명의 일부 구현예에 따르면, 개체는 크라베 질환으로 진단된다.
- [0463] 본 발명의 일부 구현예에 따르면, 개체는 레트 증후군으로 진단된다.
- [0464] 본 발명의 일부 구현예에 따르면, 개체는 카나반 질환으로 진단된다.
- [0465] 본 발명의 일부 구현예에 따르면, 개체는 척수근위축증으로 진단된다.
- [0466] 본 발명의 일부 구현예에 따르면, 개체는 파킨슨병으로 진단된다.
- [0467] 본 발명의 일부 구현예에 따르면, 개체는 저산소/허혈성 또는 신경염증성 CNS 장애로 진단된다.
- [0468] 본 발명의 일부 구현예에 따르면, 개체는 알츠하이머병으로 진단된다.
- [0469] 본 발명의 일부 구현예에 따르면, 개체는 근위축성 측색 경화증으로 진단된다.
- [0470] 본 발명의 일부 구현예에 따르면, 개체는 헌팅턴병으로 진단된다.
- [0471] 본 발명의 일부 구현예에 따르면, 개체는 리소좀 축적병으로 진단된다.
- [0472] 본 발명의 일부 구현예에 따르면, 개체는 MECP2-중복 증후군으로 진단된다.
- [0473] 본 발명의 일부 구현예에 따르면, 개체는 타협(compromised) 면역 체계를 가지지 않는다. 타협 면역 체계를 가지는 개체의 예는, 이에 제한되는 것은 아니나, AIDS 환자, 화학요법을 받은 개체, 세포, 조직 및/또는 기관 이식과 같은 면역억제 약물을 받은 개체를 포함한다.
- [0474] 본 발명의 일부 구현예에 따르면, 방법은 자기-파괴 요소를 유도할 수 있는 약물을 개체에 투여하는 것을 추가

로 포함한다.

- [0475] 본 발명의 일부 구현예에 따르면, 방법은 숙주세포 및/또는 신체 내 독소플라즈마를 지속시키기 위해 필수적인 분자를 개체에 투여하는 것을 추가로 포함한다.
- [0476] 본 발명의 일부 구현예에 따르면, 독소플라즈마를 지속시키기 위해 필수적인 분자는 항생제이다.
- [0477] 본 발명의 일부 구현예에 따르면, 독소플라즈마를 지속시키기 위해 필수적인 분자는 소분자(small-molecule)이다.
- [0478] 본 발명의 일부 구현예에 따르면, 독소플라즈마를 지속시키기 위해 필수적인 분자는 대사물질이다.
- [0479] 본 발명의 일부 구현예에 따르면, 방법은 개체에 독소플라즈마의 투여 전 및/또는 독소플라즈마의 투여 후 및/또는 독소플라즈마의 투여와 동시에, 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0480] 본 발명의 일부 구현예에 따르면, 방법은 개체에 독소플라즈마의 투여 전에 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0481] 본 발명의 일부 구현예에 따르면, 방법은 개체에 독소플라즈마의 투여 후 (또는 이어서) 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0482] 본 발명의 일부 구현예에 따르면, 방법은 개체에 독소플라즈마의 투여와 동시에 면역억제 약물을 개체에 투여하는 것을 추가로 포함한다.
- [0483] 본 발명의 일부 구현예에 따르면, 투여는 말초 투여에 의해 수행된다.
- [0484] 본 발명의 일부 구현예에 따르면, 말초 투여는 정맥내 투여를 포함한다.
- [0485] 본 발명의 일부 구현예에 따르면, 말초 투여는 경구 투여를 포함한다.
- [0486] 본 발명의 일부 구현예에 따르면, 말초 투여는 복강내 투여를 포함한다.
- [0487] 본 발명의 일부 구현예에 따르면, 말초 투여는 근육내 투여를 포함한다.
- [0488] 본 발명의 일부 구현예에 따르면, 투여는 에어로졸에 의해 수행된다.
- [0489] 본 발명의 일부 구현예에 따르면, 투여는 중추신경계 또는 그에 근접한 조직에의 직접 투여에 의해 수행된다.
- [0490] 본 발명의 일부 구현예에 따르면, 본 발명의 일부 구현예의 방법, 예를 들어, 독소플라즈마 및/또는 이를 포함하는 약학적 조성물에 의해 치료되는 질환은 위에 표 7에 열거된 질환 중 임의의 것이다.
- [0491] 표 7은 본 발명의 일부 구현예의 치료용 폴리펩티드의 투여에 의해 치료될 수 있는, 내인성 단백질의 결핍된 또는 비정상적인 발현 또는 기능과 관련된 비-제한적인 질환들을 열거한 것이다.

[0492] [표 7]

유전자 명/기호	관련 질환
TFEB	리소좀 축적 질환 및 퇴행성 신경질환
HGSNAT	점액다당류증 3C (산필립포증후군 C)
MEF2C	파킨슨병
NRTN	파킨슨병
PGF	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환
RPE65	레베르 선청성 흑암시, 망막색소변성증
GDNF	파킨슨병, 핵상마비, 다발성 경화증, 알츠하이머병, 근위축성 측삭경화증, 헌팅턴병, 망막 퇴화, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
CNGB3	색맹
BDNF	근위축성 측삭경화증, 헌팅턴병, 알츠하이머병, 척수손상, 비만, 리소좀 축적 질환.
APP	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
ASPA	카나반병
S1PR1	다발성 경화증
IDS	II 형 점액다당류증 (헌터증후군, 이두로네이트 설파타제 결핍)
HTRA2	파킨슨병, 알츠하이머병
CDNF	파킨슨병, 알츠하이머병, 근위축성 측삭경화증
DNAJC5	신경퇴행성 질환
IDUA	I 형 점액다당류증 (후를러 증후군, 후를러-샤이 증후군, 샤이 증후군)
SPON1	알츠하이머병

[0493]

유전자 명/기호	관련 질환
NMNAT2	택솔-유도 신경병증과 같은 축삭변성 관련 장애, 다발성 경화증, 몇몇 바이러스성 장애, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
FMR1	취약 x 증후군
MECP2	레트증후군
GNS	점액다당류증 3C (산필리포증후군 C)
VEGFB	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
HIF1A	알츠하이머병
SERPINF1	파킨슨병, 근위축성 축삭경화증, 다발성 경화증, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
VEGFA	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
STC1	망막 퇴화, 시신경 질환, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
NGB	시신경 위축, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
NFE2L2	
MAPK7	알츠하이머병
NMNAT1	파킨슨병, 선천성 흑내장, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
NGF	근위축성 축삭경화증, 알츠하이머병, 다운증후군, 감각신경병증
NAGLU	점액다당류증 3B (산필리포증후군 B)
CLU	알츠하이머병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
MME	알츠하이머병
CTSA	갈락토시알리도시스
PPT1	1 형 신경 세로이드 리포푸신증 (바텐병)

[0494]

유전자 명/기호	관련 질환
TIMP2	다발성 경화증, 알츠하이머병, 및 헌팅턴병, 파킨슨병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
MANF	파킨슨병, 망막색소변성증, 망막동맥폐쇄, 당뇨, 볼프람 증후군, 알츠하이머병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
TIMP1	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GAD2	파킨슨병
GALC	크라베병 (글로보이드 세포 로이코디스트로피)
GAD1	파킨슨병
NTF3	사르코-마리-투스병, 다발성 경화증, 척수손상, X-연관 부신백질이영양증, 당뇨병 신경병증, 척삭 신경병증, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GUSB	슬라이 증후군
HGF	근위축성 축삭경화증
SERPINI1	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
RGS2	불안장애
NPY	뇌전증, 외상 후 스트레스 장애
UCP2	급성 및 흥분독성 뇌손상, 파킨슨병
SST	뇌전증, 알츠하이머병,
SGSH	점액다당류증 3A (산필리포증후군 A)
CYP2J2	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GM2A	GM2 강글리오시드증 (테이-삭스병(TSD), 샌드호프-케윅츠병, GM2 활성화 결핍)
HEXA	GM2 강글리오시드증 (테이-삭스병(TSD), 샌드호프-케윅츠병, GM2 활성화 결핍)
UCHL1	알츠하이머병
HEXB	GM2 강글리오시드증 (테이-삭스병(TSD), 샌드호프-

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유전자 명/기호	관련 질환
	케이트병, GM2 활성화 결핍)
PINK1	파킨슨병
PRDX3	근위축성 축삭경화증, 파킨슨병, 알츠하이머병
PRDX1	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GLB1	GM1 갱글리오시드증
TPP1	2 형 신경 세로이드 리포푸신증 (바텐병)
ANG	근위축성 축삭경화증, 파킨슨병
HMOX1	알츠하이머병(AD), 파킨슨병(PD), 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
NRG1	샤르코-마리-투스병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
NFIL3	근위축성 축삭경화증
MAN2B1	알파-만노스 축적증
DHCR24	알츠하이머병.
DDC	파킨슨병, 방향성 L-아미노산 탈카복시화효소 결핍
TP53	뇌종양 (성상세포종양, 핍지교종, 핍지교성상세포종, 뇌실막종양, 맥락열기종양, 기타 신경상피종양(성아세포종, 제 3 뇌실 척삭모양 신경교종, 혈관중심성 신경교종), 신경세포성 및 혼합신경교세포종양, 송과체 부위 종양, 배아성종양, 두개골 및 척추주변 신경 종양(슈판세포종, 신경섬유종, 신경주막종, 악성말초신경초종양), 수막세포성종양, 중간엽종양, 일차 멜라노 병변, 기타 뇌막 관련 신생물(혈관모세포종), 혈구형성계 종양(악성 임파육종, 형질세포종, 과립구육종), 생식세포종양(배아세포종, 태생기암, 난황낭종양, 융모암, 기형종, 혼합 생식세포종양), 안장 영역 종양(두개인두종, 과립상세포종양, 과립세포종, 선하수체의 방추세포 호산과립세포종), 전이성 종양).
ADNP	알츠하이머병, 근위축성 축삭경화증, 전두측두엽 퇴화/치매(FTD), 외상성 뇌손상, 저산소/허혈성 CNS 장애,

[0496]

유전자 명/기호	관련 질환
	뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GAN	거대축삭신경병증
GAL	뇌졸중, 알츠하이머병, 아편 중독증/금단증
SMN1	척수근위축증
PROC	근위축성 축삭경화증, 알츠하이머병, 다발성 경화증, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
TRAP1	파킨슨병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
IL18BP	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
PRDX6	알츠하이머병, 파킨슨병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
TXN	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GAA	폼페병
GHRL	알츠하이머병, 파킨슨병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
CSF3	파킨슨병, 근위축성 축삭경화증, 뇌성마비, 알츠하이머병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
UBE3A	안젤만 증후군
ABCD1	부신백질이영양증
NDP	노리병, 가족성 삼출 유리체망막병증(FEVR), 내이질환
TH	파킨슨병
GCH1	파킨슨병
BCL2	근위축성 축삭경화증, 파킨슨병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
ENO2	알츠하이머병
EPO	파킨슨병, 다발성 경화증, 외상성 뇌손상, 저산소/허혈성

[0497]

유전자 명/기호	관련 질환
	CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GBA	고셔병
AGA	아스파르틸글루코사민뇨
UPF1	근위축성 축삭경화증
PSAP	파킨슨병, 탈수(demyelination) 장애, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
ANXA1	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
IGF1	근위축성 축삭경화증, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
IGF2	알츠하이머병
PARK2	파킨슨병, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
FUCA1	푸코사이드 축적증
SIRT1	헌팅턴병, 근위축성 축삭경화증, 파킨슨병, 알츠하이머병, 전두측두엽 치매, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
PARK7	근위축성 축삭경화증, 파킨슨병
ANXA2	외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
GCG	알츠하이머병, 파킨슨병, 근위축성 축삭경화증 내 뇌 인슐린 저항증
LEP	알츠하이머병, 비만, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을 포함하는 신경염증성 질환.
SH3BP5	알츠하이머병.
CNTF	파킨슨병, 핵상마비, 다발성 경화증, 알츠하이머병, 근위축성 축삭경화증, 헌팅턴병, 망막 퇴화, 외상성 뇌손상, 저산소/허혈성 CNS 장애, 뇌졸중 및 신경퇴행성 조건을

[0498]

유전자 명/기호	관련 질환
	포함하는 신경염증성 질환.
GLA	파브리병
KCNN3	알츠하이머병
ARSA	이염성 백질디스트로피, 다중 설파타제 결핍
SUMF1	다중 설파타제 결핍, 점액다당류증 III A (A 형 산필립포 증후군)
CRH	뇌부종
SMPD1	니만-피크병

[0499]

- [0500] 본 발명의 일부 구현예에 따르면, 질환(병리)은 암이 아니다.
- [0501] 본 발명의 일부 구현예의 핵산 구조물, 핵산 구조물 시스템, 또는 핵산 구조물 또는 핵산 구조물 시스템에 의해 형질전환된 독소플라즈마는 개체에 그 자체로, 적합한 담체 또는 부형제와 혼합된 약학적 조성물로 투여될 수 있다.
- [0502] 본 발명의 일부 구현예의 일 측면에 따르면, 본 발명의 일부 구현예의 독소플라즈마를 포함하는 약학적 조성물 및 약학적으로 허용가능한 담체를 포함하는 약학적 조성물이 제공된다.
- [0503] 본 발명의 일부 구현예에 따르면, 약학적 조성물은 본원에서 설명된 병리 중 임의의 것으로 진단된 개체를 치료하기 위한 것이다.
- [0504] 본 발명의 일부 구현예에 따르면, 개체의 중추신경계에 결핍된 내인성 단백질에 의해 특징지어진 병리로 진단된 개체를 치료하기 위한 것이다.
- [0505] 본 발명의 일부 구현예에 따르면, 약학적 소어물은 개체의 중추신경계 내 약학적 폴리펩티드의 투여에 의해 치료가 가능한 병리로 진단된 개체를 치료하기 위한 것이다.
- [0506] 본 발명의 일부 구현예에 따르면, 약학적 조성물은 면역억제제를 추가로 포함한다.
- [0507] 본원에서 사용된 "약학적 조성물"은 생리학적으로 적합한 담체 및 부형제와 같은 다른 화학 성분들과, 본원에서 설명된 하나 이상의 활성 성분의 제제를 말한다. 약학적 조성물의 목적은 화합물의 개체로의 투여를 촉진하는 것이다.
- [0508] 본원의 용어 "활성 성분"은 생물학적 효과에 책임이 있는 본 발명의 일부 구현예의 핵산 구조물, 핵산 구조물 시스템, 핵산 구조물 또는 핵산 구조물 시스템에 의해 형질전환된 독소플라즈마를 말한다.
- [0509] 이하, 상호교환적으로 사용될 수 있는, 구 "생리학적으로 허용가능한 담체" 및 "약학적으로 허용가능한 담체"는 개체에 유효한 자극(irritation)을 유발하지 않고, 투여된 화합물의 생물학적 활성 및 특성을 없애지 않는, 담체 또는 희석제를 말한다. 아췌버트는 이러한 구에 포함된다.
- [0510] 본원에서 용어 "부형제"는 활성 성분의 투여를 더욱 촉진하기 위한 약학적 조성물에 첨가되는 비활성 물질을 말한다. 제한 없이, 부형제의 예는, 탄산칼슘, 인산칼슘, 다양한 당류 및 전분, 셀룰로오스 유도체, 젤라틴, 식물성 오일 및 폴리에틸렌 글리콜 타입을 포함한다.
- [0511] 약물의 제형 및 투여 기술은 "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, 최신 판에서 찾을 수 있으며, 이는 본원에 참고로서 통합된다.
- [0512] 투여의 적절한 방법은, 예를 들어, 경구, 직장, 점막경유, 특히 경비, 장, 또는 척수강내, 직접 심실내, 심장내 뿐만 아니라 근육내, 피하 및 척수내 주사를 포함하는 비경구 전달, 예를 들어, 오른쪽 또는 왼쪽 심실 공동, 공통 관상동맥, 정맥내, 복강내, 비강내 또는 안내 주사를 포함한다.
- [0513] 중추신경계(CNS)로의 약물 전달을 위한 종래 접근법은 다음을 포함한다: 신경외과적 전략(예를 들어, 대뇌내 주사 또는 뇌실내 투입); BBB의 내인성 수송 경로 중 하나를 이용하려는 시도에서, 제제의 분자적 조작(예를 들어, 그 자체가 BBB를 가로지를 수 없는 제제와의 조합으로, 내피세포 표면 분자에 대한 친화도를 가지는 수송 단백질을 포함하는 키메라 융합 단백질의 생산); 제제의 지질 용해도를 증가시키기 위해 설계된 약리학적 전략(예를 들어, 지질 또는 콜레스테롤 담체에의 수용성 제제의 접합); 및 고삼투압 분열에 의한 BBB의 완전성의 일시적인 파괴(경동맥으로 만니톨 용액의 투입 또는 안지오텐신 펩티드와 같은 생물학적 활성 제제의 사용에서 기원).
- [0514] 대체적으로, 하나는 전신이 아닌, 국소로, 예를 들어, 환자의 조직 영역으로 약학적 조성물의 직접적 주사를 통해, 약학적 조성물을 투여할 수 있다.
- [0515] 용어 "조직"은 하나의 기능 또는 기능들을 수행하기 위해 설계된 세포로 구성된 유기체를 말한다. 예는, 이에 제한되는 것은 아니나, 뇌 조직, 망막, 피부 조직, 간 조직, 췌장 조직, 뼈, 연골, 연결 조직, 혈액 조직, 근육 조직, 심장 조직, 혈관 조직, 신장 조직, 폐 조직, 생식선 조직, 조혈 조직을 포함한다.
- [0516] 본 발명의 일부 구현예의 약학적 조성물은 당업계에 잘 알려진 공정에 의해, 예를 들어, 종래의 혼합, 용해, 배양, 과립화, 드라제(dragee)-생산, 분말화(levigating), 유화, 캡슐화, 포괄(entraping) 또는 동결건조 공정에 의해 만들어질 수 있다.

- [0517] 따라서 본 발명의 일부 구현예에 부합되게 사용되는 약학적 조성물은 약학적으로 사용될 수 있는 제제로의 활성 성분의 조작용을 촉진시키는, 부형제 및 보조제를 포함하는 하나 이상의 생리학적으로 허용가능한 담체를 이용한 종래 방식으로 제형화될 수 있다. 적절한 제형은 선택된 투여 방식에 의존적이다.
- [0518] 주사용으로, 약학적 조성물의 활성 성분은 수용액, 바람직하게는 헵크(Hank's) 용액, 링거(Ringer's) 용액, 또는 생리식염수와 같은 생리학적으로 호환가능한 버퍼로 제형화된다. 점막경유 투여용으로, 침투될 장벽에 적절한 침투물이 제형에 사용된다. 이러한 침투물은 일반적으로 당업계에 알려져 있다.
- [0519] 경구투여용으로, 약학적 조성물은 당업계에 잘 알려진 약학적으로 허용가능한 담체와 함께 활성 화합물을 결합하여 미리 제형화될 수 있다. 이러한 담체는 약학적 조성물을 환자에 의한 경구 섭취를 위해, 정제, 알약, 드라제, 캡슐, 액체, 젤, 시럽, 식품, 슬러리, 현탁액 등으로 제형화되게 할 수 있다. 경구 사용을 위한 약리학제 제제는 고체 부형제를 사용하여, 정제 또는 드라제 중심(core)을 얻기 위하여, 바람직한 경우 적합한 보조제를 추가한 후, 선택적으로 결과 혼합물을 갈고, 과립 혼합물을 조작하여 만들어질 수 있다. 적합한 부형제는 특히, 락토오스, 수크로오스, 만니톨 또는 소르비톨을 포함하는 당류와 같은 필러; 예를 들어, 옥수수 전분, 밀 전분, 쌀 전분, 감자 전분, 젤라틴, 트라가칸트 검, 메틸 셀룰로오스, 히드록시프로필메틸-셀룰로오스, 카르보메틸셀룰로오스 나트륨과 같은 셀룰로오스 제제; 및/또는 폴리비닐피롤리딘(PVP)와 같은 생리학적으로 허용가능한 고분자이다. 바람직할 경우, 가교된 폴리비닐 피롤리돈, 한천, 또는 알긴산 또는 알긴산 나트륨과 같은 이의 염과 같은 붕해제가 첨가될 수 있다.
- [0520] 드라제 중심은 적합한 코팅으로 제공된다. 이러한 목적을 위해, 아라비아 고무, 활석, 폴리비닐 피롤리돈, 카보폴 젤, 폴리에틸렌 글리콜, 이산화티타늄, 라커 용액 및 적합한 유기 용매 또는 용매 혼합물을 선택적으로 포함하는, 농축된 당 용액이 사용될 수 있다. 염료 또는 안료를 식별 또는 활성 화합물 투여량의 상이한 조합을 특징짓기 위하여, 정제 또는 드라제 코팅에 첨가할 수 있다.
- [0521] 경구로 사용될 수 있는 약학적 조성물은 글리세롤 또는 소르비톨과 같은, 젤라틴 및 가소제로 구성된 부드러운, 밀봉된 캡슐 뿐만 아니라, 젤라틴으로 구성된 밀어-맞춘(push-fit) 캡슐을 포함한다. 밀어-맞춘 캡슐은 락토오스와 같은 필러, 전분과 같은 바인더, 활석 또는 스테아르산염 마그네슘과 같은 윤활제 및, 선택적으로 안정제를 포함한다. 부드러운 캡슐에서, 활성 성분은 지방유, 액체 파라핀 또는 액체 폴리에틸렌 글리콜과 같은 적합한 액체에서 용해되거나 부유될 수 있다. 게다가, 안정제가 첨가될 수 있다. 경구 투여용 모든 제형은 선택된 투여 방식에 적합한 투여량이어야만 한다.
- [0522] 구강(buccal) 투여용으로, 조성물은 종래 방식으로 제형화된 정제 또는 마름모(lozenge)의 형태를 취할 수 있다.
- [0523] 비강 흡입에 의한 투여용으로, 본 발명의 일부 구현예에 따른 사용을 위한 활성 성분은 적합한 추진제, 예를 들어, 디클로로디플루오로메탄, 트리클로로플루오로메탄, 디클로로-테트라플루오로에탄 또는 이산화탄소의 사용과 함께 가압 팍 또는 분무기로부터 에어로졸 스프레이 방식의 형태로 편리하게 전달된다. 가압된 에어로졸의 경우, 투여량 단위가 계량된 양을 전달하기 위한 밸브를 제공하여 확인될 수 있다. 디스펜서에서 사용하기 위한, 예를 들어, 젤라틴의 캡슐 및 카트리지는 화합물, 및 락토오스 또는 전분과 같은 적합한 분말 베이스의 분말 혼합물을 포함하여 제형화될 수 있다.
- [0524] 본원에서 설명된 약학적 조성물은 비경구 투여, 예를 들어, 식괴(bolus) 주사 또는 연속 투입용으로 제형화될 수 있다. 주사용 제형은 단위 투여량 형태, 예를 들어, 선택적으로, 첨가된 보존제와 함께, 앰플 또는 다중투여 용기일 수 있다. 조성물은 기름기있는 또는 수용성 운반체 내 현탁액, 용액 또는 에멀전일 수 있고, 현탁, 안정화 및/또는 분산 제제와 같은 제형화 제제를 포함할 수 있다.
- [0525] 비경구 투여용 약학적 조성물은 수용성 형태의 활성 제제의 수용액을 포함한다. 추가적으로, 활성 성분의 현탁액은 적절한 기름기있는 또는 물 기반 주사 현탁액으로 제조될 수 있다. 적합한 친유성 용매 또는 운반체는 참기름과 같은 지방유, 또는 에틸 올레산염, 트리글리세라이드 또는 리포솜과 같은 합성 지방산 에스테르를 포함한다. 수용성 주사 현탁액은 카르복시메틸 셀룰로오스 나트륨, 소르비톨 또는 텍스트란과 같은, 현탁액의 점도를 증가시킬 수 있는, 물질을 포함할 수 있다. 선택적으로, 현탁액은 또한 고농축액의 제제를 허용하는 활성 성분의 용해도를 증가시키는 적합한 안정화제 또는 제제를 포함할 수 있다.
- [0526] 대체적으로, 활성 성분은 사용 전에, 적합한 운반체, 예를 들어, 멸균의, 발열물질이 없는 물 기반 용액으로 구성하기 위한 분말 형태일 수 있다.

- [0527] 본 발명의 일부 구현예의 약학적 조성물은 또한 예를 들어, 코코아 버터 또는 다른 글리세라이드와 같은 종래의 좌약 베이스를 사용하여, 좌약 또는 정제관장과 같은 직장 조성물로 제형화될 수 있다.
- [0528] 본 발명의 일부 구현예의 맥락에서 사용하기에 적합한 약학적 조성물은 활성 성분이 의도한 목적을 달성하기에 효과적인 양으로 포함된 조성물을 포함한다. 보다 구체적으로, 치료적으로 유효한 양은 장애(개체의 중추신경계에 영향을 미치는 장애)의 증상을 막고, 경감하고 또는 개선하거나, 치료되는 개체의 생존을 연장시키기에 유효한 활성 성분(예를 들어, 본 발명의 일부 구현예의 핵산 구조물, 핵산 구조물 시스템, 또는 핵산 구조물 또는 핵산 구조물 시스템으로 형질전환된 독소플라즈마)의 양을 의미한다.
- [0529] 치료적으로 유효한 양의 결정은 특히 본원에서 제공된 상세한 설명에 비추어, 당업자의 능력 범위 내에 있다.
- [0530] 본 발명의 방법에서 사용된 임의의 제제에 있어서, 치료적으로 유효한 양 또는 투여량은 시험관내 분석, 생체의 분석, 세포 배양 분석, 및/또는 동물 모델로부터 처음 추정될 수 있다. 예를 들어, 투여량은 바람직한 농도 또는 역가를 달성하기 위하여 동물 모델에서 만들어질 수 있다. 이러한 정보는 인간에서의 유용한 투여량을 보다 정확히 결정하기 위해 사용될 수 있다.
- [0531] 본원에서 설명된 활성 성분의 독성 및 치료 효능은 시험관내, 세포 배양물 내 또는 실험 동물에서의 표준 약학적 과정에 의해 결정될 수 있다. 시험관 내 및 세포 배양물 분석 및 동물 연구로부터 얻은 데이터는 인간에 사용을 위한 투여량의 범위를 정하는데 사용될 수 있다. 투여량은 이용된 투여 형태 및 활용된 투여 방식에 따라 다양할 수 있다. 정확한 제형, 투여 방식 및 투여량은 환자의 상태를 고려하여 개별 의사에 의해 선택될 수 있다(예를 들어, Fingl, et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1 참조).
- [0532] 투여량 및 간격은 생물학적 효과를 유도하거나 억제하기에 충분한 활성 성분의 조직 수준(예를 들어, 뇌 수준)을 제공하여 개별적으로 조정될 수 있다(최소유효량, MEC). MEC는 각 제제에 대하여 다양하나, 시험관 내 데이터로부터 추정될 수 있다. MEC에 도달하는데 필수적인 투여량은 개별 특징 및 투여 방식에 의존할 것이다. 검출 분석은 혈장, 조직 또는 CSF(cerebro-spinal fluid) 농도를 결정하는데 사용될 수 있다.
- [0533] 처리될 조건의 심각성 및 민감성에 따라, 투여는 며칠에서 몇주간 또는 예를 들어, 만성 질환의 경우 평생, 또는 치료에 효과가 있을 때까지, 또는 질병 상태의 축소가 달성될 때까지, 지속되는 치료 과정으로, 단일 또는 다수의 투여일 수 있다.
- [0534] 예를 들어, 만성 질환의 경우, 투여는 증상이 관리되고, 안정화되고, 및/또는 개선될 때까지 조절될 수 있다.
- [0535] 투여될 조성물의 양은, 물론, 치료받는 개체, 고통의 심각성, 투여 방식, 개체의 면역 상태, 처방하는 의사의 판단, 등에 의존적일 것이다.
- [0536] 본 발명의 일부 구현예의 조성물은, 바람직하다면, 활성 성분을 포함하는 하나 이상의 단위 투여량 형태를 포함하는, FDA 승인 키트와 같은, 팩 또는 디스펜서 장치로 주어질 수 있다. 팩은, 예를 들어, 블리스터 팩과 같은, 금속 또는 플라스틱 포일을 포함할 수 있다. 팩 또는 디스펜서 장치는 투여를 위한 설명에 동봉될 수 있다. 팩 또는 디스펜서는 또한 의약품의 제조, 사용 또는 판매를 규제하는 정부 기관이 정한 형태로 용기와 관련된 주의 사항에 의해 맞춰질 수 있는데, 주의 사항은 조성물 또는 인간 또는 수의학 투여의 형태의 기관에 의한 승인을 반영하는 것이다. 이러한 주의 사항은, 예를 들어, 처방약으로 미국 식품 의약국의 승인을 받아 표시된 것 또는 승인된 제품 삽입물의 것일 수 있다. 호환가능한 약학적 담체에서 제형화된 본 발명의 제제를 포함하는 조성물은 또한 상기 더욱 상세히 설명된 바와 같이, 제조되고, 적절한 용기에 담기고, 지시된 조건의 치료를 위해 표시될 수 있다.
- [0537] 본원에서 사용된 용어 "약"은 $\pm 10\%$ 를 말한다.
- [0538] 용어 "포함한다(comprises)", "포함하는(comprising)", "포함한다(includes)", "포함하는(including)", "가지는(having)" 및 이의 활용형태들은 "포함하나 제한되는 것은 아닌"을 의미한다.
- [0539] 용어 "구성된"은 "포함하고 제한되는"을 의미한다.
- [0540] 용어 "본질적으로 이루어진(consisting essentially of)"은 조성물, 방법 또는 구조물이 추가적인 성분, 단계 및/또는 부분을 포함하나, 추가적인 성분, 단계 및/또는 부분이 청구된 청구항, 방법 또는 구조물의 기본적인고 신규한 특성을 실질적으로 변경시키지 않는 경우에 한한다.
- [0541] 본원에서 사용된, 단수 형태 "하나의(a)", "하나의(an)" 및 "그(the)"는 문맥상 명확히 다르게 지시하지 않는 한 복수의 대상도 포함한다. 예를 들어, 용어 "하나의 화합물" 또는 "적어도 하나의 화합물"은 그 혼합물을 포

함하여, 복수의 화합물들을 포함할 것이다.

- [0542] 본원에 걸쳐, 본 발명의 다양한 구현예가 범위 형식으로 제공될 수 있다. 범위 형식에서의 설명은 단지 편의 및 간결을 위한 것임을 이해하여야만 하며, 본 발명의 범위가 융통성없는 제한으로 해석되어서는 안됨을 이해하여야만 한다. 따라서, 범위의 설명은 범위 내의 개별적인 수치 뿐만 아니라 모든 가능한 하위 범위를 개시한 것으로 간주되어야만 한다. 예를 들어, 1 내지 6과 같은 범위의 설명은 예를 들어, 1, 2, 3, 4, 5 및 6과 같은 범위 내의 개별적인 수치 뿐만 아니라, 1 내지 3, 1 내지 4, 1 내지 5, 2 내지 4, 2 내지 6, 3 내지 6 등과 같은 하위 범위를 개시한 것으로 간주되어야만 한다. 이는 범위의 폭에 관계없이 적용된다.
- [0543] 본원에서 수치 범위가 지시될 때마다, 지시된 범위 내 임의의 인용된 수치(분수 또는 정수)를 포함한다는 의미이다. 구, 제1 지시 숫자와 제2 지시 숫자 "사이의 범위에 이르는/범위(ranging/ranges between)" 및 제1 지시 숫자 "부터의 범위에 이르는/범위(ranging/ranges from)" 제2 지시 숫자"까지(to)"는 본원에서 상호교환적으로 사용되고, 이는 제1 및 제2 지시 숫자 및 그 사이의 모든 소수 및 정수를 포함하는 것을 의미한다.
- [0544] 본원에서 사용된 용어 "방법"은 이에 제한되는 것은 아니나, 알려져 있는 방식, 수단, 기술 및 과정, 또는 알려진 방식, 수단, 기술 및 과정으로부터 화학, 약리학, 생물학, 생화학 및 의학 분야 전문가에 의해 용이하게 개발된 것을 포함하는, 주어진 작업을 수행하기 위한 방식, 수단, 기술 및 과정을 말한다.
- [0545] 본원에서 사용된 용어 "치료(treating)"는 상태의 진행을 없애거나, 실질적으로 억제하거나, 느리게 하거나 역전시키는 것, 상태의 임상적 또는 미적 증상을 실질적으로 개선하는 것, 또는 상태의 임상적 또는 미적 증상의 출현을 막는 것을 포함한다.
- [0546] 특정한 서열 목록이 참조될 때, 이러한 참조는 또한, 이러한 변이의 빈도가 50 뉴클레오타이드에서 1 미만, 대체적으로, 100 뉴클레오타이드에서 1 미만, 대체적으로, 200 뉴클레오타이드에서 1 미만, 대체적으로 500 뉴클레오타이드에서 1 미만, 대체적으로 1000 뉴클레오타이드에서 1 미만, 대체적으로 5,000 뉴클레오타이드에서 1 미만, 대체적으로 10,000 뉴클레오타이드에서 1 미만이라면, 예를 들어, 대립 유전자 변이, 서열화 오류, 클로닝 오류 또는 염기 치환을 야기하는 다른 변화의 원인이 되는 경미한 서열 변이, 염기 결실 또는 염기 첨가를 포함하는, 그의 상보적 서열에 실질적으로 상응하는 서열을 포함하는 것으로 이해되어야 한다.
- [0547] 명확성을 위해 개별 구현예의 문맥으로 설명된 본 발명의 특정한 특징들은 단일의 구현예로 조합되어 제공될 수도 있음을 이해할 것이다. 반대로, 간결성을 위해 단일의 구현예의 문맥으로 설명된 본 발명의 다양한 특징들은 개별적으로 또는 임의의 적합한 하위 조합으로 또는 본 발명의 임의의 다른 설명된 구현예에 적합하게도 제공될 수 있다. 구현예가 이들 요소들 없이 동작하지 않는 것이 아닌 한, 다양한 구현예의 문맥에서 설명된 특정한 특징들은 구현예의 필수적인 특징으로 간주되어서는 안된다.
- [0548] 상술한 바 및 하기 청구범위 부분에 청구한 바와 같이 본 발명의 다양한 구현예 및 측면은 하기 실시예에서 실험적인 지지를 발견한다.
- [0549] **실시예**
- [0550] 상술한 설명과 함께 비제한적으로 본 발명의 일부 구현예를 설명하는 하기 실시예를 참조한다.
- [0551] 일반적으로, 본원에서 사용된 명명법 및 본 발명에서 사용된 실험 과정은 분자적, 생화학적, 미생물학적 및 재조합 DNA 기술을 포함한다. 이러한 기술들은 문헌에서 완전히 설명된다. 예를 들어, "Molecular Cloning: A Laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Selected Methods in Cellular Immunology", W. H. Freeman and Co., New York (1980) 참조; 이용가능한 번역분석은 특허 및 과학 문헌에 광범위하게 기재되어 있다, 예를 들어, U.S. Pat. Nos. 3,791,932; 3,839,153; 3,850,752; 3,850,578; 3,853,987; 3,867,517; 3,879,262; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; 4,098,876; 4,879,219; 5,011,771 및 5,281,521; "Oligonucleotide

Synthesis" Gait, M. J., ed. (1984); "Nucleic Acid Hybridization" Hames, B. D., and Higgins S. J., eds. (1985); "Transcription and Translation" Hames, B. D., and Higgins S. J., Eds. (1984); "Animal Cell Culture" Freshney, R. I., ed. (1986); "Immobilized Cells and Enzymes" IRL Press, (1986); "A Practical Guide to Molecular Cloning" Perbal, B., (1984) and "Methods in Enzymology" Vol. 1-317, Academic Press; "PCR Protocols: A Guide To Methods And Applications", Academic Press, San Diego, CA (1990); Marshak et al., "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996) 참조; 이들 모두는 본원에서 완전히 설명된 것처럼 참고로서 포함된다. *Toxoplasma gondii*: the model apicomplexan - Perspectives and methods. LM Weiss, K Kim, 2011. 다른 일반적인 참고는 이 문헌을 통해 제공된다. 그 안의 과정은 당업계에 잘 알려진 것으로 생각되며, 독자의 편의를 위해 제공된다. 그 안에 포함된 모든 정보는 본원에 참조로서 통합된다.

[0552] **일반 물질 및 실험 방법**

[0553] **톡소플라즈마 곤디 배양물**

[0554] 기생충을 2 mM L-글루타민, 페니실린 및 스트렙토마이신 또는 젠타마이신 항생제 믹스 및 10% 소태아혈청(FBS)로 보충된 돌베코 수정 이글 배지(Dulbecco's modified Eagle's medium, DMEM) 내 인간 포피 섬유아세포(HFF)에서 성장시켜, "완전 DMEM 배지"로 나타내었다. 배양물을 매일 모니터하고, 용해된 접시의 상청액 한 방울 또는 주사기에서 방출된 세포내 기생충 한 방울을 HFF가 있는 신선한 접시에 옮겨, 기생충을 계대시켰다.

[0555] **목적 약학적 폴리펩티드(pharmaceutical polypeptide-of-interest)에 융합된 톡소플라즈마 분비 단백질을 구성하는 이중 폴리펩티드의 발현을 위한 T. 곤디 발현 벡터의 생성**

[0556] 특정한 치료용 단백질을 발현시키는 T. 곤디의 안정한 유전자 이식 주를 생성시키기 위하여, 본 발명자들은 우선 분자 클로닝에 의해 T. 곤디 발현 구조물을 생성하였다. 구조물은 긴 개방형 해독 프레임(ORF)을 포함하는데, 이는 톡소필린 cDNA [서열번호 4481] 또는 GRA16 cDNA [서열번호 4472]에 이어지는 HA 태그 코딩 서열(서열번호 4474)에 이어지는, 쥐 MeCP2 이소폼 1 [서열번호 4476]; 인간 ASPA [서열번호 4483], 인간 SMN1 [서열번호 4479]; 인간 PARK2 [서열번호 4478]; 인간 GDNF [서열번호 4489]; 인간 TFEB (전사 인자 EB) 이소폼 1 [서열번호 4600] 서열; 인간 GALC 이소폼 1 [서열번호 4486 또는 서열번호 4601 (GALC version 2); 글리신 유연 링커(Glycine flexible linker, Gly)를 포함하는 GALC-TAT [서열번호 4490]에 이어지는 숙주세포의 리소솜에 GALC를 표적화하는 것을 돕기 위해 막을 가로지른 비고전적 운행을 촉진하는 단백질 형질도입 도메인(TAT) (서열번호 4488) 또는 "변이 GALC-TAT" (결실을 포함한 GALC-TAT) (서열번호 4487)과 같은, 관심 치료용 포유류 cDNA로 구성된다. 관심 cDNA는 또한 T. 곤디 내 이중 폴리펩티드의 발현, 안정성 및 위치화의 효율을 증가시키기 위하여 T. 곤디의 코돈 사용량에 따라 코돈-최적화될 수 있다(T. 곤디 내 발현을 위해 코돈 최적화된, 코돈 최적화된 쥐 MeCP2 이소폼 1 [서열번호 4477], 코돈 최적화된 인간 ASPA [서열번호 4602], 코돈 최적화된 인간 GALC 이소폼 1 [서열번호 4603] 및 코돈 최적화된 인간 TFEB 이소폼 1 [서열번호 4604]과 같이). T. 곤디 발현 벡터는 또한 그 적절한 발현 및 표적화를 보장하는 동일하거나 다른 톡소플라즈마 유전자 유래의 조절 요소를 포함한다. ORF의 상류는 본원에서 "톡소필린 프로모터" 또는 "톡소필린 5'-UTR"로 지칭되는 톡소필린 유전자의 내인성 5' 조절 서열(서열번호 4482) 또는 본원에서 "GRA16 프로모터" 또는 "GRA16 5'-UTR"로 지칭되는 GRA16 유전자의 내인성 5' 조절 서열(서열번호 4473) 중 하나일 수 있는 내인성 5' 조절 서열이다. ORF의 하류는 풍부한 밀집 과립 단백질 GRA2의 3'-UTR(서열번호 4491; 도 3)이다. 발현 벡터는 또한 DHFR-TS의 5' UTR (상류) [서열번호 4492] 및 DHFR-TS의 3' UTR (하류) [서열번호 4493 또는 4609]로 둘러싸인, 선택 마커 HXGPRT [서열번호 4475] 또는 DHFR-TS [서열번호 4484 또는 4606] 또는 mCherry [서열번호 4608]을 포함하는 별개의 ORF를 포함하였다.

[0557] **유전자 이식 T. 곤디의 생성**

[0558] 타입 I 균주 RH 또는 RHΔHX, 또는 타입 II 균주 Prugniald, Prugniald-GFP-Luciferase 또는 Prugniald ΔHPT(Prugniald ΔHX로도 알려진)의 T. 곤디를 유전자 이식 균주를 생성하기 위해 사용하였다. 세포의 급분열소체를 채취하거나 22-26 게이지 바늘을 이용하여 기계적으로 떼내어, 세포 파편으로부터 여과하고, 펠렛화하고, 각 30 μl (총 360 μl)에 2 mM ATP 및 5 mM GSH이 새롭게 첨가된, 300 μl 사이토믹 버퍼(120 mM KCl, 0.15 mM CaCl₂, 10 mM K₂HPO₄/KH₂PO₄ pH 7.6, 25 mM HEPES pH 7.6, 2 mM EGTA, 5 mM MgCl₂)에서 재부유하였다. 20-60 μg 플라스미드 DNA 또는 효소 ScaI로 선형화된 DNA를 BTX ECM 전기천공기로 전기천공에 의해 급분열소체로 형질감염시켰다. 형질감염된 세포의 몇몇 방울을 IFA 웰(유리 커버슬립에 뿌린 HFF 세포와 24-웰 플레이트의 면역형광 분석 웰)로 옮기고 형질감염 효율 및 일시적인 단백질 발현(플라스미드 DNA로부터의 발현)의 평가를 위해

면역형광염색하였다. 형질감염된 기생충의 나머지를 완전 DMEM 내 HFF를 포함하는 신선한 플라스크에 옮겼다. 약물-저항성 선택 마커를 사용한다면, 다음날 배지를 선택용 약물(DHFR-TS 선택용 1 μ M 피리메타민 또는 HXGPRT 선택용 25 μ g/ml 마이코페놀산 + 50 μ g/ml 잔틴)을 포함하는 신선한 배지로 바꾸었다. 기생충이 HFF로부터 탈출하기 시작한 날로부터, 세포의 기생충을 포함하는 상청액의 방울을 서택 약물을 포함하는 선택 배지 내 HFF의 두번째 플라스크로 1-2일 마다 통과시켰다. 두번째 플라스크의 기생충이 HFF로부터 탈출하기 시작하였을 때, 상청액의 방울을 두번째 플라스크로부터 세번째 플라스크 등으로 1-2일 마다 통과시켰다. 형광 단백질 선택 마커가 사용되었다면, 두번째 플라스크의 기생충이 HFF 세포의 약 50%-90%로 탈출하였을 때, 세포의 기생충을 포함하는 배지를 채취하고, 세포 파편으로부터 여과시키고, FACS 기계를 이용하여 분류하였다. 선택에 사용된 형광 단백질에 상응하는 형광을 방출하는 기생충을 채취하고 완전한 DMEM 배지 내 HFF의 다음 플라스크로 통과시켰다. 3번째-5번째 플라스크가 용해를 시작한 후(약 2-5 주), 기생충을 DNA 구조물을 그 계능에 통합시킨 기생충을 포함하는 "안정한 풀"로 간주하였다. 안정한 풀의 한 방울을 IFA(면역 형광 분석) 웰로 통과시키고, 풀 내 구조물-양성 기생충의 백분율, 계능-통합("안정한") 기생충 내 단백질 발현 및 단백질 위치화(계능 발현)를 평가하기 위하여 면역형광염색하였다. 회석을 제한하거나, 96 웰 플레이트에서 웰 당 하나의 기생충을 FACS 분류하여, 수작업 분류에 의해 클론 주를 마련하였다. 단일 기생충으로부터 유래한 것으로 추정되는 단일 플라스크로 웰을 검출하기 위한 명시야 현미경을 이용하여 육안으로 스크리닝한 후, 플레이트를 5-10일 동안 누구도 건드리지 않은 상태를 유지하였다. 단일 플라스크를 포함하는 웰을 피펫으로 힘차게 혼합하였고, 그 혼합물의 50 μ l을 새로운 접시 및 PCR 튜브로 통과시켰다. PCT 튜브에서 채취한 세포를 펠렛화하고, TE 버퍼 내 10% 단백질분해효소 K로 구성된 10 μ l 용해 버퍼에서 재부유시키고, 60 $^{\circ}$ C에서 60분 동안, 이어서 95 $^{\circ}$ C에서 10분 동안 유전자증폭장치(thermocycler)에서 배양하여, 용해물을 제조하였다. 용해물의 1 마이크로리터(1 μ l)를 유전자 구조물에 대해 특이적인 프라이머를 이용한 PCR 스크리닝용 주형으로 사용하였다. PCR-양성 클론을 IFA 벽에 통과시키고, 고정시키고, 면역형광염색하고, 형광 현미경 및 편광 현미경을 이용하여 각 클론 내 단백질 발현 및 단백질 위치를 분석하였다.

[0559] **항체**

[0560] 사용된 항체 및 각각의 농도는 다음과 같다: 항-HA (Roche, IFA: 1:1000, WB: 1:1000), 항-IMC-1 (gift from Prof. Dominique Soldati-Favre, IFA: 1:1000-1:2000), 항-MeCP2 (Cell Signaling, IFA: 1:200, WB: 1:1000, IP: 1:26), 항-NeuN (Abcam, IFA: 1:500), 항-NCoR1 (Bethyl Laboratories, WB: 1:1000), 항-TBL1 (Abcam, WB: 1:1000), 알렉사 플루오르 항-쥐 488 and 594 (Invitrogen, IFA: 1:1000), 알렉사 플루오르 항-토끼 488 and 594 (Invitrogen, IFA: 1:1000), 알렉사 플루오르 항-생쥐 488 and 594 (Invitrogen, IFA: 1:1000).

[0561] **실시예 1**

[0562] **발현, 기생충 분비 세포 기관으로의 위치화 및 숙주세포에의 치료용 목적단백질의 분비를 이끄는 T. 콘디 구조물의 생성**

[0563] **실험 과정**

[0564] 구조물을 전기천공법에 의해 RH(RHhxgprt) 또는 Pru(Pruhgxprt) 균주 T. 콘디 기생충으로 형질감염시켰다. 이는 선택 마커를 발현하는 기생충을 선택하거나(아니면 목적구조물로 공동-형질감염시킨, DHFR-TS(서열번호 4484)를 포함하는 구조물에 대한 피리메타민 선택), 또는 HXGPRT(서열번호 4475)의 발현에 기반한 선택을 위해 MPA+잔틴을 이용하는 것, 제한 회석에 의한 클로닝 또는 유동 세포 분석법, 및 PCR-기반 스크리닝의 과정이 뒤따른다. 분비 곤봉체 세포 기관, 밀집 과립 세포 기관, 기생충 액포 공간, 기생충 액포 막 또는 숙주세포 내 HA-태그 치료용 단백질의 발현 및 특이적 위치화를 특징짓기 위하여, 양성 클론을 웨스턴 블롯 분석 및 면역형광 염색에 의해 확인하였다. 확인된 양성 주를 HFF(인간 포피 섬유아세포) 세포에 더 유지시켰다.

[0565] **실험 결과**

[0566] **치료용 단백질 갈락토세레브로시다제, 갈락토세레브로시다제-TAT, GDNF, 아스파르트아실라제, MeCP2, 생존 운동 신경원 단백질 및 E3 유비퀴틴-단백질 리가아제 파크킨의 전달을 위한 구조물 및 T. 콘디의 생성** - 결과는 T. 콘디가 기생충의 내인성 단백질에 융합된 이중(포유류, 예를 들어, 인간) 치료용 단백질을 발현시키도록 조작될 수 있다는 것을 증명한다. 이러한 접근법을 이용하여, 본 발명자들은 일반적인 신경병리학과 관련된 3개의 인간 단백질, 갈락토세레브로시다제-TAT(변이 GALC-TAT 서열번호 4487), MeCP2(코돈 최적화된 서열번호 4477) 및 GDNF(서열번호 4489)를 발현시키는 3개의 신규한 안정한 T. 콘디 유전자 이식 주, 및 일반적인 신경병리학과 관련된 3개의 인간 단백질, 갈락토세레브로시다제(GLAC, 이소폼 1, 서열번호 4486), 갈락토세레브로시다제-TAT(WT

GALC-TAT 서열번호 4488), 아스파르트아실라제(ASPA 서열번호 4483) 및 생존 운동 신경원 단백질(SMN1, 서열번호 4479)을 발현시키는 안정한 T. 곤디 유전자 이식 기생충을 포함하는 추가적인 4개의 혼합-집단 풀을 생성하였다.

[0567] **바이러스성 단백질 형질도입 도메인에 의한 치료용 단백질의 분비 및 흡수 개선** - 이웃하는 세포에 의한 단백질의 흡수 뿐만 아니라, 숙주세포에서 세포외 공간으로의 갈락토세레브로시다제 단백질의 분비를 개선하기 위하여, 본 발명자들은 갈락토세레브로시다제를 바이러스성 단백질 형질도입 도메인(PTD)에 융합시켰다. Tat-PTD는 세포 배양 모델 시스템에서 효소의 분비 및 흡수 모두를 향상시킴으로써, 갈락토세레브로시다제의 교차-수정(cross-correction) 효율을 현저히(6배까지) 증가시키는 것으로 이전에 나타났다(Meng, X.-L., et al., 2013).

[0568] **치료용 단백질 갈락토세레브로시다제-TAT, 아스파르트아실라제, MeCP2 및 생존 운동 신경원 단백질의 T. 곤디 곤봉체 분비 세포 기관으로의 위치화** - 결과는 T. 곤디가 이종(포유류, 예를 들어, 인간) 치료용 단백질을 기생충의 곤봉체 분비 세포 기관으로 위치시킬 수 있으며(도 4A), 여기서 잠재적으로 숙주 세포 세포질로 방출될 수 있고, 감염된 세포 내 표적 부위로 위치할 수 있다는 것을 증명한다. 이전의 독소필린 융합체가 숙주세포로 분명히 진입한 것으로 보고된바 있는 것처럼, 갈락토세레브로시다제-TAT, 아스파르트아실라제, MeCP2 및 생존 운동 신경원 단백질을 포함하는 융합 단백질은 기생충 곤봉체에 위치하였다. 이는 면역형광 염색(IFAs)에 의해 증명되었다(도 4B-I).

[0569] 따라서, 본 발명자들은 T. 곤디가 기생충의 내인성 단백질에 융합된 이종(포유류, 예를 들어, 인간) 단백질을 발현하도록 조작될 수 있다는 점, 및 이러한 단백질이 기생충의 곤봉체 분비 세포 기관에 위치할 수 있다는 점을 증명하는데 성공하였다. 본 발명자들은 인간 단백질을 기생충에 의해 숙주세포로 자연적으로 분비되는 내인성 단백질, 독소필린에 융합되도록 조작하였는데, 이는 목적단백질(예를 들어, 치료용 단백질)의 표적화 및 분비를 위한 기생충의 단백질 분비 기계에 "타는" 것을 허용한다. 이는 T. 곤디를 본 기술의 실현가능한 기반으로 제안하는 과정에서 중요한 이정표이다.

[0570] 이러한 접근법을 이용하여, 본 발명자들은 크라베 질환과 관련된 인간 단백질 갈락토세레브로시다제-TAT(변이 GALC-TAT 서열번호 4487)를 발현시키고 곤봉체로 위치시키는 신규하고 안정한 T. 곤디 유전자 이식 주, 및 일반적인 신경병리학과 관련된 3개의 인간 단백질, 갈락토세레브로시다제-TAT(WT GALC-TAT 서열번호 4488), 아스파르트아실라제(ASPA 서열번호 4483), MeCP2(서열번호 4477) 및 생존 운동 신경원 단백질(SMN1, 서열번호 4479)을 발현시키고 곤봉체로 위치시키는 안정한 T. 곤디 유전자 이식 기생충을 포함하는 추가의 4개의 혼합-집단 풀을 생성하였다.

[0571] **치료용 단백질 아스파르트아실라제, MeCP2 및 생존 운동 신경원 단백질의 T. 곤디 밀집 과립 분비 세포 기관 및 기생충 액포 공간으로의 위치화** - 결과는 T. 곤디가 이종(포유류) 인간 치료용 단백질을 기생충의 밀집 과립 분비 세포 기관 및 기생충 액포 공간으로 위치시킬 수 있다는 것을 증명하는데(도 5A), 여기서 이들은 숙주세포 세포질로 방출될 수 있고 감염된 세포 내 표적 부위에 위치할 수 있다(도 5B-I). 기생충 밀집 과립으로부터 목적단백질의 분비를 유도하는 밀집 과립 단백질 유래 서열을 이용하는 이러한 접근법이 이례적인 것이므로, 이는 첫번째로 밀집 과립 단백질(GRA16)에의 융합에 의한 기생충 액포 공간으로의 분비되는 포유류 단백질을 발견한 것이다. 이는 면역형광 염색(IFAs)에 의해 증명되었다(도 5B-I). 그들이 융합되는, 자연적 GRA16 단백질의 알려진 위치를 기반으로(Bougdour et al. 2013), 융합 단백질이 그 후 기생충 액포 막을 통해 숙주세포로 이동할 것으로 예상된다.

[0572] 따라서, 본 발명자들은 T. 곤디가 기생충의 내인성 단백질에 융합된 이종(포유류) 단백질을 발현시키도록 조작될 수 있다는 점, 및 이들 단백질이 기생충의 밀집 과립 분비 세포 기관 및 기생충 액포 공간으로 위치화할 수 있다는 점을 증명하는데 성공하였다. 본 발명자들은 인간 단백질을 기생충에 의해 숙주세포로 자연적으로 분비되는 내인성 단백질인, GRA16에 융합되도록 조작하였는데, 이는 목적단백질(예를 들어, 치료용 단백질)의 표적화 및 분비를 위한 기생충의 단백질 분비 기계에 "타는" 것을 허용한다. 이는 T. 곤디를 본 기술의 실현가능한 기반으로 제안하는 과정에서 중요한 이정표이다.

[0573] 이러한 접근법을 이용하여, 본 발명자들은 레트 증후군과 관련된 인간 단백질 MeCP2를 발현시키고 밀집 과립 분비 세포 기관 및 기생충 액포 공간으로 위치시키는, 신규하고 안정한 T. 곤디 유전자 이식 주, 및 일반적인 신경병리학과 관련된 2개의 인간 단백질, 아스파르트아실라제 및 생존 운동 신경원 단백질을 발현시키고 밀집 과립 분비 세포 기관 및 기생충 액포 공간으로 위치시키는 안정한 T. 곤디 유전자 이식 기생충을 포함하는 추가의 2개의 혼합-집단 풀을 생성하였다.

- [0574] **유전자이식 기생충 유래 치료용 단백질 MeCP2의 숙주세포로의 분비, 및 숙주세포, 핵 내 활성 영역에의 위치화**
- 결과는 독소플라즈마 곤디 분비 폴리펩티드에 융합된 약학적 폴리펩티드(및 여기서 특히, T. 곤디 밀집 과립 단백질 GRA16에 융합된 치료용 단백질 MeCP2)로 구성된 단백질 융합물이 기생충으로부터 숙주세포로 방출될 수 있고, 숙주세포 내 치료용 단백질의 표적 부위(여기서, 핵)로 전위될 수 있음을 증명한다. 면역형광 염색(IFA s)에 의해 나타난 바와 같이 MeCP2를 포함하는 융합 단백질은 숙주세포 핵으로 위치하였다(도 5F-I). 이는 T. 곤디를 본 기술의 실현가능한 기반으로 제안하는 과정에서 중요한 이정표이다.
- [0575] 이러한 접근법을 이용하여, 본 발명자들은 레트 증후군과 관련된 인간 단백질 MeCP2를 발현시키고 숙주세포 핵으로 위치시키는, 신규하고 안정한 T. 곤디 유전자 이식 주를 생성하였다(도 5F-I).
- [0576] **실시예 2**
- [0577] **기생충 전달을 통한 갈락토세레브로시다제 결핍의 구조**
- [0578] 6-헥사데카노일아미노-4-메틸엠펙리페릴-베타-D-갈락토시드(6HMU-베타-D-갈락토시드)로 명명된 갈락토세레브로시다제의 합성 형광 물질의 효소적 분해에 기반한 갈락토세레브로시다제 효소 활성 분석은 제조자의 프로토콜에 기초한다[Otto P. van Diggelen. MOSCERDAM SUBSTRATES, Laboratory protocol for enzyme analysis for Krabbe disease; Galactocerebrosidase]. 크라베 환자-유래 섬유아세포를 이용하여, 배양물에서 크라베 질환 표현형을 구조하기 위한 GALC- 및 GALC-TAT-발현 기생충의 능력을 평가하기 위하여 분석을 사용하였다. 치료되지 않은 크라베 질환 세포(크라베 환자-유래 섬유아세포), 허위 벡터(빈 인간 발현 벡터)로 형질감염된 크라베 질환 세포 및/또는 GALC를 발현하지 않는 T. 곤디 기생충에 의해 감염된 크라베 질환 세포를 음성 대조군으로 사용한다. 양성 대조군은 야생형(WT) 세포 주, 또는 시험된 유전자 이식 기생충에 의해 발현된 융합물과 동일한, 독립형 (HA-태그) GALC 또는 GALC-TAT 유전자, 또는 독소필린/GRA16-융합 GALC 또는 GALC-TAT 유전자 중 하나의 발현을 유도하는 인간 발현 벡터로 형질감염된 크라베 질환 세포이다. 이는 어떠한 부정적 결과가 단백질 그 자체에 충분한 효과가 결여된 것, 또는 치료용 단백질의 N- 말단으로의 독소필린 또는 GRA16의 융합에 의한 치료용 단백질의 활성의 파괴에 기인할 수 있다는 가능성을 배제하고, 따라서 기생충 전달 시스템의 효율의 정량화할 수 있고 직접적인 추론을 가능하게 한다.
- [0579] 분석은 크라베 질환 환자-유래 섬유아세포에서 나타난 갈락토세레브로시다제-결핍을 구조하기 위한, 갈락토세레브로시다제-발현 기생충의 능력을 특징짓는데 사용된다. 이러한 실험은 배양물에서 보충 단백질을 세포로 전달하여, 크라베 질환을 구조할 수 있는 유전자 이식 기생충의 능력을 증명한다.
- [0580] **실시예 3**
- [0581] **기생충 전달을 통한 MECP2 결핍의 구조**
- [0582] MECP2의 변이 또는 결실을 포함하는 레트 증후군 쥐 모델 유래의 신경 및 신경교 세포는 다수의 비정상적 형태학적 및 분자적 특징들을 나타낸다[Percy, A. Rett syndrome: coming to terms with treatment. *Adv. Neurosci.* (2014), [de la Torre-Ubieta et al. Advancing the understanding of autism disease mechanisms through genetics. *Nat Med.* 2016].
- [0583] 레트 증후군 세포 배양 모델을 이용하여, 배양물 내 레트 증후군 표현형을 구조하는 MeCP2-발현 기생충의 능력을 평가하기 위하여 레트 증후군의 분자적 및 형태학적 특징적 표현형의 정량적 스코어링을 사용한다. 치료되지 않은 레트 증후군 모델 세포, 허위 벡터로 형질감염된 레트 증후군 모델 세포 및/또는 MeCP2를 발현하지 않는 T. 곤디 기생충으로 감염된 레트 증후군 모델 세포를 음성 대조군으로 사용한다. 양성 대조군은 WT 세포 주 및 독립형 (HA-태그) MECP2 코딩 서열, 또는 시험된 유전자 이식 기생충에 의해 발현된 융합물과 동일한, 독소필린/GRA16-융합 MECP2 코딩 서열 중 하나의 발현을 유도하는 인간 발현 벡터로 형질감염된 레트 증후군 모델 세포이다. 이는 어떠한 부정적 결과가 단백질 그 자체에 충분한 효과가 결여된 것, 또는 치료용 단백질의 N- 말단으로의 독소필린 또는 GRA16의 융합에 의한 치료용 단백질의 활성의 파괴에 기인할 수 있다는 가능성을 배제하고, 따라서 기생충 전달 시스템의 효율의 정량화할 수 있고 직접적인 추론을 가능하게 한다.
- [0584] 분석은 레트 증후군 세포 배양 모델에서 나타난 MeCP2-결핍을 구조하기 위한, MeCP2-발현 기생충의 능력을 특징짓는데 사용된다. 이러한 실험은 배양물에서 보충 단백질을 세포로 전달하여, 레트 증후군을 구조할 수 있는 유전자 이식 기생충의 능력을 증명한다.
- [0585] **실시예 4**

[0586] **동물 모델에서의 유전자 이식 기생충 주의 치료적 잠재력 시험**

[0587] 전체 유기체의 표현형에 영향을 미치는 능력에 대하여, 기생충의 유전자 이식 주를 시험한다. 쥐에서의 유전자 이식 기생충의 시험은 면역계 및 기능적 혈뇌 장벽(BBB)의 존재 시 시스템의 평가를 가능하게 한다. 유전자 이식 T. 곤디 기생충은 시험될 상태의 개별 동물 모델에 비강내, 경구로 (구강으로와 같이), 피하로, 근육내, 정맥내, 피부내, 복강내, 두개내 또는 대뇌내로 투여된다. 유전자 이식 T. 곤디 기생충은 급분열소체, 느린분열소체 조직 낭포 또는 집합자의 형태로 투여된다.

[0588] 기생충의 접종에 이어, 연구된 조건과 관련된 표현형(질환의 병리학적 표현에 대하여 동물 모델을 특징짓고 평가한다. 표현형은 행동, 형태학적 및 분자적 표현형을 포함한다. 유전자 이식 기생충의 효과를 치료용 폴리펩티드를 발현시키지 않는 기생충으로 처리된 동물 및 허위-처리된 동물과의 비교로 나타내었다.

[0589] 예를 들어, 치료용 단백질 MeCP2를 발현시키는 T. 곤디 기생충으로 처리된 레트 증후군의 쥐 모델은 사회적 상호작용 장애, 증가된 냄새 표시, 뒷다리 움켜잡, 감소된 수명, 불안증, 호흡 문제, 저활동성, 운동 조정력 장애, miRNA-매개 IGF1 결핍, 감소된 BDNF 수준, 외피 가소성 장애, 신경교 기능 장애, GABAergic 신경 기능 장애, 감소된 체세포 크기, 감소된 수지상극 밀도, 감소된 시냅스 수, 감소된 활성(Ca²⁺ 이미징), 감소된 sEPSC 및 sIPSC 빈도 및 진폭, 감소된 Tuk1+ 세포 수, 감소된 PAX6, SCN1A/1B 발현, 감소된 피질 뉴런 내 수지상돌기 복잡성, 감소된 피질 뉴런 내 AP 빈도, 감소된 피질 뉴런 내 전체 전사, 피질 뉴런 내 신경, 시냅스, 고-발현 유전자, 전조기 유전자(immediate early genes) 및 미토콘드리아 유전자의 감소된 발현, 감소된 피질 뉴런 내 mRNA 전사, 감소된 피질 뉴런으로부터의 BDNF 분비, 감소된 피질 뉴런 내 AKT/mTOR 경로 활성 및 감소된 피질 뉴런 내 산소 소비 및 최대 호흡을 포함하는 알려진 질환의 표현형으로 평가한다[de la Torre-Ubieta et al. Advancing the understanding of autism disease mechanisms through genetics. Nat Med. 2016.].

[0590] **실시예 5**

[0591] **맞춤형 전사 활성체-유사 이펙터(TALEs)의 전달을 위한 구조물 및 T. 곤디 주의 생성**

[0592] T. 곤디는 맞춤형 전사 활성체-유사 이펙터(TALE)를 발현시키고 분비하도록 하공한다. 맞춤형 TALE는 전사 조절 및 게놈 편집을 포함하는, 다양한 게놈 공학 응용에 사용될 수 있다. TALE의 DNA 인식 및 결합 영역은 인식된 DNA 서열의 서열을 결정하는, 34-aa 서열(단량체)의 탠덤 반복으로 구성된다. 그것들이 인식하는 뉴클레오티드를 결정하는 그들의 반복 가변 이잔기(repeat variable diresidues, RVDs)가 상이한 4개의 유형의 단량체가 있다. "NI"로 칭한 단량체(서열번호 4508)는 "A" 뉴클레오티드에 특이적이다; "HD"로 칭한 단량체(서열번호 4495)는 "C" 뉴클레오티드에 특이적이다; "NG"로 칭한 단량체(서열번호 4509)는 "T" 뉴클레오티드에 특이적이다; 그리고 "NN"로 칭한 단량체(서열번호 4494)는 "G" 또는 "A" 뉴클레오티드에 특이적이다. 더욱 최근에는, 더 높은 G-특이성을 제공하는 추가적인 RVD NH(서열번호 4504)가 나타났다. 탠덤 반복 DNA-결합 도메인은 항상 반신(half-length) 반복(0.5 반복)으로 끝난다. 맞춤형 TALE DNA-결합 도메인은 맞춤 TALE 전사 인자(TALE-TFs)를 생성하고, 합성 VP64 전사 활성체와의 융합에 의해, 게놈 유래 내인성 유전자의 전사를 조절하기 위해 사용될 수 있다. 맞춤형 TALE DNA-결합 도메인은 또한 맞춤 TALE 뉴클레아제(TALENs)를 생성하기 위해 사용될 수 있고, FokI 엔도뉴클라제의 촉매 도메인에의 융합에 의해, 비상동적 수선 또는 상동 직접 수선을 통한 게놈 편집을 촉진하는 부위-특이적 이중-가닥 파단(break)을 생성하는데 사용될 수 있다. TALE는 TALEN 백본 또는 TALE-TE 백본으로 삽입되는, 단량체 유래 DNA-결합 도메인(서열번호 4508, 4509, 4494, 4495 및 4504)을 제작하여 만들어진다. 백본은 또한 DNA 결합 도메인의 말단에 0.5 반복을 포함하므로, 4개의 TALE-TF 백본(예를 들어, 서열번호 4496, 4497, 4498 및 4499) 뿐만 아니라, 4 유형의 TALEN 백본(예를 들어, 서열번호 4500, 4501, 4502 및 4503)이 있다. 백본은 또한 시토메갈로바이러스 프로모터(CMV), Hax3 TALE 유래 비반복 N 말단(N-term), Hax3 TALE 유래 비반복 C 말단(C-term), 맞춤 TALE DNA-결합 도메인(BsaI와 같은)의 삽입에 사용되는 타입 IIIs 제한 부위, ccdB 음성 선택 유전자 및 클로람페니콜 저항 유전자를 포함하는 음성 선택 카세트(ccdB + CmR), 핵 위치화 신호(NLS), 및 FokI 엔도뉴클라제(FokI) 유래 촉매 도메인 또는 헤르페스 심플렉스 바이러스의 VP16 단백질(VP74) 유래 합성 전사 활성체에 이어진 2A 자기-절단 링커(2A) 및 향상된 녹색 형광 단백질(EGFP) 중 어느 하나를 포함한다. 모두 아데닐산중합반응 신호(polyA 신호)가 뒤따른다(Sanjana et al., *A transcription activator-like effector toolbox for genome engineering*, 2012). 결과로 생긴 TALE 서열을 상기 일반 물질 및 실험 방법에서 설명한 바와 같이 T. 곤디 내인성 분비 폴리펩티드의 코딩 서열의 하류에 삽입하고, 결과로 생긴 구조물을 TALE를 발현시키고 분비하는 유전자 이식 T. 곤디 균주를 생산하는 T. 곤디로 형질감염시킨다.

[0593] 예를 들어, 이를 필요로 하는 개체의 게놈에 TACGTACG(서열번호 4505) 서열을 표적화하기 위하여, TALE 뉴클레아제 구조물 또는 TALE 전사 인자 구조물을 사용할 수 있다. 도 6A(TALE 뉴클레아제) 및 도 6B(TALE 전사 인

자)에서 도식적으로 나타낸 바와 같이, 이러한 구조물의 개방형 해독 프레임에서, 예시적인 "표적 서열" (서열 번호 4505)를 표적하는데 특이적인 단량체를 교대로 배열한다. 이러한 구조물의 서열 정보는 서열 목록에서 이용가능하다(서열번호 4506 및 4507).

[0594] 실시예 6

포유류 치료용 단백질을 발현시키고 그것들을 그의 곤봉체 분비 세포 기관으로 위치화하는 T. 곤디 기생충의 생성

포유류 단백질을 발현시키고 그것들을 그의 곤봉체 분비 세포 기관으로 표적화하는 T. 곤디 기생충을 생성시키기 위하여, 본 발명자들은 타입 I RH△HX 급분열소체 또는 RH(pDHFR 선택 플라스미드로 공-형질감염된) T. 곤디를 곤봉체 단백질 톡소필린에 융합된 목적단백질을 코딩하는 서열을 포함하는 플라스미드로 형질감염시킨다. 톡소필린 융합 시스템에서 시험된 포유류 단백질은 다음과 같다: 신경아세포 유도 신경영양 인자(GDNF), 파킨(PARK2), 갈락토세레브로시다제(GALC), TAT 단백질 형질도입 도메인에 융합된 갈락토세레브로시다제(GALC-TAT; 서열번호 4487), 메틸 CpG 결합 단백질(MeCP2), 아스파르트아실라제(ASPA) 및 운동 뉴런의 생존(SMN1). 단백질 발현 및 표적화를 개선하기 위한 시도에서, 본 발명자들은 또한 코돈-최적화된 형태의 GALC, MECP2, ASPA를 포함하는 몇몇 단백질, 및 코돈-최적화된 형태로 시험된 추가 유전자 TFEB(서열번호 4604)를 시험하였다.

ASPA(서열번호 4483), 코돈-최적화된 ASPA (서열번호 4602), GALC(서열번호 4486 및 4601), GALC-TAT(서열번호 4488), PARK2(서열번호 4478), SMN1(서열번호 4479), GDNF(서열번호 4489), MeCP2(서열번호 4476) 및 코돈-최적화된 MeCP2(서열번호 4477)는 기생충의 융합 단백질의 가변 표적화를 나타내는데, 이는 곤봉체 표적화 뿐만 아니라, 기생충 내 소포체, 골지체, 핵, 세포질, 아피코플라스트, 미세간상체 및 다른 위치와 유사한, 다른 패턴의 표적화를 포함한다(도 9A-N).

GALC-TAT 변이 형태는 주로 곤봉체-유사 융합 단백질 위치를 생성하였다. 변이된 GALC-TAT로부터, 본 발명자들은 또한 융합 단백질을 강하게 발현시키고 이를 곤봉체에 표적화하는 클론 주를 생성하였다(도 9H).

[0599] 실시예 7

포유류 치료용 단백질을 발현시키고, 그것들을 그의 밀집 과립 분비 세포 기관에 위치시키고, 그것들을 기생충 액포로 분비하는 T. 곤디 기생충의 생성

포유류 단백질을 발현시키고 그것들을 그의 밀집 과립 분비 세포로 표적화하는 T. 곤디 기생충을 생성시키기 위하여, 타입 I RH△HX T. 곤디를 밀집 과립 단백질 GRA16에 융합된 목적단백질을 코딩하는 서열을 포함하는 플라스미드로 형질감염시켰다. GRA16 융합 시스템에서 시험된 포유류 단백질-코딩 유전자는 GALC [인간형(서열번호 4486 및 4601) 및 코돈-최적화된(서열번호 4603)], GALC-TAT (인간형 서열번호 4488), MECP2(코돈-최적화된, 서열번호 4477), ASPA [인간형 (서열번호 4483) 및 코돈-최적화된(서열번호 4602)], SMN1(인간형, 서열번호 4479) 및 TFEB(코돈-최적화된, 서열번호 4604)이었다.

GALC, 코돈-최적화된 GALC 및 GALC-TAT를 형질감염된 기생충에서 발현시켰다(도 10E, 10F 및 10H). ASPA, 코돈-최적화된 ASPA, SMN1, 코돈-최적화된 MeCP2 및 코돈-최적화된 TFEB를 발현시키고 밀집 과립에 의해 기생충 액포로 분비시켰다(도 10C, 10G, 10D, 10I, 10J).

[0603] 실시예 8

유전자 이식 T. 곤디를 이용한 포유류 치료용 단백질의 배양물 내 인간 섬유아세포로의 전달

본 발명자들은 융합 단백질을 기생충 액포로 분비할 수 있는 것에 더하여, 그것을 기생충 액포로부터 방출시키고, 면역형광 염색에 의해 검출가능한 양으로 숙주세포의 핵으로 그것을 표적화할 수 있는, 6개의 타입 I 및 타입 II 톡소플라즈마 클론 주를 조작하였다. 이들 클론 주는 다음과 같다: 코돈-최적화된 RH GRA16-MECP2(RH GRA16-MECP2opt), 코돈-최적화된 RH GRA16-TFEB(RH GRA16-TFEBopt), 코돈-최적화된 Prugniaud-GFP-Luciferase DHFR-TS GRA16-MECP2(Pru-GFP-LUC GRA16-MECP2opt), 코돈-최적화된 Prugniaud-GFP-Luciferase DHFR-TS GRA16-TFEB(Pru-GFP-LUC GRA16-TFEBopt), 코돈-최적화된 Prugniaud GRA16-MECP2(Pru GRA16-MECP2opt), 및 코돈-최적화된 Prugniaud GRA16-TFEB(Pru GRA16-TFEBopt). 융합 단백질을 발현시키는 유전자 이식 주에 더하여, 본 발명자들은 또한 HA 에피토프 태그에만 융합된 담체 단백질 GRA16을 발현시키는 2개의 대조군 주를 생성시켰다: RH GRA16-HA(RH GRA16-HAstop) 및 Prugniaud GRA16-HA(Pru GRA16-HAstop). MeCP2 및 TFEB가 모두 핵 단백질이므로, 숙주세포 핵 표적화는 그들이 세포에서 그들의 활성 부위로 표적화되는 것을 의미한다. HFF 인간 섬유아세포에서 각 주의 급분열소체를 포함하는 완전한 DMEM 내 HFF 세포의 감염, 고정, 면역형광 염색, 및 형

광 및 편광 현미경에 의한 분석에 의해, 상술한 모든 주에서 단백질의 분비 및 숙주세포 핵 표적화를 검출하였다(도 10B, 10I 및 10J).

[0606] 시험관 내 GRA16-매개 단백질 전달의 효율 및 동역학을 정량화하기 위하여, 본 발명자들은 도 11A-C에 요약된 바와 같이, 세 가지 타입 I 주, RH GRA16-HAstop, RH GRA16-MECP2opt 및 RH GRA16-TFEBopt의 급분열소체에 대하여 시간의 흐름에 따른 전달 및 감염의 다양성(MOI)을 정량화하였다.

[0607] **실시예 9**

[0608] **유전자 이식 T. 곤디를 이용한 포유류 치료용 단백질의 배양물 내 인간 뉴런으로의 전달**

[0609] 룬드 인간 중간뇌(Lund Human Mesencephalic, LUHMES) 세포로도 알려진, 불멸화 인간 도파민 신경 선구세포(Immortalized Human Dopaminergic Neuronal Precursor Cells)를 L-글루타민, N-2 무혈청 보충제 및 β FGF(베타-섬유아세포 성장 인자)가 보충된 F12 고급(advanced) DMEM 배지를 함유하는 배지에서 성장시켰다. L-글루타민, N-2 무혈청 보충제, 테트라사이클린, GDNF 및 cAMP(고리형 아데노신 일인산)가 보충된 F12 고급 DMEM 배지를 이용하여 세포를 배양물에서 형태학적으로 그리고 생화학적으로 성숙한 도파민-유사 뉴런으로 분화시켰다. 분화 6-9일차에(세포가 성숙한 뉴런인 시기), 클론 주, RH GRA16-MECP2opt, RH GRA16-TFEBopt 및 RH GRA16-HAstop의 급분열소체를 뉴런을 감염시키기 위해 사용하였다. 감염 16-22 시간 후, 뉴런을 고정시키고 면역형광 염색하고, 형광 및 편광 현미경으로 분석하였다. 시험된 모든 주는 융합 단백질의 명확한 분비를 나타냈는데, 이는 인간 뉴런의 핵을 표적화하였다(표 12A-C).

[0610] 아울러, 인간 뉴런을 RH GRA16-MECP2opt 급분열소체로 감염시키고, 감염 24시간 후에 채취하였다. 감염된 뉴런을 PBS로 씻어내고, 멸균 세포 스크레이퍼를 이용하여 긁어내고, 원심분리로 펠렛화하였고, 잔여 PBS를 제거하고, 펠렛을 액체 질소에서 스냅-동결하였다. 감염된 뉴런으로부터 추출한 핵 단백질을 MeCP2 항체에 결합된 자성 비드를 이용하여 면역침전시켰다. 면역침전된 단백질을 표준 웨스턴 블롯 프로토콜에 따라 동일한 MeCP2 항체로 면역블롯팅하였다. 결과로 생긴 블롯은 대략 75 kDa 및 대략 130 kDa의 2개의 강한 밴드를 나타냈다. ~75 kDa 밴드는 인간 뉴런 유래의 내인성 비절단 MeCP2(예측 크기: 75 kDa)를 나타내고, ~130 kDa 밴드는 기생충-전달 GRA16-MeCP2 융합 단백질(GRA16 예측 크기: 55 kDa. 융합 단백질 예측 크기: 75+55 = 130 kDa)을 나타낸다(도 14).

[0611] **실시예 10**

[0612] **유전자 이식 T. 곤디를 이용한, 포유류 MECP2의 쥐 1차 피질 및 해마 배양물로의 전달 및 전달된 MECP2의 이질염색질 DNA에의 결합**

[0613] P1(1일차) 새끼 쥐의 피질 및 해마 유래의 뉴런이 풍부한 일차 배양물을 5일 동안 배양하고, 유전자 이식 주 RH GRA16-MECP2opt의 급분열소체로 감염시켰다. 감염 12, 24 및 48 시간 후, 뉴런을 고정시키고, 면역형광 염색하고, 형광 및 편광 현미경으로 분석하였다. 열거된 시점 모두에서, GRA16-MECP2 융합 단백질을 분비하였고, 뉴런의 핵을 표적화하였으며, 또한 밀집 이질염색질 DNA의 영역에 상응하는 병소(foci)에서 나타났으며, 강한 DAPI 염색으로 인식되었다(도 13A-D). 그것이 이질염색질에 성공적으로 결합한다는 것을 시사하므로, 이는 MeCP2 기능성에 대한 고전적 마커이다. 특히, 배양 시스템에서, T. 곤디는 뉴런, 신경교 및 다른 세포 모두를 감염시킬 수 있다. 일차 배양물은 순수하게 뉴런이 아니기 때문에(NeuN 염색에 따라), 본 발명자들은 유전자 이식 T. 곤디에 의해 감염된 비-신경세포(아마도 대부분 신경교)가 또한 MeCP2 융합 단백질을 받고, 동일한 특징적인 병소 패턴을 나타낸다는 것을 알 수 있었다.

[0614] **실시예 11**

[0615] **T. 곤디 느린분열소체 낭포에서의 GRA16 및 GRA16-MECP2 융합 단백질의 발현**

[0616] 감염의 정상적인 과정 중, 기생충이 급분열소체와 같이 신체 내에서 복제하고 전파하는 초기 급성기 후에, 면역압력은, T. 곤디 급분열소체가, 조직 내, 및 대개 뇌 내, 오래 지속되는 휴지기 낭포에 있는 느린분열소체로 분화되는 것을 야기한다(Carruthers VB, Suzuki Y, 2007. Schizophr Bull. 33(3):745-51. Effects of Toxoplasma gondii infection on the brain). 그러므로, 본 발명자들은 유전자 이식 T. 곤디가 느린분열소체 형태로 분화된 후에 GRA16-융합 치료용 단백질을 계속해서 발현시키는지 조사하였다. 시험관 내 유전자 이식 T. 곤디의 느린분열소체로의 분화는 3 내지 5 일 동안의 알칼리성 배지에 의한 스트레스에 의해 유도되었다. 알칼리성 배지는 페니실린-스트렙토마이신이 보충된 10 mM HEPES 및 1% 소태아혈청을 포함하는 pH 8.1로 조정된 DMEM 배지를 포함한다(Tomita T, Bzik DJ, et al. 2013. PLoS Pathog. 9(12):e1003823. The Toxoplasma

gondii cyst wall protein CST1 is critical for cyst wall integrity and promotes bradyzoite persistence). 본 발명자들은 균주 Pru GRA16-HAstop 및 Pru GRA16-MeCP2의 분화를 시험하였다. 낭포 벽의 DBA(Dolichos Biflorus Agglutinin) 염색에 의해 식별된, 느린분열소체 낭포는 GRA16-HAstop(테이터는 나타나지 않음) 및 GRA16-MeCP2 단백질 둘 다를 계속해서 발현하였다(도 15A-C). 이러한 발견은 유전자 이식 기생충이 느린분열소체 단계로 분화한 후에도 GRA16 및 GRA16 융합 단백질을 계속해서 발현시킬 수 있음을 나타내는데, 이는 만성 감염에서, 낭포로부터의 지속적인 분비 및 단백질 전달에 있어서 중요한 것이다.

[0617] **실시예 12**

[0618] **T. 곤디에 의해 전달된 이중 폴리펩티드 및 수용체 세포 내 내인성 단백질 사이의 분자 상호작용의 조사**

[0619] 감염된 배양물 및 감염된 동물 유래의 세포 용해물 상에서 공동-면역침전을 수행하여, 본 발명자들은 유전자 이식 T. 곤디에 의해 전달된 폴리펩티드, 및 내인성 단백질과 핵산 사이의 분자 상호작용을 해독할 수 있다.

[0620] 예를 들어, 포유류 세포에서, MeCP2는 SMRT/NCOR 및 SIN3A 공-억제체 복합체 유래의 DNA 및 단백질 모두와 결합한다. DNA에의 결합은 면역형광 염색 및 염색질-면역침전에 의해 해독될 수 있고, 다른 단백질에의 결합은 면역형광 염색 및 단백질 공동-면역침전에 의해 해독될 수 있다. 전달된 융합 단백질 상에 첨가된 에피토프 태그는 숙주세포에 의해 생산된 단백질의 복사체 및 기생충에 의해 전달된 단백질의 복사체를 구별하기 위해 사용되는 반면, 단백질에 대한 항체는 그 자체로서 내인성 및 기생충-전달 단백질 모두를 해독하기 위해 사용될 수 있다 (예를 들어, 비교 분석).

[0621] **실시예 13**

[0622] **유전자 이식 T. 곤디의 이중 목적단백질을 계속적으로(/만성적으로) 전달하는 능력의 동물 모델에서의 시험**

[0623] 전체 유기체의 표현형에 영향을 미치는 능력에 대하여, 기생충의 유전자 이식 주를 시험한다. 동물 모델에서의 유전자 이식 기생충의 시험은 면역계 및 기능적 혈뇌 장벽(BBB) 내 시스템의 평가를 가능하게 한다. 이는 유전자 이식 T. 곤디로 쥐를 감염시키는 분야에 확립된 표준 감염 프로토콜에 따라 행하여졌다(Cabral CM et al., 2016, PLoS Pathog. 12(2):e1005447. Neurons are the Primary Target Cell for the Brain-Tropic Intracellular Parasite Toxoplasma gondii; Berenreiterová et al., 2011. PLoS One. 6(12):e28925. The distribution of Toxoplasma gondii cysts in the brain of a mouse with latent toxoplasmosis: implications for the behavioral manipulation hypothesis; Tait ED et al. 2010. J. Immunol. 185(3):1502-12. Virulence of Toxoplasma gondii is associated with distinct dendritic cell responses and reduced numbers of activated CD8+ T cells; Koshy AA et al. 2012. PLoS Pathog. 8(7):e1002825. Toxoplasma co-opts host cells it does not invade; Jensen KD et al. 2015. MBio. 6(2):e02280. Toxoplasma gondii superinfection and virulence during secondary infection correlate with the exact ROP5/ROP18 allelic combination). 유전자 이식 T. 곤디 기생충을 동물 모델에 비강내, 경구로(구강으로와 같이), 피하로, 근육내, 정맥내, 피부내, 복강내, 두개내 또는 대뇌내로 투여한다. 유전자 이식 T. 곤디 기생충을 급분열소체, 느린분열소체 조직 낭포 또는 접합자 형태로 투여한다. 동물 모델은 치료가 가능한 상태를 가지거나, 또는 그 밖에 유전자 이식 기생충에서 발현되는 목적단백질의 전달에 영향을 받는, 야생형 동물 또는 모델 동물일 수 있다. 급성 감염의 초기 단계 후에, 동물은 만성 느린분열소체 조직 낭포를, 주로 뇌에 발생시킨다. 이러한 전달 모드는 감염의 만성 단계에서 유전자 이식 T. 곤디 유래의 목적 단백질의 지속적인 발현 및 분비에 의존한다.

[0624] 만성 감염의 발달 동안 상이한 단계에서(균주 및 감염 경로에 의존하는, 감염 후 최초 3주 내지 2개월), 뿐만 아니라, 만성 감염이 확립되고 안정화된 후 상이한 시점에서(감염 후 수개월 내지 수년의 시간 척도), 감염된 세포의 백분율, 뇌 및 다른 조직 내 기생충 및 전달된 단백질의 분포를 평가하기 위하여, 그리고 전달된 단백질의 수준을 정량화하기 위하여, 뇌 조직 염색이 사용된다. 공동-면역침전 및 세포 형태학이 전달된 단백질과, 받아들이는(receiving) 세포 내 내인성 대응물 사이의 분자적 상호작용을 확인하기 위하여, 그리고 그들의 기능에 대한 증거를 제공하기 위하여, 사용될 수 있다.

[0625] 치료로 인한 임의의 잠재적인 독성 뿐만 아니라, 질병 표현형의 징후 및 이를 완화시키는 치료의 효능을 평가하기 위하여, 처리된 동물 모델의 상태를 만성 감염의 상이한 단계 및 생리학적, 행동학적, 세포 및 분자 측정을 이용한 질병 진행의 상이한 단계에서, 모니터링하고 특징지었다. 유전자 이식 기생충의 효과를 약학적 폴리펩티드를 발현시키지 않는 기생충이 처리된 동물 및/또는 허위-처리된 동물과의 비교로 평가한다.

[0626] 예를 들어, 치료용 단백질 MeCP2를 발현시키는 T. 곤디 기생충으로 처리된 레트 증후군의 쥐 모델은 사회적 상

호작용 장애, 증가된 냄새 표시, 뒷다리 움켜잡, 감소된 수명, 불안증, 호흡 문제, 저활동성, 운동 조정력 장애, miRNA-매개 IGF1 결핍, 감소된 BDNF 수준, 외피 가소성 장애, 신경교 기능 장애, GABAergic 신경 기능 장애, 감소된 체세포 크기, 감소된 수지상극 밀도, 감소된 시냅스 수, 감소된 활성(Ca²⁺ 이미징), 감소된 sEPSC 및 sIPSC 빈도 및 진폭, 감소된 Tuk1+ 세포 수, 감소된 PAX6, SCN1A/1B 발현, 감소된 피질 뉴런 내 수지상돌기 복잡성, 감소된 피질 뉴런 내 AP 빈도, 감소된 피질 뉴런 내 전체 전사, 피질 뉴런 내 신경, 시냅스, 고-발현 유전자, 전초기 유전자(immediate early genes) 및 미토콘드리아 유전자의 감소된 발현, 감소된 피질 뉴런 내 mRNA 전사, 감소된 피질 뉴런으로부터의 BDNF 분비, 감소된 피질 뉴런 내 AKT/mTOR 경로 활성 및 감소된 피질 뉴런 내 산소 소비 및 최대 호흡을 포함하는 알려진 질환의 표현형으로 평가한다[de la Torre-Ubieta et al. Advancing the understanding of autism disease mechanisms through genetics. Nat Med. 2016.].

[0627] **실시예 14**

[0628] **유전자 이식 T. 곤디의 이중 목적단백질을 일시적으로(/급성으로) 전달하는 능력의 동물 모델에서의 시험**

[0629] 상기 실시예 13과 유사하게, 전체 유기체의 표현형에 영향을 미치는 능력에 대하여, 기생충의 유전자 이식 주를 시험하였다. 동물 모델에서의 유전자 이식 기생충의 시험은 면역계 및 기능적 혈뇌 장벽(BBB) 내 시스템의 평가를 가능하게 하고, 이는 급분열소체, 느린분열소체 조직 낭포 또는 접합자 형태의 유전자 이식 T. 곤디의 비강 내, 경구(구강과 같이), 피하, 근육내, 정맥내, 피부내, 복강내, 두개내 또는 대뇌내 투여에 의해 수행될 수 있다. 동물 모델은 치료가 가능한 상태를 가지거나, 또는 그 밖에 유전자 이식 기생충에서 발현되는 목적단백질의 전달에 영향을 받는, 야생형 동물 또는 모델 동물일 수 있다. 이러한 실험 설계는 느린분열소체로의 분화 및 만성 감염 및/또는 만성 낭포의 확립에 의존하지 않는 일시적인 전달의 평가에 초점을 맞춘 것이다. 일부 예는 다음을 포함한다: 느린분열소체로 분화할 수 없는, 복제할 수 없는, 및/또는 몇 주 이상 시험관내 지속될 수 없는, 또는 그렇지 않으면 만성 감염을 확립할 수 없는, 약독화된 기생충에 의한 전달; 표적 조직 또는 표적 조직에 근접한 영역에의 국소 투여에 의한 전달에 뒤이은 기생충의 제거 또는 비활성화. 이는 또한 반복 투여를 위해 여러번 반복될 수 있다. 감염을 향상시키고 전에 T. 곤디에 이미 감염된 동물의 재감염을 돕기 위하여, 감염 전, 동시 또는 후에 면역억제제를 투여할 수 있다. 이러한 실험 설계는 또한 만성 감염을 확립할 수 있는 유전자 이식 T. 곤디에 의한 전달을 포함하나, 만성 감염의 확립 전 감염의 급성 단계에서 표본의 수집 또는 분석이 수행된다. 이러한 전달의 형태는 유전자 이식 주의 급분열소체의 목적단백질의 분비에 대부분 의존한다. 급성 감염 동안의 상이한 단계에서(균주 및 감염 경로에 의존하는, 감염 후 최초 수일 내지 약 2 개월), 감염된 세포의 백분율을 평가하고, 뇌 및 다른 조직 내 기생충 및 전달된 단백질의 분포를 특징짓고, 전달된 단백질의 수준을 정량화하기 위하여, 뇌 조직 염색을 사용한다. 공동-면역침전 및 세포 형태학이 전달된 단백질과, 받아들이는 세포 내 내인성 대응물 사이의 분자적 상호작용을 확인하기 위하여, 그리고 그들의 기능에 대한 증거를 제공하기 위하여, 사용될 수 있다.

[0630] 치료로 인한 임의의 잠재적인 독성 뿐만 아니라, 질병 표현형의 징후 및 이를 완화시키는 치료의 효능을 평가하기 위하여, 처리된 동물 모델의 상태를 치료 개시 후 상이한 시점에서, 및 생리학적, 행동학적, 세포 및 분자 측정을 이용한 질병 진행의 상이한 단계에서, 모니터링하고 특징지었다. 유전자 이식 기생충의 효과를 치료용 폴리펩티드를 발현시키기 않는 기생충이 처리된 동물 및/또는 허위-처리된 동물과의 비교로 평가한다.

[0631] **실시예 15**

[0632] **유전자 이식 T. 곤디의 안전성 및 조절가능성을 증가시킬 추가 변형의 도입**

[0633] 비록 기생충은 일반적으로 건강한 인간에게는 무해한 것으로 간주되나, 나아가 그 병독성을 약독화하기 위하여, 기생충에 대한 추가적인 변형이 치료용 균주에 포함될 수 있다. 그의 문(phylum)의 모델 유기체로서, 기생충을 변형시키기 위한 광범위한 고도로 발달된 유전적 도구가 있는데(Jiménez-Ruiz E, Wong EH, Pall GS, Meissner M. Parasitology. 2014, 141:1390-8. "Advantages and disadvantages of conditional systems for characterization of essential genes in Toxoplasma gondii"), 이는 약독화되고, 외인성-조절가능한 기생충을 생성하기 위해 사용될 수 있다(Moe-Behrens GH, Davis R, Haynes KA. Front Microbiol. 2013 4:5. "Preparing synthetic biology for the world"). 하나의 접근법은 조작된 영양요구체를 포함한다. 두번째로, 약독화된 기생충은 단백질 약물을 전달하는 능력에 필수적이지 않은 기생충의 특이적 병독 메커니즘을 표적화하고 방해하여 개발될 수 있다. 또 다른 하나의 접근법은 활성화 분자의 투여 시 기생충을 제거하는 유도성 "자살 스위치(suicide switches)" (자기-파괴 요소)와 같은 조작된 유도 치사(lethality)를 통한 능동적 조절을 포함할 수 있다. 일부 예는 생체 내 기생충에서 치사 또는 세포사멸 경로의 약물-유도 활성화를 위한 널리 사용되는 테트라사이클린-유도 프로모터, 또는 필수적 유전자의 유도 녹-아웃 또는 치사 또는 세포사멸 경로의 유도 활성화를

위한 라파마이신-이량화 diCre 시스템을 이용하는 것을 포함할 수 있다. 또한 이러한 약물-유도 조절은 조직 또는 세포의 약물-에의 차별적인 투과성 및 그의 신체 내 상이한 분포로 인한, 특정한 조직, 영역 또는 세포 타입으로부터의 기생충의 차별적인 제거를 가능하게 할 수 있다.

[0634] 분석 및 토론

[0635] 본 발명은 뇌 기생충 T. 곤디의 기계를 사용하는 단백질 전달 플랫폼으로, 이는 혈뇌 장벽을 침투하여 단백질을 세포, 특히 CNS 내 뉴런에 전달하게 한다.

[0636] 치료용 단백질의 CNS로의 전달을 가능하게 하기 위하여, 본 발명자들은 CNS 내 세포로의 목적단백질의 합성 및 전달을 위한 기생충 톡소플라즈마 곤디를 재전용한다(reappropriate). 따라서 본 발명자들은 단백질의 CNS 내 세포로의 특이적이고 조절된 전달을 위한 다목적 플랫폼을 확립한다.

[0637] 조작된 기생충은 다음의 신규한 능력을 가진다:

[0638] (1) 이는 다양한 치료용 이중 단백질을 합성하고, 그것들을 CNS 내 표적 세포로 특이적으로 분비하기 위하여 쉽게 변형될 수 있다.

[0639] (2) 이는 감염된 숙주에 대한 유해한 영향을 매개할 수 있는 기생충의 요소를 감소시키거나 제거하는 변형을 포함할 수 있다.

[0640] (3) 이는 숙주에서 한 번 그의 분포 및 시공간적 활성을 조절하게 하는, 조절 및/또는 자기-파괴 요소를 포함할 수 있다.

[0641] 다음은 본원에서 설명된 기생충 계통 내 변형의 비-제한적 요약이다:

[0642] (i) 선택된 치료용 단백질의, 기생충의 특정한 내인성 분비 단백질에의 융합. 그의 표적화 또는 활성화에 더 이상 필요하지 않게 된 후, 내인성 기생충 단백질로부터 치료용 단백질의 분리를 가능하게 할 수 있는 절단 부위와 같은 치료용 융합 단백질의 효율을 증가시키거나, 또는 톡소플라즈마, 및 에피토프 태그 및 형광 단백질과 같은 전달된 단백질의 효율 및 분포의 검출 및 평가를 중재할 수 있는 융합 유전자/단백질에 추가의 부수적 요소 및 변형이 추가될 수 있다.

[0643] (ii) 기생충의 치료 역할에 있어서 필수적이지 않은 병독성 유전자의 제거. 이들 변형은 환자에 대한 기생충의 잠재적인 유해한 효과를 감소시키며, 안전한 임상적 사용에 관련된다.

[0644] (iii) 기생충이 외부에서 투여된 약물에 대한 반응으로 자기-파괴하거나, 또는 기생충의 활성을 조작하도록 유도할 수 있는 조절 요소의 삽입. 이러한 요소는 본 기술의 안전성 특징을 증가시키며, 또한 시공간적 활성의 증가된 조절을 제공한다.

[0645] 본 발명의 일부 구현예의 방법으로 개발된 초기 균주는 크라베 질환용 갈락토세레브로시다제 및 갈락토세레브로시다제-TAT 단백질, 다양한 신경퇴행성 질환 및 다른 상태(파킨슨병, 핵상 마비, 다발성 경화증, 알츠하이머병, 근위축성측색경화증, 헌팅틴병, 망막 변성, 외상성 뇌 손상 및 저산소/허혈성 CNS 장애 중)용 GDNF 단백질, 카나반 질환용 아스파르트아실라제 단백질, 레트 증후군용 MeCP2 단백질, 척수근위축증용 SMN 단백질, 파킨슨병용 E3 유비퀴틴-단백질 리가아제 파킨 및 리소좀 저장 질환 및 신경퇴행성 질환용 TFEB를 기반으로 하였다. 본 발명자들이 현재 임상적으로 시험되고 보충적 기능이 알려진 많은 수의 치료용 단백질을 선택하였으나, 플랫폼은 광범위한 단백질에 적용될 수 있다.

[0646] 본 기술의 가능한 응용분야는 이에 제한되는 것은 아니나, 다음을 포함한다:

[0647] 1. 치료용 단백질의 전달을 통한 상태의 치료;

[0648] 2. 뇌 기능 증가 또는 신경-재생 촉진의 목적을 위한 건강한 개인의 뇌에의 단백질의 공급;

[0649] 3. 단백질 합성을 보충하기 위한 매우 특이적이고 효율적인 표적화된 단백질 전달을 위한 일반적인 해결책.

[0650] 비록 본 발명은 그의 특정한 구현예와 함께 설명되었으나, 많은 대안, 변경 및 변형이 당업자에게 명백하다는 것은 분명하다. 따라서, 첨부된 청구범위의 사상 및 넓은 범위 내에 있는 모든 대안, 변경 및 변형을 포함하고자 한다.

[0651] 본 명세서에서 언급된 모든 간행물, 특허 및 특허출원은 각각의 개별 간행물, 특허 또는 특허출원이 구체적이고 개별적으로 본원에 참고로 인용된 것과 동일한 정도로, 본 명세서에 참고로서 전체로서 포함된다. 아울러, 본

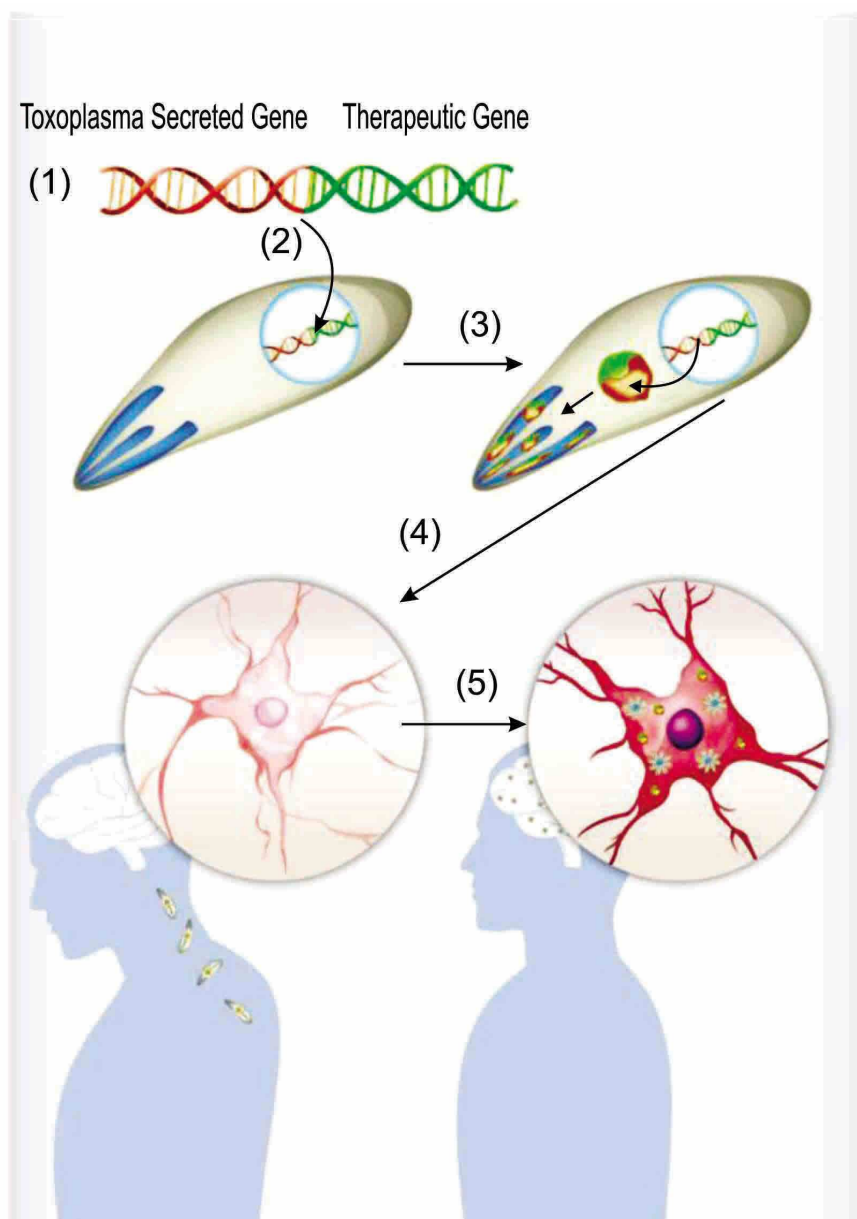
출원 내 임의의 참고문헌의 인용 또는 확인은 그러한 참고문헌이 본 발명의 선행기술로서 이용가능하다는 인정으로 해석되어서는 안된다. 섹션 제목이 사용되는 한, 그들이 반드시 제한적인 것으로 해석되어서는 안된다.

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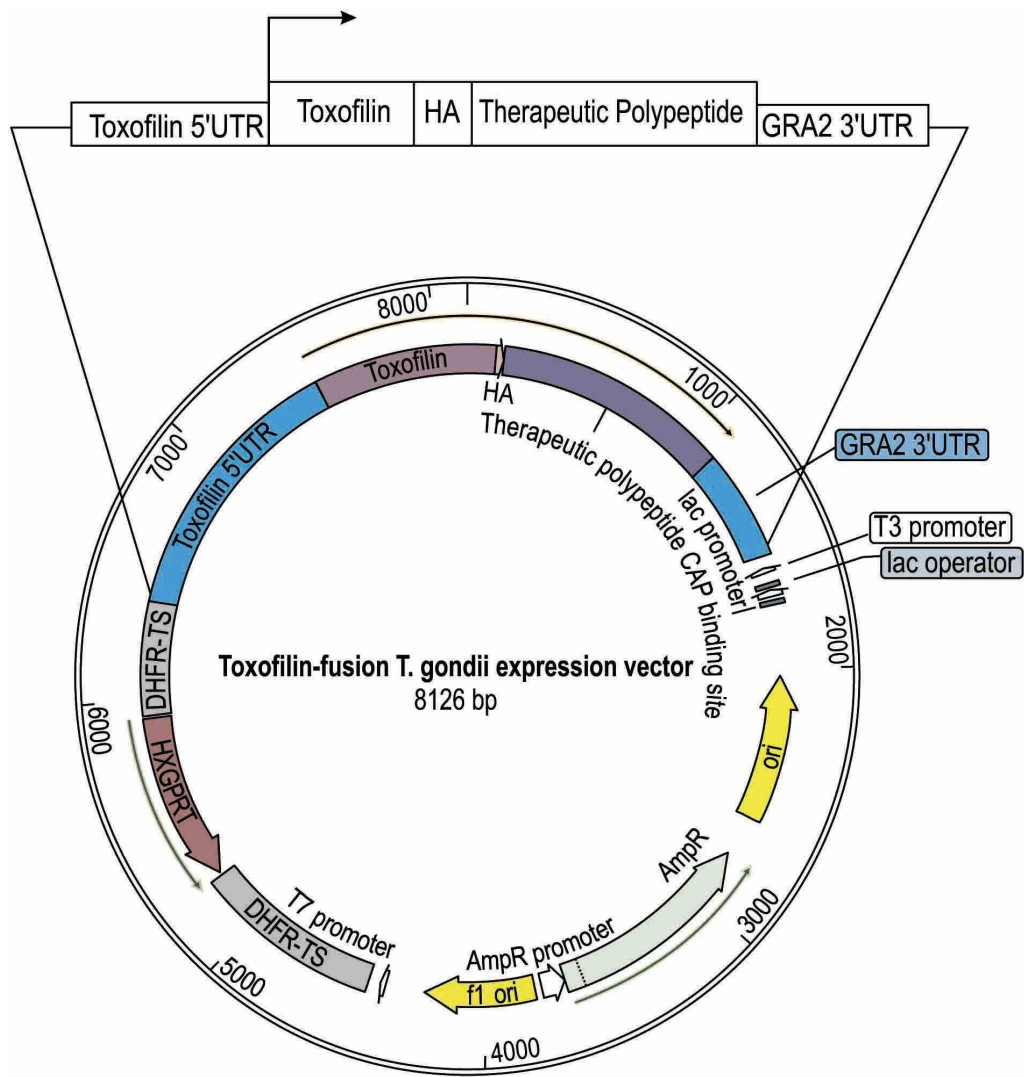
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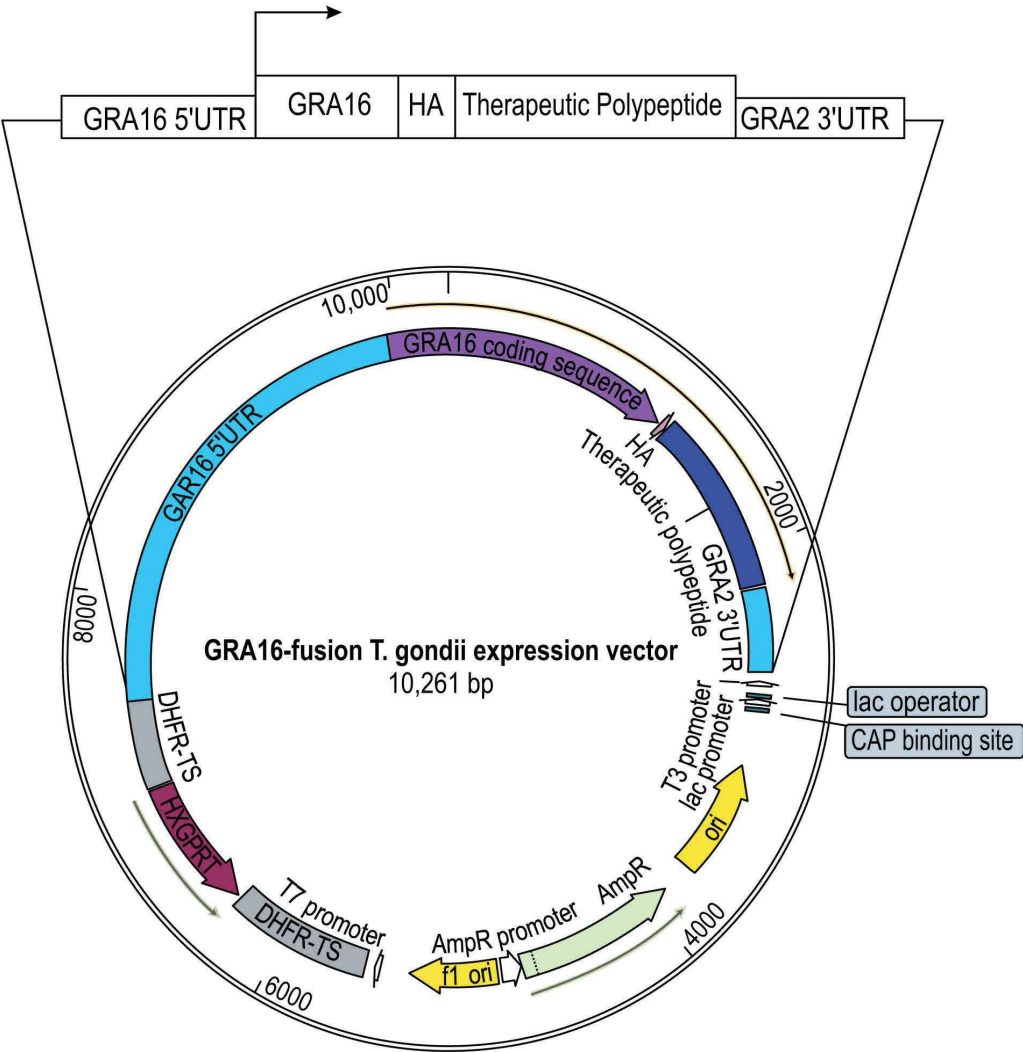
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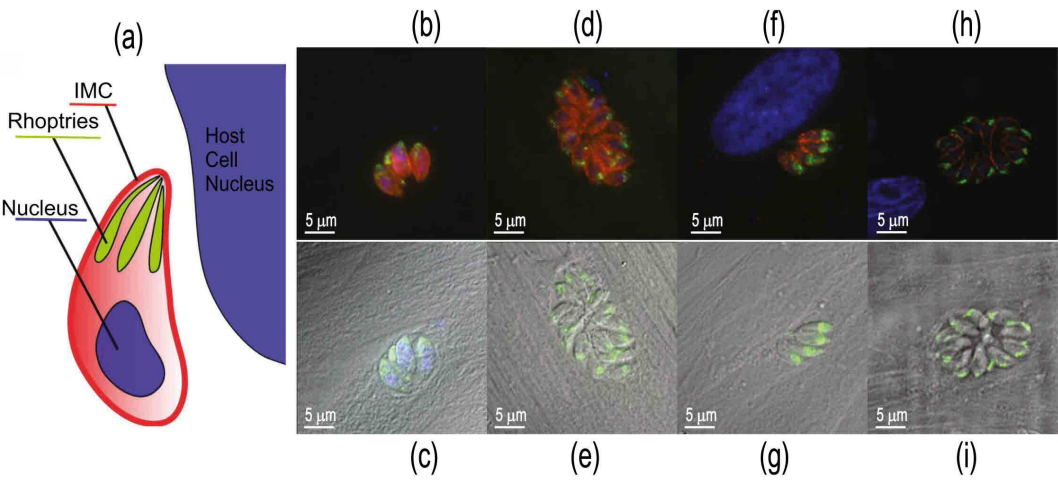
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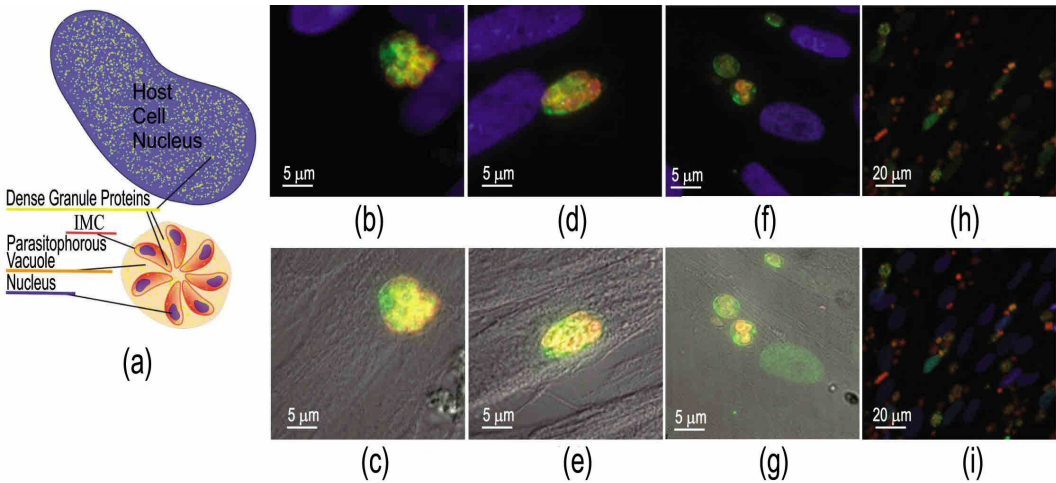
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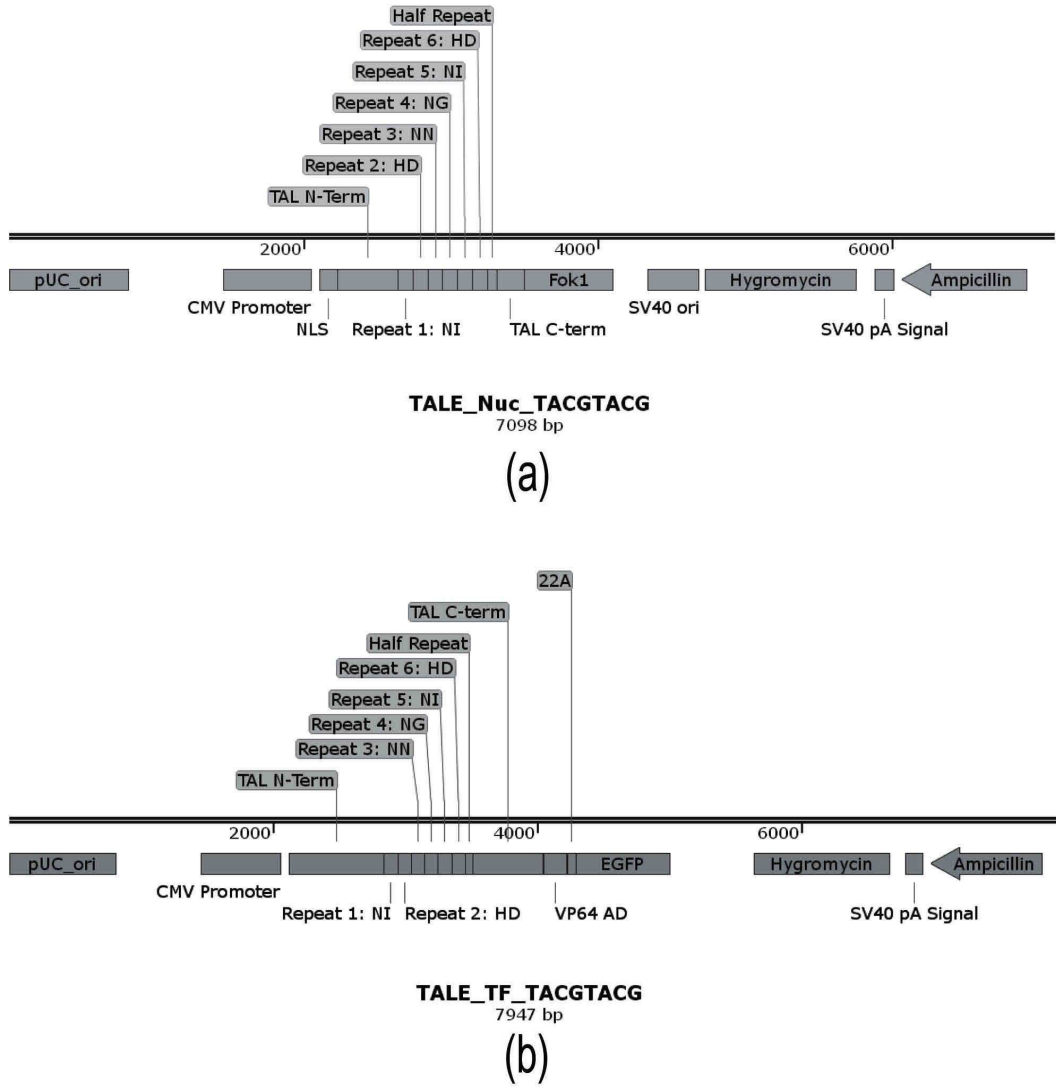
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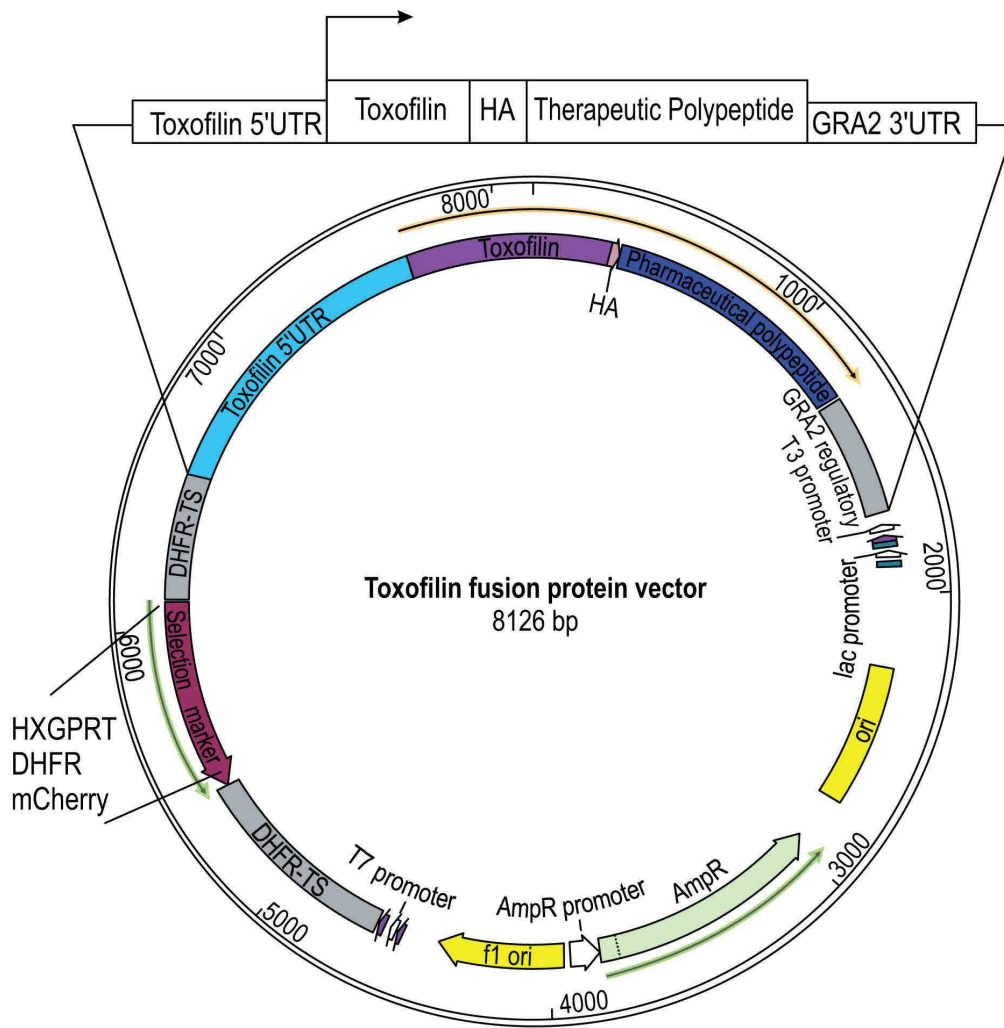
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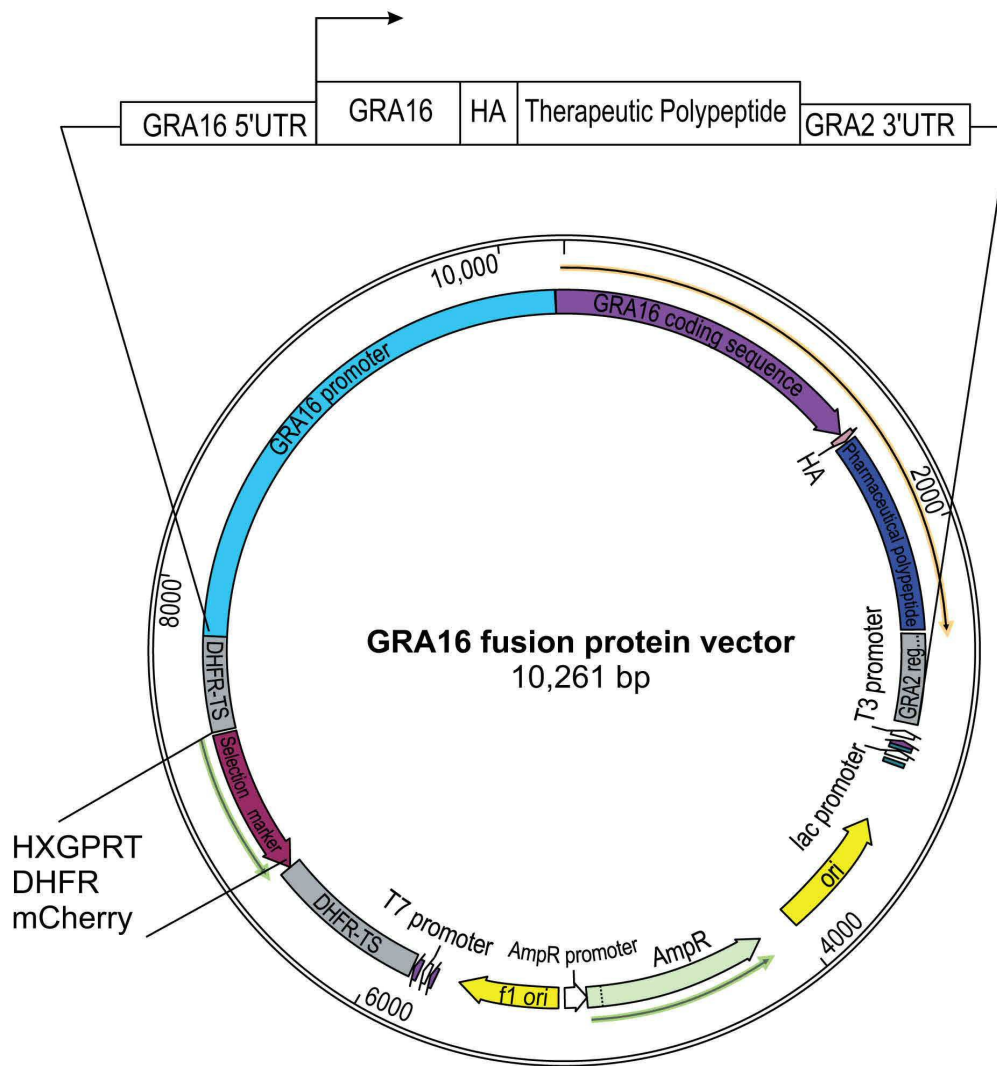
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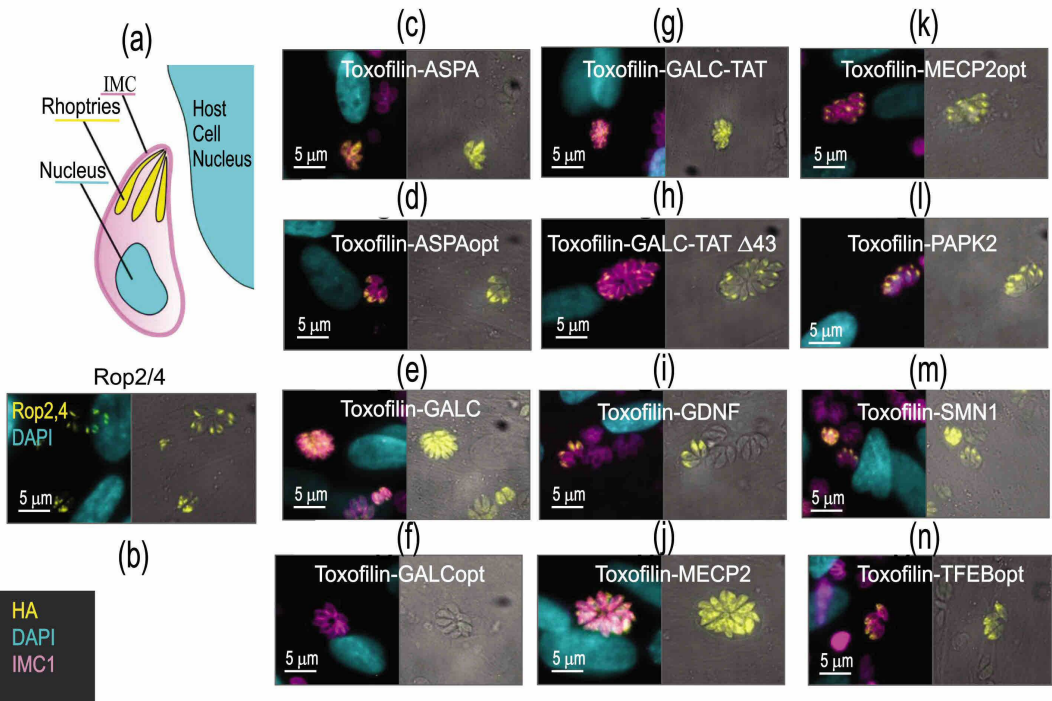
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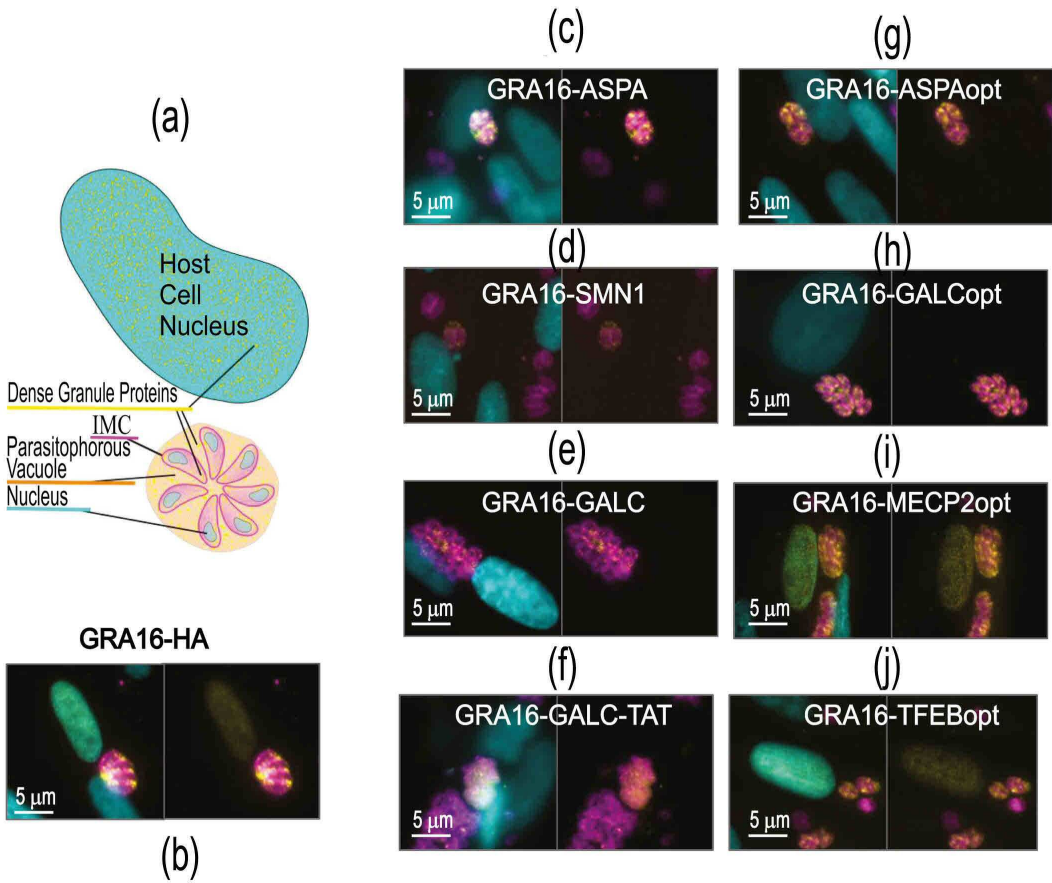
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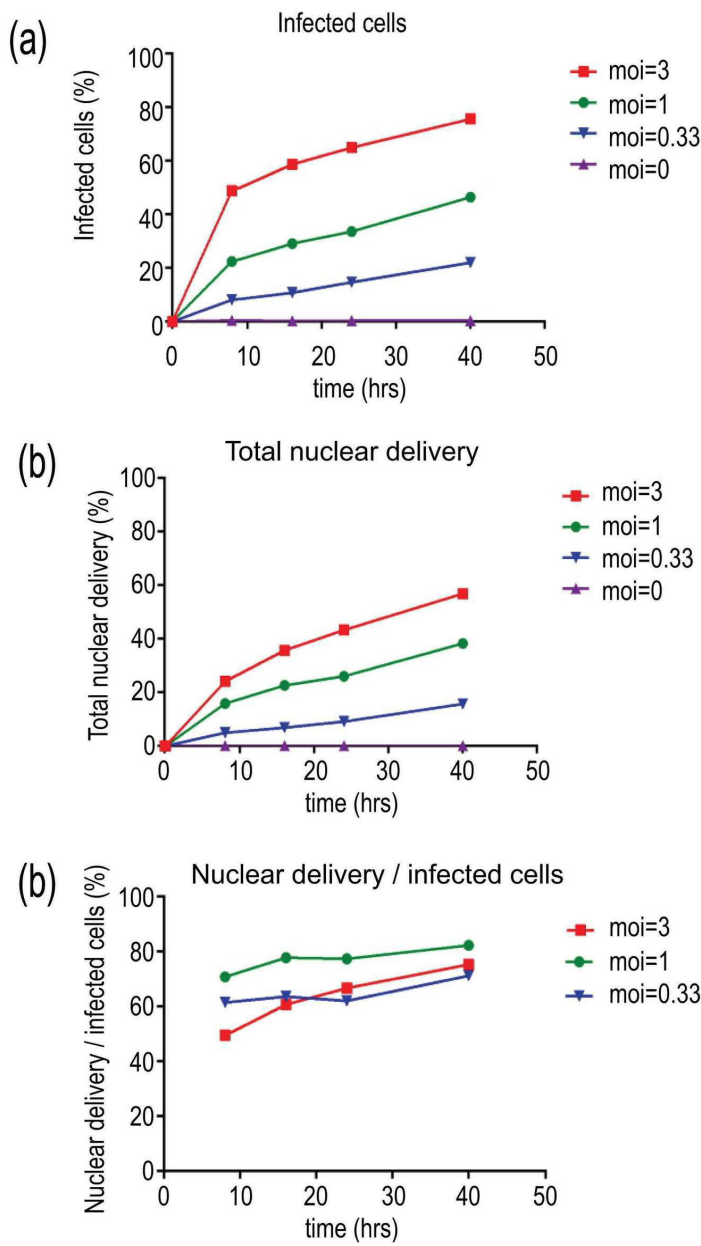
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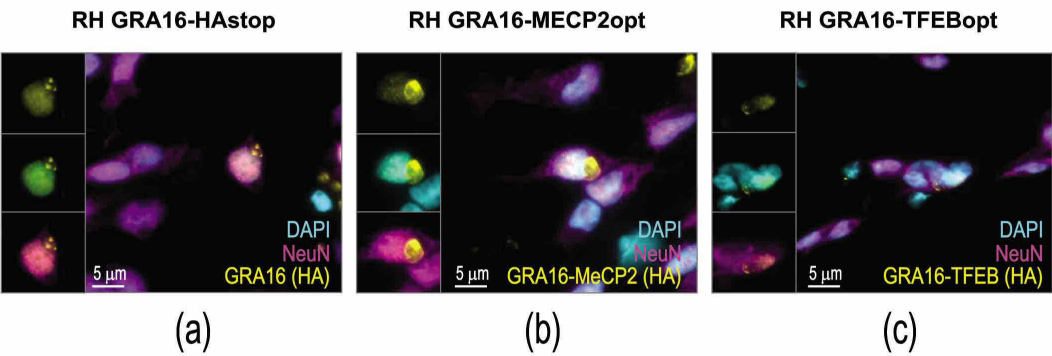
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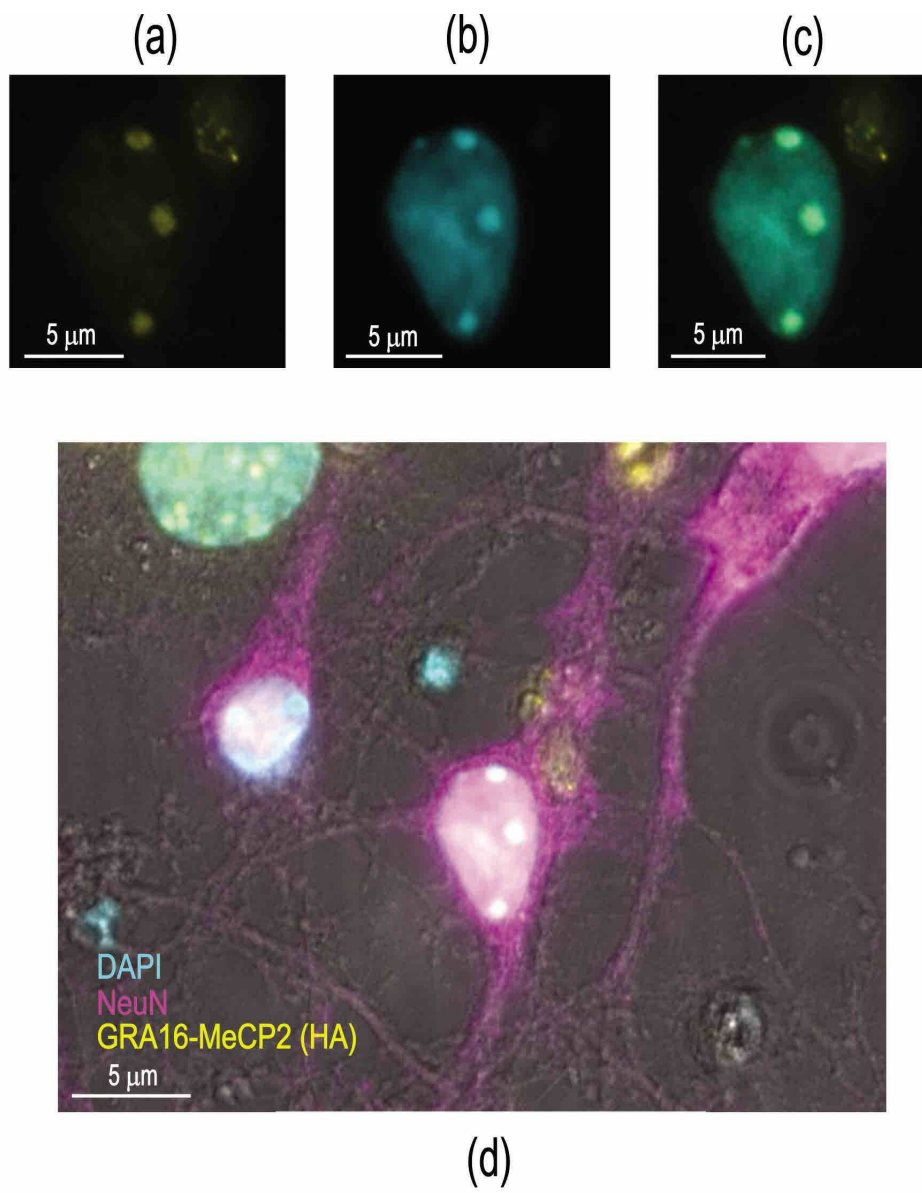
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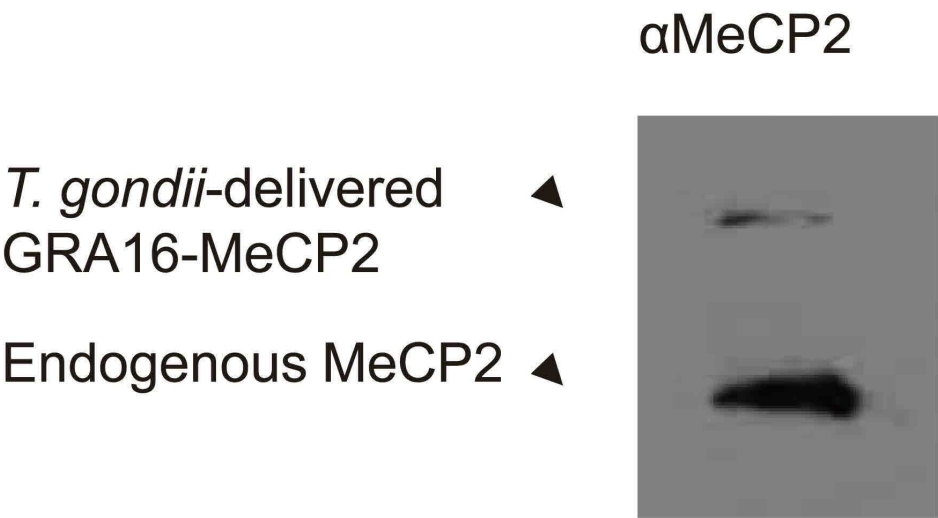
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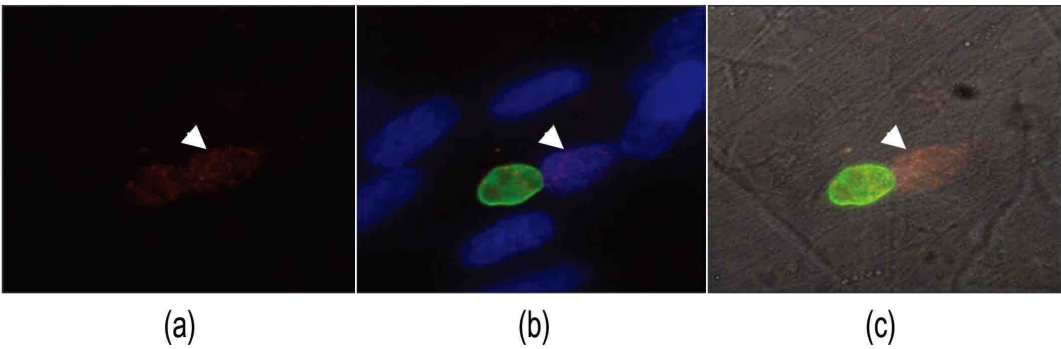
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서열 목록

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- <110> Ramot at Tel-Aviv University Ltd.
The University Court of the University of Glasgow
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- <120> ENGINEERED PARASITES FOR DELIVERING PROTEIN TO THE CENTRAL
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<212> DNA
<213> Toxoplasma gondii
<400> 7

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<210> 8

<211> 1260

<212> DNA

<213> Toxoplasma gondii

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<210> 9

<211> 1311

<212> DNA

<213> *Toxoplasma gondii*

<400> 9

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 <210> 10
 <211> 1227
 <212> DNA
 <213> *Toxoplasma gondii*
 <400> 10

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ctgggctacc agagaccaag cgaatag 1227

<210> 11
<211> 1653
<212> DNA
<213> Toxoplasma gondii
<400> 11

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<210> 12

<211> 558

<212> DNA

<213> Toxoplasma gondii

<400> 12

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ccagactttt cgagtaa 558

<210> 13

<211> 663

<212> DNA

<213> Toxoplasma gondii

<400> 13

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 aacttttttc gccgcaggcc aaaggatggg ggtgctgggg tggacaaagc ctccaagaaa 660
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<210> 14

<211> 1038

<212> DNA

<213> Toxoplasma gondii

<400> 14

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agaatgcgca aagagtga 1038

<210> 15
<211> 363
<212> DNA
<213> Toxoplasma gondii
<400> 15

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taa 363

<210> 16
<211> 675
<212> DNA
<213> Toxoplasma gondii

<400> 16

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<210> 17

<211> 711

<212> DNA

<213> *Toxoplasma gondii*

<400> 17

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<210> 18

<211> 810

<212> DNA

<213> *Toxoplasma gondii*

<400> 18

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<210> 19

<211> 957

<212> DNA

<213> Toxoplasma gondii

<400> 19

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<210> 20

<211> 903

<212> DNA

<213> Toxoplasma gondii

<400> 20

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<211> 2598

<212> DNA

<213> Toxoplasma gondii

<400> 27

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<211> 2052

<212> DNA

<213> Toxoplasma gondii

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<210> 32

<211> 1137

<212> DNA

<213> Toxoplasma gondii

<400> 32

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<210> 34

<211> 657

<212> DNA

<213> Toxoplasma gondii

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<211> 3261

<212> DNA

<213> Toxoplasma gondii

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<210> 39

<211> 993

<212> DNA

<213> Toxoplasma gondii

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<211> 660

<212> DNA

<213> Toxoplasma gondii

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<210> 41

<211> 610

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

<400> 43

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<210> 44

<211> 957

<212> DNA

<213> *Toxoplasma gondii*

<400> 44

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<211> 675
<212> DNA
<213> Toxoplasma gondii
<400> 47

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<211> 1662
<212> DNA
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<211> 2145

<212> DNA

<213> Toxoplasma gondii

<400> 50

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<211> 2634
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<213> Toxoplasma gondii
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<210> 52

<211> 873

<212> DNA

<213> Toxoplasma gondii

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<211> 2097

<212> DNA

<213> Toxoplasma gondii

<400> 53

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<210> 54

<211> 1056

<212> DNA

<213> Toxoplasma gondii

<400> 54

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<210> 55

<211> 993

<212> DNA

<213> Toxoplasma gondii

<400> 55

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<210> 56

<211> 1131

<212> DNA

<213> Toxoplasma gondii

<400> 56

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<212> DNA	
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<210> 58
<211> 597
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<213> Toxoplasma gondii
<400> 58

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<210> 59
<211> 615
<212> DNA
<213> Toxoplasma gondii
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<211> 6549

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

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<213> Toxoplasma gondii

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<212> DNA

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<211> 3000

<212> DNA

<213> Toxoplasma gondii

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<211> 1965

<212> DNA

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<210> 79
<211> 1413
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<211> 2280

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 <400> 83

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<400> 84

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<211> 882

<212> DNA

<213> Toxoplasma gondii

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<211> 1605

<212> DNA

<213> Toxoplasma gondii

<400> 87

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<211> 1428

<212> DNA

<213> Toxoplasma gondii

<400> 102

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<210> 103

<211> 1851

<212> DNA

<213> *Toxoplasma gondii*

<400> 103

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<211> 1518
<212> DNA
<213> Toxoplasma gondii
<400> 104

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<211> 1215
<212> DNA
<213> Toxoplasma gondii
<400> 105

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<210> 106

<211> 1191

<212> DNA

<213> *Toxoplasma gondii*

<400> 106

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<210> 107

<211> 1038

<212> DNA

<213> *Toxoplasma gondii*

<400> 107

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<213> Toxoplasma gondii	
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 <400> 109

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<210> 110
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 <212> DNA
 <213> *Toxoplasma gondii*
 <400> 110

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<210> 111
 <211> 489
 <212> DNA
 <213> *Toxoplasma gondii*
 <400> 111

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 <213> Toxoplasma gondii
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<210> 114

<211> 1614

<212> DNA

<213> Toxoplasma gondii

<400> 114

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<210> 115

<211> 1200

<212> DNA

<213> Toxoplasma gondii

<400> 115

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<210> 116

<211> 291

<212> DNA

<213> Toxoplasma gondii

<400> 116

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gtcttgtttg gaaagggtgaa gaactcaatt acagcttgca accttcagag gtttctggtt 180

ccattctatt ttgcgagat cccggagaga ccaataactc aggaggcgcg tcaaggagca 240

agaaaggctg ggtccttaat gccctgccgc tgtgccttg actcaggttg a 291

<210> 117

<211> 1560

<212> DNA

<213> Toxoplasma gondii

<400> 117

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<210> 118
 <211> 531
 <212> DNA
 <213> Toxoplasma gondii
 <400> 118

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<210> 119

<211> 834

<212> DNA

<213> Toxoplasma gondii

<400> 119

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<210> 120

<211> 999

<212> DNA

<213> Toxoplasma gondii

<400> 120

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<210> 121

<211> 795

<212> DNA

<213> Toxoplasma gondii

<400> 121

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<210> 122

<211> 369

<212> DNA

<213> *Toxoplasma gondii*

<400> 122

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gttgaggctc ggaaatctt caccgggattt ttacataggt tcgtcgaaga tcgacgtctc	300
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<210> 123

<211> 747

<212> DNA

<213> *Toxoplasma gondii*

<400> 123

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<210> 124

<211> 1470

<212> DNA

<213> *Toxoplasma gondii*

<400> 124

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<210> 125

<211> 615

<212> DNA

<213> Toxoplasma gondii

<400> 125

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<211> 1707	
<212> DNA	
<213> Toxoplasma gondii	
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<212> DNA

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<212> DNA

<213> *Toxoplasma gondii*

<400> 135

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<212> DNA
<213> Toxoplasma gondii
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<210> 137
 <211> 3963
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 <213> Toxoplasma gondii
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<211> 660

<212> DNA

<213> Toxoplasma gondii

<400> 138

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<210> 139

<211> 997

<212> DNA

<213> *Toxoplasma gondii*

<400> 139

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<211> 669

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1056

<212> DNA

<213> Toxoplasma gondii

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<211> 330

<212> DNA

<213> Toxoplasma gondii

<400> 143

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<210> 144

<211> 1064

<212> DNA

<213> Toxoplasma gondii

<400> 144

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<210> 145

<211> 1617

<212> DNA

<213> *Toxoplasma gondii*

<400> 145

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<210> 146

<211> 1617

<212> DNA

<213> Toxoplasma gondii

<400> 146

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<211> 1578
<212> DNA
<213> *Toxoplasma gondii*
<400> 147

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<211> 1707

<212> DNA

<213> Toxoplasma gondii

<400> 148

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<211> 1836

<212> DNA

<213> Toxoplasma gondii

<400> 152

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<210> 153

<211> 1647

<212> DNA

<213> Toxoplasma gondii

<400> 153

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<210> 154
 <211> 1608
 <212> DNA
 <213> Toxoplasma gondii

<400> 154

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<210> 155

<211> 3369

<212> DNA

<213> Toxoplasma gondii

<400> 155

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<210> 156

<211> 1308

<212> DNA

<213> *Toxoplasma gondii*

<400> 156

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<211> 2928

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1413

<212> DNA

<213> Toxoplasma gondii

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<211> 1134

<212> DNA

<213> Toxoplasma gondii

<400> 174

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<211> 480

<212> DNA

<213> Toxoplasma gondii

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 <211> 4092
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 <213> Toxoplasma gondii
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<211> 1065

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<211> 1203

<212> DNA

<213> *Toxoplasma gondii*

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<211> 3186

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1002

<212> DNA

<213> Toxoplasma gondii

<400> 201

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 <211> 2124
 <212> DNA
 <213> Toxoplasma gondii
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<211> 1827

<212> DNA

<213> Toxoplasma gondii

<400> 203

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<211> 1665

<212> DNA

<213> Toxoplasma gondii

<400> 204

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<210> 205

<211> 1300

<212> DNA

<213> Toxoplasma gondii

<400> 205

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<212> DNA

<213> Toxoplasma gondii

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<210> 207

<211> 1386

<212> DNA

<213> Toxoplasma gondii

<400> 207

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<212> DNA
<213> Toxoplasma gondii
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<213> Toxoplasma gondii
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<213> Toxoplasma gondii

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<210> 224

<211> 1896

<212> DNA

<213> Toxoplasma gondii

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<211> 396

<212> DNA

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<211> 1092

<212> DNA

<213> Toxoplasma gondii

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<211> 345

<212> DNA

<213> Toxoplasma gondii

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gctgccgaga gtaccgtcgc tggccggcgg tcgtaccaa gacatactac gcgacctgga	240

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<211> 702

<212> DNA

<213> Toxoplasma gondii

<400> 228

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gctgtgactc tctgggcagt gtttttgatt gctttttctg tgtttctcgt gctggatttc 180

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gtgcagttgc ttcttgccca ctctgtcttg agtatgtctt ggagtttcta ccgggttctg 600

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tcagcccagt tcccgctctt tgcagaagat actccgcggt ga 702

<210> 229

<211> 1440

<212> DNA

<213> Toxoplasma gondii

<400> 229

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gaggcgggtca acaaccacc gccactcgag ggagcctctg tgtcgctga aaatgccacc 240

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cctttcacgc acatacgccg cgtgtcctct gcagttcgcc gctatatcag ccgcggcacg 360

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aaagtgacgg ggaaaagcct gcttgtgagt catgcggcaa ctgtgggcgt ctcgctgtac 660

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<210> 230

<211> 681

<212> DNA

<213> Toxoplasma gondii

<400> 230

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tcctctgcct tgctcagagg caaatattat caattctgtc aggatgtgga gcacctggag 180

agagtattga aggcttccga agccgagcgg tcgagcgata tgtcttctgc agactggcgt 240

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gagcaggacg aacaactctg ttctctcgtc gggaccgtga gcaatctgaa gagcattgga 480

catgcagtcg gcgacgaagt ggatgtacac cggaagctgt tggacgattt ggacgtggac 540

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<213> *Toxoplasma gondii*
<400> 231

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<210> 232

<211> 3903

<212> DNA

<213> Toxoplasma gondii

<400> 232

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tag 3903

<210> 233

<211> 732

<212> DNA

<213> *Toxoplasma gondii*

<400> 233

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ggaagaagtc ccagcccgaa aacgggaaga ttgagagtg gagacgaagg gacatctaca 180

atgtcgccct ccgtcgcagc acgccaacag gaactagggc tgctccgtcc ggaagagagg 240

ctcattgcgg gtcaagccaa agcagcggcg ctacagactg tccatcaatt aggagcagtt 300

gttcttacc cagagcaagc taaagccgca ttgctagacg aaattctcag agccacgcaa 360

aatttggacc tcaagaagta cgagaatctc aacacggagc acaaaaaggc ctatgaacaa 420

gtccagaagg atctttcgct actgagtcg gaaacgaagg ctttgctcat tgaatatcat 480

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gcattacaat caggtgctgt gaaggctgag atccgaaaag ccaacgagca gtacaacgtc 660

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gctatgccct ag 732

<210> 234

<211> 733

<212> PRT

<213> *Toxoplasma gondii*

<400> 234

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

20 25 30

Leu Pro Ile His Ala Thr Val His Asp Ile Lys Gly Asp Trp Thr Phe

35 40 45

Tyr Leu Ser Pro Ala Val Pro Gly Asp Val Ser Asn Cys Gly Ser Pro

50 55 60

Ser Pro Asn Thr Asn Thr Ser Asn Leu Arg Glu Glu Leu Lys Asp Tyr
65 70 75 80
Lys Ser Phe Leu Ser Thr Gln Gly Gly Ile Lys Lys Glu Leu Arg Val
85 90 95
Ser Leu Thr Asp Ile Pro Val Ser Phe Ala Thr Thr Arg Thr Ala Ala
100 105 110
Ala Leu Glu Asn Pro His Arg Arg Thr Trp Lys Thr Leu Gly Val Phe
115 120 125
Asp Gly Gln Asp Lys Arg Lys Leu Val Gly Ser Trp Thr Thr Val Tyr
130 135 140
Asp Glu Gly Phe Glu Val Asp Val Gly Gly Arg Met Arg Leu Met Gly
145 150 155 160
Phe Met Lys Tyr Asn Pro Gln Asn Asn Cys Ser Ile Val Asp Gly Asp
165 170 175
Leu Glu Asn Ser Gln Gly Ile Thr Asp Cys Tyr Ala Thr Asp Pro Thr
180 185 190
Arg Thr Gln Ile Gly Trp Tyr Ile Gln Gln Ala Glu Asp Gly Ser Arg
195 200 205
Leu Ser Gly Cys Phe Tyr Ala Glu Lys Pro Lys Ala Ala Ser Ser Thr
210 215 220
Pro Ala Ala Phe Val Ala Ile Lys Glu Thr Thr Arg Val Glu Pro Ala
225 230 235 240
Ser Gly Ala Leu Ile Gly Thr Asp Leu Lys Asp Ser Thr Ser Tyr Ile
245 250 255
Ser Gln Ser Phe Val Asp Thr His Asn Ala Ser Pro Ala Ser Ser Trp
260 265 270
Arg Ala Gly Val Asn Ser Val Phe Ala Asn Met Asn Arg Arg Asp Leu
275 280 285
Ser Arg Phe Val Lys Asp Phe Gly Phe Lys Lys Met Arg Pro Ala Gly
290 295 300
Asp Ser Ala Asp Gly Leu Ser Phe Met Gln Ser Ser Thr Asp Ile Ser

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

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

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

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

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

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

Gly Tyr Val Lys Ile Ala Arg Gly Lys Asn Leu Gly Gly Ile Glu Ser
690 695 700
Gln Ala Thr Phe Ile Asp Pro Asp Phe Ser Arg Gly Gln Gly Leu Lys
705 710 715 720
Val Ala Lys Ala Ile Glu Ala Leu Lys Ser Lys Thr Met
725 730

<210> 235

<211> 753

<212> PRT

<213> Toxoplasma gondii

<400> 235

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Val Leu Phe Trp Val Asn Glu Ala Glu Pro Ala Asn Gly Asp Leu Pro

35 40 45
 Ala His Cys Leu Val Lys His Val Leu Gly Glu Trp Glu Ile Gln Glu
 50 55 60
 Gly Leu Trp Leu Pro Cys Gln Glu Glu Gly Asn Leu Thr Thr Asp Ala

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

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

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

 260 265 270
 Val Arg Lys Asn Leu Ala Ala Asp Ala Pro Trp Glu Pro Leu Asp Glu
 275 280 285

Glu Tyr Val Glu Ile Arg Gly Arg Lys Leu Arg Thr Met Glu Glu Val
 290 295 300
 Trp Ala His Ala Gly His Gln Pro Leu Leu Ile Ser Arg Gln Asn Ile
 305 310 315 320
 Glu Ser Thr His Leu Thr Leu Ser Val Arg Pro Pro Leu His Leu Leu
 325 330 335
 Ala Gly Ile Lys Pro Phe Gly Ser Pro Ala Gly Ser Asp Pro Pro Trp
 340 345 350
 Arg Thr Val Arg Asp Phe Asp Trp Ala Asn Glu Asp His Val Ala Leu
 355 360 365
 Arg Ile Gly Arg Arg Gln Ser Val Ile Pro Asp Ala Pro Asn Gln Gly
 370 375 380
 Gly Cys Gly Ser Cys Tyr Ala Ile Ala Thr Gly Thr Val Leu Thr Ser
 385 390 395 400
 Arg Leu Trp Ile Arg Tyr Ala Ala Asn Asp Asp Val Phe Gly Lys Val
 405 410 415
 Asn Val Ser Ala Phe Gln Gly Thr Ser Cys Asn Val Tyr Asn Gln Gly
 420 425 430
 Cys Gly Gly Gly Tyr Val Phe Leu Ala Leu Lys Phe Gly Gln Glu His
 435 440 445
 Gly Phe Arg Thr Glu Asp Cys Val Ser Glu Tyr His Ala Met Ala Asp
 450 455 460
 Lys His Lys Gly Ser Leu Ser Pro Asn Leu Gln Thr Cys Phe Asp Leu
 465 470 475 480
 Gly Gly Gln Leu Gly Thr Ser Ala Phe Gly Cys Gln Ala Pro Pro Ala
 485 490 495
 Arg Ala Ser Leu Pro Asp Ser Cys Asn Leu Ser Val Lys Val Thr Ser
 500 505 510
 Trp His Tyr Val Gly Gly Val Tyr Gly Gly Cys Ser Glu Asp Asp Met
 515 520 525
 Leu Arg Thr Leu Trp Glu His Gly Pro Met Ala Ala Ser Ile Glu Pro

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

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

 645 650 655
 Asn Ala Ser Lys Asp Ser Glu Arg Gly Glu Thr Leu Val Glu Ser Val
 660 665 670
 Ser Pro Val Phe Arg Gly Ser Ala Ser Gly Ser Glu Ser Gly Asn Pro
 675 680 685
 Arg Asp Ala Ala Thr Asn Glu Ser Ala Asp Met Ser Glu Ser Ala Asp
 690 695 700
 Ala Asp Ala Glu Ser Ser Ser Gly Ser Asp Asp Asp Glu Asp Gly Asp

 705 710 715 720
 Met Glu Lys Gly Asp Val Glu Ser Thr Thr Lys Gln Thr Thr Leu Phe
 725 730 735
 Arg Pro Ile Gln Arg His Gly Glu Val Leu Glu Glu Lys Arg Thr Gly
 740 745 750
 Glu

<210> 236

<211> 894

<212> PRT

<213> Toxoplasma gondii

<400> 236

Met Met Leu Leu Tyr Tyr Arg Leu Ser Ser Glu His Ala Gly Ser Tyr
1 5 10 15

Arg Gln Cys Pro Leu Ser Cys Ser Ala Leu Ser Leu Ala Glu Val Lys
20 25 30

Gln Leu Leu Ala Ala Arg Cys Gly Leu Ala Asn Glu Tyr Gly Arg Lys
35 40 45

Ile Asp Phe Arg Ile Phe Leu Ala Gly Ser Gln Val Pro Gly Gly Ala
50 55 60

Ala Glu Ala Glu Glu Leu Thr Glu Ile Val Asp Glu Asn Gln Met Ile
65 70 75 80

His Ala Tyr Ser Lys Val Val Leu Gln Arg Val Ala Ile Thr Tyr Gly
85 90 95

Gly Ser Gly Gln Ser Val Leu His Lys Ala Arg Ser Glu Leu Ser Gln
100 105 110

Glu Glu Trp Lys Thr Ala Glu Glu Arg Lys Leu Ser Ser Arg Leu Lys
115 120 125

Arg Leu Pro Pro Glu Trp Leu Cys Gly Leu Cys His Arg Val Met Thr
130 135 140

Asn Pro Val Leu Val Arg Cys Ala Thr Asn Cys Ala Gln Ser Ala Cys
145 150 155 160

His Ala Cys Leu Glu Ala His Leu Gly Pro Asn Arg Ile Cys Pro Phe
165 170 175

Cys Asn Ser Pro Phe Arg Gln Ala Ile Arg Asn Lys Arg Leu Gln Glu
180 185 190

Ile Ile Ala Leu Ala Asn Leu Ser Glu Phe Glu Ser Ala Pro Gly Ala
195 200 205

Ala Cys Ala Val Pro Gln Leu Gln Val Gln Ala Tyr Gln Ala Gly Asp
210 215 220

Pro Ala Ser Ser Ala Val Ala Pro Gly Glu Gly Ser Arg Ser Thr Asp

225 230 235 240
 Leu Ile Arg Ser Ala Cys Arg Glu Gly Pro Ser Asp Ala Ser Arg Leu
 245 250 255
 Gly Ser Gly Glu Ser His Ser Ala Thr Gly Ala Gly Val Ala Asp Arg
 260 265 270

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

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

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

 Ala Phe Gly Val Tyr Arg Ile Ser Trp Asp Asn Lys Phe Asn Pro Met
 465 470 475 480

Pro Met Leu Pro Ser Arg Lys Gln Pro Leu Cys Ser Leu Leu Gly Ala
485 490 495

His Arg Arg Gln Phe His Ser Asn Ala Ser Gly Val Pro Ala Val Pro
500 505 510

Gly Leu Leu Lys Arg Glu Val Phe Gly Gly Ala Gly Ala Gly Met Ile
515 520 525

Glu Ala Ala Val Glu Ala Ala Lys Tyr Glu Glu Val Leu Ala Cys Ile
530 535 540

Lys Asp Tyr Ala Gln Phe Gly Ser Arg Pro Ala Glu Pro Trp Gln His
545 550 555 560

Pro Ala Ser Gln Thr Ser Ser Ala Ala Ala Ala Thr Pro Gly Leu Pro
565 570 575

Lys Lys Gly Val Pro Val Gly Gly Ile Gly Gln Glu Gly Ser Arg Val
580 585 590

Pro Pro Pro Pro Pro Pro Pro Pro Gly Ser Val Gly Glu Ser Gly Phe
595 600 605

Ser Leu Ser Ser Gly Asn Gly Val Ser Val Val Glu Lys Arg Asp Val
610 615 620

Ser Ser Glu Gly Arg Gly Pro Ser Asp Gly Val Ser Ile Ser Phe Asn
625 630 635 640

Ala Arg Gly Ala Ser Leu Pro Gly Ser Leu Gly Asp Glu Arg Lys Ala
645 650 655

Leu Glu Thr Gly Val Phe Gly Ile Pro Val Ser Leu Gly Pro Pro Ser
660 665 670

Leu Gly Leu Arg Gly Asp Pro Gly Glu Pro Ser Asn Pro Tyr Leu Gly
675 680 685

Tyr Cys Ala Leu Leu Pro Leu Leu Thr Glu Glu Gln Phe Arg His Ile
690 695 700

Arg Arg Leu Gln Lys Arg Ala Met Val Leu Cys Gly Tyr Thr Gln Ser
705 710 715 720

Pro Pro Glu Ser Arg Lys Lys Arg Arg Arg Ser Gly Lys Lys Lys Arg

725 730 735
 Gly Lys His Ser Val Ser Ser His Ser Thr Gly Ser Gly Thr Leu Pro
 740 745 750
 Ser Asp Glu Pro Val Asp Gly Cys Asp Arg Val Arg Glu Glu Ala Glu
 755 760 765
 Lys Glu Gly Thr Gly Cys Met Ser Ala Asp Ala Pro Ala Val Asp Thr
 770 775 780

Asn Thr Glu Ala Leu Ser Ile Gln Asn Ala Ala Thr Ser Val Thr Arg
 785 790 795 800
 Gln Pro Leu Ser Asp Pro Asp Ser Ala Asn Ala Thr Gly Ser Arg Val
 805 810 815
 Arg Ala Gly Arg Arg Ala Leu Pro Arg Val Pro Pro Val Leu Lys Ile
 820 825 830
 Ser Arg Ile Gly Asp Lys Asn Asp Thr Asp Thr Thr Gln Asn Lys Asp
 835 840 845

Thr Gly Ser Met Gln Ser Gln Arg Ala Asn Ser Val Ile Glu Thr Cys
 850 855 860
 Ser Val Val Glu Glu Asn Thr Met Ala Lys Ile Pro Gly Ala Glu Ala
 865 870 875 880
 Lys Pro Glu Gly Val Pro Asp Asn Gly Pro Cys Glu Leu Pro
 885 890

<210> 237

<211> 219

<212> PRT

<213> *Toxoplasma gondii*

<400> 237

Met Ala Ala Arg Ala Gly Ser Ser Gly Val Ser Arg Arg Phe Leu Phe

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

Thr Pro Val Asp Leu Val Leu Asn Asp Leu Tyr Pro Leu Ile Val Lys
50 55 60
Gln Gly Leu Gly Gly Val Leu Gly Lys Ile Met Tyr Lys Val Lys Gly
65 70 75 80
Ile Met Tyr Tyr Arg Leu Ala Asp Gly Val Ala Asp Val Val Met Ser
85 90 95
Glu Leu Glu Phe Tyr Leu Phe Gly Glu Lys Gly Ala Asn Gln Ser Ser
100 105 110
Phe Lys Glu Leu Arg Lys Leu Tyr Glu Ala Tyr Met Arg Lys Phe Phe
115 120 125
Ala Glu Ser Pro Glu Asp Pro Val Asp Ala Leu Thr Thr Gly Val Trp
130 135 140
Lys Gly Leu Leu Gln Leu Phe Thr Glu Lys Leu Gln Asp Ala Phe Arg
145 150 155 160
Gly Ser Pro Lys Gly Gln Lys Met Ala Asp Leu Leu Phe Asp Ser Asn
165 170 175
Leu Thr Leu Val Lys Ser Trp Thr Asp Ala Ala His Leu Gln Ile Met
180 185 190
Gln Leu Ser Ser Ser Ser Ala Arg Ala Asn Ala Leu Arg Leu Leu Arg
195 200 205
Ala Lys Gln Lys Lys Pro Leu Ala Arg Lys Asn
210 215
<210> 238
<211> 190
<212> PRT
<213> Toxoplasma gondii
<400> 238
Met Val Arg Val Ser Ala Ile Val Gly Ala Ala Ala Ser Val Phe Val
1 5 10 15
Cys Leu Ser Ala Gly Ala Tyr Ala Ala Glu Gly Gly Asp Asn Gln Ser
20 25 30

Ser Ala Val Ser Asp Arg Ala Ser Leu Leu Gly Leu Leu Ser Gly Gly

35 40 45

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

50 55 60

Gly Asn Thr Tyr Arg Val Glu Arg Pro Thr Gly Asn Pro Asp Leu Leu

65 70 75 80

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

85 90 95

Val Asn Met Glu Glu Val Ile Asp Thr Met Lys Ser Met Gln Arg Asp

100 105 110

Glu Glu Ile Phe Phe Arg Ala Leu Asn Lys Gly Glu Thr Val Glu Glu

115 120 125

Ala Ile Glu Asp Val Ala Gln Ala Glu Gly Leu Asn Ser Glu Gln Thr

130 135 140

Leu Gln Leu Glu Asp Ala Val Ser Ala Val Ala Ser Val Val Gln Asp

145 150 155 160

Glu Met Asn Val Ile Asp Asp Val Gln Gln Leu Glu Lys Asp Lys Gln

165 170 175

Gln Leu Lys Asp Asp Ile Gly Phe Leu Thr Gly Glu Arg Glu

180 185 190

<210> 239

<211> 752

<212> PRT

<213> Toxoplasma gondii

<400> 239

Met Ser Arg Arg Met Ala Ser Arg Ser Arg Leu Leu Phe Ala Ala Phe

1 5 10 15

Cys Ala Gly Gly Val Leu Leu Gly Ala Gly Pro Pro Ala Ala Arg Gln

20 25 30

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

35 40 45

Thr Ser Ser Leu Glu Val Glu Ser Pro Glu Asn Val Gly Val His Glu
 50 55 60
 Gly Asp Glu Asn Ser Gln His Ala His Asp Glu Ile Pro Val Glu Ala
 65 70 75 80
 Ala Glu Gly Glu Glu Val Gly Ser Ser Arg Leu Ser Ser Ser Asn Arg
 85 90 95

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

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

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

 Gln Asp Pro Ala Ser Gln Arg Lys Ser Leu Gly Met Ala Ala Ser Ala

290	295	300	
Val Ala Leu Ala Phe Leu Ala Ala Gly Ala Leu Arg Ala Arg Gln Ala			
305	310	315	320
Ala Lys Ala Leu Thr His Arg Pro Ala Pro Pro Pro Ala Ser Lys Glu			
	325	330	335
Gln Gly Glu Ser Ala Gln Glu Ala Leu Glu Glu Leu Glu Pro Ala Pro			
	340	345	350
Glu Thr Gln Thr Glu Gln Val Asp Gln Ala Ser Met Pro Leu Pro Pro			
	355	360	365
Ala Pro Glu Asp Phe Asp Leu Pro Pro Met Pro Leu Pro Glu Ala Pro			
	370	375	380
Glu Asp Phe Asp Gln Ala Pro Met Pro Leu Pro Glu Ala Ala Glu Val			
385	390	395	400
Phe Asp Gln Ala Pro Met Pro Leu Pro Glu Ala Pro Glu Val Phe Asp			
	405	410	415
Gln Ala Pro Met Pro Leu Pro Glu Ala Pro Glu Val Phe Asp Gln Pro			
	420	425	430
Pro Met Pro Leu Pro Glu Ala Ala Glu Val Phe Asp Gln Ala Pro Met			
	435	440	445
Pro Leu Pro Glu Ala Pro Glu Asp Phe Asp Gln Ala Pro Glu Pro Leu			
	450	455	460
Pro Glu Ala Ala Glu Glu Phe Asp Gln Ala Pro Lys Pro Val Pro Glu			
465	470	475	480
Ala Ala Glu Glu Phe Asp Gln Pro Pro Glu Pro Leu Arg Glu Ala Ala			
	485	490	495
Glu Glu Phe Asp Gln Ala Pro Met Pro Val Pro Glu Ala Pro Glu Asp			
	500	505	510
Phe Asp Gln Ile Pro Lys Pro Val Pro Glu Ala Pro Glu Glu Phe Asp			
	515	520	525
Gln Ala Pro Met Pro Leu Pro Glu Ala Pro Glu Glu Phe Asp Gln Ile			
	530	535	540

Pro Lys Pro Val Pro Glu Ala Pro Glu Glu Phe Asp Gln Ala Pro Met
 545 550 555 560
 Pro Leu Pro Glu Ala Pro Glu Glu Ser Glu Gln Ala Pro Glu Pro Leu
 565 570 575
 Pro Glu Ala Pro Glu Glu Ser Glu Gln Ala Pro Glu Pro Leu Pro Glu
 580 585 590
 Ala Pro Glu Glu Ser Glu Gln Ala Pro Glu Pro Leu Pro Glu Ala Pro
 595 600 605

Glu Glu Ser Glu Gln Ala Pro Glu Pro Leu Pro Glu Ala Pro Glu Glu
 610 615 620
 Ser Glu Gln Ala Pro Glu Pro Leu Pro Glu Ala Pro Glu Glu Leu Asp
 625 630 635 640
 Gln Pro Pro Met Pro Leu Pro Glu Ala Pro Glu Glu Phe Asp Gln Pro
 645 650 655
 Pro Met Pro Leu Pro Glu Ala Pro Glu Glu Phe Asp Gln Ala Pro Met
 660 665 670

Pro Leu Pro Pro Ala Pro Glu Asp Phe Asp Gln Pro Ala Met Pro Leu
 675 680 685
 Pro Pro Ala Pro Glu Asp Phe Asp Gln Ala Pro Met Pro Leu Pro Gln
 690 695 700
 Ala Pro Glu Glu Leu Glu Gln Ala Pro Ala Ser His Pro Glu Glu Ala
 705 710 715 720
 Glu Gln Glu Val Pro Glu Arg Lys Thr Asp Ala Gly Ser Glu Pro Glu
 725 730 735

Lys Asp Pro Glu Thr Asn Leu Leu Glu Glu Glu Asp Glu Leu Lys Pro
 740 745 750

<210> 240

<211> 471

<212> PRT

<213> Toxoplasma gondii

<400> 240

Met Ser His Arg Met Ala Ser Arg Ser Arg Leu Leu Phe Ala Ala Phe

1 5 10 15
 Cys Ala Gly Gly Val Leu Leu Gly Ala Gly Pro Pro Ala Ala Arg Gln
 20 25 30
 Ser Ala Phe Thr Val Ala Ser Thr Val Ala Gly Gly Glu Thr Gly Tyr

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

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

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

 225 230 235 240
 Gln Leu Glu Ala Leu His Glu Met Pro Val Gly Ala Ala Ser Glu Gly
 245 250 255

Ser Ala Glu Gln Ser Ser Leu Ser His Leu Leu Ala Glu Val Val Asp
260 265 270

Ala Leu Gln Gln Pro Ser Leu Gln Asn Ile Leu Leu Gly Gly Ala Ser
275 280 285

Ala Ala Gly Leu Gly Leu Leu Gly Ala Ala Ala Ala Arg Arg Arg Arg
290 295 300

Arg Gln Ala Gln Pro Asp Thr Pro Ala Pro Pro Pro Ala Ser Glu Glu
305 310 315 320

Gln Val Glu Ser Ala Glu Glu Ala Pro Glu Lys Leu Asp Glu Ala Leu
325 330 335

Glu Thr His Pro Glu Asp Thr Gln Lys Ala Ala Pro Phe Ala Leu Leu
340 345 350

Gly Ala Pro Glu Glu Arg Glu Ser Ser Pro Glu Thr His Pro Ala Ala
355 360 365

Ser Glu Glu Ser Glu Gln Ala Pro Met Pro Leu Pro Pro Ala Pro Glu
370 375 380

Glu Leu Asp Gln Pro Pro Met Pro Leu Pro Pro Ala Pro Glu Asp Phe
385 390 395 400

Asp Gln Ala Pro Met Pro Val Pro Glu Ala Pro Glu Glu Phe Asp Gln
405 410 415

Ala Pro Met Pro Leu Pro Gln Ala Pro Glu Glu Leu Glu Gln Ala Pro
420 425 430

Ala Ser His Pro Glu Glu Ala Glu Gln Glu Val Pro Glu Arg Lys Thr
435 440 445

Asp Ala Gly Ser Glu Pro Glu Lys Asp Pro Glu Thr Asn Leu Leu Glu
450 455 460

Glu Glu Asp Glu Leu Lys Pro
465 470

<210> 241
<211> 419
<212> PRT
<213> Toxoplasma gondii

<400> 241

Met Glu Thr Gly Leu Lys Glu Arg Gly Gly Ser Arg His Ala Pro Arg

1 5 10 15

Leu Trp Arg Gly Pro Thr Arg His Leu Leu Ser Ile Arg Leu Ala Ala

20 25 30

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

35 40 45

Val Gly Ala Phe Glu Gly Gly Ile Gly Asp His Val Thr Met His Leu

50 55 60

Ile Gly Arg Ser Trp Glu Met His Gly Gly Ala Cys Phe Val Gly Arg

65 70 75 80

Pro Lys Asn Leu Val Val Asp Pro Val Phe Gly Thr Tyr Gly Arg Gln

85 90 95

Pro Gln Val Leu Glu Thr His Lys Thr Gly Pro Arg Leu Cys Lys Trp

100 105 110

Leu Asp Glu Leu Phe Glu Gln His Gln Ala Arg Arg Ser Glu Trp Glu

115 120 125

Arg Ala His Glu Ala Ala Lys Ser Gln Val Ser Met Phe Asn Ala Val

130 135 140

Arg Arg Phe Lys Asn Ala Val Thr Val Phe Pro Glu Phe Gln Val Glu

145 150 155 160

Ile Glu Ser Asn Tyr Leu Ser Leu Phe His Asp Asp Trp Tyr Gly Asn

165 170 175

Gln Leu Pro Trp Met Ala Ala Thr Val Lys Tyr Val Glu Pro Lys Asp

180 185 190

Gly Tyr Gly Val Phe Gln His Leu Asn Arg Val Phe Ala Val Pro Gly

195 200 205

Val Pro Gln Ala Gln Leu Val Phe Phe Leu Leu Tyr Pro Ala Pro Thr

210 215 220

Phe Asn Gln Pro Val Lys Leu Glu Lys Pro Gly Lys Gly Ser Ile Val

225 230 235 240

Ser Gly Phe Ile Gly Gly Thr Gly Leu Gly Ala Ser Val Ser His Met
245 250 255

Arg Arg Gly Asp Ile Gly Asp Leu Val Asp Leu Gly Arg Val Ile Tyr
260 265 270

Ala Ala Val Lys Lys Asn Phe Thr Ile Gln Ala Ser Leu Ser Asp Phe
275 280 285

Trp Leu Asn Gly Gly Asn Cys Tyr Met Gly Ser Arg Phe Lys Val Lys
290 295 300

Gly Thr Ile Gln Gly Val Thr Leu Cys Gln Phe Leu Ala Gly Glu Ala
305 310 315 320

Ser Lys Ser Val Tyr Gly Ala Tyr Lys Ala Ala Lys Leu Lys Ser Val
325 330 335

His Leu Thr Val Thr Gly Val Asp Leu Phe Asn Arg Ala Gln Pro Glu
340 345 350

Leu Arg Cys Leu Val Thr Glu Gly Leu Leu Leu His Asp Val His Asp
355 360 365

Phe Thr Val Ser Leu Ala Val Asp Thr Asn Pro Gln Leu Ile Gln His
370 375 380

Phe Gln Arg Thr Thr Arg Leu Ala Ser Met Phe Arg Trp Val Lys Leu
385 390 395 400

Ile Gly Arg Phe Leu Val Lys Ile Gly Ser Thr Phe Met Lys Pro Ser
405 410 415

Gln Lys Lys

<210> 242

<211> 436

<212> PRT

<213> Toxoplasma gondii

<400> 242

Met Arg Ala Ile Val Ala Ser Thr Gln Gln Phe Leu Arg Pro Val Gly
1 5 10 15

Ser Arg Pro Leu Ala Gly Ile Ser Ile Val Val Val Val Ala Leu Ala

20	25	30
Ile Ala Leu Gly Thr Ala Ala Asp Val Gly Arg His Val Gly Gly Phe		
35	40	45
Ser Gly Pro Phe Pro Met Thr Leu Arg Ser Gly Gln Trp Arg Leu Asp		
50	55	60
His Gly Ala Cys Phe Val Gly Lys Ala Lys Asn Leu Val Val Asp Pro		
65	70	75
80		
Leu Pro Arg Val Ser Pro Gln Gly Pro Gln Pro Leu Asp Val Thr Thr		
85	90	95
Thr Gly Ser Ala Leu Cys Trp Trp Leu Asp Ser Met Tyr Ala Ala His		
100	105	110
Met Ser Leu Lys Ala Ala Trp Glu Arg Arg His Gln Glu Ala Lys Asn		
115	120	125
Arg Thr Ser Trp Leu Asn Leu Trp Arg Arg Phe Ala Asn Trp Trp Ala		
130	135	140
Ser Phe Pro Glu Phe Gln Ile Asp Val Ser Val Leu Tyr Leu Asp Leu		
145	150	155
160		
Trp Asn Asp Asp Phe Tyr Gly His Pro Leu Pro Trp Phe Ser Ala Glu		
165	170	175
Phe Ser Tyr Thr Pro Pro Ser Gly Arg Tyr Ala Tyr Asn Leu Phe Asp		
180	185	190
Lys Leu Gln Ser His Phe Ala Ser Ala Pro Gly Thr Ala Val Gln Glu		
195	200	205
Val Phe Leu Leu Leu Ala Pro Ala Pro Thr Phe Asn Gln Pro Val Glu		
210	215	220
Lys Arg Ser Ser Ile Val Ala Arg Ala Ala Thr Val Ala Ala Gly Asn		
225	230	235
240		
Glu Leu Phe Lys Glu Ala Leu Gly His Gln Arg Val Asp Glu Val Leu		
245	250	255
Ser Met Val Pro Ala Asp Pro Phe Arg Leu Met Leu Ser Thr Ser Ala		
260	265	270

Phe Ser Phe Gln Ala Lys Ile Gly Asp Phe Trp Glu Arg Gly Leu Asp
275 280 285

Cys Met Leu Gly Ser Arg Leu Asn Leu Arg Trp Asp Gln Val Gly Thr
290 295 300

Ser Val Cys Arg Tyr Met Thr Ala Lys Ala Ser Glu Thr Gly Ser Gly
305 310 315 320

Leu Ala Ala Ser Phe Leu Asn Thr Val Glu Val Arg Val Thr Gly Met
325 330 335

Asp Phe Phe Asn His Ala Ala Pro Val Phe Lys Thr Glu Phe Ile Glu
340 345 350

Gly Ile Ile Thr Lys Arg Ala Thr Tyr Ile Pro Val Ser Met Tyr Leu
355 360 365

Ser Thr Asp Pro Thr Leu Thr His Glu Tyr Glu Ala Ala Lys Thr Val
370 375 380

Lys Arg Ala Val Gln Ala Gly Arg Val Gly Ala Ala Leu Ala Arg Gly
385 390 395 400

Leu Val Asn Phe Ala Arg Ala Thr Asn Gln Lys Ala Asp Glu Ser His
405 410 415

Glu Gly Gln Thr Lys Thr Pro Thr Ser Gly Val Arg Gly Ser Ala Gly
420 425 430

Ser Lys His Asn
435

<210> 243

<211> 408

<212> PRT

<213> Toxoplasma gondii

<400> 243

Met Gln Ala Ile Ala Arg Gly Asp Arg Ser Ser Gly Trp Ser Ser Cys
1 5 10 15

Ser Trp Leu Phe Tyr Phe Ser Phe Leu Leu Leu Thr Ser Glu Ala Val
20 25 30

Ala Ala Ala Ala Ser Leu Glu Gln Thr Ile Ser Tyr Ser Val Gln His
35 40 45

Gln Pro Gln Gln Glu Gly Ile Leu Gly Thr Gln Lys Pro Gln Thr Ala
50 55 60

Pro Thr Pro Gln Gln Leu Ile Val Pro Val Ser Tyr Leu Gly Asp Gly
65 70 75 80

Leu Ser Tyr Phe Ser Gly Val Leu Arg Arg Leu Pro Leu Asp Val Ala
85 90 95

Leu Glu Arg Leu Thr Ser Ala Arg Glu Ile Pro Thr Val Ala Gly Phe
100 105 110

Val Gln Lys Tyr Val Leu Ala Ala Gln Leu Ser Arg Ser Leu Gln Ser
115 120 125

Thr Ala Asn Gly Val Lys Lys Ile Leu Met Arg Leu Asp Ala Ala Lys
130 135 140

Asn Glu Glu Gly Phe Ile Thr Asp Leu Leu Lys Ser Ala Pro Glu Val
145 150 155 160

Gln Glu Val Leu Ser Arg Phe Leu Gly Ser Val Ala Ser Ala Leu Ala
165 170 175

Leu Leu Asp Ile Asn Gly Leu His Glu Ala Val Asp Ala Ser Leu Pro
180 185 190

Val Thr Lys Ala Val Val Met Leu Tyr Leu His Leu Val Ser Val Val
195 200 205

Pro Pro Lys Gln Arg Asp Pro Phe Ser Pro Phe Leu Leu Tyr Leu Gln
210 215 220

Asp Ala Val Gly Glu Phe Lys Ile Met Glu Asp His Val Ala Ser Val
225 230 235 240

Val Ala Gly Glu Ala Gln Glu Glu Asn Val Ile Asn Ser Gln Pro Gln
245 250 255

Gly Thr Glu Thr Ser His Arg Ala Val Val Arg Gly Gly Ile Arg Met
260 265 270

Leu Gln Ser Gly Thr Ser Glu Thr Thr Lys Leu Arg Arg Thr Trp Trp

275 280 285
 Arg Leu Phe Lys Val Ala Ala Leu Ala Val Leu Thr Met Ala Leu Leu
 290 295 300
 Lys Tyr Gly Thr Pro Arg Val Arg Ala Phe Leu Glu Arg Arg Arg Met
 305 310 315 320
 Arg Arg Gly Gly Gly Gly Asp Ser Gly Asp Phe Gly Glu Glu Gly Arg
 325 330 335
 Ser Lys Gly Asp Val Ser Thr Ser Asp Asp Met Pro Arg Glu Pro Pro
 340 345 350

 Pro Pro Tyr Val Pro Pro Met Tyr Pro Phe Ala Glu Pro Glu His Arg
 355 360 365
 Trp Ala Gly Thr Tyr Gly Thr Ser His Gly Gly Tyr Arg Val Gln Pro
 370 375 380
 Thr Ala Pro Pro Ala Pro Ala Ser Met Leu Tyr Pro Ser Leu His Arg
 385 390 395 400
 Leu Gly Tyr Gln Arg Pro Ser Glu
 405
 <210> 244
 <211> 550
 <212> PRT
 <213> Toxoplasma gondii

 <400> 244
 Met Val Thr Thr Thr Thr Pro Thr Pro Pro Gly Ala Pro Ala Val Val
 1 5 10 15
 Pro Ile Phe Asp Val Val Tyr Gln Leu Asn Pro His Val Phe Arg Ser
 20 25 30
 Arg Phe Ser Arg Arg Asn Arg Ala Arg Arg Val Ala Ser Ser Lys Ser
 35 40 45
 Arg Ser Ile Ile Arg Trp Leu Gly Tyr Leu Thr Val Leu Ala Ala Val
 50 55 60

 Ile Leu Leu Gly Ala Tyr Ala Val Arg Arg Val Ser Arg Asp Leu Ser

65	70	75	80
Asp Ser Val Arg Glu Thr Arg Arg Gly Arg Arg Ile Thr Gly Ser Val			
	85	90	95
Pro Pro Gly Thr Thr Arg Pro Arg Ser Glu Ser Cys Thr Gly Thr Gln			
	100	105	110
Val Asp Gly Gly Cys Gly Ala Asp Thr Ser Thr Asp Gly Lys Ser Glu			
	115	120	125
Ser Glu Gln Thr Glu Asn Gly Glu Asp Ser Arg Phe Ser Thr Arg Thr			
	130	135	140
Pro Ile His Val Thr Ala Ser Thr Ser Pro Phe Ala Thr Arg Lys Ala			
	145	150	155
Ala Glu Glu Arg Ser Ser Ser Pro Arg Asp Arg Lys Val Pro Glu Gly			
	165	170	175
Ala Gln Leu Pro Thr Ser Ser Thr Pro His Ala Gln Arg Lys Asp Ser			
	180	185	190
Gly Ser Asp Ser Arg Asn Pro Ser Thr Leu Ile Pro Ser Pro Gly Thr			
	195	200	205
Asn Thr Phe Asn Met Asn Phe Tyr Ile Ile Gly Ala Gly Ser Ser Ala			
	210	215	220
Leu Asp Phe Ile Phe Pro His Thr Pro Asp Ala Gln Ala Thr Val Val			
	225	230	235
Ser Pro Pro Arg Ser Ala Ala Ala Ala Pro Thr Val Glu Thr Val Pro			
	245	250	255
Arg Val Arg Thr Tyr Ser Thr Pro Thr Thr Leu Thr Leu Pro Thr Ala			
	260	265	270
Pro Ala Thr Ala Thr Ser Asn His Met His Ala Ser Ala Thr Pro Ser			
	275	280	285
Pro Pro Glu Arg Pro Gln Asn Phe Arg Gly Gly Leu Met Arg Gln Asn			
	290	295	300
Gly Met Val Glu Gly Thr Ser Leu Thr Thr Thr Glu Ala Gly Met Pro			
	305	310	315
			320

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

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

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

Ser Val Pro Thr Glu Arg Thr Ile Ser Asp Pro Gly Pro Gln Arg Ala
 515 520 525
 Gly Ala Ala Gln Ala Asp Gly Ile Gly Ala Gly Gly Pro Arg Asp Thr
 530 535 540
 Gln Ser Ala Val Thr Pro
 545 550

<210> 245

<211> 185

<212> PRT

<213> *Toxoplasma gondii*

<400> 245

Met Phe Ala Val Lys His Cys Leu Leu Val Val Ala Val Gly Ala Leu

1 5 10 15

Val Asn Val Ser Val Arg Ala Ala Glu Phe Ser Gly Val Val Asn Gln

20 25 30

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

35 40 45

Val Gly Gly Lys Gly Glu His Thr Pro Pro Leu Pro Asp Glu Arg Gln

50 55 60

Gln Glu Pro Glu Glu Pro Val Ser Gln Arg Ala Ser Arg Val Ala Glu

65 70 75 80

Gln Leu Phe Arg Lys Phe Leu Lys Phe Ala Glu Asn Val Gly Gln His

85 90 95

Ser Glu Lys Ala Phe Lys Lys Ala Lys Val Val Ala Glu Lys Gly Phe

100 105 110

Thr Ala Ala Lys Thr His Thr Val Arg Gly Phe Lys Val Ala Lys Glu

115 120 125

Ala Ala Gly Arg Gly Met Val Thr Val Gly Lys Lys Leu Ala Asn Val

130 135 140

Glu Ser Asp Arg Ser Thr Thr Thr Thr Gln Ala Pro Asp Ser Pro Asn

145 150 155 160

Gly Leu Ala Glu Thr Gln Ala Pro Val Glu Pro Gln Gln Arg Ala Ala

165 170 175

His Val Pro Val Pro Asp Phe Ser Gln

180 185

<210> 246

<211> 220

<212> PRT

<213> *Toxoplasma gondii*

<400> 246

Met Asp Arg Thr Ile Cys Pro Phe Phe Ile Gln Ser Phe Thr Met Ser
1 5 10 15

Thr Ala Leu Lys Arg Leu Ile Pro Phe Leu Val Pro Phe Val Val Phe
20 25 30

Leu Val Ala Ala Ala Leu Gly Gly Leu Ala Ala Asp Gln Pro Gly Asn
35 40 45

His Gln Ala Leu Ala Glu Pro Val Thr Gly Val Gly Glu Ala Gly Val
50 55 60

Ser Pro Val Asn Glu Ala Gly Glu Ser Tyr Ser Ser Ala Thr Ser Gly
65 70 75 80

Val Gln Glu Ala Thr Ala Pro Gly Ala Val Leu Leu Glu Ala Ile Asp
85 90 95

Ala Glu Ser Asp Lys Val Asp Asn Gln Ala Glu Gly Gly Glu Arg Met
100 105 110

Lys Lys Val Glu Glu Glu Leu Ser Leu Leu Arg Arg Glu Leu Tyr Asp
115 120 125

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

Thr Ser Ala Leu Ile Ala Gly Arg Met Phe Ser Ser Thr Leu Arg Ala
145 150 155 160

Ala Val Pro Trp Tyr Ala Val Ala Phe Asn Ala Ile Val Ala Ala Tyr
165 170 175

Tyr Ile Arg Lys Val Leu Thr Tyr Arg Arg Arg Val Met Thr Lys Arg
180 185 190

Gln Pro Phe Met Ser Ser Val Lys Asn Phe Phe Arg Arg Arg Pro Lys
195 200 205

Asp Gly Gly Ala Gly Val Asp Lys Ala Ser Lys Lys
210 215 220

<210> 247

<211> 345

<212> PRT

<213> Toxoplasma gondii

<400> 247

Met Gln Gly Thr Trp Phe Ser Leu Phe Val Val Val Met Val Ser His

1 5 10 15

Leu Ala Phe Gly Gly Glu Cys Ser Phe Gly Ser Tyr Leu Ala Asp Met

20 25 30

Ala Gly Leu Thr Gly Arg Glu Asp Lys Glu His His Ala Ala Lys Lys

35 40 45

Arg Tyr Tyr His Ser Met Tyr Gly Asn Lys Thr Pro Tyr Pro Tyr Ala

50 55 60

Asp Gly Gln Gln Gly Ser Pro Pro Pro Gln Gly Gln Leu Leu Ile Ile

65 70 75 80

Gln Asn Pro Asp Gly Ser Phe Met Ile Val Asp Gln Gln Gly Val Pro

85 90 95

Gln Ala Pro Gln Ala Ala Gly Gly Pro Gly Ser Pro Met Asn Gly Gly

100 105 110

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

115 120 125

Pro Gly His Pro Val Gln Ala Ile Pro Gln Gln Pro Leu Arg Thr Gln

130 135 140

Ala Thr Ala Thr Tyr Tyr His Pro Ala Ala Ala Pro Pro Pro Gly Pro

145 150 155 160

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

165 170 175

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

180 185 190

Tyr Ser Tyr Pro Gly Thr Thr Ser Thr Pro Thr Pro Pro Arg Pro Ala

195 200 205

Ser Tyr Gly Tyr Pro Ala Phe Pro Ala Phe Pro Arg Leu Pro Ala Phe

210 215 220

Ser Asp Ser Val Ser Val Ser Thr Glu Asp Ser Gly Leu Thr Val Val

225 230 235 240

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

 Ser Thr Ala Pro Ala Glu Ala Gly Lys Thr Glu Leu Asp Asp Gly Tyr
 305 310 315 320
 Arg Pro Pro Pro Phe Asn Pro Arg Pro Ser Pro Tyr Ala Glu Leu Leu
 325 330 335
 Lys Asp Leu Glu Arg Met Arg Lys Glu
 340 345

 <210> 248
 <211> 120
 <212> PRT
 <213> Toxoplasma gondii
 <400> 248

 Met Ala Ser Val Lys Arg Val Val Val Ala Val Met Ile Val Asn Val
 1 5 10 15

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

 Ala Ala Val Val Ala Val Val Ser Leu Leu Arg Leu Leu Arg Arg Arg

85 90 95
 Arg Arg Arg Ala Ile Gln Glu Glu Ser Lys Glu Ser Ala Thr Ala Glu
 100 105 110
 Glu Glu Glu Val Ala Glu Glu Glu
 115 120
 <210> 249
 <211> 224
 <212> PRT
 <213> Toxoplasma gondii
 <400> 249
 Met Ala His Gly Gly Ile Tyr Leu Arg Gln Lys Arg Asn Phe Cys Pro
 1 5 10 15

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

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

 Lys Arg Thr Gln Lys Arg His Arg Leu Ile Gly Ala Val Val Leu Ala
 145 150 155 160
 Val Ser Val Ala Met Leu Thr Ala Phe Phe Leu Arg Arg Thr Gly Arg
 165 170 175

Arg Ser Pro Gln Glu Pro Ser Gly Gly Gly Gly Gly Asn Asp Ala Gly
 180 185 190
 Asn Asn Ala Gly Asn Gly Gly Asn Glu Gly Arg Gly Glu Gly Gly Glu
 195 200 205

 Asp Asp Arg Arg Pro Leu His Pro Gly Ser Val Asn Glu Phe Asp Phe
 210 215 220
 <210> 250
 <211> 236
 <212> PRT
 <213> *Toxoplasma gondii*
 <400> 250
 Met Ala Arg His Ala Ile Phe Phe Ala Leu Cys Val Leu Gly Leu Val
 1 5 10 15
 Ala Ala Ala Leu Pro Gln Phe Ala Thr Ala Ala Thr Ala Ser Asp Asp
 20 25 30
 Glu Leu Met Ser Arg Ile Arg Asn Ser Asp Phe Phe Asp Gly Gln Ala

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

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

Leu Pro Glu Leu Thr Glu Gln Gln Gln Thr Gly Glu Glu Pro Leu Thr

165 170 175

Thr Gly Gln Asn Val Ser Thr Val Leu Gly Phe Ala Ala Leu Ala Ala

180 185 190

Ala Ala Ala Phe Leu Gly Met Gly Leu Thr Arg Thr Tyr Arg His Phe

195 200 205

Ser Pro Arg Lys Asn Arg Ser Arg Gln Pro Ala Leu Glu Gln Glu Val

210 215 220

Pro Glu Ser Gly Lys Asp Gly Glu Asp Ala Arg Gln

225 230 235

<210> 251

<211> 269

<212> PRT

<213> Toxoplasma gondii

<400> 251

Met Ala Leu Pro Leu Arg Val Ser Ala Thr Val Phe Val Val Phe Ala

1 5 10 15

Val Phe Gly Val Ala Arg Ala Met Asn Gly Pro Leu Ser Tyr His Pro

20 25 30

Ser Ser Tyr Gly Ala Ser Tyr Pro Asn Pro Ser Asn Pro Leu His Gly

35 40 45

Met Pro Lys Pro Glu Asn Pro Val Arg Pro Pro Pro Pro Gly Phe His

50 55 60

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

65 70 75 80

Met Pro Gln Pro Glu Val Pro Pro Leu Gln His Pro Pro Pro Thr Gly

85 90 95

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

100 105 110

Gly Met Pro Gln Pro Glu Ile Pro Pro Val His Arg Pro Pro Pro Pro

115 120 125

Gly Phe Arg Pro Glu Val Ala Pro Val Pro Pro Tyr Pro Val Gly Thr
130 135 140

Pro Thr Gly Met Pro Gln Pro Glu Ile Pro Ala Val His His Pro Phe
145 150 155 160

Pro Tyr Val Thr Thr Thr Thr Thr Ala Ala Pro Arg Val Leu Val Tyr
165 170 175

Lys Ile Pro Tyr Gly Gly Ala Ala Pro Pro Arg Ala Pro Pro Val Pro
180 185 190

Pro Arg Met Gly Pro Ser Asp Ile Ser Thr His Val Arg Gly Ala Ile
195 200 205

Arg Arg Gln Pro Ala Thr Ala Thr Thr Thr Thr Thr Thr Arg Asn Val
210 215 220

Leu Leu Arg Thr Ala Ile Leu Ala Ala Ala Ala Ala Thr Leu Ile Ala
225 230 235 240

Leu Phe Arg Gln Arg Pro Leu Phe Thr Glu Gly Val Arg Met Phe Pro
245 250 255

Asp Phe Gln Tyr Arg Phe Thr Val Gln Thr Thr Gln Asn
260 265

<210> 252
<211> 318
<212> PRT
<213> Toxoplasma gondii
<400> 252

Met Arg Ser Leu Lys Ser Ile Val Val Pro Leu Ser Ala Ala Leu Val
1 5 10 15

Ala Ala Ala Glu Leu Asp Leu Phe Leu Gly Glu Ser Gly Val Tyr Leu
20 25 30

Phe Gly Lys Ala Ser Glu Ser Asp Val Ala Leu Lys Val Pro Glu Asp
35 40 45

Pro Val Pro Glu Glu Pro Arg Arg Glu Pro Glu Lys His Val Asp Leu
50 55 60

Phe Gly Glu Asp Trp Lys Gln Phe Gly Gly Ser Gly Phe Gly Asp Phe

65					70					75					80	
Ser	Lys	Val	Glu	Phe	Glu	Asn	Leu	Phe	Ser	Gln	Val	His	Glu	Met	Met	
				85					90					95		
Arg	Arg	Leu	Met	Gly	Arg	Gly	Val	Asp	Gly	Phe	Gly	Pro	Ser	Leu	Leu	
				100					105					110		
Gly	Asp	Ser	Pro	Gly	Phe	His	Phe	Pro	Arg	Leu	Arg	Ala	Leu	Gln	Pro	
				115					120					125		
Lys	Thr	Lys	Leu	Glu	Lys	Thr	Gly	Thr	Cys	Gln	Tyr	Val	Val	Thr	Trp	
				130					135					140		
Ala	Pro	Glu	Val	Thr	Ala	Glu	Asn	Val	Arg	Val	Ile	Leu	His	Leu	Gln	
				145					150					155		
Arg	Arg	Gln	Val	Glu	Val	Gln	Tyr	Arg	Ala	Ala	Thr	Arg	Arg	Asp	Glu	
				165					170					175		
Lys	Thr	Glu	Gly	Gly	Glu	Ser	His	Ser	Met	Ser	Lys	Glu	Gln	Ser	Ser	
				180					185					190		
Gln	Leu	Met	Ser	Val	Asp	Pro	Gln	Cys	Ile	Met	Thr	Arg	Glu	Val	Val	
				195					200					205		
Ala	Gln	Lys	Leu	Ala	Gly	Trp	Thr	Asp	Asn	Thr	His	Thr	Ala	Thr	Ala	
				210					215					220		
Gly	Thr	Pro	Lys	Lys	Leu	Leu	Ile	Ser	Phe	Pro	Ser	Pro	Asp	His	Ile	
				225					230					235		
Lys	Glu	Met	Val	Lys	Glu	Gly	Tyr	Leu	Pro	Asp	Asn	Ala	Leu	Glu	Arg	
				245					250					255		
Val	Leu	Ala	Gly	Asp	Phe	Glu	Gly	Phe	Ser	Arg	Thr	Gln	Met	Cys	Leu	
				260					265					270		
Val	Ser	Gly	Arg	Asn	Arg	Thr	Glu	Cys	Ala	Phe	Ala	Glu	Gly	Gln	Glu	
				275					280					285		
Val	Glu	Leu	Glu	Glu	Lys	Pro	Leu	Pro	Ser	Asp	Ser	Ser	Pro	Val	Thr	
				290					295					300		
Ser	Val	Glu	Leu	Pro	Arg	Leu	Ser	Gln	Glu	Asp	Arg	Gly	Leu			
				305					310					315		

<210> 253

<211> 300

<212> PRT

<213> *Toxoplasma gondii*

<400> 253

Met Lys Ser Gly Ser Cys Pro Phe Thr Phe Ser Pro Thr Leu Ser His

1 5 10 15

Pro Leu Glu Ile Ala Trp Arg Ala Arg Pro Leu Gln Trp Pro Glu Ile

20 25 30

Glu Arg Gln Pro Glu Pro Ala Ala Pro Cys Gly Ala Leu Tyr Pro Ala

35 40 45

Ser Arg Val Leu Ser Phe Ser Pro Thr Met Arg Ala Ile Arg Ser Val

50 55 60

Val Gly Leu Pro Val Met Gly Ala Ala Val Phe Leu Gly Leu Leu Ser

65 70 75 80

Gly Glu Leu Pro Asn Ser Ser Val Leu Pro Val Pro Glu Val Ala Ser

85 90 95

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

100 105 110

Tyr Ala Glu Val Ala Lys Val Glu Ala Leu Thr Asn Met Ile Ser Thr

115 120 125

Pro Ile Glu Leu Phe Val Lys Asp Val Trp Gln Gln Leu Phe His Lys

130 135 140

Ser Gly Lys Pro Val Trp Glu Asn Met Leu Phe Lys Phe Gly Ser Met

145 150 155 160

Ile Arg His Arg Ala Ala His Lys Ala Thr Leu Val Ile Met Trp Glu

165 170 175

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

180 185 190

Lys Lys Leu Glu Thr Lys Phe Glu Thr Tyr Leu Arg Glu Trp Trp Met

195 200 205

Thr Val Pro Glu Asp Pro Trp Ala Ala Leu His Ala Gly Ala Trp Lys
210 215 220

Ser Leu Leu Lys Leu Tyr Asn Glu Asp Leu Glu Pro Leu Leu Arg Gly
225 230 235 240

Ser Pro Lys Leu Lys Asp Leu Glu Ser Ile Leu Phe Asp Ser Lys Leu
245 250 255

Ala Thr Ile Arg Arg Trp Thr Asp Glu Ala His Ile Glu Val Met Lys
260 265 270

Gly Arg Thr Ser Asn Met Val Pro Arg Leu Glu Ala Leu Ser Ala Lys
275 280 285

Met Ala Val Lys Gln Lys Ala Met Gln Gly Lys Gln
290 295 300

<210> 254
<211> 505
<212> PRT
<213> Toxoplasma gondii
<400> 254

Met Tyr Arg Asn His Ser Gly Ile Arg Leu Ala Cys Arg Leu Phe Glu
1 5 10 15

Val Gly Ala Leu Val Leu Ala Leu Glu Asn Val Ser Gly Ile His Arg
20 25 30

Phe Val Ala Gly Ile Glu Trp Asn Glu Gly Lys Glu Asp Phe Gln Tyr
35 40 45

Thr Thr Ser Pro Trp Val Ile Pro Pro Asp Gly Leu Val Ser Arg Arg
50 55 60

Leu Ala Glu Glu Pro Pro Arg Lys Arg Leu Arg Lys Thr Asn Lys Ser
65 70 75 80

Asp Arg Asp Ser Asp Ser Ala Gln Gly Ser Arg Thr Thr Ser Pro Gly
85 90 95

Ser Leu Gly Gly Phe Gly Ala Thr Gly Gly Arg Val Ala Ala Pro Arg
100 105 110

Ile Arg Ser Gly Val Val Ala Ser Glu Ala Ile Arg Gly Thr Ile Trp

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

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

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

 Ser Gly Gly Lys Arg Lys Pro Asp Asp Glu Asp Asp Phe Asp Cys Ser
 485 490 495
 Arg Ala Lys Arg Lys Asn Asp Gln Met
 500 505

 <210> 255
 <211> 413
 <212> PRT
 <213> Toxoplasma gondii
 <400> 255

 Met His Ser Arg Asn Cys Val Gly Gly Ser Phe Tyr Asp Gly Ala Val
 1 5 10 15
 Cys Cys Ser Pro Pro Ser Arg Ala Phe Gly Asn Met His Asn Leu Val
 20 25 30

 Leu Val Leu Leu Ala Phe Leu Ser Ser Trp Glu Asp Asn Glu Thr Arg
 35 40 45
 Arg Gly Asp Val Val Glu Gln Gln Asn Pro Phe Arg Leu Ala Ile His
 50 55 60
 Gly Lys Thr Glu Arg Asp Arg Asp Gly Asn Cys Thr Gln His Gly Val

65	70	75	80
Arg Ser Asn Asp Phe Arg Phe Val Asp Glu Gly Asp Met Ser Ala Glu			
	85	90	95
Val Gly Arg Gly Leu Ala Leu Gln Lys His Val Arg Val Pro Leu Gln			
	100	105	110
Ala Ser Ile Ala Arg Arg Leu Ser Asp Arg Glu Ser Glu Lys Arg Ser			
	115	120	125
Gln Gly Ser Asp Asn Gly Asn Gly Thr Thr Pro Pro Leu Pro Pro Arg			
	130	135	140
Arg Thr Pro Ser Pro Arg Pro Ser Gly Ala Ser Gly Val Val Gln Gln			
145	150	155	160
Gly Ala Ala Gly Val Gly Thr Pro Thr Met Leu Gly Thr Gly Gly Gln			
	165	170	175
His Leu Ser Asp Gln Gly Ala Thr Gly Ser Val Ala Pro Ser Val Gln			
	180	185	190
Ser Ser Ser Ser Ser Ala Val Ser Val Glu Gly Ala Leu Pro Leu Ile			
	195	200	205
Gln Phe Phe Gly Ser Arg Ser Ser Ser Pro Glu Val Pro Leu Cys His			
	210	215	220
Ala Cys His Thr Val Glu Ala Ala Val Gly Val Leu Gln Ser Ile Arg			
225	230	235	240
His Arg Arg Arg Ala Gly Ala Arg Glu Ala Ala Glu Arg Ile Ala Ala			
	245	250	255
Leu Glu Ser Gln His Ala Leu Leu Val Ser Ser Ser Thr Gln Gly Glu			
	260	265	270
His Ser Gln Gly Ala Arg Pro Ser Asp Ile Leu Val Ser His Arg Ala			
	275	280	285
Leu Gln Arg Ala Arg Arg Glu Ala Thr Arg Gln Glu Glu Thr Leu Arg			
	290	295	300
Gly Glu Glu Ala Ser Leu Glu Ala Phe Ile Arg Val Ala Ser Glu Lys			
305	310	315	320

Arg Glu Arg Glu Gly Gln Arg Ser Leu Glu Val Leu Arg Gln Arg Val
325 330 335

Glu Asn Gln Thr Ala Glu Leu Ala Val Leu Arg Val Glu Ala Ala Leu
340 345 350

Glu Arg Gln Arg Glu Met Val Glu Leu Glu Arg Arg Arg Gly Asp Leu
355 360 365

Leu Ala Leu Ala Leu Val Ala Glu Asp Asp Glu Glu Tyr Leu Arg Leu
370 375 380

Ser Ala Glu Glu Glu Ala Val Gln Arg Gln Ile Glu Gln Leu Ala Glu
385 390 395 400

Glu Thr Arg Arg Pro Arg Arg Gly Arg Arg Lys Pro Ala
405 410

<210> 256

<211> 501

<212> PRT

<213> Toxoplasma gondii

<400> 256

Met Glu Arg Ile Val Val Leu Val Ser Ala Thr Phe Leu Tyr Ala Val
1 5 10 15

Val Gly Arg Ala Ser Met Ala Ser Ala Glu Met Ala Ser Arg Thr Lys
20 25 30

Arg Leu Tyr Ile Leu Ile Ser Phe His Cys Val Leu Ser Glu Ile Leu
35 40 45

Ser Gly His Ala Ala Ala Glu Ala Thr Ser Lys Pro Ala Arg Gln Pro
50 55 60

Glu Gly Ala Gly Arg Ser Ala Ser Pro Ser Pro Ser Leu Ser His Ala
65 70 75 80

Ser Gly Val Val Val Gly Ala Arg Arg Arg Arg Leu Ala Glu Gly Ser
85 90 95

Pro Gly Glu Glu Pro Asp Pro Val Arg Glu Leu Leu Asp Leu Glu Glu
100 105 110

Glu Leu Glu Asn Leu His Ala Leu Arg Phe Lys Glu Arg Leu Ala Phe

115 120 125

Arg Gln Cys Val Arg His Trp Gly Thr Phe Asp Ala Tyr Cys Arg Glu

130 135 140

His Ser Arg Trp Lys Ser Lys Met Ala Ala Asp Pro Glu Arg Met Arg

145 150 155 160

Asp Ala Phe Glu Arg Lys Gln Ala Arg Lys Gln Thr Ala Cys Asn Val

165 170 175

Trp Ala Ala Leu Leu Asp Ala Ala Arg Glu Lys Ile Glu Ala Met Asp

180 185 190

Arg Glu Arg Lys Gln Met Gln Ser Arg Leu Thr Lys Glu Gln Thr Ser

195 200 205

Leu Tyr Leu Ala Ala Lys Ala Ala Arg Gly Arg Ala Gln Ile Gly Gly

210 215 220

Asp Ser Ser His Thr Ala Val Gly Glu Ala Ala Val Gly Ala Ser Thr

225 230 235 240

Arg Pro Pro Ala Thr Gly Glu Ser Pro Thr Pro Gly Asp Ser Gly Ser

245 250 255

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

260 265 270

Leu Ala Leu Gly Lys Trp His Arg Ser Arg Arg Ala Leu Lys Asp His

275 280 285

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

290 295 300

Arg Asp Arg Ala Gly Glu Ala Arg Ala Val Trp Glu Ala Gln His Leu

305 310 315 320

Gln Leu Glu Gln Asp Ala Lys Gln Ala Arg Glu Ala Val Asp Lys Phe

325 330 335

Arg Glu Arg Leu Arg Glu Leu Asn Ala Gln Lys Ala Ala His Glu Lys

340 345 350

Ala His Gly Val Ser Pro Gly Arg Arg Gly Cys Glu Asn Ala Pro Val

355 360 365
Arg Phe Ser Arg Leu Gly Ile Thr Val Asp Ala Arg Glu Ala Ala Ile

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

435 440 445
Thr Gly Ala Glu Thr Lys Ala Ser Thr Ser Thr Ser Gly Leu Ala Gly
450 455 460
Pro Ser Glu Phe Gln Asn Glu Arg Val His Cys Ala Leu Tyr Gly Thr
465 470 475 480
Asp Glu Ser Val Leu Asp Ser Ser Glu Ser Leu Ala Lys Pro Cys Phe
485 490 495
Val Lys Trp His Gly
500

<210

> 257

<211> 542

<212> PRT

<213> Toxoplasma gondii

<400> 257

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

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

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

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

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

Glu Met Pro Asn Gln Gly Ser Thr Ser Gln Ser Gly Ala Val Ala Ser

305 310 315 320

Arg Lys Arg Pro Ala Gly Gly Ala Asn Gly Pro Asp Lys Arg Arg Arg

325 330 335

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

340 345 350

Leu Ser Ser Leu Thr Glu Lys Gly Ser Thr Ala Phe Ser Thr Arg Pro

355 360 365

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

370 375 380

Met Leu Leu Asp Thr Pro Ser Tyr Pro Ile Ser Ser Val Val Ser Ser

385 390 395 400

Pro Pro Pro Ala Arg Lys Ser Ser Thr Ser Ser Ser Gln His Leu Glu

405 410 415

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

420 425 430

Asn Pro Trp Ser Thr Lys Thr Gly Leu Leu Glu Arg Arg Gly Val Ser

435 440 445

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

450 455 460

Asn Pro Ala Asp Ser Arg Lys His Ser Thr Val Thr Pro Gln Thr Thr

465 470 475 480

Pro Pro Ala Arg Lys Ser Ser Thr Ser Ser Ser Gln His Leu Glu Ala

485 490 495

Arg Leu Ser Gln Ser Arg Gly Pro Pro Arg Thr Arg Pro Pro Phe Asn

500 505 510

Pro Trp Ser Thr Lys Thr Gly Leu Leu Glu Arg Arg Gly Val Ser Glu

515 520 525

Leu Pro Pro Leu Arg Ile Val Lys Pro Pro Thr Lys Gly Asn

530 535 540

<210> 258

<211> 315

<212> PRT

<213> Toxoplasma gondii

<400> 258

Met Lys Arg Phe Trp Leu Cys Ala Leu Leu Ser Leu Leu Glu Phe Ser

1 5 10 15

Trp Gly Cys Asn Ser Leu Gly Pro Ser Leu Pro Ser Phe Gln Val Ala

20 25 30

Glu Gly Ala Phe Phe Gly Arg Leu Arg Asn Trp Phe Gly Lys Asn Ala

35 40 45

Glu Gln Lys Pro Glu Val Pro Val Ala Pro Val Ala Asp Asp Asp Ala

50 55 60

Gly Ser Glu Glu Glu Ser Ser Ser His Tyr Gly Val Lys Thr Leu Thr

65 70 75 80

Ala Ser Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Val Thr

85 90 95

Ser Thr Lys Pro Glu Gly Val Trp Glu Glu Glu Tyr Asp Ser Met Glu

100 105 110

Val Pro Tyr Thr Pro Leu Pro Pro Leu Arg Gly Ile Gly Leu Leu Gly

115 120 125

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

130 135 140

Leu Met Gly Gly Ile Gly Val Val Gln Tyr Ile Asn Ser Val Val Gln

145 150 155 160

Arg Met His Ala Arg Arg Ala Ala Asp Ala Ala Leu Arg Arg Phe Glu

165 170 175

Asp Arg Arg Glu Leu Val Arg Ala Arg Arg Arg Arg Arg Trp Ile Gln

180 185 190

Thr Phe Tyr Ser His Asn Ala Leu Gln Gln Asp Arg Ala Thr Arg Lys

195 200 205

Gly Glu Thr Gln Asn Glu Glu Ser Asn Ala Thr Leu Ala Asn Ser Ser

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

 Lys Arg Thr Asn Pro Ser Glu Thr Arg Glu Val Pro Lys Thr Arg Leu
 275 280 285
 Arg Lys Pro Thr Glu Arg Asn Thr Lys Ala Gln Val Lys Lys Lys Thr
 290 295 300
 Pro Arg Glu Asn Leu Pro Glu Phe Asp Arg Asn
 305 310 315
 <210> 259
 <211> 1904
 <212> PRT
 <213> Toxoplasma gondii
 <400> 259
 Met Lys Val Arg Ser Val Leu Ser Val Gly Phe Trp Ala Ala Ala Cys
 1 5 10 15

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

 Ser Pro Gly Glu Asp Thr Ser Gly Thr Gln Leu Pro Gln Gly Ser Thr
 85 90 95
 Gln Cys Asp Trp Arg Lys Cys Gly Thr Arg Glu Gln Val Glu Lys Thr
 100 105 110

Ile Lys Glu Ile Glu Glu Glu Trp Gly Asp Glu Ser Ala Phe Val Thr
115 120 125

Arg Lys Leu Gln Arg Arg Met Ser Thr Pro Cys Arg Leu Lys Lys His
130 135 140

Pro Cys Pro Lys Gln Arg Leu Thr Trp Glu Arg Glu Ile Arg Glu Glu
145 150 155 160

Phe Arg Arg Val Ala Pro Arg His Leu Glu Arg Ala Ala Thr Leu Arg
165 170 175

Lys Ala Leu Glu Gln Arg Pro Pro Ser Met Ser Gly Ser Leu Gly Thr
180 185 190

Gln Ser Thr Gly Gly Thr Leu Pro Gln Ala Thr Pro Glu Asp Thr Ser
195 200 205

Val Ser Arg Met Ser Ala Thr Pro Gly Asn Ala Val Glu Val Glu Leu
210 215 220

Ile Gly Phe Ala Val Gly Asn Asp Asp Thr Asp Ile Pro Val Phe Arg
225 230 235 240

Thr Pro Gly Pro Pro Gly Thr Thr Ser Ala Pro Ser Glu Pro Gln Ala
245 250 255

Gly Ile Pro Ala Thr Leu Gly Gly Lys Pro Ala Ile Leu Ile Leu Pro
260 265 270

Thr Thr Ser Asp Ala Ser Thr Gly Gly Arg Ser Ile Ser Gln Ser Gly
275 280 285

Thr Asn Leu Thr Gln Gln Ala Ser Phe Gln Gln Pro Gly Gly Thr Ala
290 295 300

Ser Gly Pro Ser Thr Ser Ser Ser Val Ser Thr Ser Gln Thr Ala Leu
305 310 315 320

Pro Pro Gly Asn Val Arg Gly Ala Ala Gly Leu Gly Thr Ser Thr Pro
325 330 335

Ser Thr Thr Asn Leu His Gln Ala Ser Ser Lys Asn Ser Thr Val Asp
340 345 350

Pro Gly Ala Ser Ser Ser Ser Gly Val Ser Gly Val Ala Gln Ala Phe

355	360	365	
Pro Gly Val Leu Pro Gly Ser Val Met His Gln Ala Leu Gln Arg Ser			
370	375	380	
Gly Leu Leu Ser Gln Pro Pro Pro Ser Glu Arg Pro Ala Ala Ser Lys			
385	390	395	400
Arg Arg Arg Lys Arg Arg Gly Gly Glu Gly Asp Leu Ala Ser Gln Gly			
405	410	415	
Val Gly Arg Thr Gly Val Asn Gln Pro Val Ala Val Asp Pro Tyr Asp			
420	425	430	
Asn Thr Pro Ser Pro Lys Leu Arg Phe Ser Pro Leu Arg Thr Ala Glu			
435	440	445	
Gly Ala Ala Gly Ala Thr Lys Pro Pro His Leu Leu Ala Ser Leu Pro			
450	455	460	
Ser Ser Asp Pro Gly Met Phe Ser Ser Thr Gly Ser Ser Pro Thr Gly			
465	470	475	480
Ser Ser Arg Leu Pro Ser Pro Gln Gly Ser Ser Ser Ser Thr Ser Leu			
485	490	495	
Ser Leu Gly Thr Ala His Arg Asn Ser Gln Thr Thr Phe Pro Leu Lys			
500	505	510	
Arg Glu Pro Leu Pro Pro Gly Thr Leu Val Glu Pro Val Val Pro Leu			
515	520	525	
Val Pro Phe Ala Ala Asn Lys Asn Gly Arg Leu Glu Thr Val Leu Ile			
530	535	540	
Pro Ser Ala Ala Val Val Ala Thr Gly Gly Ser Ser Phe Pro Gln Ser			
545	550	555	560
Gly Thr Asp Ala Thr Gln Gln Val Gly Ser Gln Gln Pro Arg Arg Thr			
565	570	575	
Ala Ser Gly Pro Pro Thr Ser Ser Phe Val Ser Ala Ser Gln Thr Ala			
580	585	590	
Leu Pro Pro Gly Asn Val Arg Gly Ala Ala Gly Pro Gly Ala Pro Pro			
595	600	605	

Pro Pro Ala Thr His Pro His Leu Ala Tyr Ser Lys Arg Ser Thr Val
610 615 620

Asp Pro Glu Pro Ser Leu Ser Arg Ser Ser Arg Gly Val Pro Gln Ala
625 630 635 640

Phe Pro Asn Leu Gln Gln Gln Pro Gln Gly Asn Val Val His Gln Pro
645 650 655

Leu Gln Gln Gln Pro Gln Gly Asn Val Val His Gln Pro Leu Gln Gln
660 665 670

Gln Pro Gln Gly Ser Leu Val His Gln Pro Leu Gln Gln Gln Pro Gln
675 680 685

Gly Thr Val Val His Gln Pro Leu Gln Leu Gln Pro Gln Gly Ser Val
690 695 700

Val His Gln Pro Leu Gln Gln Gln Thr Gln Gly Ser Leu Val His Gln
705 710 715 720

Pro Leu Gln Gln Gln Pro Gln Gly Asn Val Ala His Gln Pro Leu Gln
725 730 735

Gln Gln Pro Gln Gly Ser Val Val His Gln Pro Leu Gln Gln Gln Pro
740 745 750

Gln Gly Ser Leu Val His Gln Pro Leu Gln Met Gln Pro Gln Gly Asn
755 760 765

Val Val His Gln Pro Leu Gln Gln Gln Gln Gln Gly Ser Leu Val His
770 775 780

His Arg Pro Gln His Gln Pro Gln Gly Asn Val Val His Gln Pro Leu
785 790 795 800

Gln Gln Gln Pro Gln Gly Ser Val Val His Gln Pro Leu Gln Gln Gln
805 810 815

Pro Gln Gly Ser Leu Val His His Arg Pro Gln His Gln Pro Gln Gly
820 825 830

Asn Val Val Tyr Gln Pro Leu Gln Gln Gln Pro Gln Gly Asn Val Val
835 840 845

His Gln Pro Leu Gln Gln Gln Pro Gln Gly Ser Leu Val His Gln Pro

850	855	860	
Leu Gln His Gln Ala Gln Gly Ser Val Val Tyr Gln Pro Leu Gln Gln			
865	870	875	880
Gln Pro Gln Gly Asn Val Val His Gln Pro Leu Gln Gln Gln Pro Gln			
	885	890	895
Gly Ser Val Val Tyr Gln Pro Leu Gln His Gln Pro Gln Gly Ala Leu			
	900	905	910
Val His His Arg Pro Gln His Gln Pro Gln Gly Asn Val Val His Gln			
	915	920	925
Pro Leu Gln Gln Gln Pro Gln Gly Asn Phe Val His Gln Pro Leu Gln			
	930	935	940
Gln Gln Gln Gln Gly Ser Leu Val His His Leu His Arg Arg Pro Gln			
945	950	955	960
His Gln Pro Gln Gly Asn Val Val Tyr Gln Pro Leu Gln Gln Gln Pro			
	965	970	975
Gln Gly Ser Val Val His Gln Pro Leu Gln Gln Gln Pro Gln Gly Ser			
	980	985	990
Leu Val His Gln Pro Leu Gln Gln Gln Pro Gln Gly Asn Val Val Tyr			
	995	1000	1005
Gln Pro Leu Gln Leu Gln Pro Gln Gly Ser Val Val His Gln Pro			
	1010	1015	1020
Leu Gln Gln His Pro Gln Gly Ser Leu Val His Gln Pro Leu Gln			
	1025	1030	1035
Gln His Leu Gln Gly Ser Arg Val His Gln Pro Leu Gln Gln Gln			
	1040	1045	1050
Pro Gln Gly Ser Val Val His Gln Pro Leu Gln His Gln Ala Gln			
	1055	1060	1065
Gly Ser Val Val His Gln Pro Leu Gln Gln Gln Pro Gln Gly Ser			
	1070	1075	1080
Leu Val His Gln Pro Leu Gln Gln Gln Glu Leu Leu Pro Pro Gly			
	1085	1090	1095

Val Gln Pro Glu Thr Ser Val	Ser Trp Lys Pro Ala	Leu Ala Ser
1100	1105	1110
Ala Asp Lys Gly Gln Gln Arg	Ser Ser Gly Lys Met	Leu Met Thr
1115	1120	1125
Leu Asp Ile Pro Gly Ser Ser	Arg Arg Ala Ser Glu	Arg Ala Tyr
1130	1135	1140
Tyr Ala Pro Ser Arg Asp Gly	Ala Leu Leu Phe Asp	Gln Leu Phe
1145	1150	1155
Pro Glu Phe Pro Phe Glu Gly	Thr Ser Met Asn His	Pro Gln His
1160	1165	1170
Tyr Ala Gly His Asp Thr Ala	Asn Val Gly Asp Ser	Ser Gln Pro
1175	1180	1185
Lys Thr Ala Tyr Ser Thr Gly	Glu Val Ala Gly Pro	Ala Ser Ser
1190	1195	1200
Phe Asp Phe Leu Ser Pro Thr	Gly Trp Lys Arg Thr	Ile Arg Ser
1205	1210	1215
Ile Glu Thr Pro His Pro Gly	His Gly Ser Gln Gln	Pro Gly Gly
1220	1225	1230
Gly Gly Thr Val Leu Pro Ser	Tyr Pro Gln Leu Lys	Asp Phe Asp
1235	1240	1245
Leu Thr Leu Leu Ser Thr Pro	Met Pro Ala Pro Gln	Trp Asp Thr
1250	1255	1260
Ser Thr Asn Ala Pro Ser Glu	Asn Val Ala Ala Lys	Thr Gln Ala
1265	1270	1275
Val Pro Thr Arg Gly Asp Glu	Ser Gly Ser Val Thr	Ser Pro Tyr
1280	1285	1290
Asp Gln Leu Phe Arg Glu Ala	Ala Ala Phe Asn Glu	Ser Met Arg
1295	1300	1305
Ser Asp Glu Ala Pro Lys Ser	Tyr Leu Thr Ser Thr	Ser Met His
1310	1315	1320
Phe Gln Ser Ala Ala Pro Ser	Ser Gln Asn Arg Pro	Gly Ser Leu

1325	1330	1335
Gln Asn Lys Pro Ser Glu Ser Gly Arg Thr Ser Gly Val Ser Ala		
1340	1345	1350
Val Gly His Lys Ala Ala Ala Pro His Val Lys Pro Ser Asp Arg		
1355	1360	1365
Glu Gln Asn Pro Phe Gln Leu Phe Val Glu Pro Leu Pro Ser Ala		
1370	1375	1380
Pro Lys Pro Thr Ser Ala Phe Ala Trp Pro Glu Ala Gly Thr Ser		
1385	1390	1395
Phe Glu Pro Val Thr Ser Ala Glu Ser Met Thr Val Ser Gly Gly		
1400	1405	1410
Ser Gly Lys Lys Gln Ala Lys Arg Ser Thr Ser Pro Val Thr Ala		
1415	1420	1425
Ser Leu Glu Gln Ser Pro Phe Glu Thr Val Ser Val Ser Ser Ala		
1430	1435	1440
Thr Glu Leu Gln Ala Pro Ser Ile Ser Glu Tyr Gly Ser Pro Arg		
1445	1450	1455
Thr His Leu Ser Ser Thr Pro Ala Val Lys Gly Pro Ser Ala Gly		
1460	1465	1470
Pro Val Ser Ser Thr Ser Asn Glu Phe Gly Ser Leu Leu Ala Ala		
1475	1480	1485
Ala Leu Arg Asp Ala Gly Trp Ser Asp Gly Met Thr Glu Asp Glu		
1490	1495	1500
Ala Thr Asp Phe Val Leu Asp Ser Ile Lys Asn Leu Glu Glu Leu		
1505	1510	1515
Gln Val Ala Asn Glu Trp Asp Ala Ala Ser Thr Glu Thr Arg Pro		
1520	1525	1530
Ala Ala Glu Gly Gly Thr Gln His Ala Ser Phe Asn Leu Val Ser		
1535	1540	1545
Thr Leu Leu Gly Pro Asp Ala Thr Pro Thr Pro Pro Gly Ser Arg		
1550	1555	1560

Ser Thr Pro Pro Gly Gly Pro Thr Lys Lys Pro Ser Ala Met Gly
1565 1570 1575

Arg Gln Lys Pro Ser Ser Arg Ser Thr Ser Asp Ser Lys Val Glu
1580 1585 1590

Gly Arg Ser Ser Thr Arg Asp Ser Ser Leu Val Ala Pro Ser Thr
1595 1600 1605

Ser Ile Gly Ala Ala Val Arg Glu Arg Ser Lys Thr Ser Ser Pro
1610 1615 1620

Gly Ser Ser Ser Pro Gln Ser Lys Gln Leu Thr Glu Glu Ser Phe
1625 1630 1635

Ser Leu Gly Thr Lys Glu Asp Asp Ser Ala Ser Met Val Glu Gly
1640 1645 1650

Asp Glu Ser Gln Val Gln Ser Ser Lys Ala Thr Ala Ser Ala Thr
1655 1660 1665

Arg Arg Arg Ala Trp Gln Gly Gln Arg Leu Asn Ile Phe Gly Ile
1670 1675 1680

Gln Pro Glu Thr Pro Gly Thr Gln Pro Val Leu Gln Phe Met Arg
1685 1690 1695

Glu Ser Asn Arg Gly Ser Val Ser Thr Ala Lys Ser Pro Asp Thr
1700 1705 1710

Pro Val Thr Ser Ala Pro Gly Gly Ser Gln Gly Asp Ser Gly Asn
1715 1720 1725

Asp Gly Val Gly Leu Val Ala Gly Ser Ser Val Leu Pro Ser Ala
1730 1735 1740

Val Gln Gly Lys Ser Tyr Ala Ser Ile Ser Gly Ile Pro Ser His
1745 1750 1755

Arg Glu Ser Leu Ser Ser Ser Ile Gln Asp Val Gln Pro Gly Gly
1760 1765 1770

Val Arg Gly Ala Gly Arg Arg Thr Pro Asn Val Arg Thr Pro Val
1775 1780 1785

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

1790	1795	1800
Leu Lys Lys Thr Ser Lys Arg	Gln Thr Pro Gly Leu	Glu Gly Tyr
1805	1810	1815
Thr Pro Ser Ala Lys Thr Arg	Arg Glu Thr Gly Thr	Val Leu Pro
1820	1825	1830
Ser Ser Leu Gly Glu Trp Gln	Gly Leu Thr Leu Arg	Thr Pro Met
1835	1840	1845
Lys Ser Thr Ser Pro Gly Ala	Ser Glu Met Gln Pro	Leu Ser Ser
1850	1855	1860
Leu Val Ala Ser Thr Ser Arg	Gly Ala Leu Gln Pro	Ala Leu Pro
1865	1870	1875
Gly Ser Met Ser Pro Ser Ser	Ser Ala Arg Pro Gln	Ser Leu Arg
1880	1885	1890
Ala Pro Ser Arg Gly Ser Ser	Ser Tyr Ser Glu	
1895	1900	
<210>	260	
<211>	865	
<212>	PRT	
<213>	Toxoplasma gondii	
<400>	260	
Met Arg Pro Leu Arg Val Ala Val Ala Leu Phe Trp Ala Met Val Ala		
1	5	10
Val Val Gly Phe Trp Ala Ser Pro Asp Ser Arg Leu Thr Val Arg Gly		
	20	25
		30
Pro Gln Phe Ala Asp Ala Ala Thr Arg Gly Val Val Lys Ser Leu Lys		
	35	40
		45
Arg Ala Met Asn Gln Gly Trp Arg Asn Gly Ala His Ser Ile Cys Ala		
	50	55
		60
Ile Leu Gly Cys Asp Tyr Glu His Val Lys Ala His Leu Thr His Lys		
65	70	75
		80
Pro Thr Phe Phe His Ser Phe Lys Ala Val Cys Ala Gln Leu Asp Glu		

85

90

95

Phe Glu Glu Glu Val Thr His Ala Lys Met Arg Glu Glu Asp Leu Thr

100

105

110

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

115

120

125

Leu Ile Asn Asp Ala Leu Gly Thr Gln Phe Glu Val Pro Ala Ser Tyr

130

135

140

Val Pro His Asn Ala Lys Asn Arg His Tyr Ile Pro Gly Gln Arg Gly

145

150

155

160

Glu Gly Asp Glu Lys Glu Lys Leu Lys Thr Arg Met Arg Gly Leu Gln

165

170

175

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

180

185

190

Asp Arg Leu Ala Ala Val Arg Glu Lys His Met Ala Gln Ile Lys Glu

195

200

205

Leu Glu Asp Ala Arg His Arg Lys Phe Leu Leu Leu Gln Glu Glu His

210

215

220

Asp Arg Gln Thr Asp Gln Leu Val Ser Glu Leu Arg Leu Lys His Thr

225

230

235

240

Glu Glu Met Asp Thr Ile Arg Arg Glu Leu Ala Glu Glu Arg Arg Leu

245

250

255

Phe Glu Gln Ser Val Lys Val Trp Asp Ala Val Asn Arg Leu Leu Thr

260

265

270

Asp Ala His Val Gly Ile Glu Thr Leu Thr Asp Arg Val His Thr Met

275

280

285

Ser Gln His Val Phe Lys Leu Asn Val Phe Tyr Glu Lys Leu His Ser

290

295

300

Phe Gln Gln Thr Ala Lys Glu Asn Pro Thr Gly Ala Ala Pro Tyr Ser

305

310

315

320

Ala Leu Ser Tyr Ala Phe Gln Ser Glu Ala Ala Val Asp Gln Ala Met

325

330

335

His Gln Ile Val Ala Ile Tyr Gln Glu Ala Ser Ala Gly Val Ala Arg
340 345 350

Val Gln Glu Ile Leu Asn Gln Ala Asp Gly Val Met Ala Thr Ala Pro
355 360 365

Thr Arg Asp Asp Ala Ala Trp Phe Gln Gln Arg Gln Arg Gly Tyr Lys
370 375 380

Asp Arg Leu Glu Ser Phe Val Asn Leu Leu Ser Asp Leu Ser Val Arg
385 390 395 400

Leu Glu Asp Tyr Met Gln Thr Ala Glu Glu Arg Lys Leu Val Thr Leu
405 410 415

Phe Leu Gly Asp Glu Val Arg Thr Gln Ile Leu Ala Leu Leu Gln Glu
420 425 430

Arg Thr Thr Glu Trp Ser Thr Arg Leu Ala Thr Leu Arg Glu Arg Thr
435 440 445

Gln Gly Ile Glu Thr Ala Ala Asn Lys Phe Phe Glu Ser Ser Thr Gln
450 455 460

Leu Asp Arg Thr Thr Gly Glu Val Val Ser Ala Val Leu Gln Asn Pro
465 470 475 480

Glu Ala Phe Leu Val Gln Val Ser Thr Tyr Ala Thr Glu Ser Gly Thr
485 490 495

Leu Arg Ser Ala Ala Gly Val Ile Glu Glu Asp Leu Lys Ala Val Val
500 505 510

Lys Ala Leu Gln Asp Leu Gly Arg Glu Met Thr Gly Leu Thr Glu Gly
515 520 525

Val Ala Ser Ala Gln Leu Pro Pro Ala Val Leu Asp Phe Leu Gly Leu
530 535 540

Pro Gly Leu Phe Asn Ala Leu Gln Val Asp Met Gln Val Lys Ala Lys
545 550 555 560

Gly Gln Gln Leu Leu Gln Leu Ile Lys Gly Arg Leu Ser Gln Thr Gly
565 570 575

Glu Ile Thr Arg Lys Leu Glu Met Leu Lys Ser Glu Val Lys Asn Ile

580 585 590
 Arg Ser Pro Ala Val Arg Glu Gln Ala Glu Trp Ala Leu Thr Glu Ala
 595 600 605

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

 Ala Leu Gly Gly Ser Ala Thr Gly Ser Met Val Gly Leu Gly Gly Ser
 675 680 685
 Val Ser Gly Leu Gly Thr Asp Ser Arg Ala Ala Ile Ala Asp Leu Glu
 690 695 700
 Gln Lys Arg Gln Asn Glu Lys Glu Lys Ile Gln Glu Leu Arg His Asn
 705 710 715 720
 Leu Ser Ser Lys Gln Arg Glu Ser Val Ser Leu Asp Asn Glu Ala Arg
 725 730 735

 Arg Leu Glu Val Glu Val Ala Asn Lys Gln Arg Glu Leu Ala Glu Glu
 740 745 750
 Gln Gln Arg Val Leu Arg Val Ala Thr Leu Ala Gln Ala Leu Thr Thr
 755 760 765
 Gly Ala Ser Pro Ser Ile Gly Met Ser Met Ala Ser Met Arg Gly Gly
 770 775 780
 Leu Gly Leu Thr Gly Gly Leu Ala Gly Ser Ser Ala Ala Leu Met Thr
 785 790 795 800

 Gln Gly Ile Met Gly Ser Arg Ala Ala Gly Leu Leu Gly Gly Ser Thr
 805 810 815
 Ala Gly Leu Ala Gly Ala Ser Met Gly Gly Leu Ala Gly Gly Ser Met
 820 825 830

Gly Gly Leu Gly Gly Ala Gly Met Gly Gly Tyr Gly Gly Gly Ser Met
835 840 845

Gly Gly Leu Gly Gly Arg Ser Thr Asp Gly Gln Leu Gly Arg Gly Thr
850 855 860

Arg
865

<210> 261
<211> 637
<212> PRT
<213> Toxoplasma gondii
<400> 261

Met Arg His Ile Phe Pro Asp Asp Ser Ala Thr Ser Met Arg Ala Leu
1 5 10 15

Val Trp Gly Leu Gly Ala Arg Val Leu Trp Phe Phe Leu Ala Gly Val
20 25 30

Leu Ala Ala Thr Val Asp Ile Ala Gly Ala Asp Gly Ile Gly Gln Gly
35 40 45

Met Pro Asp Ser Gly Phe Asn His Val Asp Ala Glu Ala Gln Pro Thr
50 55 60

Val Phe Ile Arg Glu Glu His Asp Asp Ser Ala Ser Ser Glu Leu Val
65 70 75 80

Glu Asp Asp Gly Thr Tyr Ser Val Ala Arg Arg Phe Arg Leu Met Val
85 90 95

Met Ala Asp His Lys Lys Asp Gly Arg Ala Cys Glu Arg Asp Met Val
100 105 110

Leu Gln Ala Ala Asp Ile Thr Arg Leu Arg Val Gly Gly Ser Arg Thr
115 120 125

Ser Phe Ser Ala Gly Leu Val Pro Leu Val Gly Leu Pro Leu Leu Ala
130 135 140

Ala Ala Gly Leu Lys Asp Tyr Ile Leu Gly Val Asn Ala Pro Val Asp
145 150 155 160

Glu Leu Arg Leu Pro Gly Ala Arg Ala Leu Thr Pro His Asp Val Val

165 170 175
 Asp Gly Val Val Ser Val Gly Pro Gly Pro Pro Pro Arg Pro Asp Gly

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

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

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

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

Met Arg Arg Ala Ala Ala Arg Asn Leu Val Cys Ser Glu Ser Val Lys

420 425 430

Gly Gly Ser Gly Gly Ile Ser Met Cys Trp Lys Ser Ser Pro Pro Thr

435 440 445

Gly Ser Leu Leu Leu Trp His Glu Glu Val Leu Gln His Ser Cys Arg

450 455 460

Val Val Ala Ala Phe Arg Gly Ser Val Asn His Ser Val Trp Ala Asn

465 470 475 480

Phe Ala Thr Gln Gln Leu Ser Ile Gly Ser Asp Ala Pro Ser Thr Arg

485 490 495

Ser Asp Asn Val Arg Ser Val Leu Ser Lys Cys Leu Leu Leu Glu Arg

500 505 510

Asn Pro Pro Thr Tyr Gly Val Ala Leu Lys Arg Ala Thr Ile Ser Cys

515 520 525

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

530 535 540

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

545 550 555 560

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

565 570 575

Pro Gly Leu Val Gly Ala Gly Ala Ala Thr Gln Met Asp Tyr Arg Gly

580 585 590

Asn Lys Glu Thr Ser Lys Val Ile Gln Ser Ser Val Glu Phe Phe Thr

595 600 605

Val Phe Ile Val Asp Phe Gln Arg Lys Pro Ser Asp Trp Pro Val Leu

610 615 620

Leu Glu Met Arg Lys Lys Asp Ala Ala Arg Thr Arg Thr

625 630 635

<210> 262

<211> 526

<212> PRT

<213> Toxoplasma gondii

<400> 262

Met Glu Val Arg His Arg Ser Val Gln Leu Phe Trp Val Val Gly Leu

1 5 10 15

Leu Gly Phe Leu Ile Tyr Val Val Ser Leu His Gly Ser Pro Val Asn

20 25 30

Ala Ala Val Val Ala Glu Ser Glu Ser Glu Ala Gly Asp Thr Ala Leu

35 40 45

Val Leu His Asp Thr Glu Val Met Ser Ser Gly Gly Thr Ser Arg Pro

50 55 60

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

65 70 75 80

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

85 90 95

Tyr Ala Phe Gln Tyr Gly Leu Arg Arg Arg Pro Gln Asp Gly Ser Arg

100 105 110

Arg Gly Arg Gln Pro Pro Asp Glu Asp Arg Gln Arg Gly Ser Ser Pro

115 120 125

Glu Thr Ala Pro Glu Arg Gly Thr Gly Glu Ser Asp Ser Ser Gly Ser

130 135 140

Arg Ser Pro Glu Arg Phe Pro Leu Gly Ser Pro Pro Ala Ser Pro Asp

145 150 155 160

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

165 170 175

Ser Leu Leu Gly Thr Arg Ser Asp Leu Thr Arg Pro Ser Gly Ser Ser

180 185 190

Asp Glu Ala Ser Gln Val His Gly Arg Gln Gly Leu Asp Val Ser Ala

195 200 205

Ser Arg Ser Pro Pro Ser Pro Ala Ser Gly Gly Lys Pro Val Glu Gly

210 215 220

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

225						230						235						240
Val	Pro	Ala	Asp	Thr	Gln	Ser	Pro	Cys	Cys	Gly	Ala	Lys	Gly	Ser	Leu			
					245						250						255	
Pro	Lys	Glu	Thr	Ser	Pro	Thr	Arg	Asp	Ile	Gly	Thr	His	Val	Pro	Gly			
					260						265						270	
Lys	Arg	Ser	Pro	Pro	Ser	Pro	Ser	Pro	Leu	Gln	Gly	Pro	Arg	Leu	Ala			
					275						280						285	
Ser	Phe	Phe	Val	Gly	Ser	Glu	Ser	Gly	Pro	Glu	Gly	Asp	Val	Val	Ile			
					290						295						300	
Ile	His	Ser	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Gly	Ser	Ser	Gly	Leu	Gly			
					305						310						315	320
Asp	Ser	Ser	Val	Ser	Pro	Ser	Asp	Gly	Asp	Ser	Pro	Thr	Pro	Ser	Ala			
					325						330						335	
Pro	Ala	Arg	Gly	Met	Gln	Gln	Glu	Gly	Pro	Val	Gly	Gly	Ser	Ser	Ser			
					340						345						350	
Pro	Glu	Gln	Gly	Gly	Arg	Gln	Ala	Gln	Ala	Pro	Ile	Ser	Thr	Thr	Thr			
					355						360						365	
Ala	Ser	Ser	Pro	Gln	Thr	Gly	Val	Pro	Pro	Gly	Lys	Ala	Ala	Pro	Thr			
					370						375						380	
Ser	Arg	Ser	Asp	Gly	Lys	Pro	Pro	Pro	Gly	Arg	Thr	Gly	Val	Asp	Lys			
					385						390						395	400
Val	Gly	Gly	Pro	Ser	Arg	Gly	Arg	Gly	Ser	Pro	Ser	Arg	Ser	Pro	Gly			
					405						410						415	
Thr	Arg	Leu	Ser	Leu	Ser	Lys	Thr	Pro	Arg	Gly	Pro	Val	Ala	Ser	Pro			
					420						425						430	
Thr	Gly	Gly	Leu	Arg	Gly	Arg	Gly	Gly	Ser	His	Ala	Ala	Ser	Ala	Gly			
					435						440						445	
Arg	Gly	Pro	Leu	Pro	Gly	Pro	Pro	Gly	Lys	Pro	Glu	Gln	Arg	Pro	Gly			
					450						455						460	
Val	Leu	Gly	Pro	Arg	Thr	Lys	Pro	Phe	Thr	Pro	Lys	Pro	Ser	Trp	Val			
					465						470						475	480

Pro Pro Tyr Gly Thr Pro Ser Ser Arg Arg Val Gly Ser Arg Thr Arg
485 490 495

Glu Pro Pro Gln Ser Gln Glu Gln His Pro Gln Ala Pro Ser Gly Glu
500 505 510

Gly Thr Arg Asp Leu Asp Gly Arg Asp Gln Asp Asp Ser Arg
515 520 525

<210> 263

<211> 683

<212> PRT

<213> Toxoplasma gondii

<400> 263

Met Ser Ala Gln Gly Gln Gln Gly Val Arg Ser Thr Val Ala Ala Gly
1 5 10 15

Lys Asn Arg Phe Trp Gln Pro Ala Pro Ile Thr Val Leu Leu Val Leu

20 25 30

Ser Ser Ser Phe Leu Phe Ala Phe Ala Ala Asn Thr Pro Gln Asn Ser
35 40 45

Ser Thr Thr Gly Gln Ser Thr Pro Ser Asp Asp His Gly Val Ser Thr
50 55 60

Glu His Ile His Asp Ala Val Thr Val Asp Ala Ala Glu His Ala Gly
65 70 75 80

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

85 90 95

Ala Arg Val Ala Thr Leu Lys Ala Glu Thr Glu Ala Ala Val Ala Glu
100 105 110

Val Arg Arg Thr Glu Ala Met Gln Arg Glu Leu Phe Gly Arg Leu Asn
115 120 125

Ala Lys Val Arg Ala Met Asn Asp Arg Leu Asp Glu Leu Ser Asp Ala
130 135 140

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

145 150 155 160

Ala Asp Arg Glu Glu Gln Ala Lys Arg Phe Thr Thr Asp Val Glu Thr
165 170 175
Tyr Ile Ile Glu Ser Gly Leu Lys Lys Ala Val Phe Gln Gln Arg Glu
180 185 190
Ile Ala Ala Lys Leu Gln Thr Leu Ala Glu Ser Asn Gln Lys Ser Lys
195 200 205
Gln Ala Leu Asp Ala Leu Leu Gln His Val Asp Asp Glu Lys Glu Gln
210 215 220
Thr Lys Gln Trp Ile Ser Thr Val Val Arg Asp Leu Glu Lys Tyr Val
225 230 235 240
Glu Ala Arg Thr Gln Thr Thr Leu Glu Ser Leu Gln Arg Asp Ala Gln
245 250 255
Glu His Ala Asn Phe Met Gln Gln Gln Leu Asn Asp Met Lys Leu Asp
260 265 270
His Leu Leu Leu Leu Gln Ala Val Ser Ser Ala Glu Thr Gln Leu Asn
275 280 285
Glu Arg Gly Ile Ala Gly Val Asp Ile Ser Gln Leu Asp Glu Ser Ala
290 295 300
Ser Phe Glu Arg Met Met Thr Thr Phe Glu Lys Val Leu Lys Glu Gln
305 310 315 320
Leu Lys Gly Lys Phe Val Leu Pro Ile Phe Val Val Thr Gln Cys Pro
325 330 335
Asp Ser Met Glu Arg Val Ala Phe Met Asn Thr Tyr Leu Val Pro Ser
340 345 350
Lys Arg Asn Phe Arg Ala Val Phe Gln Ala Leu Gly His Thr Pro Gln
355 360 365
Ala Ser Ala Val Val Ile Arg Ile Glu Ser Val Met Val Glu Ala Trp
370 375 380
Met Glu Val Asn Gly Lys Val Thr Gly Met Gln Tyr Leu Thr Pro Pro
385 390 395 400
Ala His Glu Ala Leu Thr Val Thr Thr Lys Asp Arg Phe Gly Phe Glu

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

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

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

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

Asp Ser Thr Ser Arg Arg Gln Val Leu Val His Ile Cys Glu Ile Gly

660 665 670

Val Thr Cys Asn Ser Asp Arg His Pro Glu Ala

675 680

<210> 264

<211> 378

<212> PRT

<213> Toxoplasma gondii

<400> 264

Met Arg His Gln Glu Arg Phe Asp Leu Arg Thr Gly Val Leu Leu Cys

1 5 10 15

Ile Gly Leu Val Gly Trp Ser Gly Phe Val Val Gln His Cys Ala Cys

20 25 30

Ser Asp Gly Val Phe Ser Val Gln Ser Pro Ser Ala Pro Gln His Asp

35 40 45

Ile Leu Trp Asp Ala Arg Lys Thr Gln Asp Glu Leu Arg Ala Phe Asn

50 55 60

Gly Glu Ser Ser Gly Glu Leu Ala Lys Gly Ala Gly Ile Arg Ala Thr

65 70 75 80

Glu Gly Glu Val Phe Ala Gly Gly Arg Ala Ala Ala Gly Val Ile Ser

85 90 95

Ala Glu Ile Pro Ala Glu Glu Gly Gly Glu Ala Ala Ala Asn Pro Thr

100 105 110

Ser Glu Arg Glu Ile Glu Ala Pro Ala Ala Glu Asp Glu Ala Glu Ala

115 120 125

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

130 135 140

Glu Glu Glu Arg Leu Ser Ala Arg Ser Ala Ser Arg Pro Ser Gly Arg

145 150 155 160

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

165 170 175

Ala Gly Gly Ser Ile Leu Ala Ala Ala Val Met Met Leu Leu Ser Arg
180 185 190
Leu Ser Arg Gln Arg Ser Ile Gln Val Trp Thr Val Trp Arg Glu Glu
195 200 205
Arg Gln Ser Leu Gly Leu Ser Val Ala Ser Asp Ala Leu Val Val Ala
210 215 220
Ser Ala Leu Val Ala Leu Leu Gly Gly Lys Arg Val Val Lys Gly Val

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

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

355 360 365
Ala Ala Arg Arg Lys Lys Ser Thr Lys Ala
370 375

<210> 265

<211> 378

<212> PRT

<213> Toxoplasma gondii

<400> 265

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

1 5 10 15
 Leu Val Cys Arg Gly Ile Ala Thr Glu Gln Val Val Ala Ala Ala Ala
 20 25 30
 Lys Ser Asn Ser Glu Glu Thr Val Ser Thr Gly Ile Gly Glu Ser Ala

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

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

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

 225 230 235 240
 Val Arg Thr Leu Val Arg Thr Asp Pro Asp Lys Ala Gln Ala Ser Glu
 245 250 255

Glu Gly Arg Leu Tyr Gln Ala Lys His Phe Trp Gln Gln Leu Gln Pro
260 265 270

Glu Glu Glu Ala Leu Arg Gly Gln Leu Leu Pro Asp Val Val Arg Leu
275 280 285

Glu Gly Glu Val Arg Glu Ala Arg Asp Arg Asp Leu Pro Ser Leu Ser
290 295 300

Met Leu Tyr Gln Gln Leu Glu Gln Ala Asn Arg Arg Arg Val Val Ser
305 310 315 320

Thr Val Asp Asp Gln Leu Glu Arg Leu Asn Arg Gln Leu Pro His Met
325 330 335

Val Gly Met Asp Pro Asp Tyr Ala Glu Glu His Ile Leu Tyr Thr Gln
340 345 350

Leu Pro Leu Arg Gly Pro Ala Tyr Val Arg Met Ser Glu Asp Val Leu
355 360 365

Arg Gln Val Gln Ala Glu Pro Lys Gln Thr
370 375

<210> 266

<211> 452

<212> PRT

<213> Toxoplasma gondii

<400> 266

Met His Ser Ile Val Tyr Val Val Val Ser Val Leu Ala Val Leu Gly
1 5 10 15

Arg Val Asp Gly Gln Pro Leu Gly Ser Arg Lys Ala Lys Pro Gly Ala
20 25 30

Gly Ser Ala Pro Gly Pro Ser Val Leu Pro Ser Ser Leu Pro His Ile
35 40 45

Ile Met Gln Ser Pro Thr Lys Asn Pro Arg Lys Gln Arg Lys His Ser
50 55 60

Met Ala Ser Gly Asp Ala Gly Ala Lys Thr Ala Thr Val Ala Glu Glu
65 70 75 80

Ala Ala Lys Ala Val Gly Val Arg Gly Asp Thr Pro Gly Asp Gln Ala

85 90 95
 Ser Ala Arg Gly Pro Asp Glu Lys Glu Lys Arg Glu Thr Ala Ala Arg

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

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

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

 290 295 300
 Val Arg Leu Ala Ala Ala Ala Asp Met Val Gly Ala Asp Ile Thr Arg
 305 310 315 320
 Gln Asp Met Arg Arg Leu Thr Pro Glu Gln Gln Leu Gln Ile Val Arg
 325 330 335

Gln Gly Arg Phe Asp Glu Ala Arg Ser Leu Leu Glu Ser Thr Ser Arg
340 345 350
Glu Ala Asn Leu Leu Arg Glu Leu Tyr Val Pro Gly Ile Val Glu Ala
355 360 365
Glu Glu Glu Val Glu Arg Ala Glu Pro Gly Ser Glu Glu Leu Phe Arg
370 375 380
Arg Arg Arg Asp Leu Arg Glu Lys Lys Glu Thr Arg Leu Gly Ser Ala
385 390 395 400
Val Asp His His Leu Ala Arg Val Val Arg Glu Ile Pro Phe Ser Val
405 410 415
Gly Ile Pro Glu Glu Gln Ala Ala Gln Leu Arg Ala Pro Pro Gly Ile
420 425 430
Glu Pro Val Pro Glu His Val Leu Val Ala Met Gln Ala Ile Glu Arg
435 440 445
Ala Gln Arg Thr
450
<210> 267
<211> 218
<212> PRT
<213> Toxoplasma gondii
<400> 267
Met Tyr Thr Glu Arg Ser Ser Leu Ser Ala Ala Val Val Met Glu Lys
1 5 10 15
Glu Gly Val Thr Pro Ser Gln Cys Tyr Ala Ile Pro Pro Glu Arg Glu
20 25 30
Asp Ala Met Thr Leu Val Thr Gln Met Phe Trp Arg Trp Thr Ile Ala
35 40 45
Phe Leu Ala Leu Ile Tyr Val Val Ala Thr Gln Ala Asn Ala Ser Arg
50 55 60
Pro Ala Thr Val Arg Lys Gln Ser Asn Asp Ala Asp Gly Glu Gly Glu
65 70 75 80

Val Asp Thr Gly Val Ala Gly Arg Gln Thr Ser Met Pro Thr Thr His

85 90 95

Ile Gly Gly Leu Ala Gly Arg Gly His Arg Gly Lys Gln Thr Arg Lys

100 105 110

Gln Tyr Ile His Leu Asp Ala Leu Asn Glu Asp Val Glu Pro Glu Ile

115 120 125

Lys Glu Pro Ser Leu Arg Pro Leu Ser Gln Lys Ala Thr Arg Arg Ala

130 135 140

Lys Trp Ser Arg Leu Leu Leu Glu Leu Leu Pro Ala Ala Val Phe Val

145 150 155 160

Ser Leu Leu Ile Thr Met Met Ser Arg Ala Arg Pro Val Thr Arg Val

165 170 175

His Glu Thr Val Thr Asn Phe Leu Tyr Arg Gln Gly Val Asp Val Ser

180 185 190

Arg Gln Leu Gln Glu Leu Arg Asp Glu Arg Gln Arg Glu Ile Glu Ala

195 200 205

Glu Phe Val Asp Ile Pro Pro Asp Leu Glu

210 215

<210> 268

<211> 1086

<212> PRT

<213> Toxoplasma gondii

<400> 268

Met Ala Ile Leu Arg Leu Ser Phe Val Phe Ser Leu Ser Leu Leu Ile

1 5 10 15

Ala Leu Tyr Ser Val Trp Gln His Met Leu His Ala Arg Ala Ser Lys

20 25 30

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

35 40 45

Leu Ser Gly Ser Ser Ile Ser Ala Trp Arg Arg Val Arg Ala Val Phe

50 55 60

His	Glu	Thr	Leu	Val	Leu	Thr	Asp	Val	Asp	Asp	Thr	Leu	Trp	Ser	Ser
65				70				75				80			
Gly	Ala	Trp	Arg	Leu	Gly	Gly	Lys	Thr	Leu	Gly	Gly	Val	Asp	Glu	Asp
85				90				95							
Leu	Ser	Arg	Gly	Gln	Thr	Tyr	Pro	Gly	Ile	Gly	Ala	Leu	Tyr	Phe	Leu
100				105				110							
Leu	Ser	Ala	Gly	Pro	His	Val	Thr	Ala	Ala	Pro	Val	Asn	Lys	Phe	Leu
115				120				125							
Pro	Thr	Cys	Pro	Val	Pro	Leu	Val	Ser	Pro	Leu	Phe	Glu	Thr	Cys	Gln
130				135				140							
Val	Gly	Asp	Ala	Arg	Arg	Ser	Leu	Ala	Gly	Ala	Thr	Gly	Arg	Val	Thr
145				150				155				160			
Asp	Thr	Trp	Val	Phe	Gly	Gly	Gly	Glu	Arg	Ala	Lys	Glu	Leu	Gln	Asp
165				170				175							
Ser	Arg	Arg	Lys	Pro	Ala	Glu	Lys	Arg	Pro	Leu	Leu	Pro	Pro	Arg	Val
180				185				190							
Gly	Leu	Leu	Thr	Ala	Arg	Ala	Ser	Ser	Ala	Ala	Met	Arg	Ser	Phe	Thr
195				200				205							
Arg	Ser	Pro	Ser	Phe	Tyr	Ala	Ala	Val	Thr	Ala	Ala	Leu	Ile	His	Gly
210				215				220							
Ala	Arg	Gln	Ile	Tyr	Gly	Pro	Gly	Val	Asp	Asp	Trp	Gly	Arg	Val	Arg
225				230				235				240			
Phe	Glu	Asn	Asn	Met	Glu	Leu	Leu	Arg	Asp	Val	Ile	Gly	Gly	Gln	His
245				250				255							
Ser	Arg	Gly	Arg	Gly	Lys	Val	Ser	Gly	Phe	Lys	Glu	Ala	Leu	Glu	Arg
260				265				270							
Phe	Pro	Lys	Gln	Thr	Pro	Val	Phe	Val	Gly	Asp	Ser	Gly	Glu	Arg	Asp
275				280				285							
Val	Glu	Ala	Ala	Ala	Gly	Met	Ala	Leu	Phe	Ala	Gln	Glu	Lys	Leu	Ala
290				295				300							
Ala	Val	Phe	Val	His	Val	Val	Phe	Ser	Asn	Trp	Glu	Asn	Glu	Asn	Pro

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

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

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

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

Leu Arg Tyr Met Leu Glu Val Thr Gly Glu Ala Leu Gln Ser Val His

565 570 575

Val Glu Asn Arg Ala Ile Phe Glu Asp Gly Val Ala Ala Met Arg Thr

580 585 590

Phe His Thr Lys Ala Val Asp Ala Cys Ile Pro Ser Gly Pro Ala Glu

595 600 605

Pro Trp Thr Val Gly Glu Glu Ile Gly Ala Cys Leu Ala Leu Phe Arg

610 615 620

Thr Pro Arg Ala Ala Ala Ser Pro Pro Arg Asp Pro Thr Asp Ser Leu

625 630 635 640

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

645 650 655

Ala Arg Val Val Cys Thr Phe Val Asp Gln Leu Lys His Trp Arg Ser

660 665 670

Ala Gly Ala Asp Glu Thr Glu Val Leu Ser Leu Glu Phe Ser Val Ala

675 680 685

Leu Asn Glu Ala Val Asp Met Ser Asn Arg Pro Phe Gly Ile Gly Gly

690 695 700

Gln Pro Val Thr Ser Leu Ala Asn Leu Ser Gly Asp Ser Thr Ser Arg

705 710 715 720

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

725 730 735

Ser Pro Leu Arg Asp Ala Asp Val Ala Ser Val Phe Pro Arg Ser Leu

740 745 750

Arg Ser Arg Pro Thr Ser Gly Thr Val Asn Leu Ser Leu Pro Ile Pro

755 760 765

Pro Gly Ser Pro Gly Asn Ser Ser Phe Pro Gln Val Ser Leu Thr Gly

770 775 780

Gln Pro Gly Asp Glu Ala Asp Ala Arg Pro Ser Gly Arg Gly Asn Glu

785 790 795 800

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

805	810	815	
Pro Ala Ser Asp Pro Ala Pro Met Ser Pro Asp Arg Ala His Leu Tyr			
820	825	830	
Trp Thr Lys Glu Ala Glu Arg Gln Asn Val Glu Arg Arg Ser Ser Gly			
835	840	845	
Ala Ile Ala Thr Ser Thr Gln Ala Pro Ala Ala Ser Arg Asp Leu Pro			
850	855	860	
Asp Ser Leu Gln Ile Glu Gly Thr Val Asp Ser Pro Ser Ser Phe Gln			
865	870	875	880
Ser Arg Gly Ala Ser Ala Asp Arg Gln Arg Pro Gln Gly Arg Ile Glu			
885	890	895	
Asp Gly Ala Phe Ala Ser Pro Phe Leu Pro Gly Leu Ser Thr Thr Ala			
900	905	910	
Gly Pro Ser Gly Gln Gly Arg Thr Ser Val Asp Leu Val Arg Ser Gly			
915	920	925	
Ala Leu Ser Ser Arg Leu Asn Ala Ala Ser Gly Ala Ala Leu Gly Asp			
930	935	940	
Val Ile Ser Ala Ala Pro Ser Asp Cys Pro Phe Gly Gly Leu Arg Lys			
945	950	955	960
Leu Leu Ala Thr Met Arg Pro Ile Cys Glu His Gln Lys Lys Leu Leu			
965	970	975	
Gly Asp Ala Ser Pro Cys Ala Leu Met Ser His Leu Leu Tyr Glu Glu			
980	985	990	
Gly Leu Met His Ile Phe Ala Thr Val Thr Ala Trp Tyr Glu Asp Gly			
995	1000	1005	
Ala Arg Glu Pro Leu Tyr Ile Thr Lys Met His Leu Thr Leu Asp			
1010	1015	1020	
Pro Ala Glu Ala Lys Leu Glu Thr Leu Arg Lys Arg Glu Ser Asp			
1025	1030	1035	
Asn Phe Ala His Leu Gly Met Gly Val Leu Lys Arg Gly Arg Gly			
1040	1045	1050	

His Ser Thr Tyr Asp Ile Asp Arg Leu Gln Ala Asn His Arg Glu
1055 1060 1065

Phe Ala Arg Ser Tyr Pro Gly Phe Lys Asn Leu Ser Cys Asn Pro

1070 1075 1080

Phe Glu Ala

1085

<210> 269

<211> 921

<212> PRT

<213> *Toxoplasma gondii*

<400> 269

Met Glu Ser Asn Arg Arg Arg Ala Pro Cys Pro Pro Ala Ser Gly Val

1 5 10 15

Ser Pro Gly Ser Ile Leu Cys Leu Phe Leu Leu Ser Leu Leu Pro Cys

20 25 30

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

35 40 45

Ala Cys Val Gly Ser Pro Pro Glu Thr Ala Glu Asn Ala Thr Ala Ser

50 55 60

Leu Gly Ser Trp Glu Gln Val Pro Cys Leu Asp Ala Ala Ser Val Ser

65 70 75 80

Val Phe Thr Ser Arg Lys Glu Val Gln Ala Gly Asn Ile Leu Leu Phe

85 90 95

Leu Asp Ile Asp Asp Thr Val Ile Ala Ser Gly Gly Trp Asn Glu Val

100 105 110

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

115 120 125

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

130 135 140

His Ala Arg Asn Leu Lys Ser Gly Gln Leu Thr Glu Phe Ala Pro Pro

145 150 155 160

Ser Lys Ala Met Val Val Thr Ala Arg Pro Asn Leu Pro Val Phe Arg

165	170	175
Pro Pro Asn Leu Met Arg His Leu Thr Ser Ile Leu Thr Arg Gly Ala		
180	185	190
Arg Gln Ile Met Gly Asp Asn Ala Pro Glu Trp Gly Val Gly Ser Gln		
195	200	205
Asn Val Met Lys Pro Ala Ser Val Leu Arg Gly Thr Tyr Gly Arg Gly		
210	215	220
Glu Asn Lys Leu Ser Phe Met Thr Lys Val Leu Thr Glu Gly Arg Pro		
225	230	235
		240
Val Asn Glu Ser Arg Ile Asp Glu Asn Thr Lys Val Met Phe Val Gly		
245	250	255
Asp Ser Ala Glu Arg Asp Leu Glu Val Ala Ile Gly Leu Ser Ala Met		
260	265	270
Val Pro Asp Lys Val Ala Ala His Leu Leu His Val Val Tyr Arg His		
275	280	285
Asn Ser Gly Asp Pro Thr Gln Met His Ala Ser His Thr Val Gln Thr		
290	295	300
Gly Glu Lys Phe Asp Glu Asp Gly Val Leu Ser Lys Ala Ala Val Thr		
305	310	315
		320
Leu Gln Glu Ile Ile Ser Gly Ala Ala Arg Thr Val Ala Ala Ala Thr		
325	330	335
Arg Ala Leu Thr Glu Lys Asp Glu Arg Glu Lys His Arg Gln Thr Pro		
340	345	350
Arg Ala Phe Thr Glu Ser Gln Pro Thr Asn Lys Lys Ile Ser Phe Gln		
355	360	365
Glu Ala Leu Gly Asn Thr Thr Arg Phe Gly Ile Arg Val Gly His Ala		
370	375	380
Leu Val Asp Ala Ile Ala Leu Val Tyr Asp Val Tyr Val Thr Ser Asp		
385	390	395
		400
Asp Glu Glu Gly Pro Arg Ser Cys Ala Glu Leu Ser Ala Ser Gln Ala		
405	410	415

Phe Glu Val Gly Val Leu Thr Ala Arg Lys Ile Arg Leu Ile Leu Asp
 420 425 430

Leu Tyr Arg His Arg Trp Leu His Thr Tyr Ser Thr Phe Arg Thr Arg
 435 440 445

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

Ile Phe Phe Val Lys Cys Gly Thr Val Lys Leu Arg Val Ala His Glu
 465 470 475 480

Ala Pro Arg Gln Ala Pro Leu Asp Val Leu Leu Ser Glu Met Thr Gly
 485 490 495

Ala Arg Asp Arg Val Thr Val Arg Phe Arg Ser Val Asp Thr Leu His
 500 505 510

Ala Gly Ser Glu Leu Asp Ala Glu Thr Val Arg Ser Asn Met Leu Asp
 515 520 525

Thr Leu Gly Ile Pro Val Val Pro Tyr Val Thr Ser Ile Ser Ala Val
 530 535 540

Ala Gln Ala Tyr Val Leu Gly Ile Val Asp Leu Thr Asp Val Leu Val
 545 550 555 560

Val Val Arg Lys Thr Tyr Glu Met Leu Arg Ala Gln Gly Pro Leu Ala
 565 570 575

Gln Pro Ala Arg Leu Leu Ser Leu Leu Asp His Phe His Asp Leu Glu
 580 585 590

Ala Leu Arg Ala Met Leu Phe Pro Gly Gly Lys Gly Ala Leu Pro Ala
 595 600 605

Ser Ala Pro Val Arg Val Arg Ala Thr Val Asp Tyr Leu Asp Glu Leu
 610 615 620

Gly Lys Val Gln Lys Ala Phe Ile Lys Arg Ala Ala Tyr Leu Arg Ala
 625 630 635 640

Val Pro Thr Arg Thr Glu Met Cys Ile Arg Glu Met Glu Arg Asn Ala
 645 650 655

Glu Ser His Tyr Asp Arg Ser Leu Lys Arg Gln Arg Gly Ala Ala Gly

660	665	670
Lys Ser Ala Pro Phe Thr Arg Ser Gln Phe Ser Ala Phe Val Ser Ala		
675	680	685
Phe Ala Glu Leu Val Cys Lys Phe Asp Val Glu Leu Ser Ser Val Gln		
690	695	700
Phe Ala Gly Gly Ala Glu Val His Gly Leu Ser Val Tyr Leu Ser Arg		
705	710	715
720		
Leu Val Arg Gln Ala Val Ala Ala Thr Glu Thr Thr Pro Phe Ser Ser		
725	730	735
Ala Gln Lys Lys Lys Ala Pro Pro Glu Ser Pro Val Ser Lys Ala Val		
740	745	750
Ala Glu Leu Ala Ala Thr Asn Ala Gly Thr Glu Lys Glu Lys Lys Asp		
755	760	765
Pro Lys Asn Met Gly Arg Gly Lys Thr Ala Cys Thr Leu Ser Asp Asp		
770	775	780
Val Arg Val Thr Phe Ala Thr Met Tyr Lys Ala Phe Cys Ala Asp Val		
785	790	795
800		
Ala Arg Asp Val Cys His Leu Leu Glu Thr Arg Leu Val Thr Ser Gly		
805	810	815
Val Leu Ser Asp Phe Ile Phe Leu Ala Gln Glu Arg Gly Arg Lys Tyr		
820	825	830
Gln Gly Pro Leu Arg Leu Pro His Leu Gly Arg Val Val Phe Ile Asp		
835	840	845
Glu His Gly Leu Asp Asp Phe Glu Val Ser His Gln Lys Pro Leu Thr		
850	855	860
Asp Val Ile Gly Ser Met Gly Ala Lys Leu Asp Glu Ala Ile Met Glu		
865	870	875
880		
Gln Ala Ser Ala Gly Phe Arg Phe Ala Lys Trp Pro Gly Leu Asp Ser		
885	890	895
Trp Asn Gln Trp Thr Gln Val Ala Ala Ser Leu Gln Leu Ile Val Asp		
900	905	910

Cys Gly Leu Leu Asn Arg Gly Thr Gln

915

920

<210> 270

<211> 966

<212> PRT

<213> Toxoplasma gondii

<400> 270

Met Arg Phe Pro Pro Ala Ser Cys His Ser Ala Ser Arg Lys Glu Glu

1

5

10

15

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

20

25

30

Leu Ala Thr Pro Gly Ser Ala Pro Asn Ser Ala Pro Leu Arg Pro Arg

35

40

45

Ile Arg Arg Pro Ser Phe Ser Phe Phe Pro Arg Phe Ser Asn Ser Phe

50

55

60

Ala Ser Ala Arg Cys Leu Leu Phe Phe Ser Leu Leu Leu Phe Val Ala

65

70

75

80

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

85

90

95

Glu Ala Gly Glu Val Asp Asn Ala Gln Pro Ala Ala Asp Pro Glu Val

100

105

110

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

115

120

125

Trp Lys His Gly Leu Ser Asn Arg Ile Thr Pro Ile Val Gln Val Glu

130

135

140

Asp Val Leu Val Ser Ser Gly Gly Ile Arg Arg His Gly Asp Ala Val

145

150

155

160

Tyr Gly Glu Asp Ala Arg Leu Arg Leu Gly Glu Pro Tyr Pro Gly Thr

165

170

175

Ala Ala Leu Val Asn Leu Leu Ser Arg Gly Pro Phe Pro Ala Gly Lys

180

185

190

Thr Pro Arg Ser Ser Met Thr Arg Pro Met Val Thr Ala Pro Leu Phe

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

Phe Phe Gly Gln Glu Pro Arg Ala His Gly Pro Leu Pro Val Ile Phe
 450 455 460

Val Arg Phe Arg Asn Val Glu Ile Gln Gln Ile Val Asp Pro Trp His
 465 470 475 480

Gly His Pro Ser Arg Tyr Leu Gln Leu Gln Arg Glu Gly Lys Ala Pro
 485 490 495

Ala Ser Asn Asn Phe Ala Arg Leu Thr Pro Val Pro Pro Glu Glu Ala
 500 505 510

Ser Gly Lys Gly His Ala Phe Asp Pro Glu Lys His Leu Gln His Ala
 515 520 525

Val Pro Ile Met Thr Tyr Arg Thr Thr Val Ser Ala Ala Ala Gln Ala
 530 535 540

His Val Met Asn Leu Ile Ser Ser Ala Asp Phe Ala Glu Leu Ala Ile
 545 550 555 560

Leu Thr Val Lys Asp Leu Arg Gly Arg Gly Pro Leu Phe Gln Pro Ala
 565 570 575

Thr His Glu Tyr Val Ser Ala Leu Lys Ser Asp Trp Lys Val Tyr Val
 580 585 590

Thr Leu Ala Lys Thr Pro Asn Leu Ile Glu Asp Lys Gln Leu Ala Glu
 595 600 605

Thr His Glu Leu Ile Leu Arg Ala Asn Glu Asp Phe Ser Ala Glu Arg
 610 615 620

Met His Cys Ile Lys Lys Tyr Val Leu Thr Met Ser Gln Glu Asp Pro
 625 630 635 640

Leu Phe Asp Phe Thr Lys Thr Phe Cys Tyr Asn Phe Pro Glu Val Arg
 645 650 655

Tyr Pro Ser Ser Ala Gly Gly Ser Glu Phe Val Ala Asn Ala Val Thr
 660 665 670

Ala Gly Leu Ala Leu Arg Glu Leu Phe Asn Phe Thr Val Trp Pro Ser
 675 680 685

Arg Ser Arg Gln Glu Asn Glu Asp Glu Ala Gln Ala Ser Gly Leu Ser

690	695	700	
Ala Ala Ser Gln His Val Arg Gly Val Arg Leu Pro Ser Pro His Pro			
705	710	715	720
Pro Met Arg Lys Glu Asp Arg Pro Ala Ser Arg Ala Glu Glu Ala Arg			
	725	730	735
Arg Ala Val Leu Glu Arg Pro Leu Ser Gly Ser Leu Leu Gln Ala Ser			
	740	745	750
Gln Leu Glu Gly Gln Thr Ser Gly Asp Ala Asp Glu Asn Ala Glu Ser			
	755	760	765
Arg Leu Ala Lys Asn Gln Glu Val Val Glu Glu Gly Ala Arg Ser Val			
	770	775	780
Asp Ser Glu Lys Glu Gly Gln Gly Leu Glu Ala Gly Ser His Gly Gln			
785	790	795	800
Ser Glu His Ala Glu Val Gly Gly Arg Glu Glu Thr His Ser Glu Glu			
	805	810	815
Gly Lys Gly Ala Ala Lys Ala Val Arg Glu Glu Glu Asn Leu Asn Lys			
	820	825	830
His Gln His Ala Gly Thr Val Ala Thr Phe His Gly Thr Ile Pro Glu			
	835	840	845
Ala Phe Ala Gln Lys Met Gln Glu Asn Phe Gly Pro Arg Trp Ile Ser			
	850	855	860
Leu Leu Gln Leu Leu Gly Ser Val Ser Leu Thr Asn Asp Tyr Leu Arg			
865	870	875	880
Val Leu Ser Trp Leu Ala Ser Glu Ala Asp Ser Asp Ala Met Thr Leu			
	885	890	895
Pro Ala Arg Arg Leu Leu Val Arg Arg Asp Ala Glu Val Ser Leu Ser			
	900	905	910
Leu Ser Ala Ala Leu Arg His His Val Ala Val Phe Tyr Glu Asn Gln			
	915	920	925
Val Glu Gly Asn Leu Ser His Pro Val Val His Lys His Glu Arg Gln			
	930	935	940

Tyr Lys Val Ala Glu Glu Gly Leu Arg Arg Phe Leu Arg Asp Leu Val
945 950 955 960

Ser Tyr Ser Ser Lys Lys
965

<210> 271

<211> 186

<212> PRT

<213> Toxoplasma gondii

<400> 271

Met Met Leu Ile Ala Leu Val Cys Met Leu Val His Arg Leu Asp Leu
1 5 10 15

Gly Ala Ala Val Ser Gln Asp Gly Arg Asp Leu Phe Val Gly Leu Pro
20 25 30

Lys Gly Ala Pro Leu Gly Pro Thr Phe Ile Gly Leu Thr Thr Pro Arg
35 40 45

Pro Pro Leu Ser Ser Leu Ser Ala Leu Gln Thr Phe Gly Ala Asp Gln
50 55 60

Arg Leu Asp Arg Pro Gly Asp Ser Pro Gly Tyr Tyr Val Glu Ala Lys
65 70 75 80

Gln Phe Tyr Arg Val Pro Pro Thr Arg Ser Ser Ala Thr Arg Asn Lys
85 90 95

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

Leu Gly Thr Glu Val Ala Asp Tyr Val Asp Arg Gln His Glu Gly Glu
115 120 125

Val Thr Asp Leu Glu Tyr Asp Arg Arg Met Gln Thr Thr Arg Thr Ala
130 135 140

Leu Gly Val Thr Arg Leu Ala Ser Leu Val Leu Ala Thr Phe Gly Gly
145 150 155 160

Val Arg Phe Met Leu Asp Lys Ala Ser Lys Trp Met Lys Ala Arg Lys
165 170 175

Val Glu Asp Ser Glu Lys Ser Glu Arg Arg

180 185

<210> 272

<211> 330

<212

> PRT

<213> Toxoplasma gondii

<400> 272

Met Asn Thr Gly Cys Leu Phe Leu Pro Ala Thr Arg His Ala Ala Ile

1 5 10 15

Gln Thr Ile Cys Val Val Ala Leu Ala Arg Gln Val Ala Asp Pro Asp

20 25 30

Ala Leu Val Phe Glu Arg Asp Phe Leu Glu Phe Ile Arg Ile Leu Ser

35 40 45

Ser Thr Gln Thr Val Phe Ser Ser Phe Gly Cys Pro Arg Ser His Val

50 55 60

Ala Leu Leu Ala Gln Ser Val Glu Arg Val Arg Glu Ala Asn Ala Val

65 70 75 80

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

85 90 95

Asp Asp Ala Gly Cys Ser Cys Ala Phe Phe Val Phe Thr Gly Arg Ala

100 105 110

Met Val Trp Arg Val Ser Ile Gly Cys Ala Val Leu Ala Thr Val Leu

115 120 125

Val Ala Gly His Glu Pro Val Ala Ser Ala Pro Tyr Lys Ala Tyr Gly

130 135 140

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

145 150 155 160

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

165 170 175

Glu Glu Lys Lys Leu Pro Leu Phe Phe Ile Asp Val Glu Asp Asn Lys

180 185 190

Gly Gln Gly Arg Asn Ser Glu Lys Gly Ala Thr Asp Asp Asp Val Ala

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

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

305 310 315 320
Glu Asn Ser Thr Arg Ala Ala Ser Ala Val
325 330

<210> 273

<211> 219

<212> PRT

<213> Toxoplasma gondii

<400> 273

Met Thr Arg Gly Phe Ala Phe Cys Leu Leu Phe Leu Ala Leu Phe Gly
1 5 10 15
Leu Phe Ser Val Ala Pro His Ser Ile Glu Ala Gly Glu Thr Pro Glu
20 25 30
Glu Thr Glu Ala Val Val Ala Ala Thr Glu Gln Gly Ala Ala Glu Val

35 40 45
Asp Glu Ala Thr Asp Glu His Glu Glu Asp Asp Asp Asp His Arg
50 55 60
Ala Asp Phe Glu Ser Leu Leu Gln Met Met Ser Lys Asp Met His Met
65 70 75 80

Asp Leu Ala Asn Asn Asn Met Ala Gly Val Ala Lys Val Leu Lys Glu
 85 90 95
 Leu Thr Asp His Ile Asp Ala Ala His Lys His Asp Pro Glu Ala His
 100 105 110
 Glu His Lys His Pro Leu Leu Lys Lys Ile Leu Thr Lys Arg Thr His
 115 120 125
 Asp Lys Met Val Thr Thr Leu Gln Lys Ile Tyr Ser Asn Val Pro Arg
 130 135 140
 Glu Glu Ile Asn Asp Gln Leu Gln Ala Val Met Ser Leu Leu Glu His
 145 150 155 160
 Val Lys Gln Asp Pro Asn Met Ser Pro Lys Gln Leu Leu Glu Lys Thr
 165 170 175
 Ala His Gln Leu Gly Met Pro Leu Thr Pro Asp Met Tyr Glu Asp Met
 180 185 190
 Gln Lys His Met Gly Trp Ala Ala Lys Leu Phe Gln Tyr Ile Ala Pro
 195 200 205
 Gly Gly Leu Asp Glu Glu Lys Ala Glu Glu Leu
 210 215
 <210> 274
 <211> 203
 <212> PRT
 <213> Toxoplasma gondii
 <400> 274
 Met Trp Leu Pro Val Tyr Val Pro Leu Leu Leu Val Phe Gly Val Ser

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

Ala Leu Val Val Ile Asp Ala Gly Ser Ser Ser Thr Arg Thr Asn Val

65 70 75 80

Phe Leu Ala Lys Thr Arg Ser Cys Pro Asn Lys Gly Arg Ser Ile Asp

85 90 95

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

100 105 110

Arg Val Val Leu Glu Glu Trp Leu Asp Thr Tyr Ala Gly Lys Asp Trp

115 120 125

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

130 135 140

Met His Glu Gly Ala Lys Lys Leu Met Gln Leu Leu Glu Glu Asp Thr

145 150 155 160

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

165 170 175

Lys Ala Leu Gly Ile Pro Ser Met Leu Cys Ser Thr Ala Gly Val Arg

180 185 190

Asp Phe His Glu Trp Tyr Arg Asp Ala Leu Phe

195 200

<210> 275

<211> 333

<212> PRT

<213> Toxoplasma gondii

<400> 275

Met Trp Leu Pro Val His Val Pro Leu Leu Leu Val Phe Gly Val Ser

1 5 10 15

Leu Ser Leu Pro His Gly Ser Leu Gly Thr Asp Ser Ser Ser Leu Arg

20 25 30

Gly Val Asp Ala Asp Thr Glu Lys Arg Ile Asn Val Gly Lys Thr His

35 40 45

Leu Gln Thr Leu Arg Asn Leu Glu Thr Arg Cys His Asp Ser Leu Gln

50 55 60

Ala Leu Val Val Ile Asp Ala Gly Ser Ser Ser Thr Arg Thr Asn Val
65 70 75 80
Phe Leu Ala Lys Thr Arg Ser Cys Pro Asn Arg Gly Arg Ser Ile Asp
85 90 95
Pro Asp Ser Ile Arg Leu Ile Arg Glu Gly Lys Arg Phe Thr Gly Leu
100 105 110
Arg Val Val Leu Glu Glu Trp Leu Asp Thr Tyr Ala Gly Lys Asp Trp
115 120 125
Glu Ser Arg Pro Val Asp Ala Arg Leu Leu Phe Gln Tyr Val Pro Gln
130 135 140
Met His Glu Gly Ala Lys Lys Leu Met Gln Leu Leu Glu Glu Asp Thr
145 150 155 160
Val Ala Ile Leu Asp Ser Gln Leu Asn Glu Glu Gln Lys Val Gln Val
165 170 175
Lys Ala Leu Gly Ile Pro Val Met Leu Cys Ser Thr Ala Gly Val Arg
180 185 190
Asp Phe His Glu Trp Tyr Arg Asp Ala Leu Phe Val Leu Leu Arg His
195 200 205
Leu Ile Asn Asn Pro Ser Pro Ala His Gly Tyr Lys Phe Phe Thr Asn
210 215 220
Pro Phe Trp Thr Arg Pro Ile Thr Gly Ala Glu Glu Gly Leu Phe Ala
225 230 235 240
Phe Ile Thr Leu Asn His Leu Ser Arg Arg Leu Gly Glu Asp Pro Ala
245 250 255
Arg Cys Met Ile Asp Glu Tyr Gly Val Lys His Cys Arg Asn Asp Leu
260 265 270
Ala Gly Val Val Glu Val Gly Gly Ala Ser Ala Gln Ile Val Phe Pro
275 280 285
Leu Gln Glu Gly Thr Val Leu Pro Ser Ser Val Arg Ala Val Asn Leu
290 295 300
Gln Arg Glu Arg Leu Leu Pro Glu Arg Tyr Pro Ser Ala Asp Val Val

305					310				315				320			
Ser	Val	Ser	Phe	Met	Gln	Leu	Gly	Arg	Pro	Val	Arg	Arg				
				325				330								
<210>	276															
<211>	439															
<212>	PRT															
<213>	Toxoplasma gondii															
<400>	276															
Met	Thr	Ala	Thr	Pro	Ala	Gly	Thr	Leu	Val	Arg	Leu	Tyr	Ser	Ser	Leu	
1				5				10				15				
Val	Ser	Gly	Gln	His	Lys	Ser	Ala	Asp	Gly	Asp	Cys	Asn	Phe	Ala	Phe	
			20			25			30							
Ser	Pro	Tyr	Ala	Val	Ser	Ala	Val	Leu	Ala	Gly	Leu	Tyr	Phe	Gly	Ala	
35						40						45				
Arg	Gly	Thr	Ser	Arg	Glu	Gln	Leu	Glu	Asn	His	Tyr	Phe	Asp	Gly	Arg	
50					55			60								
Ser	Ala	Ala	Asp	Ala	Ala	Ala	Cys	Leu	Asn	Glu	Ala	Ile	Pro	Ala	Val	
65	70				75				80							
Ser	Gln	Lys	Glu	Glu	Gly	Val	Asp	Pro	Asp	Ile	Gln	Ser	Ser	Val	Val	
85				90				95								
Leu	Gln	Ala	Ala	Asn	Arg	Leu	Tyr	Ala	Ser	Lys	Glu	Leu	Met	Glu	Ala	
100				105				110								
Phe	Leu	Pro	Gln	Phe	Arg	Glu	Phe	Arg	Glu	Thr	Leu	Glu	Lys	Ala	Leu	
115			120			125										
His	Thr	Glu	Ala	Leu	Leu	Ala	Asn	Phe	Lys	Thr	Asn	Ser	Asn	Gly	Glu	
130		135			140											
Arg	Glu	Lys	Ile	Asn	Glu	Trp	Val	Cys	Ser	Val	Thr	Lys	Arg	Lys	Ile	
145	150				155				160							
Val	Asp	Leu	Leu	Pro	Pro	Ala	Ala	Val	Thr	Pro	Glu	Thr	Thr	Leu	Leu	
165				170				175								
Leu	Val	Gly	Thr	Leu	Tyr	Phe	Lys	Gly	Pro	Trp	Leu	Lys	Pro	Phe	Val	
180			185			190										

Pro Cys Glu Cys Ser Ser Leu Ser Lys Phe Tyr Arg Gln Gly Pro Ser
195 200 205

Gly Ala Thr Ile Ser Gln Glu Gly Ile Arg Phe Met Glu Ser Thr Gln
210 215 220

Val Cys Ser Gly Ala Leu Arg Tyr Gly Phe Lys His Thr Asp Arg Pro
225 230 235 240

Gly Phe Gly Leu Thr Leu Leu Glu Val Pro Tyr Ile Asp Ile Gln Ser
245 250 255

Ser Met Val Phe Phe Met Pro Asp Lys Pro Thr Asp Leu Ala Glu Leu
260 265 270

Glu Met Met Trp Arg Glu Gln Pro Asp Leu Leu Asn Asp Leu Val Gln
275 280 285

Gly Met Ala Asp Ser Ser Gly Thr Glu Leu Gln Asp Val Glu Leu Thr
290 295 300

Ile Arg Leu Pro Tyr Leu Lys Val Ser Gly Asp Thr Ile Ser Leu Thr
305 310 315 320

Ser Ala Leu Glu Ser Leu Gly Val Thr Asp Val Phe Gly Ser Ser Ala
325 330 335

Asp Leu Ser Gly Ile Asn Gly Gly Arg Asn Leu Phe Val Ser Asp Val
340 345 350

Phe His Arg Cys Leu Val Glu Ile Asp Glu Glu Gly Thr Asp Ala Ala
355 360 365

Ala Gly Ala Ala Ala Gly Val Ala Cys Val Ser Leu Pro Phe Val Arg
370 375 380

Glu His Lys Val Ile Asn Ile Asp Arg Ser Phe Leu Phe Gln Thr Arg
385 390 395 400

Lys Leu Lys Cys Val Gln Gly Leu Arg Ala Gly Asn Ser Pro Ala Met
405 410 415

Arg Lys Asp Asp Asp Ile Leu Phe Val Gly Arg Val Val Asp Val Gly
420 425 430

Val Leu Gln Ser Gly Gly Glu

435

<210> 277

<211> 318

<212> PRT

<213> *Toxoplasma gondii*

<400> 277

Met Gly Lys Asn Pro Leu Leu Phe Leu Ala Gly Val Leu Val Cys Ser

1 5 10 15

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

20 25 30

Pro Arg Asn Leu Glu Leu Asn Cys Gly Gly Asp His Val Thr Tyr Ala

35 40 45

Asn His Cys Ile Arg Glu Cys His Gly Val Gly Leu Leu His Asp Gly

50 55 60

Pro Cys Ala Asp Gln Glu Asp Gln Gly Ser Ser Val Asn Glu Pro Ser

65 70 75 80

Glu Val Ala Asp Thr Thr Glu Gln Pro Ser Ile Thr Pro Ser Gly Glu

85 90 95

Glu Asp Arg Pro Pro Lys Asp Ala Pro Lys Glu Arg Lys Arg Leu Arg

100 105 110

Gly Cys Ala Cys Thr Arg Glu Leu Arg Leu Asn Cys Gly Val Asp Gly

115 120 125

Val Thr Tyr Ser Asn His Cys Val Arg Lys Cys Glu Arg Val Lys Leu

130 135 140

Leu His Glu Gly Pro Cys Arg Gly Gly Pro Gly Arg Thr Leu Phe Ser

145 150 155 160

Gln Gln Asp Asp Glu Ser Glu Asn Asp Ala Leu Glu Glu Glu Glu Gln

165 170 175

Arg Leu Gln Arg Thr Gln Ser Ser His Gln His Asp Asp Ala Glu Asn

180 185 190

Gly Ala Arg Ala Glu His Glu Gln Arg Leu Lys Gly Cys Pro Cys Pro

195 200 205

Leu Asn Leu Met Leu Asn Cys Gly Val Asp Gly Val Thr Tyr Asp Asn

210

215

220

His Cys Leu Arg Arg Cys Arg Arg Val Glu Leu Lys His Glu Gly Pro

225

230

235

240

Cys Glu Ala Asp Glu Gln Lys Gln Leu Pro Val Gln His Gly Asp Asn

245

250

255

Glu Ile Asp Val Pro Glu Arg Arg Ile Glu Asp Leu Lys Asp Cys Ala

260

265

270

Cys Pro Leu Ile Leu Thr Pro Asn Cys Gly Thr Asp Arg Lys Thr Tyr

275

280

285

Pro Asn Asn Cys Val Arg Glu Cys Ala Gly Val Lys Leu Leu His Glu

290

295

300

Gly Pro Cys Glu Gly Asp Thr Glu Glu Ile Trp Asp Asp Gln

305

310

315

<210> 278

<211> 87

<212> PRT

<213> Toxoplasma gondii

<400> 278

Met Pro Leu Pro Gln Ala Pro Glu Glu Leu Glu Gln Ala Pro Ala Ser

1

5

10

15

His Pro Glu Glu Ala Glu Gln Glu Val Pro Glu Arg Lys Thr Asp Ala

20

25

30

Gly Ser Glu Pro Glu Lys Asp Pro Glu Thr Asn Leu Gln Ala Ser Glu

35

40

45

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

50

55

60

Lys Cys Thr Asp Lys Arg Asp Glu Val Asp Leu Asp Val Leu Glu Ala

65

70

75

80

Glu Met Leu Glu Lys Ala Pro

85

<210> 279

<211> 383

<212> PRT

<213> *Toxoplasma gondii*

<400> 279

Met Asp Val Arg Tyr Gln Thr Arg Gly Ala Val Ala Ala Val Tyr Val

1 5 10 15

Leu Phe Arg Thr Val Val Gly Ala Val Leu Gly Leu His Cys Leu Lys

20 25 30

Ile Val Ser Ala Glu Val Gly Leu Thr His Gly Ile Met Ser Thr Glu

35 40 45

Phe Glu Val Glu Leu Arg Gly His Asn Trp Val Ile Asp Ser Gly Ala

50 55 60

Cys Leu Leu Gly Gln Pro Arg Asn Leu Val Val Asp Pro Val Leu Asp

65 70 75 80

Ser Glu Phe Met Thr Pro Gln Lys Leu Leu Thr Asp Arg Thr Gly Pro

85 90 95

Glu Leu Cys Ser Trp Leu Glu Lys Ile His Arg Gln His Met Glu Gln

100 105 110

Lys Pro Ala Trp Leu Ala Ala Tyr Gln Lys Phe Glu Lys Arg Phe Phe

115 120 125

Leu Leu Arg Leu Leu Gly Met Val Gly Lys Pro Ile Thr Phe Phe Pro

130 135 140

Glu Phe Thr Val Arg Ile Ile Val Lys His Phe Ser Leu Trp Gly Asp

145 150 155 160

Asp Arg Trp Gly Asn Ala Gln Pro Trp Ile Ala Ala Thr Phe Glu Tyr

165 170 175

Ala His Pro Glu Gly Ala Gly Gly Glu Leu Phe Leu His Ile Glu Lys

180 185 190

Val Phe Ser Met Glu Phe Ser Gly Arg Val Ala Lys Leu Val His Ile

195 200 205

Leu Leu Asn Pro Ser Ala Thr Phe Asn Gln Tyr Val Glu Leu His Arg

210 215 220
 Arg Lys Ser Ser Gly Val Pro Gly Asp Ser Gly Val Ser Gly Ile Arg
 225 230 235 240
 Arg Thr Leu Tyr Glu Arg Asp Leu Asn Ile Ser His Phe Pro Thr Ala

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

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

 370 375 380
 <210> 280
 <211> 224
 <212> PRT
 <213> Toxoplasma gondii
 <400> 280
 Met Ala Thr Thr His Leu Asn Lys Ser Val Ile Ala Gly Gly Ser Ile
 1 5 10 15
 Lys Thr Ile Lys Ala Leu Lys Lys Tyr Trp Asn Ser Pro Val Ser Asp
 20 25 30
 Ile Asp Asp Asn Ser Ser Glu Ala Lys Tyr Thr Met Leu Gln Met Ala

35 40 45
 Ile Leu Leu Asn Lys Lys Asn Val Val Glu Tyr Leu Ile Ser Gln Lys
 50 55 60
 Asp Val Asp Leu Thr Thr Arg Ala Thr Asp Gly Thr Thr Ala Leu Met
 65 70 75 80
 Thr Ala Val Gly Lys Asn Val Pro Val Asp Trp Ile Arg Ala Met Leu
 85 90 95
 Glu Arg Gly Ala Ala Asp Asn Ile Asn Val Glu Asp Asn Glu Gly His
 100 105 110

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

 Gly Gly Met Ser Pro Gly Leu Asp Glu His Pro Gly Ile Trp Ala Thr
 180 185 190
 Met Cys Gly Cys Gly Gly Arg Gln Gly Lys Asn Gly Thr Glu Val Val
 195 200 205
 Glu Val Val Asp Ala Gly Lys Ala Glu Leu Asn Pro Ala Gln Ala Ser
 210 215 220
 <210> 281
 <211> 553
 <212> PRT
 <213> Toxoplasma gondii
 <400> 281
 Met Thr Thr Gln Thr Thr Thr Lys Gly Ser Ser Arg Ile Ser Arg Cys

 1 5 10 15
 Thr Val Ala Leu Val Phe Ala Leu Ser Ala Cys Ala Thr Asp Ala Leu

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

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

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

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

 260 265 270

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

515 520 525
 Pro Ser Phe Trp Gly Glu Ala Asp Asn Tyr Gly Thr Ser Val Ile Leu
 530 535 540
 Asp Ser Ala Asn Ile Asp Lys Asp Phe
 545 550
 <210> 282
 <211> 569
 <212> PRT
 <213> *Toxoplasma gondii*
 <400> 282
 Met Ile Cys Ser Ile Met Gly Gly Leu Arg Ser Leu Arg Ala Ala Arg
 1 5 10 15
 Pro Tyr Ser His Gln Ser Asn Thr Glu Thr Lys His Met Gly Leu Val
 20 25 30
 Gly Val Ala Ser Leu Leu Val Leu Val Ala Asp Cys Thr Ile Phe Ala
 35 40 45
 Ser Gly Leu Ser Ser Ser Thr Arg Ser Arg Glu Ser Gln Thr Leu Ser
 50 55 60
 Ala Ser Thr Ser Gly Asn Pro Phe Gln Ala Asn Val Glu Met Lys Thr
 65 70 75 80
 Phe Met Glu Arg Phe Asn Leu Thr His His His Gln Ser Gly Ile Tyr
 85 90 95
 Val Asp Leu Gly Gln Asp Lys Glu Val Asp Gly Thr Leu Tyr Arg Glu
 100 105 110
 Pro Ala Gly Leu Cys Pro Ile Trp Gly Lys His Ile Glu Leu Gln Gln
 115 120 125
 Pro Asp Arg Pro Pro Tyr Arg Asn Asn Phe Leu Glu Asp Val Pro Thr
 130 135 140
 Glu Lys Glu Tyr Lys Gln Ser Gly Asn Pro Leu Pro Gly Gly Phe Asn
 145 150 155 160
 Leu Asn Phe Val Thr Pro Ser Gly Gln Arg Ile Ser Pro Phe Pro Met
 165 170 175

Glu Leu Leu Glu Lys Asn Ser Asn Ile Lys Ala Ser Thr Asp Leu Gly
 180 185 190
 Arg Cys Ala Glu Phe Ala Phe Lys Thr Val Ala Met Asp Lys Asn Asn
 195 200 205
 Lys Ala Thr Lys Tyr Arg Tyr Pro Phe Val Tyr Asp Ser Lys Lys Arg
 210 215 220
 Leu Cys His Ile Leu Tyr Val Ser Met Gln Leu Met Glu Gly Lys Lys
 225 230 235 240
 Tyr Cys Ser Val Lys Gly Glu Pro Pro Asp Leu Thr Trp Tyr Cys Phe
 245 250 255
 Lys Pro Arg Lys Ser Val Thr Glu Asn His His Leu Ile Tyr Gly Ser
 260 265 270
 Ala Tyr Val Gly Glu Asn Pro Asp Ala Phe Ile Ser Lys Cys Pro Asn
 275 280 285
 Gln Ala Leu Arg Gly Tyr Arg Phe Gly Val Trp Lys Lys Gly Arg Cys
 290 295 300
 Leu Asp Tyr Thr Glu Leu Thr Asp Thr Val Ile Glu Arg Val Glu Ser
 305 310 315 320
 Lys Ala Gln Cys Trp Val Lys Thr Phe Glu Asn Asp Gly Val Ala Ser
 325 330 335
 Asp Gln Pro His Thr Tyr Pro Leu Thr Ser Gln Ala Ser Trp Asn Asp
 340 345 350
 Trp Trp Pro Leu His Gln Ser Asp Gln Pro His Ser Gly Gly Val Gly
 355 360 365
 Arg Asn Tyr Gly Phe Tyr Tyr Val Asp Thr Thr Gly Glu Gly Lys Cys
 370 375 380
 Ala Leu Ser Asp Gln Val Pro Asp Cys Leu Val Ser Asp Ser Ala Ala
 385 390 395 400
 Val Ser Tyr Thr Ala Ala Gly Ser Leu Ser Glu Glu Thr Pro Asn Phe
 405 410 415
 Ile Ile Pro Ser Asn Pro Ser Val Thr Pro Pro Thr Pro Glu Thr Ala

420 425 430
 Leu Gln Cys Thr Ala Asp Lys Phe Pro Asp Ser Phe Gly Ala Cys Asp
 435 440 445
 Val Gln Ala Cys Lys Arg Gln Lys Thr Ser Cys Val Gly Gly Gln Ile
 450 455 460
 Gln Ser Thr Ser Val Asp Cys Thr Ala Asp Glu Gln Asn Glu Cys Gly

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

 530 535 540
 Pro Ser Phe Trp Asp Glu Ala Glu Glu Asn Ile Glu Gln Asp Gly Glu
 545 550 555 560
 Thr His Val Met Val Glu Gly Asp Tyr
 565
 <210> 283
 <211> 714
 <212> PRT
 <213> Toxoplasma gondii
 <400> 283
 Met Cys Pro Arg Val Ser Val Asp Ala Val Thr Val Leu Gly Thr Ala
 1 5 10 15
 Leu Leu Leu Cys Leu Glu Gly Thr Arg Leu Ser Ser Ile Val Pro Pro

 20 25 30
 Ser Ser Val Pro Phe Ala Leu Pro Ala Gln Cys Leu Asn Ala Asn Gln
 35 40 45
 Arg Leu Gln Gln Gly Val Met Ala Arg Ala Trp Ser Ala Thr Gln Ser
 50 55 60

Asp Asp Asp Glu Ser Pro Ala Pro Ile Phe Pro Glu Ser Asp Cys Thr
 65 70 75 80
 Tyr Pro Ala Asp Asn Asn Phe Glu Lys Ile Ile Thr Thr Ala His Leu

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

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

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

 275 280 285
 Ala Leu Thr Asp Asn Asp Arg Glu Lys Leu Thr Lys Gly Val Ser Gly
 290 295 300
 Phe Gly Leu Thr Ile Asn Ile Leu Ala Gly Glu Ala Val Ala Cys Cys

305 310 315 320
 Pro Ser Ala Leu Lys Asp Ala Leu Ala Ala Val Pro Lys Pro Val Leu
 325 330 335
 Leu Pro Ser Ala Ala Val Pro Gly Val Ile Gly Val Ala Glu Ser Glu

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

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

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

 530 535 540
 Ala Asn Arg Leu Cys Thr Thr Arg Gly Val Leu Ser Ala Arg Ala Ala
 545 550 555 560

Glu Ser Asn Ala Ala Asn Thr Asp Ala Ala Gly Ala Ala Thr Ala Ala
 565 570 575
 Asp Thr Phe Cys Leu Ser Val Val Arg Gly Cys Pro Val Met Phe Pro
 580 585 590
 Pro Ser Ala Val Glu Ile Asn Ala Asp Gln Gly Asp Glu Asp Thr Val
 595 600 605
 Asn Leu Val Lys Ala Ala Ala Ser Gly Asn Ala Ala Val Ile Gly
 610 615 620
 Pro Asp Gly Glu Lys Cys Asn Phe Val Cys Val Asp Ala Ser Asn Asn
 625 630 635 640
 Ser Ala Gln Ser Ala Thr Asn Gly Ala Val Ser Thr Asp Ala His Ala
 645 650 655
 Ala Glu Asp Asp Ala Leu Ala Ala Lys Ser His Ala Glu Ala Val Ala
 660 665 670
 Asn Leu Lys Thr Glu Glu Phe Glu Leu Lys Ser Phe Glu Tyr Leu Pro
 675 680 685
 Lys Ser Gly Val Val Cys Gly Tyr Thr Cys Val Ser His His Asp Glu
 690 695 700
 Thr Glu Gly Gly Thr Val Phe Glu Gly Ala
 705 710
 <210> 284
 <211> 877
 <212> PRT
 <213> Toxoplasma gondii
 <400> 284
 Met Lys Pro Ser Ser Leu Arg Ile Leu Leu Val Ala Trp Thr Ile Ile
 1 5 10 15
 Ser Asp Ala Glu Leu Asn His Phe Ser Ser Gln Ala Pro Leu Ser Trp
 20 25 30
 Pro Arg Cys Val Val Val Ser Ala Ala Asp Asp Ala Gln Arg Asp Arg
 35 40 45
 Gly Asp Thr Thr Ala Ala Ser Ser Ser Arg Asp Glu Glu Leu Glu Ala

50 55 60
 Ala Gly Pro Ala Asp Glu Ala Lys Lys Ala Ala Gly Glu Asn Ala Arg

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

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

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

 260 265 270
 Ile Glu Leu Ala Trp Glu Ser Gly Glu Gly Gly Glu Lys Pro Tyr Met
 275 280 285
 Lys Cys Glu Glu Gly Gly Leu Tyr Val Pro Val Ile Val Thr Asn Val
 290 295 300

Glu Asp Gln Glu Pro Tyr Arg Val Glu Leu Ser Pro Thr Lys Phe Trp
 305 310 315 320
 Ser Ala Ala Ser Ser Arg Thr Gly Arg Leu Tyr Val Ile Pro Glu Gln

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

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

 450 455 460
 Leu Ser Arg Asp Arg Val Thr Pro Gln Gly Leu Thr Glu Gln Glu Ser
 465 470 475 480
 Arg Thr Val Gly Lys Thr Glu Glu Thr Asp Thr Ala Ala Ser Arg Ser
 485 490 495
 Ala Glu Leu Thr Gly Ala Thr Arg Gly Leu Val Leu Met Phe Leu Thr
 500 505 510
 Glu Glu Asp Gly Leu Gly Phe Glu Leu Pro Leu Pro Val Leu Val Asp

 515 520 525
 Arg Val Leu Phe Met Val Lys Gln Thr Gln Glu Ala Ala Pro Leu His
 530 535 540
 Leu Leu Ala Tyr Leu Thr Val Arg Pro Cys Lys Arg Pro Ile His Asp

545 550 555 560
 Pro Ile Phe Gly Gln Ser Tyr Glu Pro Val Gln Glu Thr Thr Val Lys
 565 570 575
 Asn Arg Met Gly Gly Gly Gly Glu Gly Ser Gly Lys Glu Ser Gly Gly

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

 645 650 655
 Thr Gln Cys Ile Val Ala Ala Ala Pro Ala Thr Pro Lys Ser Asp Ser
 660 665 670
 Pro Asn Arg Pro Arg Leu Arg Ala Arg Leu Val Cys Pro Ser Leu Glu
 675 680 685
 His Leu Phe Ile Leu Leu Arg Glu Lys Asp Ala Ser Asp Arg Glu Tyr
 690 695 700
 Asn Ala Phe Lys Arg Thr Lys Asn Arg Gln Met Ile Lys Gly Ala Val

 705 710 715 720
 Val Gly Leu Phe Gly Leu Phe Leu Ala Tyr Arg Gly Leu Val Gly Leu
 725 730 735
 Thr Arg Asn Pro Met Met Ala Arg Glu Leu Phe Ala His Val Ile Gly
 740 745 750
 Arg Glu His Val Gly Asn Gln Pro Tyr His Phe Phe Pro Ser Glu Arg
 755 760 765
 Gln Leu Tyr Arg Phe Val Gly Leu Arg Ser Leu Gly Arg Ala Leu Gln

 770 775 780
 Phe Arg Arg Tyr Asn Glu Ala Met Gly Asn Ala Gly Val Arg Ala Gln
 785 790 795 800

Val Gly Ile Ser Leu Trp Thr Val Ser Leu Leu Ala Leu Thr Ala Leu
805 810 815
Leu Ala Ile Arg Leu Gly Arg Gly Thr Arg His Phe Val Arg Asn Arg
820 825 830
Lys Arg Val Ser Asn Ile Lys Gly Glu Leu Gln Arg Arg Pro Ile Ile
835 840 845
His Glu Glu Gln Ala Pro Val Pro Glu Leu Glu Glu Ala Glu Asp Glu
850 855 860
Cys Ser Thr Val Asp Val Thr Tyr Leu Ser Phe Leu Tyr
865 870 875
<210> 285
<211> 290
<212> PRT
<213> *Toxoplasma gondii*
<400> 285
Met Ser Ser His Asp Leu Arg Leu Cys Arg Pro Arg Arg Gln Ser Lys
1 5 10 15
Gly Ser Arg Gln Ser Pro Ala Phe Ser Ala Gly Arg Leu Cys Ser Ser
20 25 30
Trp Gly Ser Leu Cys Val Cys Arg Arg Val Pro Arg Thr Lys Leu Gly
35 40 45
Gly Ser Pro Ala Pro Arg Thr Ala Gly Ile His Arg Asp Ser Lys Cys
50 55 60
Cys Ala Thr Ala Met Met Pro Phe Pro Lys Arg Ser Leu Ser Leu Val
65 70 75 80
Cys Leu Leu Phe Cys Val Val Thr Ala Ala Gly Thr Leu Pro Arg Gln
85 90 95
Pro Val Ala Asp Ala Phe Arg Leu Glu Asn Gln Gly Val Gln Asp Ser
100 105 110
His Ala Asn Ser Asp Ala Met Gln Pro Ser Leu Gly Ser Ala Thr Asn
115 120 125
His Lys Ala Thr Gly Thr Thr Ser Phe Val Ser Val Asn Glu Asn Glu

130 135 140

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

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

 Met Leu Ala Gly Thr Glu Arg Thr Cys Arg Thr Gly Gln Gln Lys Phe
 275 280 285
 Lys Lys
 290
 <210> 286
 <211> 698
 <212> PRT
 <213> Toxoplasma gondii
 <400> 286

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

35	40	45	
Tyr Pro Ala Trp Phe Asp Glu Ser Leu His Pro Ser Lys Phe Pro Asn			
50	55	60	
Ala Gln Glu Ala Leu Ser Gln Ile Leu Tyr Tyr Leu Asp Glu Phe His			
65	70	75	80
Glu Asn Lys Tyr Ser Gly Asp Phe Ser Val Ile Thr Gly His Leu Asp			
85	90	95	
Ala Phe Leu Lys Gly Asp Pro Ser Leu Ile Leu Lys Thr His Glu Phe			
100	105	110	
Ile Leu Leu Ala Ala Val Asn Gly Asp Ser Gln Gln Ile Ile Ala Lys			
115	120	125	
Ile Met Ala Met Ser Gln Pro Thr Gln Glu Ile Ile Gln Ala Ile Ile			
130	135	140	
Gln Gln Tyr Ala Asp Ala Asp Asn Gly Ser Ser Asn Asp Thr Pro Thr			
145	150	155	160
Asn Phe Ser Arg Met Ala Ser Glu Ala Ala Ala Ala Arg Arg Glu Pro			
165	170	175	
Ser Ile Ala Asp Asp Leu Gly Leu Gly Arg Ser Ser Ser Ala Val Gly			
180	185	190	
Gly His Leu Ala Pro Val Leu Gln Lys Val Gln Asp Glu Leu Ser Gln			
195	200	205	
Ile Lys Ala Glu Leu Arg Lys Thr Lys Asn Ala Leu Thr Glu Ser Glu			
210	215	220	
Ser Gln Arg Glu Thr Leu Ser Asp Lys Leu Gln Leu Ala Glu Lys Glu			
225	230	235	240
Arg Glu Glu Glu Lys Thr Lys Arg Met Val Leu Glu Gln Gln Leu Ser			
245	250	255	
Ala Lys Lys Asp Val Leu Val Lys Asp Phe Thr Glu Gln Ile Glu Asp			
260	265	270	
Ser Asp Lys Gln Arg Ala Lys Leu Lys Glu Glu Leu Glu Asn Glu Lys			
275	280	285	

Lys Glu Arg Lys Lys Ala Asp Glu Lys Asn Arg Ala Val Val Ala Glu

290

295

300

Leu Lys Glu Glu Met Asp Leu Leu Lys Gln Glu Ala Arg Arg Val Ser

305

310

315

320

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

325

330

335

Ala Ala Leu Lys Glu Lys Met Thr Gln Leu Glu Leu Gln Asn Lys Ala

340

345

350

Tyr Met Asp Arg Ile Val Glu Gly Glu Ala Asp Ser Val Gly Ala Leu

355

360

365

Gly Leu Arg Lys Gln Ile Asp Ser Tyr Lys Glu Arg Val Ala Asp Val

370

375

380

Glu Glu Arg Leu Ser Ser Met Thr Ala Glu Lys Glu Ala Leu Ser Asn

385

390

395

400

Leu Lys Glu Glu Val Glu Lys Gln Leu Ser Ala Ala Glu Lys Lys Leu

405

410

415

Glu Val Lys Glu Leu Glu Val Ala Gln Leu Glu Ala Lys Ile Glu Ala

420

425

430

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

435

440

445

Lys Asn Lys Gly Arg Asp Ile Ala Glu Glu Leu Ala Asn Met Ala Lys

450

455

460

Lys Asn Lys Ala Asp Gly Val Asp Thr Ala Ala Arg Ile Ala Glu Leu

465

470

475

480

Ser Asn Glu Val Asp Asp Leu Lys Arg Val Lys Gln Arg Leu Glu Lys

485

490

495

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

500

505

510

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

515

520

525

Val Glu Lys Thr Ala Lys Gln Glu Glu Glu Ile Lys Gln Leu Arg Glu

530 535 540
 Ser Lys Asp Asp Met Ala Lys Gln Met Met Glu Ala Leu Ser Lys His

 545 550 555 560
 Glu Lys Gly Ser Gly Gly Asp Glu Thr Ser Ala Ala Lys Val Ala Met

 565 570 575
 Leu Glu Thr Gln Leu Glu Phe Glu Lys Lys Gln Ala Ser Met Arg Glu

 580 585 590
 Asp Ile Val Arg Ala Lys Val Glu Lys Glu Met Glu Asn Val His Ser

 595 600 605
 Thr Leu Lys Asn Gln Leu Gln Leu Arg Glu Arg Glu Ser Asn Phe Tyr

 610 615 620
 Arg Lys Ala Val Glu Glu Asn Ala Glu Ser Ser Lys Lys Glu Met Lys
 625 630 635 640
 Leu Leu Ser Ser Val Leu Tyr Asp Leu Gly Leu Arg Phe His Arg Leu

 645 650 655
 Gln Ala Tyr Cys Asp Gln Leu Lys Asn Glu Asn Glu Ala Ile Gln Leu

 660 665 670
 Arg Val Arg Leu His Gln Gln Ser Asn Ala Ser Met Ala Asp Ser Ile

 675 680 685
 Ala Thr Asp Ser Val Thr Pro Arg Glu Ala

 690 695
 <210> 287
 <211> 351
 <212> PRT
 <213> Toxoplasma gondii
 <400> 287
 Met Phe Gly Glu Leu Cys Val Glu Leu Ala Phe Pro Phe Leu Arg Gln
 1 5 10 15
 Ala Val Ser Val Met Phe Ser Arg Ala Ser Leu Gly Arg Pro Gly Val

 20 25 30
 Pro Arg Leu Pro Gly Arg Pro Val Cys Leu Leu Leu Phe Ala Ser Leu

35	40	45	
Cys Ser Cys Leu Val Gln Lys Cys Thr Phe Leu Pro Val Ser Ala Phe			
50	55	60	
Arg Arg Ser Glu Gly Asn Leu Ser Arg Gly Leu Ser Ala Glu Gln His			
65	70	75	80
Ile Arg Asn Lys Ser Gly Arg Arg Gln Leu Ser Glu Ile Asp Gly Gly			
85	90	95	
Asn His Phe Asp Val Glu Pro Ala Ser Phe Leu Gly Leu Leu Gly Glu			
100	105	110	
Ser Pro Glu Asp Ala Asp Ser Ser Ser Thr Lys Ala Glu Asp Ser Asp			
115	120	125	
Ser Glu Gly Gly Thr Ser Pro Ala Ala Thr Glu Asp Gln Asn Gly Asn			
130	135	140	
Glu Ser Asp Ser Gln Gln Ser Glu Ser Ser Gly Ala Val Glu Lys Arg			
145	150	155	160
Thr Ala Ala Lys Glu Ala Pro Glu Ala Gln Pro Glu Lys Gln Glu Glu			
165	170	175	
Pro Ser Lys Asn Glu Ala Gln Glu Ala Lys Gly Thr Ala Ala Ala Ala			
180	185	190	
Ser Arg Gln Asp Asp Thr Val Ile Gly Glu Gly Lys Asn Pro Glu Glu			
195	200	205	
Leu Thr Asp Asp Asp Phe Lys Gln Met Ser Thr Ser Gln Gly Leu Ser			
210	215	220	
Ile Leu Phe Ser Gln Gly Lys Gly Met Met Gln Glu Val Gln His Thr			
225	230	235	240
Leu Asp Gly Val Asn Ala Val Val Ser Ile Thr Glu Leu Met Gly Lys			
245	250	255	
Val Arg Glu Asp Ile Arg Lys Asp Val Glu Ala Leu Asn His Thr Val			
260	265	270	
Thr Glu Glu Tyr Gln Asn Ile Glu Gln Leu Arg Gln Leu Gln Asp Ala			
275	280	285	

Gln Thr Ala Val Leu Arg Ser Gln Leu Asn Tyr Leu Ile Pro Leu Asn

290

295

300

Arg Gln Glu Ala Ala Ala Leu Pro Glu Met Pro Gly Glu Val Leu Gln

305

310

315

320

Ser Gly Ser Ser Ser Leu Ser Phe Tyr Ser Leu Phe Gly Ser Val Cys

325

330

335

Ala Ala Val Val Ser Val Leu Leu Ser Ala Ala His Val Ser Ser

340

345

350

<210> 288

<211> 330

<212> PRT

<213> Toxoplasma gondii

<400> 288

Met Lys Leu Ala Ala Val Ser Ser Ala Ala Phe Ala Ala Ala Phe Phe

1

5

10

15

Pro Ala Val Val Asn Ala Arg Lys Val Gly Asn Pro Ala Ala Gln Pro

20

25

30

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

35

40

45

Leu Glu Leu Val Glu Val Pro Cys Asn Ser Val His Val Gln Gly Val

50

55

60

Met Thr Pro Asn Gln Met Val Lys Val Thr Gly Ala Gly Trp Asp Asn

65

70

75

80

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

85

90

95

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

100

105

110

Asp Gly Val Pro Ser Asp Lys Ala Gly Lys Cys Phe Leu Lys Asn Phe

115

120

125

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

130

135

140

Ile Lys Ser His Asn Asp Ala Phe Met Phe Val Cys Ser Ser Asn Asp
 145 150 155 160
 Gly Ser Ala Leu Gln Cys Asp Val Phe Ala Leu Asp Asn Thr Asn Ser
 165 170 175
 Ser Asp Gly Trp Lys Val Asn Thr Val Asp Leu Gly Val Ser Val Ser
 180 185 190

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

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

Asn Gly Arg Leu Pro Ser Asp Asp Glu Ala
 325 330

<210> 289

<211> 376

<212> PRT

<213> Toxoplasma gondii

<400> 289

Met His Thr Lys Met Thr Asp Gly Ala Lys Leu Tyr Arg Arg Ser Met
 1 5 10 15
 Thr Thr Ala Thr Thr Thr Gly Phe Phe Leu Leu Ala Cys Trp Phe Leu

20	25	30	
Pro Ser Ser Cys Ile Gln Gly Ser Glu Ala Leu Ser Thr Thr Ala Thr			
35	40	45	
Thr Gln Pro Ile Ser Asn Val Thr Arg Tyr Pro Glu Gln His Thr Val			
50	55	60	
Ala Arg Ser Ala Ala Asp Val Ala Lys Ala Leu Ala Glu Lys Val Ala			
65	70	75	80
Arg Glu Ala Met Lys Asn Ala Tyr Asn Asp Val Phe Arg Asn Trp Thr			
85	90	95	
Gly Ile Ala His Pro Asp Phe His Asn Gly Asp Ala Glu Thr Cys Lys			
100	105	110	
Ile Val Leu Ser Phe Asp Val Ala Lys Lys Lys Asn Ala Met Gly Ser			
115	120	125	
Val Thr Lys Ile Leu Ser Val Thr Val Asn Asn Ala Arg Gly Gln Leu			
130	135	140	
Thr Val Lys Tyr Leu Glu Arg Pro Asn Val Arg Asn Ala Thr Asn Val			
145	150	155	160
Arg Arg Ala Ser Ser Trp Val Arg Arg Lys Leu Ala Leu Glu Thr Ala			
165	170	175	
Asp Glu Val Val Ser Val Thr Glu Thr Ile Asp Val Pro Gln Ala Cys			
180	185	190	
Ile Ala Asp Asn His Ser Arg Tyr Phe Val Val Thr Arg Arg Lys Asn			
195	200	205	
Val Ile Asp Thr Arg Val Phe Ala Val Val Ile Glu Leu Glu Leu His			
210	215	220	
Pro Gly Pro Tyr Leu Val Pro Arg Asp Ile Ser Arg Ile Ala Glu Leu			
225	230	235	240
Asp Arg Ile Leu Lys Glu His Glu Arg Glu Thr Phe Thr Glu Gly Lys			
245	250	255	
Trp Val Thr Leu Pro Gly Cys Met Met Leu Ile Arg Val Arg Glu Thr			
260	265	270	

Leu Lys Arg Ala Pro Arg Leu Thr Ile Asp Ala Tyr Arg Gly Ser Val
275 280 285

Gln Phe Arg Glu Asp Glu Leu Lys Ser Leu Gly Ser Gln Ala Leu Pro
290 295 300

Gln Gly Cys Thr Trp Asp Gly Pro Ser Ala Val Gly Val Val Thr Arg
305 310 315 320

His Asp Arg Ser Ala Asp Ala Asn Leu Trp Asp Val Leu Leu Phe Met
325 330 335

Ala Asp Ala Pro Ser His Val Gln Phe Glu Tyr Thr Leu Pro Lys Glu
340 345 350

Ala Asp Val Glu Arg Asn Ser Asp Leu Ser Ser Gly Phe Ala Ser Gly
355 360 365

Pro Gly Glu Gln Asp Asp Asn Ile
370 375

<210> 290

<211> 456

<212> PRT

<213> *Toxoplasma gondii*

<400> 290

Met Gly Gln Ala Leu Phe Leu Thr Val Leu Leu Pro Val Leu Phe Gly
1 5 10 15

Val Gly Pro Glu Ala Tyr Gly Glu Ala Ser His Ser His Ser Pro Ala
20 25 30

Ser Gly Arg Tyr Ile Gln Gln Met Leu Asp Gln Arg Cys Gln Glu Ile
35 40 45

Ala Ala Glu Leu Cys Gln Gly Gly Leu Arg Lys Met Cys Val Pro Ser
50 55 60

Ser Arg Ile Val Ala Arg Asn Ala Val Gly Ile Thr His Gln Asn Thr
65 70 75 80

Leu Glu Trp Arg Cys Phe Asp Thr Ala Ser Leu Leu Glu Ser Asn Gln
85 90 95

Glu Asn Asn Gly Val Asn Cys Val Asp Asp Cys Gly His Thr Ile Pro

100	105	110	
Cys Pro Gly Gly Val His Arg Gln Asn Ser Asn His Ala Thr Arg His			
115	120	125	
Glu Ile Leu Ser Lys Leu Val Glu Glu Gly Val Gln Arg Phe Cys Ser			
130	135	140	
Pro Tyr Gln Ala Ser Ala Asn Lys Tyr Cys Asn Asp Lys Phe Pro Gly			
145	150	155	160
Thr Ile Ala Arg Arg Ser Lys Gly Phe Gly Asn Asn Val Glu Val Ala			
165	170	175	
Trp Arg Cys Tyr Glu Lys Ala Ser Leu Leu Tyr Ser Val Tyr Ala Glu			
180	185	190	
Cys Ala Ser Asn Cys Gly Thr Thr Trp Tyr Cys Pro Gly Gly Arg Arg			
195	200	205	
Gly Thr Ser Thr Glu Leu Asp Lys Arg His Tyr Thr Glu Glu Glu Gly			
210	215	220	
Ile Arg Gln Ala Ile Gly Ser Val Asp Ser Pro Cys Ser Glu Val Glu			
225	230	235	240
Val Cys Leu Pro Lys Asp Glu Asn Pro Pro Val Cys Leu Asp Glu Ser			
245	250	255	
Gly Gln Ile Ser Arg Thr Gly Gly Gly Pro Pro Ser Gln Pro Pro Glu			
260	265	270	
Met Gln Gln Pro Ala Asp Arg Ser Asp Glu Arg Gly Gly Gly Lys Glu			
275	280	285	
Gln Ser Pro Gly Gly Glu Ala Gln Pro Asp His Pro Thr Lys Gly Gly			
290	295	300	
Asn Ile Asp Leu Pro Glu Lys Ser Thr Ser Pro Glu Lys Thr Pro Lys			
305	310	315	320
Thr Glu Ile His Gly Asp Ser Thr Lys Ala Thr Leu Glu Glu Gly Gln			
325	330	335	
Gln Leu Thr Leu Thr Phe Ile Ser Thr Lys Leu Asp Val Ala Val Gly			
340	345	350	

Ser Cys His Ser Leu Val Ala Asn Phe Leu Asp Gly Phe Leu Lys Phe
355 360 365

Gln Thr Gly Ser Asn Ser Ala Phe Asp Val Val Glu Val Glu Glu Pro
370 375 380

Ala Gly Pro Ala Val Leu Thr Ile Gly Leu Gly His Lys Gly Arg Leu
385 390 395 400

Ala Val Val Leu Asp Tyr Thr Arg Leu Asn Ala Ala Leu Gly Ser Ala
405 410 415

Ala Tyr Val Val Glu Asp Ser Gly Cys Ser Ser Ser Glu Glu Val Ser
420 425 430

Phe Gln Gly Val Gly Ser Gly Ala Thr Leu Val Val Thr Thr Leu Gly
435 440 445

Glu Ser Pro Thr Ala Val Ser Ala
450 455

<210> 291

<211> 198

<212> PRT

<213> Toxoplasma gondii

<400> 291

Met Ala Leu Ser Ser Leu Asn Asn Ile Arg Pro Phe Ser Gly Leu Leu
1 5 10 15

Gly Cys Gly Leu Leu Phe Gly Ala Leu Val Val Val Val Ala Cys Val
20 25 30

Phe Ser Val Pro Val Glu Ala Gly Val Leu Arg Lys Val Ala Gly Ala
35 40 45

Gly Ser Leu Gln Ala Ser Ile Gly Glu His Asp Phe Phe Asn Asp Tyr
50 55 60

Asp Gln Asp Glu Glu Tyr Arg Lys Arg Gln Gln Glu Leu Gln Asn Gln
65 70 75 80

Ser Pro Glu Glu Val Glu Glu Ala Lys Arg Lys Tyr His Glu Glu Leu
85 90 95

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

Arg Leu Met Gln Gln Arg Lys Lys Asp Gln Glu Glu Arg Glu Leu Ala
165 170 175
Arg Lys Asn Ser Asp Lys Val Met Glu Glu Leu Lys Glu Lys Leu Ala
180 185 190

Arg Arg Arg Lys Ser Met
195

<210> 292

<211> 204

<212> PRT

<213> Toxoplasma gondii

<400> 292

Met Gln Leu Lys Lys Leu Ser Val Val Ser Ile Thr Leu Leu Gly Leu
1 5 10 15

Phe Lys Phe Val Asn Gly Val Ser Glu Gly Val Val Val Pro Val Arg
20 25 30

Phe Gly Ser Glu Thr Ala Arg Ala Asp Leu Leu Asn Gln Val Ser Glu
35 40 45

Thr Val Phe Ser Leu Val Glu Thr Thr Glu Asp Asp Lys Ser Ala Ala
50 55 60

Ser Ile Val Arg Gly Ala Phe Arg Ser Ala Leu Lys Glu Ile Leu Val
65 70 75 80

Ala Val Lys Gly Glu Val Gln Gln Thr Cys Glu Glu Leu Ala Asp Leu
85 90 95

Ala Ala Arg Lys Ile His Glu Ala Glu Glu Arg Gly Glu Gly Arg Leu

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

 Glu Arg Lys Phe Val Asp Thr Leu Lys Thr Leu Ala Lys Gly Ala Leu
 145 150 155 160
 Lys Thr Phe Val Glu Pro Met Lys Ala Ala Leu Val Asp Gly Ile Arg
 165 170 175
 Pro Met Leu Pro Lys Ile Lys Glu Val Ala Ile Asp Val Phe Arg Gln
 180 185 190
 Ala Cys Glu His Ala Glu Glu Lys Leu Gln Asp Ala
 195 200
 <210> 293
 <
 211> 2182
 <212> PRT
 <213> Toxoplasma gondii
 <400> 293
 Met Ala Ile Leu Arg Ser Gly Ile Ala Val Ala Thr Leu Cys Val Ala
 1 5 10 15
 Leu Gly Phe Thr Ser Gln Arg Gly Val Val Ala Glu Thr Cys Pro Ala
 20 25 30
 Arg Phe Thr Ala Trp Thr Tyr Cys Gly Gly Gln Asn Ala Met Gln Glu
 35 40 45
 Arg His Asn Val Ala Cys Ala Asn Ile Val Glu Ser Arg Glu Cys Glu

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

Trp Thr Glu Trp Thr Tyr Cys Asn Ser Lys Gly Ile Gln Gln Arg His

115 120 125

Asn Ala Ser Cys His Val Val Glu Ile Arg Gly Cys Gly Asp Val Pro

130 135 140

Glu Gly Cys Gly Glu Phe Gly Pro Trp Ser Pro Pro Leu Asp Asp Phe

145 150 155 160

Asn Asn Cys Lys His Gly Val Val Tyr Arg Arg Lys Arg Glu Gly Cys

165 170 175

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

180 185 190

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

195 200 205

Glu Gly Tyr Glu Gly Asp Gly Leu Thr Cys Glu Pro Val Asn Pro Cys

210 215 220

Lys Asn His Asn Cys Ser Glu His Ala Val Cys Phe Ala Asp Gly Leu

225 230 235 240

Gln Ala Lys Cys Arg Cys Glu Lys Gly Tyr Asp Gly Lys Glu Gly Ala

245 250 255

Gly Thr Gln Asp Asp Pro Cys Ile Asp Arg Asp Glu Cys Ala Thr Asn

260 265 270

Thr His Gln Cys Pro Ala His Ser Thr Cys Arg Asn Thr Glu Gly Ser

275 280 285

Tyr Asp Cys Asp Cys Lys Thr Gly Tyr Ala Met Ser Glu Thr Gly Ser

290 295 300

Cys Glu Asp Val Asn Glu Cys Ala Thr Glu Asn Ser Cys Pro Glu Asn

305 310 315 320

Ser Ser Cys Val Asn Thr Ala Gly Ser Phe Glu Cys Val Cys Asn Glu

325 330 335

Gly Phe Arg Met Asn Ala Glu Thr Gln Gln Cys Glu Asp Ile Asp Glu

340 345 350

Cys Ala Glu Glu Gly Gly Cys Ser Ala Asn Ala Thr Cys Thr Asn Ser

355 360 365
Val Gly Ser Tyr Ser Cys Ser Cys Pro Glu Gly Tyr Lys Gly Glu Gly

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

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

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

565 570 575
Ala His Ala Val Cys Arg Asn Thr Val Gly Ser Phe Ser Cys Asn Cys
580 585 590
Glu Glu Gly Tyr Gly Asn Leu Asp Glu His Arg Ala Cys His Asp Ile
595 600 605

Asn Glu Cys Glu Ala Glu Pro Glu Arg Ile Pro Pro Asn Ala Thr Cys
 610 615 620
 Val Asn Thr Asp Gly Ser Phe Glu Trp Ser Cys Asn Ala Gly Tyr Glu

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

 690 695 700
 Asp Glu Asn Gly Gly Ile Cys Thr Asn Thr Glu Gly Ser Tyr Thr Cys
 705 710 715 720
 Ser Cys Lys Glu Gly Tyr Arg Gln Leu Ala Asp Gly Thr Cys Glu Asp
 725 730 735
 Ile Asp Glu Cys Ala Ser Gly His Glu Cys His Glu Ser Ala Thr Cys
 740 745 750
 His Asn Thr Ala Gly Ser Tyr Thr Cys Ser Cys Asn Pro Gly Phe Ser

 755 760 765
 Gly Asp Gly His Glu Cys Ala Asp Ile Asn Glu Cys Glu Thr Asn Ala
 770 775 780
 His Asp Cys Gly Ser His Thr Thr Cys Glu Asn Thr Val Gly Ser Phe
 785 790 795 800
 Val Cys Asn Cys Lys Glu Gly Phe Val His Ser Asp Glu Lys Thr Cys
 805 810 815
 Arg Asp Val Asp Glu Cys Ala Glu Asn Lys His Asp Cys Ser Val His

 820 825 830
 Ala Thr Cys Asn Asn Thr Glu Gly Ser Phe Glu Cys Ser Cys Lys Ala
 835 840 845
 Gly Phe Glu Gly Asn Gly Lys Glu Cys Ser Asp Ile Gln Phe Cys Ser

850 855 860
 Ala Gly Arg Ser Asp Cys Ala Ala Asn Ala Asp Cys Ala Glu Asn Glu
 865 870 875 880
 Ala Gly Thr Asp Tyr Ala Cys Ser Cys His Ala Gly Tyr Arg Gly Ser

 885 890 895
 Gly His Thr Ser Lys Gly Ala Ala Asp Gly Cys Val Asp Ile Asp Glu
 900 905 910
 Cys Thr Glu Gly Val Asp Thr Cys Pro Arg Gln Gly Gly Arg Cys Val
 915 920 925
 Asn Thr Pro Gly Ser Tyr Arg Cys Glu Cys Glu Glu Gly Tyr Thr Tyr
 930 935 940
 Thr Thr Lys Glu Asp Gly Thr Val Glu Cys Val Asp Ile Asn Glu Cys

 945 950 955 960
 Gly Val Ser Glu Met Asn Thr Cys Ala Ser Lys Ala Asn Gly Gly Val
 965 970 975
 Cys Thr Asn Thr Met Gly Ser Tyr Thr Cys Ser Cys Leu Pro Gly Tyr
 980 985 990
 Thr Pro Ser Asp Asp Gly Arg Val Cys Thr Asp Ile Asp Glu Cys Ala
 995 1000 1005
 Thr Glu Asn Gly Gly Cys Ser Glu His Ser Gln Cys Arg Asn Leu

 1010 1015 1020
 Pro Gly Ser Tyr Glu Cys Val Cys Asp Ala Gly Tyr Glu Lys Val
 1025 1030 1035
 Glu Gly Ser Glu His Leu Cys Gln Asp Ile Asp Glu Cys Ala Ala
 1040 1045 1050
 Gly Thr Ala Thr Ile Pro Asn Asn Ser Asn Cys Val Asn Thr Ala
 1055 1060 1065
 Gly Ser Tyr Glu Phe Ala Cys Lys Pro Gly Phe Glu His Lys Asp

 1070 1075 1080
 Asn Ala Cys Ser Lys Ile Asp Tyr Cys Gly Arg Gly Gly Cys Asn
 1085 1090 1095

Ser Leu	Ala Thr	Cys Glu	Glu Thr	Ala Asp	Gly Thr	Asp Tyr	Val
1100		1105		1110			
Cys Thr	Cys Pro	Lys Gly	Phe Val	Thr Gln	Asn Glu	Gly Arg	Gly
1115		1120		1125			
Ala Asp	Gly Cys	Thr Asp	Val Asp	Glu Cys	Ala Glu	Asn Gly	Cys
1130		1135		1140			
Ala Ala	Tyr Gly	Ser Glu	Gly Val	Ile Cys	Glu Asn	Thr Pro	Gly
1145		1150		1155			
Ser Phe	Asn Cys	Ser Cys	Ala Asn	Gly Tyr	Leu Leu	Asn Asn	Gly
1160		1165		1170			
Val Cys	Glu Glu	Ile Asp	Glu Cys	Ala Gly	Ser Ser	Ser Asn	Thr
1175		1180		1185			
Cys Ala	Asp Glu	Gly Gly	Ile Cys	Thr Asn	Thr Pro	Gly Ser	Tyr
1190		1195		1200			
Thr Cys	Ser Cys	Lys Pro	Gly Tyr	Asp Gln	Gln Gly	His Asp	Cys
1205		1210		1215			
Val Asp	Ile Asn	Glu Cys	Thr Thr	Gln Glu	Pro Cys	Gly Asp	Asn
1220		1225		1230			
Ala Asp	Cys Glu	Asn Thr	Ser Gly	Ser Tyr	Ile Cys	Lys Cys	Lys
1235		1240		1245			
Ala Gly	Phe Glu	Met Arg	Asp Asn	Gln Cys	Val Asp	Ile Asp	Glu
1250		1255		1260			
Cys Ala	Thr Asn	Thr Asn	Glu Cys	His Asn	His Arg	Gly Arg	Cys
1265		1270		1275			
Ile Asn	Thr His	Gly Ser	Tyr Thr	Cys Glu	Cys Ile	Ala Gly	Phe
1280		1285		1290			
Ile Gly	Asp Gly	Lys Ile	Cys Ile	Asn Lys	Asn Glu	Cys Gln	Ser
1295		1300		1305			
Gly Asp	Phe Glu	Cys Gly	Pro Asn	Ser His	Cys Val	Asp Thr	Glu
1310		1315		1320			
Gly Ser	Tyr Lys	Cys Asp	Cys Asn	Ser Gly	Tyr Lys	Gln Asp	Pro

1325	1330	1335
Glu Asn Pro Asp Ser Cys Ile	Asp Arg Asp Glu Cys	Glu Ile Glu
1340	1345	1350
Gly Ala Cys Asp Glu Asn Ala	Asp Cys Thr Asn Leu	Pro Gly Ser
1355	1360	1365
Phe Ser Cys Thr Cys Arg Ala	Gly Tyr Arg Gln Glu	Gly Glu Leu
1370	1375	1380
Cys Val Lys Met Asn Leu Cys	Ala Asp Asp Glu Asn	Gly Gly Cys
1385	1390	1395
Ser Pro His Ala Asp Cys Glu	His Leu Asp Lys Ile	Val Cys Thr
1400	1405	1410
Cys Arg Pro Gly Tyr Glu Gly	Asp Gly Ile Thr Cys	Thr Asp Ile
1415	1420	1425
Asp Glu Cys Ala Leu Asn Thr	Asp Asn Cys Asp Ser	His Ala Thr
1430	1435	1440
Cys Glu Asn Thr Asp Gly Ser	Tyr His Cys Ala Cys	Gly Ser Gly
1445	1450	1455
Phe Thr Gly Asp Gly Phe Thr	Cys Glu Asp Ile Asn	Glu Cys Glu
1460	1465	1470
Thr Gly Glu His Glu Cys Asp	Ser Asn Ala Thr Cys	Glu Asn Ile
1475	1480	1485
Val Gly Ser Tyr Ser Cys His	Cys Pro Thr Gly Phe	Ala Gly Asp
1490	1495	1500
Gly Arg Ser Cys Ser Pro Val	Glu Val Val Pro Gly	Gln Glu Ser
1505	1510	1515
Cys Asn His Trp Ser Ala Phe	Thr Arg Cys Asp Pro	Glu Thr His
1520	1525	1530
Leu Ser Ser Arg Tyr Cys Val	Asp Leu Pro Asp Lys	Val Glu Ser
1535	1540	1545
Ile Thr Cys Glu Val Gly Ser	Leu Pro Gln Pro Pro	Thr Val Ala
1550	1555	1560

Pro Gly	Glu Gly Gly	Glu Glu	Asp Gly	Asn Ala	Cys Gly	Pro Trp
1565		1570		1575		
Gly Pro	Trp Ser	Pro Cys	Pro Gly	Glu Gly	Asn Asn	Met Ser Thr
1580		1585		1590		
Arg Arg	Arg Glu	Asp Thr	Glu Ser	Glu Ala	Cys Val	Asn Gln Val
1595		1600		1605		
Glu Thr	Met Glu	Cys Pro	Thr Gln	Ala Gly	Gln Ala	Cys Gly Asn
1610		1615		1620		
Tyr Gly	Ala Phe	Ser Asp	Cys Gly	Val Pro	Leu Arg	Gly Phe Ala
1625		1630		1635		
Met Ala	Phe Pro	Glu Asn	Cys Pro	Glu Leu	Val Ala	Phe Ala Ala
1640		1645		1650		
Cys Asp	Ala Pro	Ala Pro	Pro Gln	Glu Asp	Arg Cys	His Ser Phe
1655		1660		1665		
Ser Ala	Trp Ser	Lys Cys	Thr His	Ile Pro	Gly Thr	Thr Leu Tyr
1670		1675		1680		
Glu Gln	Thr Arg	Ser Cys	Asp Gly	Met Asp	Leu Thr	Glu Ser Arg
1685		1690		1695		
Phe Cys	Thr Pro	Asp Asp	Glu Val	Gly Ser	Asp Val	Ser Thr Asp
1700		1705		1710		
Val Ala	Ser Glu	Cys Gly	Ser Leu	Gly Glu	Phe Gly	Glu Cys Val
1715		1720		1725		
Asn Gly	Leu Gln	Glu Arg	Ser Tyr	Ser Asp	Cys Pro	Asp His Lys
1730		1735		1740		
Glu Val	Arg Gln	Cys Ser	Asp Glu	Ser Cys	Ser Ala	Phe Gly Glu
1745		1750		1755		
Trp Ser	Pro Cys	Gly Glu	Pro Gln	Gln Gly	Leu Arg	Ile Arg Lys
1760		1765		1770		
Arg Arg	Ala Cys	Asp Asn	Val His	Cys Ala	Cys Val	Glu Ala Glu
1775		1780		1785		
Val Cys	Gly Asp	Ala Thr	Pro Glu	Ile Glu	Glu Glu	Glu Gly Glu

1790	1795	1800
His Phe Pro Pro Glu Glu Gly	Glu Val Leu Pro Pro	Tyr Glu Glu
1805	1810	1815
Gly Pro Gly Glu Gly Glu Leu	Leu Pro Pro Glu Glu	Glu Ile Pro
1820	1825	1830
Glu Gly Glu His Val Pro Glu	Glu Glu Ile Pro Glu	Gly Glu His
1835	1840	1845
Val Pro Glu Glu Glu Ile Pro	Glu Gly Glu His Ile	Pro Glu Glu

1850	1855	1860
Leu Pro Glu Gly Glu His Val	Pro Glu Glu Glu Ile	Pro Glu Gly
1865	1870	1875
Glu His Val Pro Glu Glu Glu	Ile Pro Glu Gly Glu	His Ile Pro
1880	1885	1890
Glu Glu Leu Pro Glu Gly Glu	His Val Pro Glu Glu	Glu Ile Pro
1895	1900	1905
Glu Gly Glu His Val Pro Glu	Glu Glu Ile Pro Glu	Gly Glu His

1910	1915	1920
Ile Pro Glu Glu Leu Pro Glu	Gly Glu His Val Pro	Glu Glu Phe
1925	1930	1935
Pro Glu Gly Glu His Ile Pro	Glu Glu Leu Pro Glu	Gly Glu His
1940	1945	1950
Ile Pro Glu Glu Phe Pro Glu	Gly Glu His Ile Pro	Glu Glu Leu
1955	1960	1965
Pro Glu Gly Glu His Val Pro	Glu Glu Glu Ile Pro	Glu Gly Glu

1970	1975	1980
His Ile Pro Glu Glu Phe Pro	Glu Gly Glu His Val	Pro Glu Glu
1985	1990	1995
Glu Ile Pro Glu Gly Glu His	Ile Pro Glu Glu Glu	Phe Pro Glu
2000	2005	2010
Gly Glu His Val Pro Glu Glu	Glu Ile Pro Glu Gly	Glu His Val
2015	2020	2025

Pro Glu Glu Glu Leu Pro Gly Gly Glu Leu Ile Pro Glu Glu Glu

2030

2035

2040

Ile Pro Glu Gly Glu His Ile Pro Glu Glu Leu Pro Glu Gly Glu

2045

2050

2055

His Val Pro Glu Glu Glu Ile Pro Glu Gly Glu His Val Pro Glu

2060

2065

2070

Glu Glu Ile Pro Glu Gly Glu His Val Pro Glu Glu Glu Ile Pro

2075

2080

2085

Glu Gly Glu His Ala Pro Glu Glu Glu Thr Pro Ala Pro Glu Glu

2090

2095

2100

Thr Glu Lys Glu Glu Glu Glu Gly Val Pro Val Ala Ala Ile Ala

2105

2110

2115

Gly Gly Val Val Gly Gly Val Leu Leu Ile Ala Gly Gly Ala Gly

2120

2125

2130

Ala Ala Val Tyr Ala Ser Gln Gly Gly Val Glu Ala Ala Glu Asp

2135

2140

2145

Glu Val Met Phe Glu Ser Glu Glu Asp Gly Thr Gln Ala Gly Glu

2150

2155

2160

Asn Arg Glu Ser Glu Thr Val Ile Glu Ile Glu Asp Asp Ala Trp

2165

2170

2175

Ala Asp Met Asp

2180

<210> 294

<211> 468

<212> PRT

<213> Toxoplasma gondii

<400> 294

Met Val Gly Val Phe Gln Leu Cys Leu Leu Thr Cys Leu Leu Cys Leu

1

5

10

15

Leu Lys Gly Ser Asp Ala Ile Gln Leu Arg Gln His Arg Asn Gly Leu

20

25

30

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

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

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

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

465

<210> 295

<211> 968

<212> PRT

<213> Toxoplasma gondii

<400> 295

Met Ser Glu Ala Ala Tyr Ser Ala Glu Arg Gly Trp Asp Pro Glu Thr

1

5

10

15

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

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

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

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

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

 500 505 510

Gly Arg Val His Cys Pro Ile Ser Lys Ser Ser Asp Leu Gly Ser Arg
 515 520 525
 Phe Pro Thr Phe Thr Glu Phe Glu Ser Pro Glu Ser Met Asn Asn Phe
 530 535 540
 Cys Glu Asn Gly Leu Pro Phe Trp Gln Glu Lys Arg Glu Pro Leu Val
 545 550 555 560
 Asp Cys Arg Gln Val Ile Pro Lys Asn Ala Ser Thr Thr Asp Cys Pro
 565 570 575
 Gly Arg Cys His Lys Ala Val Val Asn Cys Met Val Ser Asn Asp Ser
 580 585 590
 Leu Asp Asn Cys Ile Asn Glu Ala Leu Ser Ala Gly Asp Phe Ala Glu
 595 600 605
 Asn Cys Glu Leu Gln Ser Ser Val Lys Leu Gly Lys Gly Leu Met Phe
 610 615 620
 Cys Lys Arg Ile Arg Thr Asp Cys Glu Tyr Ser Glu Trp Ser Glu Trp
 625 630 635 640
 Ser Glu Cys Ser Arg Thr Cys Arg Ser Gly Asp Asp Glu Glu Ser Val
 645 650 655
 Arg Val Arg Gly Arg Lys Leu Leu Val Ala Ala Glu His Gly Gly Ser
 660 665 670
 Cys Asp Ala Asp Ile Glu Asp Ser His Gly Gly Ser Leu Ser Asp Val
 675 680 685
 Gln Leu Cys Asp Trp Leu Pro Pro Cys Asp Ala Leu Ala Asp Thr Glu
 690 695 700
 Thr Tyr Val Ile Met Pro Lys Pro Glu Pro Lys Leu Ala Asp Trp Ser
 705 710 715 720
 Ala Thr Arg Thr Thr Thr Thr Val Ile Pro Gly Leu Gln Asn Glu
 725 730 735
 Asn Lys Ile Leu Cys Thr Ile Val Asp Met Ala Asp Phe Ser Lys Ser
 740 745 750
 His Arg Gly Tyr Asp Thr Glu Thr Glu Ser Cys Lys Cys Pro Tyr Asn

755 760 765
Ala Arg Val Cys Ser Arg Thr Glu Ala Val Asn Ser Arg Asp Asn Trp
770 775 780
Asp Glu Leu Met Gln Thr Val Cys Glu Ser Asn Gly Gln Gly Gln Ile
785 790 795 800
Leu Ala Gln Gly Met Glu Thr Phe Ser Cys Ser Asp Arg Val Phe Arg
805 810 815
Ser Phe Arg Gly Thr Leu Gly Gln Thr Pro Glu Ala His Cys Lys Ser

820 825 830
Glu Asp Ala Thr Tyr Ile Phe Cys Glu Asp Gly Ala Ile Asp Asn Asp
835 840 845
Leu Ile Phe Thr Glu Val Met Met Ser Ile Ile Thr Gly Val Val Met
850 855 860
Gly Ile Ala Val Val Tyr Trp Ala Ile Gln Tyr Ser Gly Asp Val Gln
865 870 875 880
Lys Val Leu Gly Leu Ala Gly Arg Tyr Val Glu Leu Thr Asn Leu Leu

885 890 895
His Glu Val Ser Gln Glu Pro Gln Ala His Glu Glu Glu Lys Ala Glu
900 905 910
Glu Gly Glu Gly Pro Asp Glu Asp Ala Glu Pro Glu Ala Ala Val Glu
915 920 925
Gly Asn Asn Glu Phe Asp Cys Asn Pro Arg Ala Lys Glu Glu Asn Gly
930 935 940
Glu Glu Ser Glu Gln Asp Ala Ser Asp Ser Glu Ser Gly Ser Asp Asp

945 950 955 960
Asp Asp Asp Ile Val Ser Glu Glu

965

<210> 296

<211> 2924

<212> PRT

<213> Toxoplasma gondii

<400> 296

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

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

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

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

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

 485 490 495

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

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

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

 675 680 685
 Pro Ala Ile Pro Pro His Thr Ser Gln Ser Leu Leu Glu Gln Leu Gln
 690 695 700
 Arg Cys Arg Phe Ala Thr Arg Pro Ala Thr Ala Pro Leu Gln Gln Tyr
 705 710 715 720
 Glu Asp Glu Ile Asp Val Gln Leu Pro Asp Tyr Gly Ala Val Ile Ile
 725 730 735
 Pro Leu Gly Cys Asp Lys Leu His His Arg Glu Val Val Gln Ala Leu

740	745	750	
Val Gly Ser Ala Ser Ser Ile Met Leu Gly Val His Glu Pro Gly Cys			
755	760	765	
Arg Tyr Glu Asp Ala Thr Glu Thr Val Gln Arg Glu Cys Lys Ala Ala			
770	775	780	
Val Ser Ala Arg Lys Thr Thr Cys Glu Ile Asp Ser Ser Leu Phe Thr			
785	790	795	800
Ser Lys Asp Ile Leu Cys Asn Thr Ser Thr Ile Lys Leu Ile Ile Arg			
805	810	815	
Gly Thr Cys Ile Pro Gly Pro Tyr Leu Pro Thr Asp Tyr Thr Cys Ala			
820	825	830	
Leu Tyr Pro Thr Thr Gly Val Val Ser Arg Asp Gly Arg Ser Cys Thr			
835	840	845	
Cys Pro Asn Ser Ala Tyr Pro Cys Thr Tyr Glu Glu Gly Gln Leu Thr			
850	855	860	
Ala Ser Arg Trp Lys Asn Glu Val Asn Thr Gly Ala Thr Val Ser Leu			
865	870	875	880
Ala Asn Ser Val Val Trp Thr Ala Pro Pro Gly Thr Ser Glu Tyr Thr			
885	890	895	
Tyr Thr His Thr Asp Ala Tyr Asp Tyr Val Cys Ser Thr Asp Glu His			
900	905	910	
His Phe Val Leu Cys Lys Asp Leu Thr Pro Ser Ala Leu Pro Leu Thr			
915	920	925	
Glu Arg Glu Pro His Cys Leu Asn Ser Phe Ser Val Lys Pro Asp Ala			
930	935	940	
Ser Thr Val Asp Asp Arg Asp Cys Gln Asp Gln Cys Ala Ser Leu Phe			
945	950	955	960
Ala Thr Arg Cys Arg Gln Ser Phe Tyr Lys Trp Leu Cys Val Ala Gln			
965	970	975	
Gly Leu Pro Glu Cys Tyr Ile Pro Asn Thr Asp Ser Phe Thr Cys Gln			
980	985	990	

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

995	1000	1005
Cys Ser Gly Ala Tyr Pro Pro	Cys Ser Arg Asn Glu	Ala Asn Ala
1010	1015	1020
Thr Arg Leu Asp Trp Ile Thr	Ala Phe Arg Ala Leu	Ser His Lys
1025	1030	1035
Lys Gly Val Val Val Ala Arg	Gly Lys Gln Ala Leu	Trp Thr Glu
1040	1045	1050
Asn Pro Asp Arg Trp Arg Tyr	Glu Asn Gly Met Leu	Gln Gly Gly

1055	1060	1065
Gly Cys Leu Asn Asn Ser Trp	Phe Val Gly Val Phe	Cys Gly Ala
1070	1075	1080
His Leu Ser Val Thr Pro Pro	Ala Arg Gly Asp Val	Leu Pro Ile
1085	1090	1095
Cys Ser Ser Ala Ala Lys Val	Glu Asn Pro Asp Thr	Pro His Pro
1100	1105	1110
Ala Cys Arg Val Leu Cys Ala	Gln Val Leu Asn Glu	Cys Lys Lys

1115	1120	1125
Val Phe Ser Thr Thr Glu Gly	Ala Ser Ala Tyr Ala	Ser Val Phe
1130	1135	1140
Asp Cys Phe Lys Ala Arg Gly	Lys Gly Thr Thr Leu	Asp Asn Cys
1145	1150	1155
Thr Tyr Glu Leu Gly Pro Glu	Asn Arg Ala Thr Gly	Val Ala Glu
1160	1165	1170
Leu His Thr Gly Trp Thr Val	Ala Ser Ala Ser Trp	Ser Arg Val

1175	1180	1185
Leu Phe Asp Val Glu Phe Ala	Asp Pro Pro Val Val	Phe Leu Gly
1190	1195	1200
Ile Pro Arg Asp Thr Gln Pro	Phe Tyr Thr Pro Ser	Val Arg Leu
1205	1210	1215
Val Thr Lys Thr Ser Phe Glu	Val Lys Leu Tyr Arg	Asn Asn Cys

1220 1225 1230
Gly Leu Asp Asp Thr Arg Ser Ser Ser Ala Pro Val Ser Trp Met

1235 1240 1245
Ala Ile Pro Glu Gly Ala Tyr Leu Thr Asp Phe Val Glu Asn Pro

1250 1255 1260
Val Arg Val Met Lys Leu Pro Met Thr Thr Arg Thr Pro Thr Val

1265 1270 1275
Leu Thr Phe Ser Leu Pro Gly Leu Lys Glu Pro Glu Glu Met Val

1280 1285 1290
Ala Leu Ala Gln Val Gln Asp Leu Thr Pro Thr Ser Val Ser Thr

1295 1300 1305
Asp Arg Val Ala Val Val Ile Ser Asn Leu Lys Thr Asn Ser Leu

1310 1315 1320
Glu Leu Ser Leu Val Val Asp Glu Ser Val Asn Phe Ser Thr Val

1325 1330 1335
Ala Val Gly Ile Leu Ile Ser Gly Lys Gln Asn Pro Asp Leu Ala

1340 1345 1350
Ala Gly Leu Ser Pro Leu Leu Asn Arg Tyr His Leu Gln Thr Phe

1355 1360 1365
Arg Ile Pro Ala Ala Ala Tyr Ser Ala Thr Ser Ile Leu Gly Glu

1370 1375 1380
Gly Leu Tyr Leu Ser Gly Gly Ile Met Pro His Val Phe Ala Ala

1385 1390 1395
Ala Ile Gln Thr Arg Ser Arg Thr Lys Glu Leu Asp Glu Ser Asp

1400 1405 1410
Arg Val Val Ile Ser Arg Arg Ala Thr Thr Thr Pro Ser Thr Trp

1415 1420 1425
Ser Ala Leu Leu Trp Lys Lys Thr Cys Asp Ala Lys Asp Met Phe

1430 1435 1440
Glu Ala Val Glu Asn Pro Ser Asp Leu Ile Ile Ala Gly Ile Tyr

1445 1450 1455

Val Glu	Ala Arg Lys Asp Glu	Pro Ser Ala Ile Leu	Gly Asn Arg
1460	1465	1470	
His Asp	Leu Cys Leu Ser Phe	Ile Gly Gln Ser Phe	Glu Ser Gly
1475	1480	1485	
Val Val	Ala Thr Cys Met Gly	Ala Cys Arg Ser Ala	Leu Pro Ala
1490	1495	1500	
Ser Val	Gln Leu His Cys Gln	Asp Glu Cys Ala Leu	Asn Ile Phe
1505	1510	1515	
Ala Pro	Ser Val His Thr Lys	Cys Met Ser Asp Cys	Glu Ser Leu
1520	1525	1530	
Leu Val	Ala Gln Tyr Glu Glu	Cys Ala Gly Gln Cys	Thr Ala Thr
1535	1540	1545	
Gly Thr	Ala Ser Cys Gln Arg	Lys Cys Lys Gln Phe	Leu Gly Asn
1550	1555	1560	
Lys Cys	Asp Ser Thr Ala Ser	Ser Asp Val Ala Ala	Cys Leu Glu
1565	1570	1575	
Phe Val	Thr Pro Pro Ser Val	Phe Glu Gln Cys Thr	Leu Leu Val
1580	1585	1590	
Glu Tyr	Ser Val Ser Glu Gly	Gly Ala Ser Asp Gly	Leu Glu Ile
1595	1600	1605	
Glu Glu	Glu Thr Thr Pro Ser	Gln Thr Tyr Glu Asn	Cys Ile Ile
1610	1615	1620	
Val Asp	Met Arg Asp Gly Arg	Phe Thr Ala Phe Thr	Gly Trp Asp
1625	1630	1635	
Ser Arg	Val Ala Ser Cys Lys	Cys Pro Asn Asp Phe	Arg Ala Cys
1640	1645	1650	
Thr Ser	Glu Thr Val Asn Thr	Gln Asn His Trp Arg	Thr Glu Leu
1655	1660	1665	
Leu Ala	Ser Ala Gly Leu Cys	Lys Glu Gln Pro Asp	Gly Arg Phe
1670	1675	1680	
Asn Ala	Val Thr Gln Gln Leu	Trp Ser Thr Thr Gly	Asp Leu Cys

1685	1690	1695
Ala Leu Ala Ala Asp Glu Gln	Gln Pro Pro Ile Ser	Trp Thr Ser
1700	1705	1710
Asn Met Leu Pro Ala Tyr Val	Asp Gln Asp Val Val	Leu Asp Asn
1715	1720	1725
Ser Thr Ile Arg Ser Gly Asp	Tyr Gln Cys Arg Glu	Ile Trp His
1730	1735	1740
Tyr Val Val Cys Pro Ala Ala	Ala Thr Ser Thr Thr	Thr Gln Glu
1745	1750	1755
Pro Pro Val Pro Pro Phe Thr	Ala Thr Leu Lys Thr	Ala Ile Val
1760	1765	1770
Gly Glu Trp Gly Glu Trp Ser	Ala Cys Thr Gly Thr	Cys Phe Ser
1775	1780	1785
Gln Trp Trp Thr Pro Lys Arg	Thr Arg Thr Arg Leu	Val Leu Ala
1790	1795	1800
Glu Leu Ser His Ser Gln Ile	Pro Ser Val Ser Glu	Thr Ala Thr
1805	1810	1815
Cys Leu Asp Leu Pro Pro Cys	Gly Thr Val Cys Trp	Glu Arg Glu
1820	1825	1830
Trp Thr Glu Trp Ser Glu Cys	Lys Leu Phe Thr Ile	Val Met Gly
1835	1840	1845
Gln Gly Leu Glu Tyr Phe Arg	Gln Gln Ile Lys Pro	Ile Phe Asp
1850	1855	1860
Phe Val Glu Glu Ala Cys Gly	Leu Asp Glu His Glu	Arg Tyr Glu
1865	1870	1875
Arg Cys Gly Glu Glu Gln Asn	Asn Gly Glu Thr Pro	Ala Thr Ser
1880	1885	1890
Thr Leu Gln Thr Asp Ser Leu	Leu Glu Thr Arg Ser	Leu Thr Val
1895	1900	1905
Ser Arg Gly Thr Ala Ala Arg	Ala Leu Ser Arg Val	Ser Met Asp
1910	1915	1920

Pro Ala	Leu Glu	Pro Pro	Ser Phe	Ala Ser	Leu His	Gly Thr	Arg
1925			1930			1935	
Ser His	Val Pro	Ala Ser	Ile Asp	Ala Lys	Ile Ile	Glu Arg	Arg
1940			1945			1950	
Lys Gly	Ile Met	Ser Arg	Arg Arg	Arg Ser	Val Pro	Pro Ser	Gly Tyr
1955			1960			1965	
Leu Glu	Glu Thr	Ala Glu	Gln Val	Ala Arg	Gly Gly	Glu Ser	Glu
1970			1975			1980	
Gln Ser	Glu Lys	Ala Ser	Gln Asn	Gly Ser	Arg Arg	His Arg	Ala
1985			1990			1995	
Ser Arg	Lys Gln	Lys Arg	Gly Leu	Glu Ser	Ile Tyr	Ser Asp	Ala
2000			2005			2010	
Ser Val	Arg Gly	Ser Gly	Glu Ser	Thr Leu	His Gly	Thr Gly	Thr
2015			2020			2025	
Asn Ala	Tyr Arg	Asp Gln	Ile Glu	Trp Thr	Ser Lys	Ser Ser	Ser
2030			2035			2040	
Arg Ser	Ala Ile	Leu Asp	Ser Gly	Ala Arg	Gly Ala	Glu Ala	Gly
2045			2050			2055	
Thr Ser	Leu Leu	Gln Lys	Ala Arg	Arg Ala	Arg Arg	Gly Ala	Gly
2060			2065			2070	
Arg Phe	Arg Lys	Ser Arg	Ser Gln	Ala Arg	Asn Gln	Thr Pro	Asp
2075			2080			2085	
Lys Ser	Cys Ser	Val Val	Ser Glu	Trp Ser	Gly Cys	Asp Ser	Pro
2090			2095			2100	
Cys Leu	Pro His	Lys Gly	Ser Thr	Pro Arg	Arg Tyr	Arg Leu	Ala
2105			2110			2115	
Val Pro	Gly Gln	Asn Glu	Ala Asn	Tyr Cys	Thr Val	Pro Leu	Ser
2120			2125			2130	
Gly Lys	Glu His	Leu Cys	Thr Asp	Leu Pro	Gln Cys	Ala His	Pro
2135			2140			2145	
Asn Phe	Asp Cys	Ala Lys	Val Thr	Ala Ser	Arg Leu	Thr Asp	Glu

2150	2155	2160
Asp Ile Ala Ala Cys Lys Ala Val Cys Val Glu Val Val Lys Thr		
2165	2170	2175
Cys Glu Thr Met Met Ser Ala Val Phe Ser Leu Tyr Thr Ser Leu		
2180	2185	2190
Glu Gln Cys Ala Leu Val Gln Phe Gln Glu Tyr Glu Gln Phe Pro		
2195	2200	2205
Gly Gln Cys His Ile Pro Glu Glu Tyr Thr Ser Thr Arg Arg Pro		
2210	2215	2220
Thr Lys Cys Phe Pro Ser Arg Thr Arg Arg Arg Val Ala Ser Gly		
2225	2230	2235
Glu Leu Pro Phe Ile Phe Gln Val Ser Thr Ala Ser Gly Thr Ser		
2240	2245	2250
Pro Ser Ala Thr Ser Asp Ala Ala Ser Ser Val Ala Glu Ser Phe		
2255	2260	2265
Val Ser Thr Gly Thr Ala Ser Ala Pro Ser Ser Arg Val Met Asn		
2270	2275	2280
Ala Leu Ala Phe Glu Ala Ser Ala Ser Gln Thr Ser Ile Asp Ser		
2285	2290	2295
Cys Glu Cys Tyr Asp Pro Ala Asp Glu Pro Cys Thr Ala Gln Glu		
2300	2305	2310
Ala Arg Asp Ser Leu Phe Asp Ser Leu Tyr Leu Phe Leu Thr His		
2315	2320	2325
Pro Leu Cys Ala Glu Ser Pro Ala Ala Glu Gly Ala Leu Phe Thr		
2330	2335	2340
Met Ser Glu Pro Asn Gln Thr Ala Asp Ala Ala Ser Tyr Phe Ala		
2345	2350	2355
Leu Arg Gly Leu Gly Arg Met His Cys Pro Val Pro Met Tyr Lys		
2360	2365	2370
Ser Ser Thr Glu Val Lys Gly Val Leu Thr Pro Lys Arg Val Thr		
2375	2380	2385

Phe Ser	Glu Phe Lys Thr Lys	Glu Asp Leu Asn Glu	Phe Cys His
2390	2395	2400	
Lys Gly	Leu Ser Asn Trp Arg	Gln Asn Val Pro Pro	Glu Ile Ile
2405	2410	2415	
Gly Ser	Ala Ser Phe Pro Asn	Cys Met Leu Val Thr	Pro Arg Glu
2420	2425	2430	
Gly Ala	Glu Pro Gln Asp Cys	Ala Leu Leu Cys Ser	Glu Thr Met
2435	2440	2445	
Ser Ser	Cys Ser Ala Ala Ser	Leu Ser Phe Val Glu	Leu Ser Gln
2450	2455	2460	
Cys Val	Gln Asp Lys Leu Thr	Glu Ser Asp Phe Tyr	Ser Lys Cys
2465	2470	2475	
Ser Ala	Pro Glu Val Leu Ala	Pro Gly Glu Gly Ile	Ile Leu Cys
2480	2485	2490	
Lys Lys	Lys Val Ser Thr Cys	Asp Tyr Thr Glu Trp	Ser Glu Trp
2495	2500	2505	
Ser Thr	Cys Thr Ala Thr Cys	Phe Asn Trp Asp Glu	Gly Val Ile
2510	2515	2520	
Pro Leu	Arg Val Arg Ser Arg	Asp Phe Ala Ser Ser	Ser Ala Glu
2525	2530	2535	
Ser Arg	Val Leu Cys Arg Leu	Glu Ser Gln Asn Asp	Ala Ile Gln
2540	2545	2550	
Thr Glu	Lys Cys Asp Trp Met	Pro Val Cys Pro Glu	Ala Glu Ser
2555	2560	2565	
Glu Glu	Glu Asp Asp Ala Thr	Gly Gly Val Glu Pro	Arg Gly Glu
2570	2575	2580	
Pro Ile	Val Pro Pro Trp Ser	Pro Glu Arg Pro Thr	Asp Glu Asn
2585	2590	2595	
Asn Gln	Ala Met Gly Ser Glu	Asp Ile Val Pro Gly	Thr Val Glu
2600	2605	2610	
Cys Tyr	Val Thr Asn Met Gly	Thr Ile Met Thr Ser	Tyr Tyr Arg

2615	2620	2625
Gly Tyr Asn Gln Glu Tyr His	Gly Cys Asn Cys Pro	Gly Gly Arg
2630	2635	2640
Arg Pro Cys Thr Arg Ala Glu	Ala Val Ala Ser Leu	Asp Leu Trp
2645	2650	2655
Ala Lys Asp Ser Gly Gly Leu	Cys Asp Gln Asp Met	Ala Thr Met
2660	2665	2670
Ile Ser Ala Ala Glu Gly Glu	Ala Phe Phe Cys Ala	Thr Gly Ser

2675	2680	2685
Phe Gly Lys Ile Asp Thr Ser	Leu Ser Glu Ser Ser	Cys Ala Ser
2690	2695	2700
Ser Glu Tyr Gln Tyr Val Leu	Cys Glu Gly His Pro	Tyr Glu Gly
2705	2710	2715
Ile Ala Asn Leu Thr Thr Trp	Val Ile Cys Leu Leu	Leu Gly Val
2720	2725	2730
Gly Gly Gly Ile Cys Phe Val	Leu Ser Cys Val Gln	Tyr Ser Ser

2735	2740	2745
Asp Ile Gln Lys Leu Leu Gly	Leu Ala Gly Ser Tyr	Pro Val Leu
2750	2755	2760
Val Gln Asn Val Thr Glu Leu	Gln Glu Arg Glu Ser	His Lys Leu
2765	2770	2775
Arg Arg Gln Gly Asn Ile Ser	Ala Thr Ser Glu His	Ser Asp Ala
2780	2785	2790
His Ala Pro Ser Leu Ser Asp	Ser Gly Trp Asp Met	Asp Gly Asn

2795	2800	2805
Gln Ser Ala Gly Ser Ala Phe	Pro Glu Glu Glu Pro	Trp Gln Phe
2810	2815	2820
Glu Asp His Asp Glu Glu Pro	Leu Leu Ser Thr Arg	Lys Tyr Ser
2825	2830	2835
Arg Asn Ser Gly Ser Ala Glu	Ile Pro Glu Pro Ser	Glu Ile Gly
2840	2845	2850

Gln Thr Ser Pro Thr Gln Gln Arg Val Pro Arg Ala Ser Leu Ala

2855 2860 2865

Ala Gln Arg Ser Thr Cys Gln Leu Ser Ser Arg Leu Gly Gln Ala

2870 2875 2880

Asn Ser Pro Glu Gln Ser Leu Glu Arg Arg Ser Leu Lys Leu Arg

2885 2890 2895

Asp Ser His Ala Asp Val Glu Leu Gln Arg Thr Leu Arg Lys Glu

2900 2905 2910

Met Lys Gly Asn Gln Val Trp Asp Lys Thr Val

2915 2920

<210> 297

<211> 668

<212> PRT

<213> Toxoplasma gondii

<400> 297

Met Val Val Ser Cys Leu Cys Thr Ala Met Ser Ser Ala Leu Ser Gln

1 5 10 15

Arg Asn Cys Ile Leu Ile Ser Cys Arg Leu Gly Arg Gln Arg Ser Arg

20 25 30

Pro Pro Asp Ala Met Lys Val Tyr Ala Pro Val Phe Thr Cys Arg Arg

35 40 45

Gln Phe Leu Tyr Glu Lys Tyr Thr Arg Arg Arg Cys Thr Thr Leu Gly

50 55 60

Gly Leu Val Ala Leu Cys Val Ile Phe Thr Ala Glu Ala Ile Ser Arg

65 70 75 80

Ser Gln His Pro Tyr Gly Thr Ser Arg Ser Asp Leu Ser Pro Pro Ala

85 90 95

Thr Val Asp Ser Thr Ser Tyr Gly Met Ser Ile Leu Glu Ala Gly Gly

100 105 110

Pro Ser Asp Glu Val Ala Ile Pro Ser Asp Arg Leu Gln Thr Phe Arg

115 120 125

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

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

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

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

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

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

625 630 635 640

Leu Val Val Val Ile Gly Leu Gly Phe Ile Gly Arg Lys Phe Tyr Arg

645 650 655

Ala Leu Pro Ala Glu Arg Thr Arg Asp Asn Tyr Leu

660 665

<210> 298

<211> 351

<212> PRT

<213> Toxoplasma gondii

<400> 298

Met Asp Ala Leu Lys Thr Val Phe Asn Arg Arg Ile Ala Leu Pro Val

1 5 10 15

Val Val Ala Ala Ala Leu Leu His Asn Ser Ala Glu Ala Leu Gln Ser

20 25 30

Pro Gly Leu Arg Arg Gln Leu Val Asn Ser His Ser Phe Ala Glu Val

35 40 45

Glu Thr Thr Gly Tyr Ser Cys Phe Glu Lys Gly Lys Glu Tyr Val Gly

50 55 60

Phe Ser Leu Thr Glu Phe Ala Lys Val Gly Asp Ala Ala Leu Cys Gln

65 70 75 80

Gln Arg Cys Asn Gln His Pro Gln Cys Gly Phe Phe Thr Phe Tyr Ser

85 90 95

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

100 105 110

Asn Asn Ala Asn Ala Val Ser Gly Pro Lys Arg Cys Pro Leu Cys Leu

115 120 125

Val Asp Asn Tyr Asp Phe Arg Gly Glu Thr Asn Met His Lys Ser Gly

130 135 140

Ala Pro Gly Leu Asn Thr Leu Leu Ala Cys Gln Gln Gly Cys Ala Ala

145 150 155 160

Glu Pro Lys Cys Lys Ala Phe Leu Phe Glu Lys Arg Pro Arg Thr Cys
165 170 175

His Phe Lys Thr Ser Asp Asn Tyr Leu Lys Ser Phe His Pro Asp Thr
180 185 190

Ser Tyr Ile Ala Gly Pro Lys Thr Cys Thr Asp Glu His Trp Cys Ile
195 200 205

Met Lys Asp Ile Gly Tyr Lys Gly Thr Asp Ser Lys Ala Thr Lys Ala
210 215 220

Asn Ser Ala Ala Glu Cys Gln Gln Met Cys Leu Asn Asp Glu Arg Cys
225 230 235 240

Asp Phe Phe Thr Trp Gln Gln Ala Gly Lys His Cys Trp Phe Lys Ala
245 250 255

Gly Ala Ser Thr Ala Ser Thr Lys Tyr Asn Arg Ala Gly Asp Tyr Ser
260 265 270

Ala Pro Lys His Cys Gly Leu Pro Thr Thr Cys Val Lys Glu Arg Thr
275 280 285

Lys Tyr Ala Gly Glu Thr Val Ala Thr Phe Pro Lys Ser Glu Val Gly
290 295 300

Thr Phe Glu Ser Cys Gln Met Lys Cys Trp Lys Thr Ser Lys Cys Val
305 310 315 320

Phe Met His Phe Asn Asn Asp Gly Cys Thr Leu Ser Gly Ile Asn Ala
325 330 335

Thr Ala Gln Thr Asp Ala Asn Ser Lys Ala Gly Asp Ile Thr Cys
340 345 350

<210> 299

<211> 351

<212> PRT

<213> Toxoplasma gondii

<400> 299

Met Glu Thr Val Thr Thr Leu Phe Asn Arg Lys Ile Ala Leu Ser Phe
1 5 10 15

Val Val Ala Ala Ala Leu Leu His Asn Ser Ala Glu Ala Leu Gln Ser

20	25	30
Pro Gly Leu Arg Arg Gln Leu Val Asn Val His Ser Phe Ala Glu Val		
35	40	45
Glu Thr Thr Gly Tyr Ser Cys Leu Glu Lys Asp Lys Glu Tyr Val Gly		
50	55	60
Phe Ser Leu Thr Glu Phe Thr Glu Val Gly Asp Ala Gly Leu Cys Gln		
65	70	75
Gln Arg Cys Asn Gln His Pro His Cys Ser Phe Phe Thr Phe Tyr Ser		
85	90	95
Asn Gly Asn Arg Cys Val Leu Gln Ser Arg Lys Pro Ser Gln Glu Lys		
100	105	110
Asn Asn Ala Asp Ala Val Ser Gly Pro Lys Arg Cys Pro Leu Cys Leu		
115	120	125
Val Asp Ser Phe Asp Phe Arg Gly Glu Ala Asn Leu His His Lys Gly		
130	135	140
Ala Pro Gly Leu Asn Thr Leu Leu Ala Cys Gln Gln Gly Cys Ala Ala		
145	150	155
Glu Pro Arg Cys Lys Gly Phe Leu Phe Glu Lys Arg Pro Arg Thr Cys		
165	170	175
His Phe Lys Thr Asn Asp Asn Tyr Leu Lys Ala Leu Asp Pro Asp Thr		
180	185	190
Ser Tyr Ile Ala Gly Pro Lys Thr Cys Thr Asp Glu His Trp Cys Ile		
195	200	205
Met Lys Asp Ile Gly Tyr Arg Gly Thr Asp Ser Lys Glu Thr Arg Ala		
210	215	220
Asn Ser Ala Ala Glu Cys Gln Gln Met Cys Leu Asn Asp Glu Arg Cys		
225	230	235
Asp Phe Phe Thr Trp Gln Gln Ala Gly Lys Tyr Cys Trp Phe Lys Ala		
245	250	255
Gly Ala Ser Thr Ala Ser Thr Lys Tyr Asn Arg Ala Gly Asp Tyr Ser		
260	265	270

Ala Pro Lys His Cys Gly Leu Pro Thr Thr Cys Val Lys Glu Arg Thr
 275 280 285
 Lys Tyr Ala Gly Glu Thr Val Ala Thr Phe Pro Lys Ser Glu Val Gly
 290 295 300

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

<210> 300

<211> 603

<212> PRT

<213> Toxoplasma gondii

<220><221> misc_feature

<222> (317)..(560)

<223> Xaa can be any naturally occurring amino acid

<400> 300

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

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

Asn Asn Ala Asp Ala Val Ser Gly Pro Lys Arg Cys Pro Leu Cys Leu
 115 120 125

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

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

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

 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 325 330 335
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 340 345 350
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

355					360					365				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
370					375					380				

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
385						390						395				400
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
						405						410				415
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
						420						425				430
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
						435						440				445

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
450				455				460								
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
465				470				475				480				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				485				490				495				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
500				505				510								

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
515				520				525								
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
530				535				540								
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
545				550				555				560				
Phe	Arg	Lys	Pro	Val	Ala	Ser	Ile	Cys	His	Ser	Pro	Arg	Thr	Lys	Lys	
565				570				575								

Gly Asp Gln Thr Val Ser His Glu Ile Val Arg Pro Val Asn Thr Cys
580 585 590
Arg Arg Val Thr Pro Glu Arg Gly Asp Ser Glu
595 600

<210> 301

<211> 769

<212> PRT

<213> *Toxoplasma gondii*

<400> 301

Met Arg Leu Gln Arg Glu Ala Val Phe Gly Leu Met Phe Ala Cys Gly

1 5 10 15

Met Trp Met Trp Pro Ser Glu Val Ala Gly Gly Gly Trp Ser Ile Val

20 25 30

Asp Ala Leu Arg Lys Arg Tyr Asp Thr Ser Arg Gly Gly Asp Ala Asn

35 40 45

Gly Val Asp Thr Ser Gly Val Glu Asp Val Ile Gln Ser Glu Ser Ala

50 55 60

Ile Gly Ala Ala Glu Gly Cys Thr Asn Gln Leu Asp Ile Cys Phe Leu

65 70 75 80

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

85 90 95

Gln Phe Leu His Thr Phe Leu Met Val Leu Pro Ile Gly Pro Glu Glu

100 105 110

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

115 120 125

Asp Leu Gln Ser Pro Asn Ala Val Asp Lys Gln Leu Ala Ala His Ala

130 135 140

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

145 150 155 160

Leu Lys Ala Cys Lys Gln Ile Leu Phe Thr Gly Ser Arg Pro Gly Arg

165 170 175

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

180 185 190

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

195 200 205

Gly Ile Val Thr Val Leu Ala Val Gly His Tyr Val Lys His Ser Glu

210	215	220	
Cys Arg Ser Met Cys Gly Cys Ser Gly Thr Ser Asp Asp Asp Ser Pro			
225	230	235	240
Cys Pro Leu Tyr Leu Arg Ala Asp Trp Gly Gln Leu Ala Thr Ala Ile			
	245	250	255
Lys Pro Met Leu Lys Glu Val Cys Lys Thr Leu Pro Gln Asp Ala Ile			
	260	265	270
Cys Ser Asp Trp Ser Ala Trp Ser Pro Cys Ser Val Ser Cys Gly Asp			
	275	280	285
Gly Ser Gln Ile Arg Thr Arg Thr Glu Val Ser Ala Pro Gln Pro Gly			
	290	295	300
Thr Pro Thr Cys Pro Asp Cys Pro Ala Pro Met Gly Arg Thr Cys Val			
305	310	315	320
Glu Gln Gly Gly Leu Glu Glu Ile Arg Glu Cys Ser Ala Gly Val Cys			
	325	330	335
Ala Val Asp Ala Gly Cys Gly Val Trp Gly Glu Trp Ser Ala Trp Ser			
	340	345	350
Ala Ser Cys Gly Asn Ala Thr Arg Lys Arg Glu Arg Thr Arg Tyr Asn			
	355	360	365
Asp Pro Pro Pro Gln Gly Ala Gly Arg Arg Cys Glu Asn Gln Asp Pro			
	370	375	380
Pro Val Leu Gln Glu Gln Thr Glu Glu Ala Thr Leu Ala Pro Cys Ile			
385	390	395	400
Thr Ile Pro Pro Thr Pro Pro Glu Trp Ala Ala Trp Ser Asp Cys Thr			
	405	410	415
Val Thr Cys Gly Gly Gly Asn Arg His Arg Val Arg Asn Ala Leu Pro			
	420	425	430
Pro Gly Leu Gly Ser Gln Asn Gly Glu Ser Asp Glu Ser Leu Val Ser			
	435	440	445
Lys Leu Trp Pro Gly Thr Asp Leu Arg Gln Glu Glu Ala Cys Asn Thr			
	450	455	460

Ser Pro Cys Pro Ile Asn Ala Thr Cys Gly Gln Phe Glu Glu Trp Ser
465 470 475 480

Thr Cys Ser Val Ser Cys Gly Gly Gly Leu Lys Thr Arg Ser Arg Asn
485 490 495

Pro Trp Asn Glu Asp Gln Gln His Gly Gly Leu Ser Cys Glu Gln Gln
500 505 510

His Pro Gly Gly Arg Thr Glu Thr Ile Thr Cys Asn Pro Gln Ala Cys
515 520 525

Pro Val Asp Glu Arg Pro Gly Glu Trp Ala Glu Trp Gly Glu Cys Ser
530 535 540

Val Thr Cys Gly Asp Gly Val Arg Glu Arg Arg Arg Gly Lys Ser Leu
545 550 555 560

Val Glu Ala Lys Phe Gly Gly Arg Thr Ile Asp Gln Gln Asn Glu Ala
565 570 575

Leu Pro Glu Asp Leu Lys Ile Lys Asn Val Glu Tyr Glu Pro Cys Ser
580 585 590

Tyr Pro Ala Cys Gly Ala Ser Cys Thr Tyr Val Trp Ser Asp Trp Asn
595 600 605

Lys Cys Val Cys Pro Met Gly Tyr Gln Ala Arg His Ala Ala Val Lys
610 615 620

Phe Asp Tyr Arg Asn Lys Pro Cys Asp Leu Pro Thr Phe Glu Thr Lys
625 630 635 640

Ala Cys Ser Cys Gly Glu Thr Asn Pro Val Pro Ser Glu Gly Thr Thr
645 650 655

Pro Gly Ala Pro Gly Ala Thr Gly Pro Glu Gln Pro Asn Gln Arg Pro
660 665 670

Leu Pro Glu Gly Ser Asp Glu Asn Glu Thr Pro Thr Asn Glu Glu Gly
675 680 685

Glu Gln Ser Lys Lys Glu Ser Gly Ser Gly Ile Ala Gly Ala Ile Ala
690 695 700

Gly Gly Val Ile Gly Gly Leu Ile Leu Leu Gly Ala Ala Gly Gly Ala

705 710 715 720
Ser Tyr His Tyr Tyr Leu Ser Ser Ser Val Gly Ser Pro Ser Ala Glu
725 730 735

Ile Glu Tyr Glu Ala Asp Asp Gly Ala Thr Lys Val Val Met Glu Glu
740 745 750
Glu Lys Glu Thr Leu Val Pro Val Asp Asp Asp Ser Asp Met Trp Met
755 760 765
Glu

<210> 302

<211> 383

<212> PRT

<213> *Toxoplasma gondii*

<400> 302

Met	Arg	Gly	Gly	Thr	Ser	Ala	Leu	Leu	His	Ala	Leu	Thr	Phe	Ser	Gly
1				5					10					15	
Ala	Val	Trp	Met	Cys	Thr	Pro	Ala	Glu	Ala	Leu	Pro	Ile	Gln	Lys	Ser

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

[illegible]

Cys Ser Cys Glu Lys Gln Gly His Arg Cys Asp Lys Asn Ala Glu Cys

145 150 155 160

Val Glu Asn Leu Asp Ala Gly Gly Gly Val His Cys Lys Cys Lys Asp

165 170 175

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

180 185 190

Arg Gly Asn Ala Lys Cys Gly Pro Asn Gly Thr Cys Ile Val Val Asp

195 200 205

Ser Val Ser Tyr Thr Cys Thr Cys Gly Asp Gly Glu Thr Leu Val Asn

210 215 220

Leu Pro Glu Gly Gly Gln Gly Cys Lys Arg Thr Gly Cys His Ala Phe

225 230 235 240

Arg Glu Asn Cys Ser Pro Gly Arg Cys Ile Asp Asp Ala Ser His Glu

245 250 255

Asn Gly Tyr Thr Cys Glu Cys Pro Thr Gly Tyr Ser Arg Glu Val Thr

260 265 270

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

275 280 285

Glu Lys Cys Glu Lys Glu Phe Gly Ile Ser Ala Ser Ser Cys Lys Cys

290 295 300

Asp Asn Gly Tyr Ser Gly Ser Ala Ser Ala Thr Ser His His Gly Lys

305 310 315 320

Gly Glu Ser Gly Ser Glu Gly Ser Leu Ser Glu Lys Met Asn Ile Val

325 330 335

Phe Lys Cys Pro Ser Gly Tyr His Pro Arg Tyr His Ala His Thr Val

340 345 350

Thr Cys Glu Lys Ile Lys His Phe Ala Leu Asp Gly Ala Gly Asn His

355 360 365

Asp Thr Thr Thr Tyr Val Ala Arg Arg Arg Tyr Pro Ala Ser Leu

370 375 380

<210> 303

<211> 580

<212> PRT

<213> Toxoplasma gondii

<400> 303

Met Arg Ala Ser Leu Pro Val His Leu Val Val Cys Thr Gln Leu Ser

1 5 10 15

Ala Val Trp Phe Gly Val Ala Lys Ala His Gly Gly His Arg Leu Glu

20 25 30

Pro His Val Pro Gly Phe Leu Gln Gly Phe Thr Asp Ile Thr Pro Ala

35 40 45

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

50 55 60

Asp Leu Ser Cys Val His Ser Asp Asn Lys Gly Ser Arg Ala Pro Thr

65 70 75 80

Ile Gly Glu Pro Val Pro Asp Val Ser Leu Glu Gln Cys Ala Ala Gln

85 90 95

Cys Lys Ala Val Asp Gly Cys Thr His Phe Thr Tyr Asn Asp Asp Ser

100 105 110

Lys Met Cys His Val Lys Glu Gly Lys Pro Asp Leu Tyr Asp Leu Thr

115 120 125

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

130 135 140

His Val Ser Tyr Glu Gly Ala Pro Asp Val Met Thr Ala Met Val Thr

145 150 155 160

Ser Gln Ser Ala Asp Cys Gln Ala Ala Cys Ala Ala Asp Pro Ser Cys

165 170 175

Glu Ile Phe Thr Tyr Asn Glu His Asp Gln Lys Cys Thr Phe Lys Gly

180 185 190

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

195 200 205

Gly Pro Lys Gln Phe Cys Asp Glu Gly Gly Lys Leu Thr Gln Glu Glu

210	215	220	
Met Glu Asp Gln Ile Ser Gly Cys Ile Gln Leu Ser Asp Val Gly Ser			
225	230	235	240
Met Thr Ala Asp Leu Glu Glu Pro Met Glu Ala Asp Ser Val Gly Ala			
245	250	255	
Cys Met Glu Arg Cys Arg Cys Asp Gly Arg Cys Thr His Phe Thr Phe			
260	265	270	
Asn Asp Asn Thr Arg Met Cys Tyr Leu Lys Gly Asp Lys Met Gln Leu			
275	280	285	
Tyr Ser Ser Pro Gly Asp Arg Thr Gly Pro Lys Ser Cys Asp Ser Ser			
290	295	300	
Cys Phe Ser Asn Gly Val Ser Tyr Val Asp Asp Pro Ala Thr Asp Val			
305	310	315	320
Glu Thr Val Phe Glu Ile Ser His Pro Ile Tyr Cys Gln Val Ile Cys			
325	330	335	
Ala Ala Asn Pro Leu Cys Thr Val Phe Gln Trp Tyr Ala Ser Glu Ala			
340	345	350	
Lys Cys Val Val Lys Arg Lys Gly Phe Tyr Lys His Arg Lys Thr Gly			
355	360	365	
Val Thr Gly Val Thr Val Gly Pro Arg Glu Phe Cys Asp Phe Gly Gly			
370	375	380	
Ser Ile Arg Asp Arg Glu Glu Ala Asp Ala Val Gly Ser Asp Asp Gly			
385	390	395	400
Leu Asn Ala Glu Ala Thr Met Ala Asn Ser Pro Asp Phe His Asp Glu			
405	410	415	
Val Glu Cys Val His Thr Gly Asn Ile Gly Ser Lys Ala Gln Thr Ile			
420	425	430	
Gly Glu Val Lys Arg Ala Ser Ser Leu Ser Glu Cys Arg Ala Arg Cys			
435	440	445	
Gln Ala Glu Lys Glu Cys Ser His Tyr Thr Tyr Asn Val Lys Ser Gly			
450	455	460	

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

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

<210> 304

<211> 181

<212> PRT

<213> Toxoplasma gondii

<400> 304

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

Ala Asp Arg Gln Ala Glu His Pro Gly Ala Pro Thr Gln Ser Glu Met
 65 70 75 80
 Lys Glu Phe Gln Glu Glu Ile Lys Glu Gly Val Glu Glu Thr Lys His

85 90 95
 Glu Gly Asp Pro Glu Met Thr Arg Leu Met Val Thr Glu Lys Gln Glu
 100 105 110
 Ser Lys Asn Phe Ser Lys Met Ala Lys Ser Gln Ser Phe Ser Thr Arg
 115 120 125

 Ile Glu Glu Leu Gly Gly Ser Ile Ser Phe Leu Thr Glu Thr Gly Val
 130 135 140
 Thr Met Ile Glu Leu Pro Lys Thr Val Ser Glu His Asp Met Asp Gln
 145 150 155 160
 Leu Leu His Asp Ile Leu Ala Ala Gly Gly Val Val Gly Leu Asp Ser
 165 170 175
 Glu Val Lys Leu Ala
 180
 <210> 305
 <211> 349
 <212> PRT
 <213> Toxoplasma gondii
 <400
 > 305
 Met Arg Leu Phe Arg Cys Cys Ala Ala Ala Val Val Ala Ala Glu Ser
 1 5 10 15
 Leu Leu Trp Leu Lys Asn Gly Ser Pro Phe Phe Ala Phe Leu Pro Gly
 20 25 30
 Asn Gly Glu Ile Ala Asp Asn Cys Ser Gly Asn Pro Cys Gly Gly Thr
 35 40 45
 Ala Ala Gly Thr Cys Ile Asn Thr Pro Ser Gly Tyr Asp Cys Arg Cys
 50 55 60

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

Cys Asn Glu Thr Asn Ser Gly Tyr Ile Cys Arg Cys Asn Gln Gly Tyr
 115 120 125

Arg Ile Ser Leu Asp Gly Thr Gly Asn Val Thr Cys Ile Val Arg Gln
 130 135 140

Glu Ser Gly Cys Glu Glu Asn Gly Cys Gly Pro Pro Asp Ala Val Gln
 145 150 155 160

Ser Cys Arg Arg Leu Thr Gly Thr Ala Gly Arg Leu Cys Val Cys Lys
 165 170 175

Glu Asn Phe Ile Ala Thr Ile Asp Ala Ser Ala His Ile Thr Cys Lys
 180 185 190

Arg Val Pro Pro His Tyr Arg Lys Pro Pro Phe Glu Phe Gly Lys Gly
 195 200 205

Gly His Pro Val Asp Ser Glu Pro Ser Lys Arg Gln Arg Glu Asp Glu
 210 215 220

Gly Glu Ser Arg Glu Pro Glu Ser Asp Ser Thr Glu Pro Gly Arg Asp
 225 230 235 240

Gln Glu Arg Arg Thr Pro Leu Glu Glu Ser Gln Glu Pro Glu Gly Ser
 245 250 255

Thr Pro Asp Ser Gln Gln Ser Arg Gly Gly Ser Gly Ser Asp Ser Thr
 260 265 270

Glu Ser Glu Glu Gln Gly Lys Glu Arg Glu Glu Gly Ser Gly His Ala
 275 280 285

Gly Ala Ile Ala Gly Gly Val Ile Gly Gly Leu Leu Leu Leu Ser Ala
 290 295 300

Ala Gly Ala Gly Val Ala Tyr Met Arg Lys Ser Gly Ser Gly Gly Gly
 305 310 315 320

Glu Glu Ile Glu Tyr Glu Arg Gly Ile Glu Ala Ala Glu Ala Ser Glu
 325 330 335

Val Glu Val Leu Val Asp Leu Asp Ser Lys Thr Trp Asp
 340 345

<210> 306

<211> 340

<212> PRT

<213> Toxoplasma gondii

<400> 306

Met Gly Gly Trp Glu Ser Lys Asp Ala Cys Glu Ser Gly Gly Thr Ala

1 5 10 15

Phe Cys Gly Thr Val Ala Asn Ser Ala Gly Cys Ile Ala Leu Ser Lys

20 25 30

Glu Phe Tyr Cys Thr Cys Leu Pro Gly Phe Gln Pro Glu Gly Arg Arg

35 40 45

Met Asn Ser Ser Cys Val Asp Ile Asp Glu Cys Ala Arg Gly Ile Gly

50 55 60

Leu Cys Phe Ser Lys Ile Glu Asn Ser Glu Cys Val Asn Thr Pro Gly

65 70 75 80

Ser Phe Glu Cys Arg Cys Asn Glu Tyr Arg Thr Leu Lys Asn Asn Val

85 90 95

Cys Glu Asp Ile Asn Glu Cys Leu Asp Asn Arg Gly Gly Cys Ala Glu

100 105 110

His Thr Asp Cys Ile Asn Asn Asp Gly Ala Ala Val Thr Cys Arg Cys

115 120 125

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

130 135 140

Asp Ile Asn Glu Cys Glu Glu Pro Asp His Cys Pro Glu Asn Ser Val

145 150 155 160

Cys Val Asn Thr Pro Gly Ser Tyr Arg Cys Glu Cys Lys Thr Gly Phe

165 170 175

Ala Lys Asp Ala Glu Gly Met Cys Thr Gly Lys Asp Phe Cys Val Thr

180 185 190

Gly Glu Asn Gly Cys Asp Pro Asn Phe Ala Thr Cys Thr Pro Val Val

195 200 205

Gly Ser Tyr Ala Cys Ala Cys Lys Asp Gly Phe Gln Gly Ser Gly Arg

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

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

Ser Phe Arg Gly

340

<210> 307

<211> 684

<212> PRT

<213> Toxoplasma gondii

<400> 307

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

50 55 60
 Lys Lys Tyr Asp Ala Cys Gly Ser Arg Glu Tyr Ser Asp Lys Gly Leu
 65 70 75 80

Lys Trp Thr Phe Cys Pro Glu Asp Phe Cys Cys Ser Lys Thr Ala Cys
 85 90 95
 Phe Tyr Gly Ser Cys Gly Ser Trp Cys His Asp Asn Trp Ala Leu Cys
 100 105 110
 Ser Ser Ser Ile Ile Tyr His Asp Glu Tyr Ser Tyr Gly Lys Cys Asn
 115 120 125
 Cys Lys Arg Phe Gln Glu Asn Cys Asp Val Asn Ala Ile Cys Val His
 130 135 140
 Ala Asn Arg Glu Asp Gly Gly Ala Tyr Cys Gln Cys Lys Glu Gly Tyr
 145 150 155 160
 Trp Gly Asp Gly Lys Ser Cys Lys Ile Asp Phe Cys Gln Leu Gln Pro
 165 170 175
 Cys Gly Ala Gly Thr Cys Thr Arg Thr Asp Glu Gly Tyr Lys Cys Asp
 180 185 190
 Cys Pro Glu Thr His Lys Leu Ile Val Val Glu Asp Lys Glu Thr Cys
 195 200 205
 Lys Ala Lys Pro Asp Phe Cys Ala Glu Glu Pro Cys Gly Pro Pro Ser
 210 215 220
 Met Val Glu Asn Cys Val Asn Thr Asp Asp Ser Tyr Glu Cys Val Cys
 225 230 235 240
 Lys Gln Gly Tyr Glu Val Arg Asn Gly Arg Cys Glu Glu Ile Asp Leu
 245 250 255
 Cys Ala Asp Lys Pro Cys Gly Pro Asp Glu Gly Val His Glu Cys Val
 260 265 270
 Thr Glu Arg Gln Pro Lys Leu Arg Tyr Arg Cys Thr Cys Lys Ala Gly
 275 280 285
 Phe Asp Leu Thr Thr Leu Pro Asp Gly Val Ser Gln Lys Cys Leu Lys
 290 295 300
 Asn Phe Cys Tyr Glu Glu Pro Cys Gly Thr Arg Asp Leu Val Glu Ser
 305 310 315 320
 Cys Lys Ser Lys Ala Tyr Gly Tyr Ser Cys Leu Cys Ala Ala Gly Ala

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

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

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

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

 565 570 575

Gln Cys Leu Pro Glu Ser Thr Asp Gln Thr Asp Phe Asp Ser Lys His
580 585 590
Lys Pro Glu Asp Asn Lys Gly Arg Tyr Ser Lys Gly Thr Ile Ala Leu
595 600 605
Val Val Val Gly Cys Val Ala Leu Leu Gly Ile Ile Ala Gly Gly Ile
610 615 620
Ser Tyr Ala Arg Asn Arg Gly Gly Glu Arg Asp Asp Glu Asp Leu Ala
625 630 635 640
Pro Pro Pro Arg Ser Thr Arg Glu Arg Arg Leu Ser Ser Met Gly Glu
645 650 655
Gly Phe Glu Asn Ala Ser Trp Ala Ser Ser Val Ser Met Ile Pro Ser
660 665 670
Ala Pro Ala Pro Pro Pro Ser Gly Gly Ile Trp Ser
675 680
<210> 308
<211> 300
<212> PRT
<213> Toxoplasma gondii
<400> 308
Met Arg Val Ser Phe Asn Val Pro Leu His Arg Thr Gly Phe Val Leu
1 5 10 15
Val Cys Val Ile Gly Ser Leu Cys Trp Cys Ile Ala Pro Ala Pro Glu
20 25 30
Cys Val Phe Pro Ala Thr Gly Leu Gly Pro Ala Ala Trp Asn His Pro
35 40 45
Gly Ser Leu Ala Gln Met Arg Ala Glu Ser Lys Gly Val Leu Ser Val
50 55 60
Thr Gly Ile Cys Asp Arg Asn Pro Cys Gly Pro His Gly Asn Cys Ile
65 70 75 80
Pro Asn Leu Ser Thr Tyr Thr Tyr Thr Cys Ser Cys Glu Gly Gly Tyr
85 90 95
Val Glu Ala Ala Val Ser Gly Lys Pro Thr Cys Gln Arg Lys Asp Pro

100 105 110
 Cys Asp Thr Ser Pro Cys Gly Thr Lys Glu Ala Val Lys Glu Cys Arg
 115 120 125
 Pro Asn Gly Gln Tyr Tyr Ala Cys Ile Cys Gln Ala Gly Tyr Gln Val

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

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

 260 265 270
 Phe Ala Val Val Tyr Leu Thr Ser Ser Arg Gln Ser Pro Asn Ser Asn
 275 280 285
 Asp Ala Leu Tyr Ala His Asp Phe Glu Gly Met Tyr
 290 295 300
 <210> 309
 <211> 999
 <212> PRT
 <213> Toxoplasma gondii
 <400> 309
 Met Val Pro Leu Ser Arg Met Ala Met Val Ser Val Ala Tyr Phe Ile
 1 5 10 15

Leu Gly Ala Leu Val Tyr Gly Ser Ala Asn Val Phe Gly Glu Met Gln

20 25 30

Pro Arg Gln Leu Ala Lys Ser Ser Thr Asp Asp Pro Thr Ile His Asp

35 40 45

Glu Gly His Gly Ala Ala Ala Pro Ser Thr Pro Arg Ala Gly Thr Glu

50 55 60

Leu Met Thr Pro His Pro Leu Ala Ser Arg Ala Lys Ala Val Thr Ser

65 70 75 80

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

85 90 95

Thr Thr Thr Glu His Ala Pro Lys Asn Pro Gly Leu Leu Gly Lys Pro

100 105 110

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

115 120 125

Thr Thr Met Glu Pro Lys Ala Ala Ser Gln His Ala Asp Arg Ser Gly

130 135 140

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

145 150 155 160

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

165 170 175

Ala Pro Leu His Arg Gln Pro Met Thr Arg Ala Thr Pro Val Gly Pro

180 185 190

Lys Pro Ala Asp Pro Ala Gly Lys Ala Val Lys Lys Ala Ala Thr Gly

195 200 205

Ile Pro Lys Pro Ala Ala Pro Gly Gly Lys Ala Val Lys Val Thr Pro

210 215 220

Val Ala Arg Lys Pro Val Ala Pro Lys Ala Ala Ala Pro Asp Gly Lys

225 230 235 240

Ala Val Lys Lys Ala Thr Val Val Val Pro Lys Pro Ala Ala Pro Ser

245 250 255

Gly Lys Ala Val Lys Lys Pro Val Val Ser Val Pro Lys Pro Ala Thr

260 265 270
Leu Gly Gly Lys Ala Val Lys Lys Pro Ala Ala Gly Val Pro Lys Pro

275 280 285
Ala Ala Pro Asp Gly Lys Ala Val Arg Lys Pro Val Val Gly Val Pro

290 295 300
Lys Pro Ala Ala Pro Asp Gly Lys Ala Ala Lys Lys Pro Ala Ser Gly

305 310 315 320
Val Pro Lys Pro Ala Asp Pro Ala Gly Lys Ala Val Lys Lys Ala Ala

325 330 335
Thr Gly Ile Pro Lys Pro Ala Ala Pro Gly Gly Lys Ala Val Lys Val

340 345 350
Thr Pro Val Ala Arg Lys Pro Val Ala Pro Lys Ala Ala Ala Pro Asp

355 360 365
Gly Lys Ala Val Lys Lys Ala Thr Val Val Val Pro Lys Pro Ala Ala

370 375 380
Pro Ser Gly Lys Ala Val Lys Lys Pro Val Val Ser Val Pro Lys Pro

385 390 395 400
Ala Thr Leu Asp Gly Lys Ala Val Arg Lys Pro Val Val Gly Val Pro

405 410 415
Lys Pro Ala Ala Pro Asp Gly Lys Ala Val Lys Lys Pro Val Val Gly

420 425 430
Val Pro Lys Pro Ala Ala Pro Asp Asp Thr Gly Ile Asn Lys Ala Thr

435 440 445
Leu Val Thr Arg Lys Pro Glu Ala Pro Asp Val Lys Val Val Lys Lys

450 455 460
Ala Thr Val Val Val Pro Lys Pro Glu Ala Pro Asp Ile Lys Val Met

465 470 475 480
Thr Asp Gln Thr Pro Thr Thr Pro Pro Ser Pro Pro Val Arg Ala Arg

485 490 495
Ala Ala Ser Ala Thr Thr Ile Val Thr Ala Pro Ala Pro Val Pro Thr

500 505 510

Arg Pro Val Leu Thr Thr Thr Ser Thr Ala Ala Thr Val Thr Thr Ile
515 520 525

Lys Thr Glu Thr Pro Arg Ala Ala Ser Arg Leu Gln Gln Asp Leu Asn

530 535 540

Ala Phe Cys Thr Thr Gln Phe Gln Lys Leu Cys Ser Glu Thr Ile Asp
545 550 555 560

Gly Gly Arg Tyr Cys Gly Val Ser Gly Ala Val Ala Arg Phe Gly Pro
565 570 575

Gly Gly His Asp Ser Asp Ser Gln Trp Arg Cys Tyr Glu Glu Ser Ile
580 585 590

Met Asn Thr Thr Thr Lys Gly Val Gln Cys Met Asp Asp Cys Gly Asn

595 600 605

Gln Met Gln Cys Val Gly Ala Val Ser Val Lys Thr Val Ala Thr Pro
610 615 620

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

Cys Ser Ser Phe Gln Arg Ser Ala Asp Ala Leu Cys Asn Phe Lys Arg
645 650 655

Thr Gly Asn Val Ala Arg Tyr Asp Pro Gly Arg Thr Arg Trp Met Cys

660 665 670

Phe Asn Pro Val Asp Ile Ser Leu Glu Gly Gln Ser Tyr Cys Ala Asn
675 680 685

Asn Cys Gly Gly Phe Thr Pro Cys Ala Gly Gly Leu Ser Pro Gly Glu
690 695 700

Ile Pro Thr Arg Thr Val Tyr Ile Ile Gln Gln Ser Asp Thr Ala Glu
705 710 715 720

Ala Phe Ala Ala Leu His Pro Cys Arg His Asp Glu Ile Cys Ile Pro

725 730 735

Ser Thr Val Tyr Pro Pro Ala Cys Val Lys Ala His Lys Ile Ile Ala
740 745 750

Ile Gln Gln Leu Ser Lys Gln Gln Glu Ala Met Asp Asn Tyr Cys Gln

755 760 765
 Thr Glu Met Asp Gln Met Cys Arg Val Gly Lys Trp Thr Thr Tyr Cys
 770 775 780
 Tyr Gln Leu Trp Leu Ser Arg Met Val Ser Thr Glu Glu Asp Glu Glu

 785 790 795 800
 Pro Lys Trp Arg Cys Tyr Pro Phe Ala Leu Leu Asn Phe Ser Asp Leu
 805 810 815
 Ser Thr Cys Ile Asp Gly Cys Ser Asn Arg Val Pro Cys His Gly Ala
 820 825 830
 Pro Ser Pro Thr Ser Thr Leu Thr Thr Glu Phe Ser Lys Leu Lys Thr
 835 840 845
 Ile Ala Glu Asn Ile Ala Phe Cys Ser Pro Phe Gln Lys Ala Ala Asn

 850 855 860
 Asp His Cys Asn Lys Arg Tyr Gly Glu Gly Trp Val Ala Arg Gln Asp
 865 870 875 880
 Val Thr Thr Asp Asp Trp Ala Cys Phe Gln Thr Thr Lys Leu Pro Thr
 885 890 895
 Tyr Arg Trp Thr Gly Cys Val Asp Asn Cys Gly Asn Thr Ser Leu Cys
 900 905 910
 Ala Ala Gly Val Pro Glu Gln Leu His Ser Ala Ala Ala Glu Ala Phe

 915 920 925
 Val His Pro Asp Pro Ala Leu Glu Arg Val Val Glu Ser Val Pro Ser
 930 935 940
 Pro Cys Leu Thr Gly Glu Ser Cys Thr Pro Thr Ala Met Asn Pro Pro
 945 950 955 960
 Tyr Cys Ser Glu Thr Arg Pro Asn Pro Gln Pro Ala Pro Leu Arg Asp
 965 970 975
 His Thr Ile Arg Asn Ala Leu Asp Cys Ser Lys Gly Ala Pro Leu Ala

 980 985 990
 Arg Arg Asn Pro Thr Ser Lys
 995

<210> 310

<211> 608

<212> PRT

<213> *Toxoplasma gondii*

<400> 310

Met Tyr Pro Ile Ala Pro Ser Phe Ala Met Val Gly Ser Val Gly Ser

1 5 10 15

Ile Arg Arg Thr Ser Arg Cys Pro Ser Lys Thr Ala Ser Cys Phe Arg

20 25 30

Leu Tyr Val Phe Pro Leu Val Pro Pro Thr Asn Met Ala Lys Ala Lys

35 40 45

Thr Val Gly Val Arg Leu Ile Gly Val Thr Thr Cys Val Ala Phe Ala

50 55 60

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

65 70 75 80

Tyr Arg Val Ala Gln Arg Pro Gly Ser Leu His Phe Ala Arg Met His

85 90 95

Asp Arg Phe Val Asn Lys Asp Arg Glu Ala Glu Glu His Lys Val Ala

100 105 110

Ala Leu Glu Arg Asn Thr Thr Pro Glu Asn Ile Ser Ser Gln Met Asp

115 120 125

Ser Asn Lys Thr Thr Ala Pro Ser Pro Glu Pro Gly Thr Ser Lys Arg

130 135 140

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

145 150 155 160

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

165 170 175

Gln Gln Cys Ala Lys Gly Val Leu Gly Lys Thr Tyr Cys Thr Asp Gly

180 185 190

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

195 200 205

Trp His Cys Phe Lys Gly Ala Glu Ile Ala His Ser Gln Arg Gln Val

210 215 220
 Lys Cys Val Asp Asn Cys Gly Asn Leu Met Lys Cys Phe Gly Asp Val

 225 230 235 240
 Asn Ser Ser Gln Thr Ala Lys Val Ala Met Pro Gly Met Asp Glu Trp

 245 250 255
 Ile Asp Lys Arg Lys Trp Thr Tyr Cys Ser Pro Tyr Gln Gln Ala Ala

 260 265 270
 Asp Ala Leu Cys Asn Leu Lys His His Gly Asp Val Ala Arg Tyr Asp

 275 280 285
 His Val Arg Gln Arg Trp Met Cys Leu Asp Leu Asn Asp Val Ala Leu

 290 295 300
 Asp Gly Ile Ser Tyr Cys Ala Asp Asn Cys Gly Gly Pro Thr Ser Cys
 305 310 315 320
 Val Gly Gly Leu Leu Pro Gly Glu Leu Pro Gln Arg Ser Val Arg Ile

 325 330 335
 Val Arg His Arg Asp Met Glu Ser Ala Phe Glu Ala Ile Gln Pro Cys

 340 345 350
 Pro Asn Ala Gly Asp Ile Cys Val Ala Ser Thr Val Asn Pro Pro Ala

 355 360 365
 Cys Leu Pro Gln Val Gln Thr Leu Val Leu Gln Arg Leu Pro Ala Gln
 370 375 380
 Gln Arg Ala Leu Asp Thr Met Cys Gln Asp Ala Met Asp Glu Glu Cys
 385 390 395 400
 Arg Lys Gly Lys Gln Thr Glu Asp Cys Phe Gly Leu Trp Leu Ala Arg

 405 410 415
 Tyr Glu Leu Glu Ser Ser Pro Gly Gly Ala Gly Ala Trp Arg Cys Tyr

 420 425 430
 Pro Glu Ser Arg Leu Asp Phe Thr Gln Leu Ser Ser Cys Ile Asp Gly
 435 440 445
 Cys Gly Asn Pro Ile Ser Cys Arg Gly Gln Pro Ala Glu Val Ser Pro

 450 455 460

Ala Phe Ile Asp Leu Pro Ala Leu Asp Lys Val Ala Gly Asp Met Ser
 465 470 475 480
 Tyr Cys Ser Ala Tyr Gln Arg Ala Gly Asn Ala Tyr Cys Ala Gln Lys

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

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

<210> 311

<211> 654

<212> PRT

<213> Toxoplasma gondii

<400> 311

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

Phe	Tyr	Phe	Thr	Tyr	Ile	Pro	Glu	Arg	Lys	Gln	Cys	Tyr	Leu	Lys	Asp
65				70				75				80			
Asn	Gln	Ala	Pro	Asn	Gly	Thr	Val	Thr	Asn	Pro	Leu	Ala	Ile	Ser	Gly
85				90				95							
Pro	Lys	Phe	Cys	Tyr	Pro	Thr	Gly	Thr	Cys	Phe	Glu	Tyr	Met	Thr	Asp
100				105				110							
Tyr	Val	Gly	Tyr	Asp	Val	Gln	Lys	Ile	Glu	Asp	Gln	Ser	Val	Ser	Gln
115				120				125							
Ala	Asp	Asp	Cys	Gln	Arg	Leu	Cys	Ala	Ser	Asn	Asp	Gln	Cys	Phe	Phe
130				135				140							
Trp	Thr	Phe	Ile	Pro	Ser	Lys	His	Asn	Cys	Tyr	Leu	Lys	His	Asn	Gly
145				150				155				160			
Ala	Thr	Val	Gly	Arg	Thr	Pro	His	Ser	Glu	Ala	Ile	Ser	Gly	Pro	Lys
165				170				175							
Ser	Cys	Thr	Gly	Gly	Ser	Pro	Asn	Asp	Gln	Gly	Val	Pro	Cys	Tyr	Glu
180				185				190							
Pro	Asp	Thr	Asp	Tyr	Phe	Gly	Tyr	Asp	Ile	Lys	Ile	Phe	Asp	Asn	Asn
195				200				205							
Leu	Val	Gly	Thr	Ala	Ala	Glu	Cys	Tyr	Gly	Leu	Cys	Leu	Ser	Phe	Ala
210				215				220							
Glu	Cys	Lys	Phe	Trp	Thr	Trp	Val	Pro	Ala	Leu	Arg	Asn	Cys	Tyr	Leu
225				230				235				240			
Lys	Ser	Glu	Tyr	Ala	Pro	Leu	Gly	Arg	Val	His	Ala	Pro	Gly	Thr	Ile
245				250				255							
Ser	Gly	Pro	Arg	Asp	Cys	Asn	Gly	Ser	Asn	Leu	Pro	Pro	Phe	Val	Pro
260				265				270							
Pro	Pro	Pro	Ile	Tyr	Pro	Pro	Thr	His	Pro	His	Pro	Pro	Pro	Ser	Pro
275				280				285							
Tyr	Pro	Pro	Tyr	Pro	Gly	His	Thr	Ser	Thr	Thr	Thr	Pro	Ala	Thr	Pro
290				295				300							
Pro	Ala	Glu	Ser	Cys	Tyr	Lys	Ala	His	Val	Asp	Phe	Pro	Thr	Gly	Thr

305 310 315 320
 Leu Lys Gln Ile Val Thr Asp Asp Ala Tyr Ala Cys Gln Lys Leu Cys
 325 330 335
 Gln Ala Glu Ala Ala Cys Phe Phe Phe Thr Tyr Lys Ala Asp Ile Leu
 340 345 350
 Glu Cys Ala Leu Lys Gly Ser Phe Ala Ala Asn Ala Pro Ile Pro Arg
 355 360 365
 Arg His Ala Leu Ser Gly Ser Lys Tyr Cys Ala Asp Lys Met Pro Pro
 370 375 380

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

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

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

Ala Lys Glu Glu Gly Thr Cys Val Ser Gly Pro Lys Thr Cys Ala Asp
565 570 575

Lys Pro Thr Asp Pro Cys Phe Lys Glu Gly Phe Tyr Phe Gly Gln Val
580 585 590

Leu Lys Arg His Asn Ala Val Ala Ser Ala Lys Glu Cys Gln Thr Leu
595 600 605

Cys Ala Thr Phe Pro His Ser Cys Val Gly Phe Thr Tyr Glu Ser Ala
610 615 620

Ser Gln Lys Cys Phe Leu Met Ser Gln Thr Asp Gly Leu Glu Leu Ser
625 630 635 640

Asp Gly Phe Val Ser Gly Leu Arg Gln Cys Pro Ala Thr Pro
645 650

<210> 312
<211> 470
<212> PRT
<213> Toxoplasma gondii
<400> 312

Met Ser His Glu Asn Ala Phe His Pro Ser Arg Met Gln Ser Phe Ser
1 5 10 15

Leu Arg Cys Arg Pro Ser Ser Leu Tyr His Ala Ala Gly Ser Asp Glu
20 25 30

Glu Pro Ala Ala Val Ser Thr Pro Ala Ala Gly Arg Thr Ser Gly Val
35 40 45

Val Gln Ala Val Gln Arg Arg Glu Gly Lys Ala Phe Ala Ala Gly Gln
50 55 60

Pro Val Arg Cys Arg Ala Leu Leu Thr Arg Arg Ser Ser Arg Leu Leu
65 70 75 80

Leu Ala Gly Arg Leu His Leu Arg Ser His His Ala Leu Thr Ser Ile
85 90 95

Ala Ala Val Phe Leu Met Phe Ala Ala Tyr Cys Pro Ser His Ile Asp
100 105 110

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

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

420 425 430
 Asn Asp Gly Glu Gly Val Asn Ala Gly Ala Ile Ala Gly Gly Val Ile
 435 440 445
 Gly Gly Val Val Gly Ile Gly Ile Cys Gly Ala Gly Ala Phe Phe Phe
 450 455 460

Met Lys Lys Ser Gln His

465 470

<210> 313

<211> 717

<212> PRT

<213> Toxoplasma gondii

<400> 313

Met Cys Leu Leu Ser Ser Leu Phe Ser Pro Ser Ser Val Ser Ala Ser

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

65 70 75 80
 Trp Leu Cys Arg Phe Ser Phe Trp Asp Gly Pro Cys Val Asp Arg Gln
 85 90 95

His Asn Gly Ile Gly Pro Trp Arg Phe Cys Pro Ser Gly Ser Cys Cys
 100 105 110
 Ser Lys Val Lys Cys Ala Tyr Gly Ser Cys Gly Gly Ser Trp Cys Ala
 115 120 125
 Ala Trp Asn Ser Gly Leu Cys Val Phe His Asn Gly Asp Tyr Glu Ser
 130 135 140
 Asp Arg Cys Thr Cys Glu Lys Tyr Gly Gly Gln Cys Ser Lys Asn Gly
 145 150 155 160
 Ser Cys Lys Arg Leu Asp Thr Pro Glu Gly Gly Ala Phe Cys Tyr Cys
 165 170 175
 Asn Pro Gly Tyr Val Gly Asp Gly Arg Thr Cys Glu Ser Asp Pro Cys
 180 185 190
 Tyr Gly Ser Pro Cys Ala Pro Gly Thr Cys Ser Arg Met Gly Asn Ser
 195 200 205
 Tyr Val Cys Gly Cys Pro Pro Gly Tyr Thr Gln Asp Thr Ser Arg Gly
 210 215 220
 His Ala Arg Cys Val Glu Lys Ala Asp Ser Cys Arg Ala Gln Pro Cys
 225 230 235 240
 Gly Ser Asp Thr Val Ala Tyr Asp Cys Val Ser Phe Asp Ser Gly Ala
 245 250 255
 Tyr Glu Cys Ile Cys Lys Asp Gly Tyr Ala Ser Asn Gly Thr Lys Cys
 260 265 270
 Glu Lys Gln Asp Trp Cys Lys Asp Asn Pro Cys Gly Asp Ala Asn Ala
 275 280 285
 Val Tyr Asp Cys Ile Ser His Glu Thr Gly Tyr Thr Cys Gln Cys Gln
 290 295 300
 Lys Gly Tyr Ile Gln Val Val Thr Asp Glu Gly Gln Gln Lys Cys Ala
 305 310 315 320
 Lys Asn Pro Cys Ser Tyr Asp Pro Cys Gly Thr Ser Asp Leu Val Lys
 325 330 335
 Glu Cys Ile Asn Lys Ser Asp Gly Thr Tyr Gly Cys Val Cys Ala Asp

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

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

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

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

 580 585 590

Leu Gln Thr Met Tyr Gly Lys Pro Arg Cys Val Pro Gly Pro Ser Ser
 595 600 605
 Tyr Asp Ser Asp Glu Glu Glu Thr Ser Ser Ser Ser Ser Thr Thr Ser
 610 615 620
 Glu Glu Glu Gly Thr Ser Thr Val Met Ile Ala Gly Cys Val Val Gly
 625 630 635 640
 Gly Val Val Leu Leu Gly Ala Val Ala Tyr Met Gly Arg Arg Gly Asn
 645 650 655
 Asp Glu Glu Glu Asp Glu Gln Pro Arg Pro Pro Ala Gly Gly Pro Gln
 660 665 670
 Gly Pro Tyr Met Gly Gln Gln Gly Tyr Gly Gln Gly Gln Asn Leu Met
 675 680 685
 Pro Pro Gly Met Asp Pro Ala Met Gly Arg Asn Ser Met Met Ala Arg
 690 695 700
 Gln Gln Tyr Ala Met Asp Thr Arg Asn Ser Phe Trp Gly
 705 710 715
 <210> 314
 <211> 759
 <212> PRT
 <213> Toxoplasma gondii
 <400> 314
 Met Ala Gly Pro Tyr Arg Tyr Ser Gly Leu Asp Arg Phe Ser Leu Pro
 1 5 10 15
 Cys Leu Ser Pro Ala Ser Ala Leu Arg Val Val Gly Ser Ser Glu Thr
 20 25 30
 Lys Ala His Leu Val Lys Met Arg Gly Ala Arg Asp Ala Leu Leu Ser
 35 40 45
 Leu Ser Arg Ile Ser Leu Leu Ala Ala Leu Ala Gly Leu Ala Cys Cys
 50 55 60
 Arg Ala Met Val Val Leu Ser Ser Ala Phe Ala Thr Thr Val Val Glu
 65 70 75 80
 Lys His Pro Gly Ser Leu His Pro Glu Ser Gly Glu Ala Pro Ala Thr

	85	90	95
Ala Ser Ser Leu Val Gln Ile Glu Ala Ala Gln His Thr Ser Leu Val			
	100	105	110
Ser Ser Ala Ala Ala Arg Thr Val Phe Gln Pro Pro Ser Glu Glu Ser			
	115	120	125
Trp Leu Cys Arg Leu Ser Thr Asn Asn Gly Pro Cys Ser Lys Asn Ser			
	130	135	140
Ser Asp Pro Glu Ile Gly Gln Trp Arg Phe Cys Pro Pro Gly Arg Cys			
145	150	155	160
Cys Ser Met Ser Lys Cys Gly Pro Ala Gly Cys Ser Ile Gly Trp Cys			
	165	170	175
Glu Gly Trp Gly Asn Pro Leu Cys Trp Ile Lys Asp Asp Thr Tyr Ser			
	180	185	190
Asp Gly Lys Cys Thr Cys Glu Lys Tyr Arg Asp Arg Cys Ser Pro Asn			
	195	200	205
Ala Asp Cys Leu Glu Tyr Asn Val Glu Arg Gly Gly Ala Tyr Cys Val			
	210	215	220
Cys Lys Asp Gly Tyr Tyr Gly Asp Gly Lys Val Cys Glu Phe Asp Pro			
225	230	235	240
Cys Ser Gly Asn Pro Cys Asn Pro Gly Ser Cys Arg Arg His Gly Thr			
	245	250	255
Ser Tyr Ser Cys Ala Cys Pro Asp Thr Tyr Ala Val Thr Ser Thr Ser			
	260	265	270
Ser Gly Glu Arg Cys Glu Val Lys Arg Asn Phe Cys Leu Gly Glu Pro			
	275	280	285
Cys Gly Ser Ser Glu Val Ala Ala Asp Cys Val Ser Phe Asp Ser Gly			
	290	295	300
Glu Tyr Glu Cys Ile Cys Lys Ser Ser Tyr Val Ser Asp Gly Lys Gly			
305	310	315	320
Cys Val Lys Phe Asp Pro Cys Glu Tyr Asn Pro Cys Gly Thr Ser Glu			
	325	330	335

Ala Val Lys Ser Cys Thr His Val Asn Gly Asp Glu Tyr Lys Cys Glu
340 345 350

Cys His Glu Gly Tyr Asn Leu Thr Asn Asp Ser Asp Gly Asn Met Val
355 360 365

Cys Ala Lys Asp Pro Cys Tyr Gly Asn Pro Cys Gly Leu Pro His Leu
370 375 380

Val Ala Ser Cys Ala Arg Arg Thr Pro Asp Ser Thr Ser Ser Ala Thr
385 390 395 400

Tyr Thr Cys Leu Cys Thr Ala Ala Gly His Leu Gln Val Asp Pro Val
405 410 415

Thr Gly Ala Gln Ser Cys Thr Gln Gly Asp Pro Cys Ala Ser Asn Pro
420 425 430

Cys Gly Ser Asp Ala Val Val Asp Phe Cys Ile Ser Glu Asp Asp Thr
435 440 445

Tyr Arg Cys Val Cys Lys Thr Gly Tyr Ala Ser Val Glu Ile Asn Gly
450 455 460

Arg Lys Gln Cys Lys Arg Gly Asp Pro Cys Glu Leu Lys Val Cys Gly
465 470 475 480

Glu Asp His Leu Val Glu Ser Cys Ser Thr Asn Asn Lys Leu Tyr Ser
485 490 495

Cys Asp Cys Thr Ser Leu Ala Ile Lys Gly Leu Asn Asp Glu Lys Lys
500 505 510

Pro Val Cys Ile Ser Arg Glu Glu Cys Glu Ser Val Cys Gly Pro Leu
515 520 525

Lys Gly Val Lys Gln Cys Asn Gln Lys Met Gly Val Leu Glu Cys Val
530 535 540

Cys Asp Met Gly Tyr Ile Leu Ser Thr Gln Asn Gly Lys Lys Gln Cys
545 550 555 560

Val Gln Gly Asp Ala Cys Leu Asn Gln Pro Cys Gly Thr Pro Glu Ser
565 570 575

Thr Leu Ala Cys Thr Ala Asn Gly Ser His Tyr Ser Cys Ser Cys Asn

580 585 590
 Glu Gly Tyr Glu Leu Arg Met Arg Pro Asp Gly Thr Gln Val Cys Ala
 595 600 605
 Ser Ala Gly Asp Cys Thr Gly Ser Pro Cys Gly Ala Ser Thr Ser Ile
 610 615 620

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

 Leu Ala Leu Gly Ala Ala Leu Trp Phe Ser Asn Ser Gln Glu Glu Gln
 690 695 700
 Thr Met Gly Ser Gly Gly Met Gly Gly Met Asp Asp Pro Met Gln Gly
 705 710 715 720
 Pro Met Gly Pro Met Gly Met Gly Gly Pro Met Gly Pro Gly Gly Pro
 725 730 735
 Met Gly Pro Met Gly Pro Pro Gly Pro Arg Gln Ser Tyr Ala Ala Tyr
 740 745 750

 Pro Ser Gly Ser Met Trp Ser
 755
 <210> 315
 <211> 351
 <212> PRT
 <213> Toxoplasma gondii
 <400> 315
 Met Asp Ala Leu Lys Thr Val Phe Asn Arg Arg Ile Ala Leu Pro Val
 1 5 10 15
 Val Val Ala Ala Ala Leu Leu His Asn Ser Ala Glu Ala Leu Gln Ser
 20 25 30

Pro Gly Leu Arg Arg Gln Leu Val Asn Ala His Ser Phe Ala Glu Val
35 40 45

Glu Ser Thr Gly Tyr Ser Cys Leu Glu Lys Gly Lys Glu Tyr Val Gly
50 55 60

Phe Ser Leu Thr Glu Phe Thr Glu Val Gly Asp Ala Ala Leu Cys Gln
65 70 75 80

Gln Arg Cys Asn Gln His Pro Gln Cys Gly Phe Phe Thr Phe Tyr Ser
85 90 95

Asn Gly Asn Arg Cys Val Leu Gln Ser Arg Lys Pro Ser Gln Glu Lys
100 105 110

Asn Asn Ala Asn Ala Val Ser Gly Pro Lys Arg Cys Pro Leu Cys Leu
115 120 125

Val Asp Ser Phe Asp Phe Arg Gly Glu Lys Asn Met His Asp Asn Gly
130 135 140

Val Pro Gly Ile Lys Thr Val Val Glu Cys Gln Met Gly Cys Ala Ala
145 150 155 160

Glu Pro Lys Cys Lys Gly Phe Leu Phe Gln His Lys Thr Lys Gln Cys
165 170 175

His Phe Lys Thr Ser Asp Asn Tyr Leu Lys Ser Leu His Pro Asp Asn
180 185 190

Glu Tyr Val Ala Gly Pro Lys Thr Cys Thr Gly Glu His Trp Cys Ile
195 200 205

Met Lys Asp Ile Gly Tyr Glu Ala Met Tyr Thr Arg Arg Ser Gln Thr
210 215 220

Asn Ser Ala Glu Glu Cys Gln Asn Lys Cys Leu Asn Asp Glu Gln Cys
225 230 235 240

Gln Tyr Phe Thr Trp Gln Val Ser Asn Lys His Cys Trp Leu Lys His
245 250 255

Gly Pro Thr Ile Ala Asn Ser Lys Tyr Asn Arg Gln Gly Asp His Ser
260 265 270

Ala Pro Lys His Cys Gly Leu Pro Thr Thr Cys Val Lys Glu Arg Thr

275 280 285
Lys Tyr Ala Gly Glu Thr Val Ala Thr Phe Pro Lys Ser Glu Val Gly
290 295 300

Thr Phe Glu Ser Cys Gln Met Lys Cys Trp Lys Thr Ser Lys Cys Val
305 310 315 320

Phe Met His Phe Asn Asn Asp Gly Cys Thr Leu Ser Gly Ile Asn Ala
325 330 335

Thr Ala Gln Thr Asp Ala Asn Ser Lys Ala Gly Asp Ile Thr Cys
340 345 350

<210> 316

<211> 407

<212> PRT

<213> Toxoplasma gondii

<400> 316

Met Lys Thr Arg Ser Phe Asn Gln Ala Glu Leu Lys Arg Glu Arg Val

1 5 10 15
Asp Val Arg Lys Cys Glu Lys Asn Asp Thr Val Ser Cys Ala Gly Val

20 25 30
Ser Phe Cys Ser Glu Gly Leu Glu Leu Arg Arg Gln Asp Met Asp Met

35 40 45
Thr Pro Phe Val Glu Asp Asn Ala Glu Ala His Val Cys Tyr Glu Pro

50 55 60
Asp Val Glu Tyr Val Asp His Thr Asn Leu Ala Ile Glu Gly Gly His

65 70 75 80
Val His Ser Pro Ser Ser Cys Gln Asp Leu Cys Gln Arg Tyr Gln Asp

85 90 95
Cys Tyr Phe Trp Thr Trp Asn Ser Val Lys Lys Asp Cys Tyr Leu Lys

100 105 110
Asn Ser Thr Ala Leu Phe Ser Arg Gln Lys Asn Tyr Asp Thr Arg Asn

115 120 125
Lys Ile Ser Gly Pro Lys Trp Cys Met Met Pro His Pro Leu Arg Cys

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

Trp Thr Lys Asn Glu Thr Thr Glu Lys Leu Ile Ser Gly Pro Lys Asp

385 390 395 400

Cys Ser Cys Ser Gly Leu His

405

<210> 317

<211> 1161

<212> PRT

<213> Toxoplasma gondii

<400> 317

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

1 5 10 15

His Gly Lys Ser Ile His Arg Ser Ser Ile Val Val Val Thr His Cys

20 25 30

Ser His Arg Leu Ser Leu Ser Pro Leu Asn Arg Pro Ala Leu Phe Pro

35 40 45

Ser His Ser Asp Arg Tyr Thr Val Pro Trp Arg Cys Arg Pro Ser Ser

50 55 60

Trp Arg Leu Trp Ile Thr Phe Val Cys Leu Ser Thr Leu His Met Phe

65 70 75 80

Gly Leu Ser Ser Ala Val Lys Arg Asp Gly Glu Val Pro Thr Ala Asn

85 90 95

Leu Arg Ala Ser Leu Ser Pro Asp Ser Ser Lys Glu Asn Ala Met Leu

100 105 110

Leu Ser Ala Ile Gly Gly Ile Gly Pro Thr Glu Ser Arg Leu Gln His

115 120 125

Ile Pro Phe Ser Thr Thr Arg Tyr Leu Pro Ile Arg Ser His Val Leu

130 135 140

Gln Ser Thr Val Glu Arg Ile Glu Ser Pro Glu Ala Leu Asn Glu Val

145 150 155 160

Pro Thr Lys Val Glu Arg Asn Glu Phe Thr Glu Lys Gly Asp Lys Thr

165 170 175

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

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

 290 295 300
 Asp Ser Ser Ser Asn Thr Gln Ala Asp Asp Ser Gln Arg Gln Ser Leu
 305 310 315 320
 Gly Asp Ser Ser Ala Leu Asp Leu Phe Gly Ser Asp Thr Gly Asp Thr
 325 330 335
 Gly Asp Ile Phe Gly Phe Ser Asn Ser Ser Ser Asp Gly Gly Asn Ala
 340 345 350
 Ala Ala Asn Asp Gly Gly Leu Phe Ser Ser Ser Gly Met Gly Pro Thr

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

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

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

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

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

Gly Thr His Phe Leu Val Arg Leu Phe Ala Gly Gly Lys Met Thr Tyr

675 680 685

Gln Val Thr Ala Lys Arg Ser Glu Val Glu Lys Met Arg Asn Met Gly

690 695 700

Ile Asp Val Lys Thr Gln Leu Lys Met Gln Leu Gly Gly Val Ser Gly

705 710 715 720

Gly Ala Gly Gln Gly Thr Ser Ser Lys Lys Asn Gln Ser Ser Ser Glu

725 730 735

Tyr Gln Met Asn Val Gln Lys Glu Thr Leu Val Ile Gly Gly Arg Pro

740 745 750

Pro Gly Asn Val Ser Asp Pro Ala Ala Leu Ala Ala Trp Ala Asp Thr

755 760 765

Val Glu Glu Leu Pro Met Pro Val Lys Phe Glu Val Gln Pro Leu Tyr

770 775 780

His Leu Leu Pro Val Glu Lys Gln Glu Ala Phe Lys Gln Ala Val Thr

785 790 795 800

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

805 810 815

Thr Gly Val Thr Arg Asn Leu Pro Lys Gln Leu Thr Gln Ala Thr Gln

820 825 830

Val Ala Trp Ser Gly Pro Pro Pro Gly Phe Ala Lys Cys Pro Glu Gly

835 840 845

Gln Val Val Ile Leu Gly Phe Ala Met His Leu Asn Phe Lys Glu Pro

850 855 860

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

865 870 875 880

Cys Asp Gly Val Gly Thr Ala Ser Ser Glu Thr Asp Glu Gly Arg Ile

885 890 895

Tyr Ile Leu Cys Gly Glu Glu Pro Ile Asn Glu Ile Gln Gln Val Val

900 905 910

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

915	920	925	
Pro Asp Glu Thr Val Val Val Gly Gly Phe Gly Ile Ser Val Arg Gly			
930	935	940	
Gly Ser Asp Gly Leu Asp Ser Phe Ser Ile Glu Ser Cys Thr Thr Gly			
945	950	955	960
Gln Thr Ile Cys Thr Lys Ala Pro Thr Arg Gly Ser Glu Lys Asn Phe			
965	970	975	
Leu Trp Met Met Cys Val Asp Lys Gln Tyr Pro Gly Leu Arg Glu Leu			
980	985	990	
Val Asn Val Ala Glu Leu Gly Ser His Gly Asn Ala Asn Lys Arg Ala			
995	1000	1005	
Val Asn Ser Asp Gly Asn Val Asp Val Lys Cys Pro Ala Asn Ser			
1010	1015	1020	
Ser Ile Val Leu Gly Tyr Val Met Glu Ala His Thr Asn Leu Gln			
1025	1030	1035	
Phe Val Arg Asp Lys Phe Leu Gln Cys Pro Glu Asn Ala Ser Glu			
1040	1045	1050	
Cys Lys Met Thr Gly Lys Gly Val Asp His Gly Met Leu Trp Leu			
1055	1060	1065	
Phe Asp Arg His Ala Leu Phe Gly Trp Ile Ile Cys Lys Thr Val			
1070	1075	1080	
Asn Glu Pro Ala Met His Val Ala Thr Asp Val Gly Lys Ala Lys			
1085	1090	1095	
Gly Asn Gly Lys Lys Arg Lys Gly Lys Lys Gly Lys Asn Lys Thr			
1100	1105	1110	
Asn Ala Pro Asn Glu Val Glu Glu Gly Gln Gln Leu Gly Ala Asp			
1115	1120	1125	
Ser Pro Ser Gln Val Ser Val Pro Ala Asp Ala Asp Ser Gly Pro			
1130	1135	1140	
Thr Ser Lys Thr Met Ser Ser Leu Lys Leu Ala Pro Val Lys Leu			
1145	1150	1155	

Leu Asp Leu

1160

<210> 318

<211> 351

<212> PRT

<213> *Toxoplasma gondii*

<400> 318

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

1 5 10 15

Val Val Ala Ala Val Leu Leu Gln Ile Arg Ala Val Ala Leu Gln Ser

20 25 30

Pro Gly Leu Arg Asn Gln Val Val Asn Ala His Ser Phe Ala Glu Val

35 40 45

Glu Thr Thr Gly Tyr Ser Cys Leu Glu Lys Asp Lys Glu Tyr Val Gly

50 55 60

Phe Ser Leu Thr Glu Phe Thr Glu Val Gly Asp Ala Gly Leu Cys Gln

65 70 75 80

Gln Arg Cys Asn Gln His Pro His Cys Ser Phe Phe Thr Phe Tyr Ser

85 90 95

Asn Gly Asn Arg Cys Val Leu Gln Ser Arg Lys Pro Ser Gln Glu Lys

100 105 110

Asn Asn Ala Asp Ala Val Ser Gly Pro Lys Arg Cys Pro Leu Cys Leu

115 120 125

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

130 135 140

Ala Pro Gly Leu Asn Thr Leu Leu Glu Cys Gln Gln Gly Cys Ala Ala

145 150 155 160

Glu Pro Arg Cys Lys Gly Phe Leu Phe Glu Lys Arg Pro Arg Thr Cys

165 170 175

His Phe Lys Thr Asn Asp Asn Tyr Leu Lys Ala Leu Asp Pro Asp Thr

180 185 190

Ser Tyr Ile Ala Gly Pro Lys Thr Cys Thr Asp Glu His Trp Cys Ile

195					200					205						
Met	Lys	Asp	Ile	Gly	Tyr	Arg	Gly	Thr	Asp	Ser	Lys	Glu	Thr	Arg	Ala	
210					215					220						
Asn	Ser	Ala	Ala	Glu	Cys	Gln	Gln	Met	Cys	Leu	Asn	Asp	Glu	Arg	Cys	
225					230					235					240	
Asp	Phe	Phe	Thr	Trp	Gln	Gln	Ala	Gly	Lys	Tyr	Cys	Trp	Phe	Lys	Ala	
245					250					255						
Gly	Ala	Ser	Thr	Ala	Ser	Thr	Lys	Tyr	Asn	Arg	Ala	Gly	Asp	Tyr	Ser	
260					265					270						
Ala	Pro	Lys	His	Cys	Gly	Leu	Pro	Thr	Thr	Cys	Val	Lys	Glu	Arg	Thr	
275					280					285						
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Ala	Thr	Phe	Pro	Lys	Ser	Glu	Val	Gly	
290					295					300						
Thr	Phe	Glu	Ser	Cys	Gln	Met	Lys	Cys	Trp	Lys	Thr	Ser	Lys	Cys	Val	
305					310					315					320	
Phe	Met	His	Phe	Asn	Asn	Asp	Gly	Cys	Thr	Leu	Ser	Gly	Ile	Asn	Ala	
325					330					335						
Thr	Ala	Gln	Thr	Asp	Ala	Asn	Ser	Lys	Ala	Gly	Asp	Ile	Thr	Cys		
340					345					350						
<210>	319															
<211>	293															
<212>	PRT															
<213>	Toxoplasma gondii															
<400>	319															
Met	Ala	Arg	Val	Arg	Thr	Leu	Ala	Asp	Leu	Arg	Thr	Glu	Asp	Glu	Ala	
1	5				10				15							
Asp	Glu	His	Thr	Pro	Leu	Tyr	Asn	Ala	Glu	Thr	Gly	Ser	Arg	Asp	Ser	
20					25					30						
Asp	Ser	Thr	Ser	Ser	Gly	Gly	Ala	Ala	Pro	Arg	Ser	Met	Pro	Ile	Arg	
35					40					45						
Phe	Leu	Glu	Leu	Leu	Phe	Pro	His	Phe	Ser	Leu	Arg	Ser	Val	Val	Leu	

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

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

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

 225 230 235 240
 Ser Ile Gly Met Leu Tyr Asn Lys Glu Leu Asn Asp Lys Pro Val Trp
 245 250 255
 Tyr Pro Trp Ala Ser Ala Ala Ala Ile Gly Ile Leu Leu Ala Leu Pro
 260 265 270
 Ala Ala Cys Phe Pro Ile Leu Tyr Ala Val Asp Arg His Cys His Arg
 275 280 285
 Asp Leu Ser Tyr Ile
 290
 <210

> 320

<211> 534

<212> PRT

<213> Toxoplasma gondii

<400> 320

Met Glu Val Ser Arg Ser His Arg Trp Pro Leu Gly Ser Ser Pro His

1 5 10 15

Ser Ser Ser Pro Ala Leu Cys Trp Ser Cys Val Ser Arg Phe Ser Arg

20 25 30

Ser Ile Cys Arg Arg Gly Gly Arg Phe Pro Pro Leu Tyr Phe Ser Arg

35 40 45

Ser Ser Phe Leu Leu Arg Val Leu Pro Leu Val Leu Tyr Ser Leu Val

50 55 60

Ser Gly Pro Ser Pro Val Ser Leu Ser Phe Ser Pro Ser Ala Phe Ser

65 70 75 80

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

85 90 95

Asp Ala Ala Gly Asp Ala Ser Ser Ser Leu Pro Asp Gly Glu Pro Leu

100 105 110

Asp Ser Thr Ser Glu Thr Ala Ala Ser Glu Ser Glu Lys Arg Ser Glu

115 120 125

Asp Lys Thr Gln Leu Thr Glu Glu Gln Met Lys Glu Lys Ala Arg Lys

130 135 140

Ala Ala Glu Ala Ala Ala Ala Thr Ala Lys Ala Leu Glu Leu Gly

145 150 155 160

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

165 170 175

Leu Ser Thr His Ser Ala Ala Ser Asp Ala Ala Asp Ala Ala Asp Arg

180 185 190

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

195 200 205

Ala Asp Asp Met Arg Tyr Gln Ser Asn Pro Glu Asn Ser Thr Asp Gly

210 215 220
 Glu His Ala Ser Ser Glu Glu Glu Glu Lys Pro Ile Pro Val Asp Gly
 225 230 235 240
 Gly Asp Cys Ile Ile Phe Ala Ala Glu Glu Gly Asp Arg Asp Ser Cys

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

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

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

 435 440 445
 Asp Ser Ser Trp Thr Pro Arg His Cys Leu Val Ala Asp Phe Tyr Leu
 450 455 460

Cys Lys Arg Leu Pro His Lys Arg Lys Lys Val Asn Cys Glu Met Ser
 465 470 475 480
 Gly Trp Ser Glu Trp Ser Pro Glu Cys Val Asn Gly Thr Gln Met Arg
 485 490 495
 Lys Asn Arg Ile Thr Arg Ser Gly Gln His Gly Gly Arg Ala Cys Val
 500 505 510
 Trp Asp Gly Lys Gln Pro Val His Ala Glu Val Thr Glu Leu Arg Ser
 515 520 525
 Cys Asn Gln Pro Ser Ser
 530
 <210> 321
 <211> 761
 <212> PRT
 <213> Toxoplasma gondii
 <400> 321
 Met Gly Ser Ser His Ala Ile Val Ala Cys Ala Ala Leu Ile Val Leu
 1 5 10 15
 Leu Ser Thr Asn Ala Arg Gly Leu Arg Val Arg Lys Asp Lys Asp Val
 20 25 30
 Leu Leu Ala Thr Ser Phe Leu Ser His His Gly Glu Tyr Gln Asn Pro
 35 40 45
 Thr Gly Thr Tyr Asn Leu Ile Lys Glu Ile Arg Arg Val Glu Ala Glu
 50 55 60
 Ile Glu Asp Glu Val Glu Thr Leu Asn Arg Asp Arg Arg Leu His Arg
 65 70 75 80
 Gly His Asn Lys Tyr Ala Asp Asp Asp Ile Arg Gln Gly Leu Lys Gly
 85 90 95
 Glu Gln Asp Met Gly Ala Ser Glu Asn Ile Pro Val Ala Glu Leu Glu
 100 105 110
 Pro Gln Asp Leu Asp Arg Glu Ala Lys Tyr Pro Val Arg Met Leu Ile
 115 120 125
 Val Asp Lys Arg Ser Asp Asp Asp Asp Glu Glu Thr Lys Thr Ser Phe

130 135 140
 Val Glu Thr Ala Leu His Ser Asp Leu Ala Gln Arg Val Val Lys Glu

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

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

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

 340 345 350
 Gly Tyr Ser Ser Asp Ala Val Arg Cys Ile Asp Tyr Cys Val Lys Arg
 355 360 365
 Gly Ala Asp Ile Val Asn His Ser Trp Gly Gly Ser Trp Pro Ser Glu
 370 375 380

Ala Leu Arg Glu Ala Val Val Arg Thr Ala Asn Asn Gly Leu Ile His
385 390 395 400
Ile Phe Ala Ala Gly Asn Asp Gly Val Asp Ile Asp Gln Thr Ala Phe
405 410 415
Tyr Pro Ala Ala Phe Ser Thr Glu Ala Asp Gly Leu Ile Thr Val Ala
420 425 430
Asn Val Lys Gly Asp Pro Asp His Gly Gly Lys Arg Ile Ile Glu Leu
435 440 445
Asp Arg Ser Ser Asn Tyr Gly Ile Gln Arg Val Gln Val Ala Cys Pro
450 455 460
Gly Met Trp Ile Leu Ser Thr Val Pro Thr Ser Gly Ser Ser Gln Glu
465 470 475 480
Pro Tyr Ala Glu Lys Ser Gly Thr Ser Met Ala Ala Pro Ala Leu Ser
485 490 495
Gly Ile Val Ala Leu Met Leu Ala Val Asn Pro Gly Leu Ser Thr Arg
500 505 510
Gln Val Arg Glu Gly Leu Arg Gln Cys Ser Val Gln Gln Pro Leu Leu
515 520 525
Gln Gly Lys Val Glu Trp Gly Ser Met Pro Asp Ala Lys Arg Cys Val
530 535 540
Glu Tyr Ala Leu Thr Thr His Ala Glu Gly Arg His Lys Ser Phe Ile
545 550 555 560
Arg Glu Pro Ser Thr Glu Thr Ser Thr Pro Pro Pro Pro Pro Ala
565 570 575
Gln Pro Thr Pro Gln Pro Gln Pro His Pro Pro Pro Gln Pro Glu Thr
580 585 590
Pro Pro Cys Ala Pro Ser Pro Pro Pro Thr Pro Pro Cys Ala Pro
595 600 605
Ser Pro Ser Pro Pro Thr Pro Pro Pro Gly Ser Pro His Lys Pro Glu
610 615 620
Pro Gln Thr Pro Val Tyr Pro Glu Val Pro Arg Ser Thr Arg Ser Pro

625 630 635 640
Pro Pro Ser Pro Pro Pro Thr Glu Ser Ala Pro Glu Ala Pro Pro Ser
645 650 655
Asp Thr Pro Ser Cys Arg Val Pro Pro Cys Ser Ser Ser Pro Arg Ser
660 665 670
Gly Ser Gln Pro Lys Pro Pro Gln Asp Asn Thr Thr Thr Pro Lys Met
675 680 685
Pro Ser Leu Ser Ser Pro Pro Thr Glu His Ser Thr Ala Gln Pro Pro
690 695 700
Lys His Glu Asn Asp Ala Arg Glu Gln Glu Pro Pro Thr Asp Glu Asp
705 710 715 720
Asp Phe Ser Ser Val Lys Gly Lys Lys Leu Gly Ala Tyr Glu Ser Asp
725 730 735
Gly Ser Pro Arg Ala Ser Ser Cys Ala Gly Ala Gly Val Leu Gly Val
740 745 750
Phe Phe Met Val Val Gly Leu Thr Val
755 760
<210> 322
<211> 2340
<212> PRT
<213> Toxoplasma gondii
<400> 322
Met Val Ser Ala Arg Lys Phe Leu Thr Ser Phe Asn Arg Glu Gln Gly
1 5 10 15
Gly Glu Asn Ser Leu Cys Phe Ser Pro Phe Phe Ser Pro Leu Phe Arg
20 25 30
Ser Ser Val Ala Glu Ala Glu Thr Arg Pro Asp Ser Ser Ser Asp Pro
35 40 45
Val Asn Asp Gly Asp Ser Thr Ser Gly Gly Glu Thr Pro Asp Pro Leu
50 55 60
Pro Thr Leu Ala Glu Val Arg Ala Ala Leu Ala Ser Thr Val Ala Gln
65 70 75 80

Ser Arg Thr Phe Pro Arg Arg Leu Ala Ala Lys Asn Gly Glu Gln Val

85 90 95

Glu Asp Gly Asp Glu Glu Leu Ala Glu Arg Lys Arg Val Arg Lys Pro

100 105 110

Pro Arg Asp Thr Ser Ala Tyr Ser Val Phe Ser Val Pro Ala Leu Lys

115 120 125

Leu Glu Gly Val Ala Ile Ala Asp Gln Glu Glu Ala Val Gly Ser Phe

130 135 140

Ala Val Ser Val Gly Cys Gly Phe Phe His Asp Pro Pro Ala Ile Pro

145 150 155 160

Gly Val Ala His Gln Leu Glu His Leu Ile Phe Leu Gly Ala Glu Gly

165 170 175

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

180 185 190

Thr His Asn Ala His Thr Thr Ala Glu Leu Thr Thr Phe Phe Val Ala

195 200 205

Ala Pro Thr Asp Thr Leu Pro Glu Leu Leu Asp Arg Leu Leu Leu His

210 215 220

Leu Phe His Pro Leu Leu Ala Ala Glu Gln Phe Ala Ser Glu Val Met

225 230 235 240

Ala Val Gln Phe Glu His Glu Lys Asn Gln Pro Asp Val Ala Arg Val

245 250 255

Leu Leu Glu Leu Ala Met Ala Val Thr Pro Ser Leu Ala Ser Pro Ala

260 265 270

Ser Ser Ala Thr Gln Asp Glu Val Pro Thr Ser Phe Tyr Arg Pro Glu

275 280 285

Val Ala Arg Lys Phe Gly Thr Gly Asp Phe Asp Thr Leu Cys Lys Thr

290 295 300

Pro Leu Glu Gln Gly Leu Asp Val Leu Lys Ala Leu Arg Glu Phe His

305 310 315 320

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

325 330 335
Arg Arg Ser Val Pro Ile Ile Val Glu Gly Ala Val Asp Ala Ser Gly

340 345 350
Gln Ser Leu Arg Ile Pro Ala Glu Val Glu Ala Ala Ala Glu Arg Glu

355 360 365
Ala Glu Lys Arg Ser Val Tyr Thr Pro Lys Glu Ile Gly Glu Met Val

370 375 380
Val Arg Ile Leu Ser Lys Tyr Val Gln Ala Asn Ser Pro Glu Thr Glu

385 390 395 400
Ala His Ala Asp Lys Thr Lys Thr Pro His Asn Lys Gly Asn Ser Phe

405 410 415
Ser Ala Ser Ser Ser Ser Asp Leu Thr Pro Gln Arg Thr Pro Ser Asp

420 425 430
Ala Ser Ser Ser Ala Ser Pro Ser Val Ser Ser Ala Pro Ala Ser Ser

435 440 445
Gln Ala Lys Arg Arg Asn Glu Val Leu Lys Thr Val Arg Leu His Ala

450 455 460
Gly Glu Arg Gln Lys Glu Ala Ser Gln Val Ala Ser Leu Leu Glu Ala

465 470 475 480
Ala Val Gly Glu Asp Ala Tyr Arg Ser Arg Pro Asn Ala Thr Ala Glu

485 490 495
Asp Ser Ser Pro Thr Asp Gly Glu Ser Asp Ala Ser Gly Lys Leu Tyr

500 505 510
Arg Val Phe Arg Gln His Gly Trp Gly Lys Arg Leu Leu Val Val Trp

515 520 525
Glu Arg Arg Thr Asn Trp Thr Val Arg Gly Tyr Asp Glu Val Phe Gln

530 535 540
Pro Thr Ala Leu Leu Glu Tyr Leu Leu Glu Tyr Pro Gly Glu Ala Ala

545 550 555 560
Leu Leu Asn Arg Leu Lys Ala Gln Gly Leu Ile Ala Asp Ala Glu Tyr

565 570 575

Val Asp Tyr Thr Thr Ser Gln Lys Ala Phe Val Ala Leu Leu Phe Glu
580 585 590

Leu Thr Asp Glu Gly Glu Glu Lys Phe Glu Asp Val Val Ser Ala Thr
595 600 605

Leu Ala Tyr Ala Glu Gln Leu Arg Thr Ser Val Thr Glu Thr Tyr Ile
610 615 620

Leu Asp Phe Phe Asp Glu Phe Ala Arg Val Ala Asn Arg Ser Trp Thr
625 630 635 640

Tyr Lys Asp Pro Glu Asp Ala Val Ser Ala Val Ile Ala Ala Ala Glu
645 650 655

Lys Leu Ala Val Leu Pro Gln Arg Pro Asp Met Val Ile Ala Gly Gly
660 665 670

Glu Phe Val Ser Leu Pro Gly Asp Arg Thr Leu Leu Val Asp Val Leu
675 680 685

Lys Glu Glu Leu Glu Ser Phe Gly Arg Ala Arg Ala Ser Ala Ile Val
690 695 700

Val Leu Pro Glu Asp Thr Ala Arg Gly Ser Ala Glu Val Val His Ala
705 710 715 720

Phe Arg Pro Tyr Gly Val Gln Phe Ser Val Ser Ala Leu Pro Ser Leu
725 730 735

Ala Gln Ala Glu Lys Val Gly Glu Arg Ile Ser Arg Thr Asp Ala Ala
740 745 750

Glu Lys Met Glu Leu Leu His Ala Glu Leu Ala Ser Glu Asp Leu Ile
755 760 765

Ser His Ser Met Ile Glu Ser Ser Ala Phe Pro Leu Pro Pro Val Leu
770 775 780

Ala Cys Asn Val Ala Ala Thr Val Ala Leu Thr Pro Arg Arg Val Pro
785 790 795 800

Glu Ile Cys Gln Ser Leu Ser Pro Val Gln Phe Pro Ile Lys Gly Gly
805 810 815

Arg Ser Asp Ser Glu Leu Arg Glu Ser Ser Glu Leu Pro Leu Gly Pro

820	825	830	
Arg Ser Glu Ser Leu Glu Asp Ala Glu Val Glu Glu Glu Arg Lys Lys			
835	840	845	
Leu Glu Ala Ser Gly Pro Pro Cys Val Leu Val Thr Glu Glu Ser Phe			
850	855	860	
Ser Val Phe Trp Lys Asn Ala Glu Pro Phe Asn Lys Pro Ile Val Arg			
865	870	875	880
Gly Tyr Phe Lys Leu Arg Val Ser Ala Glu Asp Ala Thr Ala Gln Asn			
885	890	895	
Thr Leu Tyr Gly Lys Ile Phe Ala Thr Leu Ala Gly Glu Arg Ala Arg			
900	905	910	
Thr Ala Leu Ala Ser Phe Gln Gly Cys Gly Val Asp Leu Leu Met Ser			
915	920	925	
Phe Thr Asn Gly Ala Leu Val Leu Glu Ile Gln Ala Phe Ser Glu Leu			
930	935	940	
Phe Ala Pro Val Leu Ala Arg Leu Ile Glu Val Leu Lys Glu Ser Gln			
945	950	955	960
Asp Asn Val Lys Gln Ser Asp Phe Asn Lys Ile Phe Asn Thr Leu Lys			
965	970	975	
Val Gln Leu Ser Asp Phe Ser Thr Val Thr Pro Phe Glu Leu Ala Leu			
980	985	990	
Asp Val Ala Leu Ser Val Val Arg Arg Asn Arg Phe Ser Gln Leu Asp			
995	1000	1005	
Leu Arg Ser Ala Val Thr Asp Ala Ser Ser Gln Phe Glu Asp Phe			
1010	1015	1020	
Lys Val Phe Leu Glu Lys Val Leu Thr Lys Asn Ala Leu Asp Val			
1025	1030	1035	
Phe Ile Met Gly Asp Ile Asp Tyr Glu Glu Ala Arg Lys Leu Ala			
1040	1045	1050	
Glu Asp Phe Arg Ala Ala Leu Ser Lys Gln Pro Leu Pro Phe Ser			
1055	1060	1065	

Glu Ser	Ala Gly Ser Glu Ile	Leu Asn Leu Ala Asp	Asp Ile Glu
1070	1075	1080	
Ile Arg	Phe Ser Asn Pro Ile	Pro Glu Asp Ala Thr	Asn Ala Tyr
1085	1090	1095	
Val Ser	Leu Tyr Val Thr His	Pro Pro Pro Asp Met	Met Glu Met
1100	1105	1110	
Val Val	Tyr Ser Leu Ile Gly	Glu Val Ile Ser Ser	Pro Phe Phe
1115	1120	1125	
Asp Thr	Ile Arg Thr His Trp	Met Asp Gly Tyr Val	Ala Ala Ala
1130	1135	1140	
Ala Val	Arg Glu Val Pro Pro	Ala Met Thr Leu Ala	Thr Ile Val
1145	1150	1155	
Gln Gly	Ser Gln Arg Lys Pro	Asp Glu Leu Glu Arg	His Val Cys
1160	1165	1170	
Ala Phe	Leu Ala Glu Met Glu	Glu Asn Ile Gly Ser	Ser Met Thr
1175	1180	1185	
Thr Glu	Ala Phe Leu Glu Arg	Leu Arg Trp Leu Ser	Ser Ser Lys
1190	1195	1200	
Phe His	Arg Ser Ala Thr Ser	Phe Ser Asp Tyr Phe	Gly Glu Val
1205	1210	1215	
Thr Ser	Gln Ile Ala Ser Arg	Asn Phe Cys Phe Ile	Arg Glu Gln
1220	1225	1230	
Leu Ala	Arg Leu Ala Thr Glu	Lys Phe Leu Ser Cys	Pro Ala Ile
1235	1240	1245	
Leu Lys	Ser Tyr Met Asn Ser	Leu Val Asp Arg Ala	Asn Arg Lys
1250	1255	1260	
Arg Ile	Thr Val Lys Ile Glu	Gly Asn Ser Ser Ser	Ser Glu Thr
1265	1270	1275	
Ala Ser	His Gln Arg Glu Ile	Arg Ala Pro Ser Ser	Thr Leu Pro
1280	1285	1290	
Asn Arg	Cys Gly Leu Pro Gly	Leu Ser Pro Ser Ala	Ser Pro Ser

1295	1300	1305
Ala Glu Val Arg Gln Ala Pro	Ser Leu Ser Thr Gln	Thr Ser Ala
1310	1315	1320
Leu Arg Pro Arg Pro Leu Ser	Glu Lys Arg Glu Thr	Thr Gln Ser
1325	1330	1335
Ser Glu Pro Glu Ala Pro Glu	Thr Ser Ser Gln Asp	Gly Gln Arg

1340	1345	1350
Ser Val Lys Ala Asn Ser Pro	Lys Pro Leu Asn Ala	Ala Gly Ser
1355	1360	1365
Val Gly Thr Ala Gly Lys Val	Glu Gly Lys Ser Arg	Lys Val Ala
1370	1375	1380
Ser Arg Val Asp Thr Pro Gly	Asn Glu Arg Arg Thr	Tyr Ala Ser
1385	1390	1395
Leu Phe Gly Thr Gln Asn Val	Leu Arg Ser Ser Arg	Ile Gln Ser

1400	1405	1410
Asp Phe Ser Ser Pro Ile Phe	Ser Leu Gly Asp Asp	Ala Asp Ala
1415	1420	1425
Leu Ser Leu Ile Gln Val Glu	Ala Arg Val Ser Thr	Ser Asn Ser
1430	1435	1440
Lys Pro Lys Ala Val Leu Gly	Ala Arg Arg Gly Asp	Gly Gln Ser
1445	1450	1455
Pro Thr Val Ala Ser Pro Ser	Gly Ala Ala Pro Lys	Arg Pro Ala

1460	1465	1470
Pro Pro Ala Gly Pro Arg Asp	Lys Ser Gly Glu Ala	Ser Glu Thr
1475	1480	1485
Thr Gly Thr Glu Gly Met Glu	Val Thr Glu Ile Ala	Ser Asp Val
1490	1495	1500
Glu Gly Gln Ala Glu Glu Gly	Asp Val Pro Ile Glu	Phe Leu Pro
1505	1510	1515
Leu Ala Arg Gln Ile Thr Pro	His Ile Leu Glu Arg	Cys Ala Ala

1520	1525	1530
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Asp Gln Asn Ala Ala Gly Ala	Lys Arg Ile Val Val	Asp Asn Phe
1535	1540	1545
Phe Thr Asp Pro Val Glu Ala	Arg Arg Ser Ile Leu	Glu Asn Leu
1550	1555	1560
Glu Ala Lys Leu Ser Ser Thr	Ser Ser Leu Phe Ser	Leu Ser Pro
1565	1570	1575
Ser Ser His Pro Ser Pro Pro	Leu Trp Leu Ala Tyr	Ser Arg Ser
1580	1585	1590
Glu Ser Cys Ser Ile Arg Thr	Ser Thr Ile Ser Arg	Ala Glu Glu
1595	1600	1605
Val Cys Gly Ala Trp Arg Glu	Ser Ala Pro Glu Ala	Val Leu Ile
1610	1615	1620
Val Ser Pro Glu Gln Pro Pro	Ala Gly Met Pro Ser	Leu Pro Pro
1625	1630	1635
Thr Leu Gly Asp Ala Glu Pro	Pro Ala Ala Ala Val	Pro Leu Ser
1640	1645	1650
Pro Ser Gly Ala Glu Thr Gly	Val Pro Leu Val Pro	Glu Ser Pro
1655	1660	1665
Gly Ser Pro Ala Ala Ala Gly	Arg Gln Ala Ala Thr	Lys Ala Pro
1670	1675	1680
Thr Glu Ser Glu Ala Ser Ala	Ala Thr Glu Gly Asp	His Pro Arg
1685	1690	1695
Val Gly Thr Ser Ala Glu Ala	Arg Thr Arg Gln Leu	Pro Thr Ala
1700	1705	1710
Glu Gln Gln Thr Leu Glu Gln	Arg Lys Ala Leu Leu	Glu Ala Arg
1715	1720	1725
Leu Arg Arg Leu Glu Met Gln	Thr Ile Ala Gln Arg	Ala Gln Leu
1730	1735	1740
Leu Lys Gln Arg Leu Asp Ala	Met Lys Gln Tyr Gly	Thr Arg Pro
1745	1750	1755
Thr Thr Ile Phe Asn Thr Trp	Leu Gly Pro His Lys	Arg Gly Phe

1760	1765	1770
Leu Gln Ser Val Gly Gly Gly Thr Gly Ala Ser Ser Gly Ala Phe		
1775	1780	1785
Pro Val Ser Ala Val Ser Gly Arg Ser Ser Thr Ala Thr Arg Thr		
1790	1795	1800
Gln Ala Ala Ser Asp Leu His Gly Ser Arg Arg Leu Pro Ser Ala		
1805	1810	1815
Leu His Gln Ala Ala Asp Pro Leu Ala Phe Lys Arg Thr Leu Glu		
1820	1825	1830
Thr Leu Lys Trp Arg Glu Gln Gly Leu Leu Gln Arg Gln Ala Glu		
1835	1840	1845
Leu Arg Thr Gln Leu Arg Lys Val Asn Ala Phe Gly Ser Thr Ala		
1850	1855	1860
Gly Asp Ser Thr Ala Pro Asn Leu Gly Leu Ala Glu Asp Lys Asn		
1865	1870	1875
Leu Arg Leu Val Glu Asn Val Thr Val Ala Ser Gly Ala Ser Leu		
1880	1885	1890
Gly Ser Arg Asp Gln Thr Ala Ile Ala His Gln Thr Asp Val Leu		
1895	1900	1905
Pro Pro Pro Arg Ala Ser Ile Pro Thr Val Pro Thr Leu Thr Pro		
1910	1915	1920
Ala Pro Ser Pro Val Ala Phe Ala Ala Leu Pro Gln Ile His Gln		
1925	1930	1935
Gln Leu Pro Gly Val Asp Val Gly Ala Glu Ile Pro Arg Pro Val		
1940	1945	1950
Thr Pro Val Ser Thr Asp Ile Ser Ala Ser Ala Ser Ala Phe Val		
1955	1960	1965
Pro Gly Ser Val Gln Ala Ser Leu Ser Gln Ser Pro Ala Ala Ser		
1970	1975	1980
Val Lys Gly Ala Gly Ala Pro Pro Leu Pro Leu Ala His Gln Pro		
1985	1990	1995

Phe Ala Ser Leu Pro Pro Ala Pro Gln Leu Pro Gln Glu Pro Arg

2000 2005 2010

Val Gln Glu Ala Asn Val Gly Ser Pro Ser Pro Pro Thr Val Val

2015 2020 2025

Pro Gly Val Pro Thr Val Gly Ala Thr Ala Pro Thr Val Gly Glu

2030 2035 2040

Gly Ala Thr Thr Leu Gly Ala Gly Ala Pro Ala Val Ala Ser Pro

2045 2050 2055

Ala Pro Thr Val Gly Ala Ala Pro Gln Ala Val Thr Tyr Thr Ala

2060 2065 2070

Pro Thr Met Gly Ala Gly Ala Pro Thr Val Ala Ser Leu Ala Pro

2075 2080 2085

Thr Val Gly Ala Ala Pro Gln Ala Val Thr Tyr Thr Ala Pro Thr

2090 2095 2100

Thr Gly Ala Gly Ala Pro Ala Val Ala Ser Leu Ala Pro Thr Val

2105 2110 2115

Gly Ala Ala Pro Gln Ala Val Thr Tyr Thr Ala Pro Thr Ile Gly

2120 2125 2130

Ala Gly Ala Pro Ala Val Ala Ser Pro Ala Pro Thr Val Gly Ala

2135 2140 2145

Ala Pro Gln Ala Val Thr Tyr Thr Ala Pro Thr Ile Gly Ala Gly

2150 2155 2160

Ala Pro Ala Val Ala Ser Leu Ala Pro Thr Val Gly Ala Ala Pro

2165 2170 2175

Gln Ala Val Thr Tyr Thr Ala Pro Thr Ile Gly Ala Gly Ala Pro

2180 2185 2190

Ala Val Ala Ser Pro Ala Pro Thr Val Gly Ala Ala Pro Gln Ala

2195 2200 2205

Val Thr Tyr Thr Ala Pro Thr Ile Gly Ala Gly Ala Pro Ala Val

2210 2215 2220

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

2225 2230 2235
 Tyr Thr Ala Pro Thr Ile Gly Ala Gly Ala Pro Ala Val Ala Ser

 2240 2245 2250
 Pro Ala Pro Thr Val Gly Ala Ala Pro Gln Ala Val Thr Tyr Thr
 2255 2260 2265
 Ala Pro Thr Met Gly Ala Gly Ala Pro Ala Ala Val Ala Ser Leu
 2270 2275 2280
 Ala Arg Gly Pro Ser Phe Asp Tyr Gln Ala Gly Val Val Ser Arg
 2285 2290 2295
 Ala Val Gly Gly Ala Ser Gln Pro Gln Ala Glu Gln Ala Ala Ser

 2300 2305 2310
 Tyr Val Ser Asp Pro Ala Ser Val Ala Arg Val Ser Ser Ala Ser
 2315 2320 2325
 Ile Leu Pro His Ala Ala Val Pro Val Val His Ala
 2330 2335 2340
 <210> 323
 <211> 376
 <212> PRT
 <213> Toxoplasma gondii
 <400> 323
 Met Ala Asp Glu Glu Val Gln Ala Leu Val Val Asp Asn Gly Ser Gly
 1 5 10 15

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

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

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

Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ser Ser Leu Ser Thr
 340 345 350
 Phe Gln Gln Met Trp Ile Thr Lys Glu Glu Tyr Asp Glu Ser Gly Pro
 355 360 365
 Ser Ile Val His Arg Lys Cys Phe
 370 375
 <210> 324
 <211> 256
 <212> PRT
 <213> Toxoplasma gondii
 <400> 324
 Met Ser Pro Leu Gly Phe Gly Ala Phe Leu Ser Pro Leu Leu Leu Phe
 1 5 10 15

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

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

 Met Pro Gly Ala Glu Arg Cys Arg Asp Ser Ala Ala Leu Thr Ala Met
 145 150 155 160
 Leu Lys Thr His Lys Ala Gln Gly Lys Leu Ile Ala Ala Ile Cys Ala

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

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

<210> 325

<211> 475

<212> PRT

<213> Toxoplasma gondii

<400> 325

Met Phe Arg Leu Leu Val Pro Thr Tyr Tyr Ser Tyr Ser Val Pro Leu

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

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

Asp Gly Thr Lys Asn Glu Trp Gly Trp Cys Lys Ser Lys Leu Gly Ala

130 135 140

Asn Ala Ile Leu Ala Val Ser Met Ala Cys Cys Arg Ala Gly Ala Ala

145 150 155 160

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

165 170 175

Pro Thr Asp Lys Met Val Met Pro Val Pro Phe Phe Asn Val Ile Asn

180 185 190

Gly Gly Ser His Ala Gly Asn Lys Val Ala Met Gln Glu Phe Met Ile

195 200 205

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

210 215 220

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

225 230 235 240

Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro Asn Ile Ser

245 250 255

Gly Ala Thr Glu Ala Leu Asp Leu Leu Met Glu Ala Ile Lys Val Ser

260 265 270

Gly His Glu Gly Lys Val Lys Ile Ala Ala Asp Val Ala Ala Ser Glu

275 280 285

Phe Phe Leu Gln Asp Asp Lys Val Tyr Asp Leu Asp Phe Lys Thr Pro

290 295 300

Asn Asn Asp Lys Ser Gln Arg Lys Thr Gly Glu Glu Leu Arg Asn Leu

305 310 315 320

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

325 330 335

Phe Asp Gln Asp Asp Phe His Ser Tyr Ala Gln Leu Thr Asn Glu Val

340 345 350

Gly Glu Lys Val Gln Ile Val Gly Asp Asp Leu Leu Val Thr Asn Pro

355 360 365

Thr Arg Ile Glu Lys Ala Val Gln Glu Lys Ala Cys Asn Gly Leu Leu

370 375 380
 Leu Lys Val Asn Gln Ile Gly Thr Val Ser Glu Ser Ile Glu Ala Cys

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

 450 455 460
 Gln Tyr Ala Gly Ala Gly Phe Arg His Pro Asn
 465 470 475
 <210> 326
 <211> 433
 <212> PRT
 <213> Toxoplasma gondii
 <400> 326
 Met Leu Cys Ile Val Glu Arg Ile Ala Met Pro Thr Arg Gly Val Asn
 1 5 10 15
 Pro Ser Ala Ala Asn Gly Lys Leu Pro Pro Arg Thr Arg Ser Ala Thr
 20 25 30
 Gly Cys Arg Val Tyr Ile His Pro Met Val Lys Phe Ile Ser Leu Leu

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

100	105	110	
Arg Phe Asp Ser Ile Gly Val Glu Asn Thr Glu Ala Asn Arg Ala Phe			
115	120	125	
Tyr Arg Asp Leu Leu Phe Ser Thr Lys Gly Leu Gly Gln Tyr Ile Ser			
130	135	140	
Gly Ala Ile Leu Phe Glu Glu Thr Leu Tyr Gln Lys Ser Pro Ser Gly			
145	150	155	160
Val Pro Met Val Asp Leu Leu Lys Ala Glu Gly Ile Ile Pro Gly Ile			
	165	170	175
Lys Val Asp Lys Gly Leu Glu Thr Leu Pro Leu Thr Asp Asp Glu Lys			
180	185	190	
Ala Thr Met Gly Leu Asp Gly Leu Ser Glu Arg Cys Lys Lys Tyr Tyr			
195	200	205	
Glu Ala Gly Ala Arg Phe Ala Lys Trp Arg Ala Val Leu Ser Ile Asp			
210	215	220	
Pro Ala Lys Gly Lys Pro Thr Asn Leu Ser Ile Thr Glu Val Ala His			
225	230	235	240
Gly Leu Ala Arg Tyr Ala Ala Ile Cys Gln Ala Asn Arg Leu Val Pro			
245	250	255	
Ile Val Glu Pro Glu Ile Leu Thr Asp Gly Ser His Asp Ile Thr Val			
260	265	270	
Cys Ala Glu Val Thr Glu Arg Val Leu Ala Ala Val Phe Lys Ala Leu			
275	280	285	
Asn Asp His His Val Leu Leu Glu Gly Ala Leu Leu Lys Pro Asn Met			
290	295	300	
Val Thr His Gly Ser Asp Cys Pro Lys Pro Ala Ser His Glu Glu Ile			
305	310	315	320
Ala Phe Tyr Thr Val Arg Ser Leu Lys Arg Thr Val Pro Pro Ala Leu			
325	330	335	
Pro Gly Val Met Phe Leu Ser Gly Gly Gln Ser Glu Glu Asp Ala Ser			
340	345	350	

Leu Asn Leu Asn Glu Met Asn Lys Met Gly Pro His Pro Phe Gln Leu

355 360 365
Ser Phe Ser Tyr Gly Arg Ala Leu Gln Ala Ser Cys Leu Lys Ala Trp

370 375 380
Lys Gly Val Pro Glu Asn Lys Ala Lys Ala Gln Gln Val Leu Met Glu

385 390 395 400
Arg Ala Arg Ala Asn Gly Glu Ala Gln Leu Gly Lys Tyr Gly Gly Gly

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

420 425 430
Tyr

<210> 327

<211> 489

<212> PRT

<213> Toxoplasma gondii

<400> 327

Met Ala Leu Leu Thr Thr Val Arg Asp Ser Cys Phe Tyr Phe Pro Gln
1 5 10 15

Lys Thr Ala Ser Arg His Val Phe Leu Ala Cys Val Thr Ala Leu Leu
20 25 30

Gln Arg Ser Asp Pro Thr Phe Phe Cys Glu Gln Ser Thr Ser Met Gln
35 40 45

Pro Glu Ala Asp Ser Ala Trp Gln Pro Asp Ala Gly Thr Val Ser Leu
50 55 60

Leu Thr Arg Val Lys Asp Leu Arg Val Ala Ile Ala Pro Val Leu Trp
65 70 75 80

Lys Ser Ala Glu Ala His Glu His Arg His His Pro Ser Ala Cys Cys
85 90 95

Gly Pro Val Glu Arg Asn Leu Leu Gln Tyr Thr Ala Arg Pro Ala Pro
100 105 110

Pro Pro Phe Pro Asp Leu Ala Pro Ser Leu Leu Trp Pro Arg Ala Arg
115 120 125

Leu Arg Thr Lys Lys Ile Ala Gly Arg Ser Tyr Thr Thr Pro Asp Cys
130 135 140

Arg His Phe Ala Lys Met Val Cys Lys Leu Gly Ile Asn Gly Phe Gly
145 150 155 160

Arg Ile Gly Arg Leu Val Phe Arg Ala Ala Met Glu Arg Gly Asp Val
165 170 175

Glu Val Leu Ala Ile Asn Asp Pro Phe Met Ser Leu Asp Tyr Met Val
180 185 190

Tyr Leu Leu Arg Tyr Asp Ser Val His Gly His Tyr Pro Gly Glu Val
195 200 205

Ser His Lys Asp Gly Lys Leu Ile Val Gly Gly Lys Ala Val Thr Val
210 215 220

Phe Asn Glu Lys Glu Pro Thr Ala Ile Pro Trp Gly Gln Ala Gly Val
225 230 235 240

His Tyr Ile Cys Glu Ser Thr Gly Ile Phe Leu Thr Lys Glu Lys Ala
245 250 255

Gln Ala His Leu Thr Asn Gly Ala Lys Lys Val Ile Met Ser Ala Pro
260 265 270

Pro Lys Asp Asp Thr Pro Met Phe Val Met Gly Val Asn Asn Asp Gln
275 280 285

Tyr Lys Ser Ser Asp Val Ile Val Ser Asn Ala Ser Cys Thr Thr Asn
290 295 300

Cys Leu Ala Pro Leu Ala Lys Ile Val His Asp Lys Phe Gly Ile Val
305 310 315 320

Glu Gly Leu Met Thr Thr Val His Ala Met Thr Ala Asn Gln Leu Thr
325 330 335

Val Asp Gly Pro Ser Lys Gly Gly Lys Asp Trp Arg Ala Gly Arg Ser
340 345 350

Ala Gly Val Asn Ile Ile Pro Ala Ser Thr Gly Ala Ala Lys Ala Val

355 360 365
 Gly Lys Ile Ile Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ala Phe
 370 375 380
 Arg Val Pro Val Pro Asp Val Ser Val Val Asp Leu Thr Cys Lys Leu
 385 390 395 400
 Ala Lys Pro Ala Lys Tyr Glu Asp Ile Val Ala Ala Val Lys Glu Ala
 405 410 415
 Ala Thr Ser Gly Pro Met Lys Gly Ile Ile Ser Tyr Thr Asp Glu Glu
 420 425 430

 Val Val Ser Ser Asp Phe Val His Cys Lys Phe Ser Ser Val Phe Asp
 435 440 445
 Ile Asn Ala Gly Ile Met Leu Asn Asp Thr Phe Val Lys Leu Val Ser
 450 455 460
 Trp Tyr Asp Asn Glu Trp Gly Tyr Ser Asn Arg Leu Val Glu Leu Ala
 465 470 475 480
 His Tyr Met Ser Val Gln Asp Gly Ala
 485
 <210> 328
 <211> 116
 <212> PRT

 <213> Toxoplasma gondii
 <400> 328
 Met Pro Lys Cys Met Ile Phe Cys Pro Val Ala Ala Thr Pro Ala Gln
 1 5 10 15
 Gln Asp Ala Leu Leu Lys Asp Ala Glu Lys Ala Val Ala Asp Ala Leu
 20 25 30
 Gly Lys Pro Leu Ser Tyr Val Met Val Gly Tyr Ser Gln Thr Gly Gln
 35 40 45
 Met Arg Phe Gly Gly Ser Ser Asp Pro Cys Ala Phe Ile Arg Val Ala
 50 55 60

 Ser Ile Gly Gly Ile Thr Ser Ser Thr Asn Cys Lys Ile Ala Ala Ala

65 70 75 80
 Leu Ser Ala Ala Cys Glu Arg His Leu Gly Val Pro Lys Asn Arg Ile
 85 90 95
 Tyr Thr Thr Phe Thr Asn Lys Ser Pro Ser Glu Trp Ala Met Gly Asp
 100 105 110
 Arg Thr Phe Gly
 115
 <210> 329
 <211> 471
 <212> PRT
 <213> Toxoplasma gondii
 <400> 329

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

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

Ile Glu Lys Met Thr Gly Pro Ala Val Thr Glu Val Glu Gly Ser Ala
 130 135 140
 Glu Asp Lys Val Thr Lys Glu Ala Pro Ile Ala Phe Val Ala Glu Leu
 145 150 155 160

Ala Ser Lys Asp Ser Asp Met Ala Lys Leu Phe Glu Glu Val Ala Asn
165 170 175

Glu Ser Arg Gln Leu Gly Arg Phe Leu Ala Lys Tyr Gly Ala Ser Asp
180 185 190

Glu Lys Ile Tyr Ser Leu Arg Tyr Glu Glu Gly Thr Glu Ala Phe Thr
195 200 205

Gly Lys Thr Lys Asp Glu Leu Lys Lys Phe Val Asp Thr Glu Ser Phe
210 215 220

Pro Leu Leu Gly Pro Ile Asn Ala Glu Asn Phe Arg Lys Tyr Ile Asp
225 230 235 240

Arg Asp Leu Asp Leu Val Trp Leu Cys Gly Thr Glu Lys Asp Phe Asp
245 250 255

Glu Ala Lys Thr Ala Val Arg Glu Ala Ala Lys Lys Leu Arg Asp Thr
260 265 270

Arg Ser Phe Val Trp Leu Asp Thr Asp Gln Phe Lys Gly His Ala Glu
275 280 285

Asn Ala Leu Gly Ile Thr Glu Phe Pro Gly Leu Val Phe Gln Ser Lys
290 295 300

Lys Gly Arg Phe Val Leu Pro Glu Ala Thr Thr Ser Leu Lys Asp Ala
305 310 315 320

Ala Lys Ile Ser Gln Phe Phe Asp Asp Val Glu Ala Gly Lys Ile Asp
325 330 335

Arg Ser Leu Lys Ser Glu Pro Val Pro Glu Lys Gln Asp Glu Ala Val
340 345 350

Lys Val Val Val Gly Lys Asn Phe Glu Glu Met Val Ile Gln Lys Asp
355 360 365

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

Ser Phe Glu Pro Ile Tyr Lys Glu Phe Ala Glu Lys Tyr Lys Asp Val
385 390 395 400

Asp His Leu Val Val Ala Lys Met Asp Gly Thr Ala Asn Glu Thr Pro

405 410 415
 Leu Glu Glu Phe Ser Trp Ser Ser Phe Pro Ser Ile Phe Phe Val Lys
 420 425 430
 Ala Gly Glu Lys Thr Pro Met Lys Phe Glu Gly Ser Arg Thr Val Glu
 435 440 445

 Gly Leu Thr Glu Phe Val Asn Lys His Gly Ser Lys Pro Leu Lys Lys
 450 455 460
 Asp Asp Lys Gly Glu Glu Leu
 465 470
 <210> 330
 <211> 645
 <212> PRT
 <213> Toxoplasma gondii
 <400> 330
 Met Ala Glu Lys Ala Leu Thr Arg Ala Thr Thr Pro Thr Gly Ser Trp
 1 5 10 15
 Arg Arg Pro Glu Pro Val Asp Arg Ala Asp Pro Glu Asn Arg Arg Asp
 20 25 30

 Ser Leu His Ala Gly Ala Pro Tyr Ala Ser Glu Gly Gln Gly Gly Arg
 35 40 45
 Lys Thr Glu Ser Gly Arg Ser Pro Glu Ser Leu Ser Leu Phe Ser Arg
 50 55 60
 Gln Phe Leu Ala Glu Ser Arg Thr Pro Gln Ser Ser Trp Ser Arg Ser
 65 70 75 80
 Arg Pro Ser Ser Ser Ala Pro Ala Ser Ser Leu Arg Pro Ser Pro Ser
 85 90 95

 Ser Asp Pro Ser Pro Arg Ala Ser Ser Ser Ser Ser Cys Pro Ala Cys
 100 105 110
 Ser Cys Gly Leu Ser Ser Cys Leu Ser Thr Asp Ser Pro Gly Ser Arg
 115 120 125
 Thr Ser Ala Ser Gly Val Pro Asp Lys Phe Lys Arg Ser Cys Ala Tyr
 130 135 140

Ser Gly Lys Pro Pro Pro Ser Lys Lys Arg Arg Leu Leu Pro Ala Ala
145 150 155 160

Gln Leu Ala Ser Pro Thr Cys Thr Leu Lys Gly His Val Tyr Arg Cys
165 170 175

Pro Leu Glu Arg Lys His Ser Leu Pro Thr Pro Ser Val Phe Leu Glu
180 185 190

Lys Asp Gly Ser Leu Ser Ser Ser Ala Leu Arg Ile Leu Ser Arg Leu
195 200 205

His Val Lys Tyr Val Pro Ser Glu Asp Pro His Lys Val Thr Ser Gly
210 215 220

Ser Ser Gly Phe Val Arg Thr Ala Ser Phe Ser Ala Ser Val Lys Ser
225 230 235 240

Gly Gln Leu Gly Gly Arg Ala Ser Pro Pro Gln Thr Lys Thr Gly Leu
245 250 255

Asn Pro Leu Ile Ser Leu Leu Cys Cys Leu Pro Leu Leu Glu Pro Ser
260 265 270

Ser Arg Pro Ser Cys Phe Phe Phe Leu Ser Pro Ser Ala Leu Leu Thr
275 280 285

Pro Ser Ser Ser Arg Ala Ser Ser Ser Ser Ser Ser Lys Pro Pro Tyr
290 295 300

Pro Ser Asp Arg Val Arg Pro Gly Gly Leu Thr Gly Asp Ala Phe Lys
305 310 315 320

Leu Ser Arg Leu Gln Leu Leu Tyr Asp Ser Leu Pro Leu Cys Cys Gln
325 330 335

Pro Leu Ala Cys Ser Ser Ser Leu Val Ser Arg Phe Ser Ser Leu Asp
340 345 350

Gln Ser Phe Gly Val Pro Ser Ala Ser Pro Ala Phe Val Pro Ile Asn
355 360 365

Thr Trp Ala Phe Phe Leu Ser Leu Leu Ala Thr Val Thr Ser Ser Pro
370 375 380

Leu Pro Cys Val Ser Pro Ser Ser Val Ser Pro Ser Ser Ser Phe

385 390 395 400
 Glu Ser Ser Asp Gly Phe Ser Ser Leu Ser Arg Ser Ala Ser Pro Arg
 405 410 415

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

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

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

 Thr His Ser Gln Glu Asn Ile Glu Ala Asp Ala Glu Leu Ala Trp Thr
 610 615 620
 Thr Trp Ile Glu Gln Gly Gly Arg Val Ala Glu Leu Thr Asn Pro Ala
 625 630 635 640

Phe Asp Arg Pro Phe

645

<210> 331

<211> 182

<212> PRT

<213> Toxoplasma gondii

<400> 331

Met Lys Ile Gln Ser Ile Val Thr Lys Thr Thr Lys Ala Ala Leu Thr

1 5 10 15

Ala Ala Ile Asp Thr Leu Leu Ala Lys Gly Ala Asp Ala Pro Ala Val

20 25 30

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

35 40 45

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

50 55 60

Leu Cys Phe Pro Asn Phe Pro Leu Leu Glu Arg Leu Ala Gln His Cys

65 70 75 80

Ser Ser Gly Thr Leu Leu Lys Gly Glu Asp Thr Leu Cys Arg Asp Pro

85 90 95

Lys Ala Ser Ser Cys His Leu His Leu Arg Leu Arg Phe Leu Glu Val

100 105 110

Val Ala Val Cys Phe Val Leu Pro Arg Lys Gln Ala Asp Leu Arg Leu

115 120 125

Pro Leu Tyr Arg Phe Gln Ala Gly Val Arg Arg Pro Cys Leu His Ala

130 135 140

Pro Arg Ala Leu Asn Glu Ala Pro Leu Lys Phe Asp Val Ala Leu Phe

145 150 155 160

Val Gln Phe Val Leu His Ile Lys Ala Phe Cys Cys Glu Ser His Asp

165 170 175

Ser Cys Cys Arg Pro Thr

180

<210> 332

<211> 216

<212> PRT

<213> Toxoplasma gondii

<400> 332

Met Lys Val Ala Ser Gly Ser Ala Ile Val Gly Leu Leu Leu Gly Ala

1 5 10 15

Ala Val Pro Val Val Tyr Ala Gly Pro His Gly Gly His Arg Pro Gln

20 25 30

Lys Lys Gly Gly Tyr Thr Thr Thr Thr Thr Leu Pro Pro Asn Pro Met

35 40 45

Asp Val Arg Thr Glu Cys Phe Gln Val Pro Tyr Ser Val Glu Lys Thr

50 55 60

Cys Tyr Lys Asp Glu His Ile Ser Arg Pro Tyr Thr Cys Pro Ser Ser

65 70 75 80

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

85 90 95

Cys Thr Gln Leu Val Lys Lys Glu Val Gln Tyr Gln Cys Pro Lys Ala

100 105 110

Thr Lys Gln Thr Leu Cys Ser Gln Ile Pro Val Thr Leu Asn Lys Thr

115 120 125

Cys Lys Lys Gln Val Thr Asn Lys Val Pro Ser Ser Cys Pro Lys Ile

130 135 140

Leu Thr Val Pro Glu Cys Glu Ile Gln Ser Arg Pro Ser Gln Asp Val

145 150 155 160

Cys Tyr Glu Ser Glu Ala Tyr Thr Gln Glu Tyr Asp Cys Trp Gly Ser

165 170 175

Glu Leu His Arg Glu Cys Glu Val Asp Met Arg Val Val Asp Thr Gln

180 185 190

Cys Asn Arg Ile Val Asp Ser Pro Val Leu Tyr Glu Tyr Glu Asp Thr

195 200 205

Val Val Glu Arg Val Cys Ser Thr

210 215

<210> 333

<211> 952

<212> PRT

<213> *Toxoplasma gondii*

<400> 333

Met His Pro Ser Gly Gly Gln Phe Val Pro Thr Pro Gln Arg His Gly

1 5 10 15

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

20 25 30

Arg Thr Arg Glu Trp Ala Val Ser Gln Arg Ser Leu Val Phe Pro Val

35 40 45

Ala Val Ala Ala Val Arg Gly Glu Thr Ala Pro Ile Ala Gly Arg Ala

50 55 60

Ser Gln Cys Pro Arg Leu Leu Val Pro Phe Ser Trp Val Leu Phe Leu

65 70 75 80

Glu Gln Arg Pro Glu Leu Ser Leu Thr Lys Val Val Phe Leu Leu Trp

85 90 95

Asn Leu Tyr Phe Val Ser Leu Ser Pro Leu Arg Pro Phe Thr Gly Ser

100 105 110

Leu His Pro Arg Pro Val Val Lys Met Val Asn Phe Ser Val Glu Gln

115 120 125

Met Arg Glu Ile Met Gly Asn Pro Lys Asn Ile Arg Asn Met Ser Val

130 135 140

Ile Ala His Val Asp His Gly Lys Ser Thr Leu Thr Asp Ser Leu Val

145 150 155 160

Ser Lys Ala Gly Ile Ile Ser Ala Lys Ala Ala Gly Asp Ala Arg Phe

165 170 175

Thr Asp Thr Arg Ala Asp Glu Gln Glu Arg Cys Ile Thr Ile Lys Ser

180 185 190

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

195 200 205

Ala Gln Pro Tyr Leu Ile Asn Leu Ile Asp Ser Pro Gly His Val Asp
210 215 220

Phe Ser Ser Glu Val Thr Ala Ala Leu Arg Val Thr Asp Gly Ala Leu
225 230 235 240

Val Val Val Asp Thr Ile Glu Gly Val Cys Val Gln Thr Glu Thr Val
245 250 255

Leu Arg Gln Ala Leu Ala Glu Arg Ile Arg Pro Val Leu His Val Asn
260 265 270

Lys Val Asp Arg Ala Leu Leu Glu Leu Gln Met Asp Gly Glu Glu Ile
275 280 285

Tyr Gln Thr Phe Ser Arg Thr Ile Glu Asn Val Asn Val Ile Ile Ser
290 295 300

Thr Tyr Asn Asp Glu Leu Met Gly Asp Val Gln Val Tyr Pro Glu Lys
305 310 315 320

Gly Thr Val Ser Phe Gly Ser Gly Leu His Gly Trp Ala Phe Thr Val
325 330 335

Glu Arg Phe Ser Lys Ile Tyr Ala Lys Lys Phe Asp Val Pro Lys Glu
340 345 350

Lys Met Met Glu Arg Leu Trp Gly Asn Asn Phe Tyr Asn Ala Lys Glu
355 360 365

Lys Lys Trp Thr Lys Thr Gln Ser Glu Asn Thr Arg Arg Ala Phe Cys
370 375 380

Gln Phe Ile Met Asp Pro Ile Cys Thr Leu Phe Thr Ser Ile Met Asn
385 390 395 400

Asp Glu Lys Glu Lys Tyr Thr Lys Met Leu Gly Ser Leu Gly Ile Glu
405 410 415

Leu Lys Gly Asp Asp Arg Asp Leu Thr Gly Lys Ala Leu Leu Lys Arg
420 425 430

Val Met Gln Leu Trp Leu Pro Ala Gly Asp Thr Leu Leu Glu Met Val
435 440 445

Val Arg His Leu Pro Ser Pro Phe Ala Ala Gln Lys Tyr Arg Val Glu

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

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

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

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

 Ser Pro Asn Lys His Asn Arg Leu Tyr Met Val Ala Glu Pro Phe Pro
 690 695 700

Asp Gly Leu Ala Asp Ala Ile Glu Ala Gly Gln Val Asn Ala Arg Asp
 705 710 715 720
 Asp Pro Lys Glu Arg Ala Asn Ala Leu Ala Glu Lys Phe Asp Phe Asp
 725 730 735
 Lys Asn Ala Ala Leu Lys Ile Trp Cys Phe Gly Pro Glu Thr Thr Gly
 740 745 750

 Ala Asn Met Leu Ile Asp Thr Thr Gln Gly Val Gln Tyr Leu Asn Glu
 755 760 765
 Ile Lys Glu His Cys Asn Ser Ala Phe Gln Trp Ala Ser Lys Glu Gly
 770 775 780
 Val Leu Cys Glu Glu Asn Met Arg Gly Ile Arg Phe Asn Leu Thr Asp
 785 790 795 800
 Val Thr Met His Ala Asp Ala Ile His Arg Gly Ala Gly Gln Ile Met
 805 810 815

 Pro Thr Cys Arg Arg Val Leu Tyr Ala Cys Gln Leu Ala Ser Ala Pro
 820 825 830
 Arg Leu Gln Glu Pro Met Phe Leu Val Asp Ile Thr Cys Pro Gln Asp
 835 840 845
 Ala Val Gly Gly Ile Tyr Ser Thr Leu Asn Thr Arg Arg Gly His Val
 850 855 860
 Phe His Glu Glu Gln Arg Ser Gly Thr Pro Leu Val Glu Ile Lys Ala
 865 870 875 880

 Tyr Leu Pro Val Ala Glu Ser Phe Gly Phe Thr Thr Ala Leu Arg Ala
 885 890 895
 Ala Thr Ser Gly Gln Ala Phe Pro Gln Cys Val Phe Asp His Trp Ser
 900 905 910
 Thr Leu Asn Gly Asp Pro Leu Glu Lys Gly Ser Lys Met Glu Glu Leu
 915 920 925
 Val His Asn Ile Arg Thr Arg Lys Asn Leu Lys Pro Glu Ile Pro Pro
 930 935 940

 Phe Glu Asn Tyr Tyr Asp Lys Leu

Ser Thr Gly Gln Ile Ala Asp Ile Gln Phe Glu Ser Val Lys Phe Asn
210 215 220

Glu Glu Lys Lys Gln Leu Cys Leu Ser Leu His Val Val Pro Gly Pro
225 230 235 240

Asp Glu Gln Ser Pro Ala Leu Ala Glu Glu Glu Lys Leu Gly Pro Glu
245 250 255

Glu Ile Pro Ser Arg Ala Gln Val Leu Pro Pro Ser Gly Val Glu Gly
260 265 270

Asp Asp Phe Gly Glu Gly Asp Asp Asp Gln Thr Ile Thr Pro Trp Asp
275 280 285

Val Gln Ala Ala Glu Gly Gly Ile Asp Tyr Asn Lys Leu Leu Arg Lys
290 295 300

Phe Gly Cys Ser Ser Ile Thr Pro Glu Leu Ile Ser Arg Ile Glu Ala
305 310 315 320

Leu Thr Gly Lys Arg Ala His His Leu Leu Arg Arg Gly Ile Phe Phe
325 330 335

Ser His Arg Asp Leu Asn Leu Leu Leu Asp Ser Leu Glu Lys Arg Gln
340 345 350

Ala Arg Leu Ala Ser Gly Lys Arg Glu Asp Gly Pro Gly Ser Glu Gly
355 360 365

Leu Ser Gly Pro Gly Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser
370 375 380

Glu Ala Leu His Ile Gly His Leu Val Pro Phe Met Phe Thr Lys Tyr
385 390 395 400

Leu Gln Asp Val Phe Asp Val Pro Leu Val Ile Gln Leu Thr Asp Asp
405 410 415

Glu Lys Phe Leu Phe Lys Asp Ser Leu Thr Leu Glu Glu Thr His Arg
420 425 430

Leu Ala Phe Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Pro
435 440 445

Asp Lys Thr Phe Ile Phe Ser Asp Leu Ser Tyr Ile Gln His Leu Tyr

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

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

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

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

Gln

<210> 335

<211> 475

<212> PRT

<213> *Toxoplasma gondii*

<400> 335

Met Glu Arg Gly Gln Met Leu Glu Pro Lys Glu Thr Ala Lys Ala Leu

1 5 10 15

Ser Ala Thr Ser Ser Gly Tyr Tyr Ser Asp His Val Asp Gln Asn Glu

20 25 30

Gln Val Arg Leu Leu Asn Arg Leu Ala Asn Ala Glu Gly Ser Ser Gln

35 40 45

Val Lys Gln Asp Ala Val Leu Ala Asn Pro Pro Asp Trp Lys Thr Leu

50 55 60

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

65 70 75 80

Ile Asn Pro Leu Cys Leu Asp Glu Phe Ala Glu Met Leu Ala Ala Asp

85 90 95

Pro Asp Leu Val Arg Ala Leu Val Ala Leu Val Arg Leu Glu Gly Asn

100 105 110

Leu His Thr Val Gln Tyr Val Leu Thr Val Leu Cys Glu Val Val Arg

115 120 125

Asp Asp Ser Ser Lys Tyr Glu Ala Leu Cys Ser Ala Val Ala Asp Ser

130 135 140

Glu Val Phe Glu Ala Phe Arg Gln Leu Leu Glu Val Ala Asn Leu Asp

145 150 155 160

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

165 170 175

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

180 185 190

Gln Gly Leu Leu His Gly Arg Ala Ala Asn Lys Phe Leu Leu Ser Glu

195 200 205

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

210	215	220	
Arg Pro Met Ile Trp Asp Cys Arg Gly Phe Pro Glu Leu Val Leu Arg			
225	230	235	240
Asn Leu Ser Leu Thr Leu Pro Ala Ser Val Leu Tyr Lys Ala Met Phe			
	245	250	255
Cys Val Trp Leu Leu Thr Phe His Asp Ala Phe Leu Pro Gln Leu Asn			
	260	265	270
Glu Lys Gly Ile Val Val Ala Val Cys Val Val Leu Lys Glu Ser Arg			
	275	280	285
Val Glu Lys Val Ile Arg Val Gly Leu Gly Val Leu His Asn Leu Leu			
	290	295	300
Lys Cys Asp Ala Ser Val Glu Thr Val Ile Glu Gln Asn Val Ala Gln			
305	310	315	320
Val Leu Ala Leu Leu Glu Phe Glu Lys Trp Arg Asp Gly Asp Met Tyr			
	325	330	335
Asp Asp Ile Arg Leu Ala Thr Ser His Leu Glu Gln Lys Ile Arg Gln			
	340	345	350
Phe Asn Asn Phe Asp Arg Tyr Cys His Glu Leu Asp Lys Gly Gln Leu			
	355	360	365
Thr Phe Ser Val Leu His Ser Glu Lys Phe Trp Arg Glu Asn Val Met			
370	375	380	
Ala Phe Glu Asn Asp Glu Phe Arg Ala Ile Lys Lys Leu Val Lys Leu			
385	390	395	400
Leu Asp Thr Ser Thr Asp Lys Thr Thr Leu Ala Val Ala Cys Tyr Asp			
	405	410	415
Leu Gly Glu Phe Ala Arg Leu His Pro Ala Gly Lys Lys Val Cys Gln			
	420	425	430
Gln Leu Lys Val Lys Asp Arg Val Met Leu Met Ile Ser Asp Lys Asp			
435	440	445	
Arg Glu Val Ala Gly Glu Ala Leu Leu Cys Ile Gln Lys Leu Met Leu			
450	455	460	

Asn Asn Trp Gln Asp Val Ala Glu Leu Gly Lys

465 470 475

<210> 336

<211> 616

<212> PRT

<213> *Toxoplasma gondii*

<400> 336

Met Ala Pro Arg Gly Glu Ala Ala Ala Pro Glu Gly Asp Ala Glu Met

1 5 10 15

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

20 25 30

Ser Gly Thr Lys Met Tyr Glu Leu Val Arg Val Gly Trp Gln Arg Leu

35 40 45

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

50 55 60

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

65 70 75 80

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

85 90 95

Phe Asp Gly Ile Gln Arg Pro Leu Glu Arg Ile Ala Gln Val Ala Gln

100 105 110

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

115 120 125

Lys Leu Trp Glu Tyr Asn Pro Val Ala Asn Val Gln Val Gly Asp Ile

130 135 140

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

145 150 155 160

Leu Glu His Arg Ile Met Ile Pro Pro Lys Ile Gln Gly Lys Val Ser

165 170 175

Trp Ile Ala Pro Ala Gly Ser Tyr Thr Val Lys Asp Thr Ile Met Thr

180 185 190

Leu Glu Tyr Arg Gly Glu Gln Ile Pro Ile Gln Met Ala His Asp Trp

195 200 205
 Pro Val Arg Glu Pro Arg Pro Cys Leu Glu Lys Leu Ser Gly Asn Thr

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

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

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

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

Trp Thr Thr Ser Phe Ser Lys Tyr Ile Arg Ala Leu Glu Pro Phe Phe
 450 455 460
 Asp Ser Tyr Asp Ala Glu Phe Ser Ser Leu Arg Gln Lys Ile Ser Asp

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

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

 595 600 605
 Gly Leu Arg Gly Leu Val Glu Lys
 610 615
 <210> 337
 <211> 505
 <212> PRT
 <213> Toxoplasma gondii
 <400> 337
 Met Ala Ala Gln Ala Ala Lys Ala Asp Ala Ala Leu Ala His Ala Ala
 1 5 10 15
 Ala Ala Ser Arg Asp Tyr Arg Val Ala Pro Arg Leu Asp Tyr Arg Thr
 20 25 30

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

35 40 45

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

50 55 60

Arg Glu Gly Gln Val Leu Glu Val Arg Gly Lys Arg Ala Val Val Gln

65 70 75 80

Val Phe Glu Gly Thr Ser Gly Ile Asp Thr Arg Gln Cys His Ala Glu

85 90 95

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

100 105 110

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

115 120 125

Leu Ala Glu Glu Phe Leu Asp Ile Asn Gly Cys Pro Ile Asn Pro Gln

130 135 140

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

145 150 155 160

Asp Val Met Asn Ser Val Val Arg Gly Gln Lys Ile Pro Leu Phe Ser

165 170 175

Ala Ala Gly Leu Pro His Asn Glu Ile Gly Ala Gln Ile Cys Arg Gln

180 185 190

Ala Ser Leu Val Ala Gly Lys Asp Val Lys Asp His Ser Asn Glu Asn

195 200 205

Phe Ala Val Val Phe Gly Ala Met Gly Val Asn Met Glu Thr Ala Arg

210 215 220

Phe Phe Arg Gln Asp Phe Glu Glu Asn Gly Ser Met Glu Arg Val Ala

225 230 235 240

Leu Phe Leu Asn Leu Ala Asn Asp Pro Thr Ile Glu Arg Ile Ile Thr

245 250 255

Pro Arg Leu Ala Leu Thr Thr Ala Glu Tyr Leu Ala Tyr Glu Arg Glu

260 265 270

Met His Val Phe Val Ile Leu Thr Asp Met Thr Ala Tyr Ala Asp Ala

275 280 285
Leu Arg Glu Val Ser Ala Ala Arg Glu Glu Val Pro Gly Arg Arg Gly

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

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

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

485 490 495
Arg Asn Asp Lys Arg Val Pro Pro Ser
500 505

<210> 338

<211> 404

<212> PRT

<213> *Toxoplasma gondii*

<400> 338

Met Leu Gly Ser Ser Glu Gly Gly Ala Arg Gly Cys Pro Tyr Trp Ile

1 5 10 15

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

20 25 30

Ser Leu Lys His Ala Val Leu Gly Ser Arg Asn Ala Leu Cys Asp Glu

35 40 45

Ala Cys Leu Leu Asp Ile Pro His Leu Lys Phe Gly Thr Phe Asp Asp

50 55 60

Leu Ile Arg Ser Val Asp Ile Leu Gln Lys Gln Asp Ala Tyr Val Glu

65 70 75 80

Ser Val Ile Arg Arg Ile Glu Arg Gln Ala Val Glu Ile Asp Pro Asp

85 90 95

Cys Glu Leu Lys Val Val Trp Gln Arg His Ser Leu Thr Val Asp Gln

100 105 110

Tyr Ile Arg Arg Phe Gln Trp Asp Asp Ala Lys Phe Pro Arg Leu Arg

115 120 125

Ala Ile Pro Glu Asn Leu Asp Ala Leu Val Gln Ser Val Thr Lys Thr

130 135 140

Asp Asp Glu Val Arg Ala Lys Val Ala Val Trp Gln Glu Val Arg Gln

145 150 155 160

Gln Met Ala Asn Ser Ala Ser Gly Lys Lys Thr Gly Pro Ala Thr Tyr

165 170 175

Phe Gln Arg Asp Leu Ile Asp Val Leu Ser Pro Asp Thr Val Arg Asp

180 185 190

Asp Asp Phe Leu Val Thr Glu His Leu Thr Thr Ala Val Val Val Val

195 200 205

Pro Arg Gly Gln Glu Arg Glu Trp Glu Gln Ser Tyr Glu Ser Leu Asp

210 215 220

Ala Phe Val Val Pro Arg Ser Ser Arg Lys Phe Asn Val Ala Glu Asp

225 230 235 240

Ala Asp Gly Asn Ala Leu Trp Arg Val Ile Leu Phe Thr Ser His Leu

245 250 255

Gln Ala Phe Arg Gln Ala Ala Gln Ala Lys Lys Phe Val Val Arg Asp

260 265 270

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

275 280 285

Arg Val Glu Ala Glu Lys Thr Lys Gln Glu Thr Phe Leu Ser Arg Val

290 295 300

Cys Phe Ala Ala Phe Ser Asp Ile Phe Val Ala Trp Met His Leu Lys

305 310 315 320

Val Met Arg Thr Phe Cys Glu Ala Val Leu Arg Phe Gly Val Pro Pro

325 330 335

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

340 345 350

Lys Leu Arg His Glu Leu Asp Lys Leu Phe Ser Pro Lys Gly Gly Phe

355 360 365

Gly Asn Ser Tyr Phe Ser Gly Lys Asp Asp Pro Gly Ser Asp Asp Glu

370 375 380

Asp Phe Tyr Pro Tyr Ile Trp Leu Ala Leu Gln Pro Phe Gly Ser His

385 390 395 400

Arg Ala Ser Ala

<210> 339

<211> 396

<212> PRT

<213> Toxoplasma gondii

<400> 339

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

1 5 10 15

Cys Arg Gly Leu Arg Ser Ala Phe Leu Thr Glu Glu Asp Tyr Lys Lys
 20 25 30
 Leu Ser Ala Ala Asp Ser Leu Glu Asp Leu Arg Ser Ala Leu Glu Glu
 35 40 45
 Thr Asp Tyr Gly Pro Phe Met Gln Asp Glu Pro Leu Pro Leu Ala Val
 50 55 60
 Pro Thr Leu Ser Gln Lys Cys Arg Glu Lys Met Ala Ser Glu Phe Arg

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

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

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

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

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

 385 390 395
 <210> 340
 <211> 345
 <212> PRT
 <213> *Toxoplasma gondii*
 <400> 340
 Met Leu Ser Phe Glu Phe Ser Ser Gly Val Tyr Met Arg Asn Asn Ser
 1 5 10 15
 Ser Ala Ala Leu Gln Glu Thr Gly Val Trp His Asn Ala Trp Arg Ala
 20 25 30
 Arg Ser Lys Leu Pro Thr Ala Phe Phe Ile Asp Ile Ser Ser Phe Ser
 35 40 45

 Val Gly Ser Phe Phe Ser Ser His Ser Leu Ala Asn Asn Thr Ser Ser
 50 55 60
 Thr Pro Pro Phe Val Cys Lys Lys Arg Phe Val Thr Ala Pro Ile Tyr
 65 70 75 80

Leu Arg Phe Pro Arg Tyr His Glu Glu Glu Phe Ala Ile Phe Phe Pro
 85 90 95
 Thr Leu Ser Ser Ser Pro Ala Pro Ala Pro Leu Gly Lys Met Ala Met
 100 105 110

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

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

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

 Gly Val Val Leu Met Thr Arg Asp Gly Arg Ile Thr Cys Asp Asn Thr
 305 310 315 320
 Phe Asp Ala Arg Leu Arg Met Val Ile Val Glu Cys Ala Pro Ala Ile

	325	330	335
Arg His Thr Leu Phe Pro Ser His Gln			
	340	345	
<210> 341			
<211> 195			
<212> PRT			
<213> Toxoplasma gondii			
<400> 341			
Met His Gln Phe Arg Cys Leu Ala Arg Ile Lys Lys His Tyr Cys Gly			
1	5	10	15
Gly Asp Thr Val Glu Asn His Ser Asp Lys Asn Lys Glu Leu Gln Leu			
	20	25	30
Glu Gln Ile Phe Ala Pro Ala Thr Val Cys Gly Leu Ser Arg Leu Arg			
	35	40	45
Pro Ala Ala Gly Cys Ser Lys Val Val Leu Val Ser Lys Ile Leu Leu			
	50	55	60
Val Leu Ala Lys Met Ala Pro Val Leu Gly Arg Val Gln Gly Thr Asp			
65	70	75	80
Leu Lys Val Ala Val Ile Gly Asp Glu Asp Thr Val Ala Gly Phe Leu			
	85	90	95
Met Ala Gly Ile Gly Met Arg Asp Gly Leu Gly Arg Thr Asn Phe Phe			
	100	105	110
Ile Val Asp Ser Lys Thr Lys Arg Gln Asp Val Glu Asp Ala Phe Arg			
	115	120	125
Thr Met Thr Glu Arg Pro Asp Ile Gly Ile Val Leu Ile Asn Gln His			
	130	135	140
Val Ala Asp Asp Ile Arg Tyr Met Val Asp Leu His Thr Lys Ile Ile			
145	150	155	160
Pro Thr Ile Leu Glu Ile Pro Ser Lys Asp Lys Pro Tyr Asp Pro Ser			
	165	170	175
Lys Asp Ser Val Met Gln Arg Ile Lys Phe Phe Phe Gly Gly Glu Leu			
	180	185	190

Pro Thr Ser

195

<210> 342

<211> 131

<212> PRT

<213> Toxoplasma gondii

<400> 342

Met Ala Ala Ala Lys Gly Ser Asn Ala Leu Ile Gln Gln Leu Leu Glu

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

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

130

<210> 343

<211>

157

<212> PRT

<213> Toxoplasma gondii

<400> 343

Met Phe Trp Ser Ala Phe Leu Gln Cys Asp Pro Asn Ser Thr Phe Phe

1 5 10 15

Gly Phe Met Gly Ile Thr Ala Ala Met Val Phe Ser Asn Leu Gly Ala
20 25 30
Ala Tyr Gly Thr Ala Lys Ser Gly Val Gly Ile Ser Ser Met Gly Val
35 40 45
Met Arg Pro Asp Leu Val Met Arg Ser Ile Ile Pro Val Val Met Ala
50 55 60
Gly Ile Leu Gly Ile Tyr Gly Leu Ile Ile Ser Ile Val Ile Asn Gly
65 70 75 80
Ser Met Asp Thr Pro Asp Thr Tyr Ser Ser Tyr Ala Gly Tyr Gly His
85 90 95
Leu Ala Ala Gly Leu Thr Val Gly Leu Ser Ala Met Ala Ala Gly Leu
100 105 110
Ala Ile Gly Ile Val Gly Asp Ala Gly Val Arg Ala Asn Ala Gln Gln
115 120 125
Pro Lys Leu Leu Arg His Asp Ala Tyr Pro His Phe Arg Arg Gly Ser
130 135 140
Trp Thr Leu Arg Ser Tyr His Trp Thr Cys Arg Arg Tyr
145 150 155
<210> 344
<211> 162
<212> PRT
<213> Toxoplasma gondii
<400> 344
Met Glu Arg Ala Ser Ala Ala Ala Ala Thr Arg Ser Pro Ile Phe Ala
1 5 10 15
Ser Ala Leu Thr Lys Arg Lys Pro Leu Leu Leu Leu Gly Phe Ala
20 25 30
Val Val Leu Thr Phe Phe Thr Cys Gly Val Pro Thr Thr Ser Leu Arg
35 40 45
Leu Arg Gly Pro Lys Phe Thr Leu Gln Asp Met Lys Lys Ala Ile Lys
50 55 60
Asp Ala Lys Asp Gly Val Lys Gly Val Glu Asp Ala Lys Lys Lys His

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

Ser Lys Glu Gly Glu Lys Ala Asp Glu Val Leu Lys Arg Cys Gly Thr
145 150 155 160
Val Val

<210> 345

<211> 571

<212> PRT

<213> *Toxoplasma gondii*

<400> 345

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

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

100	105	110	
Val Pro Gly Pro Ser Gln Pro Ile Pro Ser Gly Thr Asp Ser Thr Pro			
115	120	125	
Glu Gly Trp Glu Thr Val Gln Ser Gly Asp Val Pro Pro Gly Glu Pro			
130	135	140	
Glu Pro Lys Ala Pro Thr Arg Ser Pro Arg Gln Arg Ala Arg Asp Met			
145	150	155	160
Phe Gly Arg Val Gly Arg Phe Phe Gly Gly Ala Arg Arg Phe Val Gly			
165	170	175	
Arg Gly Trp Arg Arg Phe Thr Thr Gly Met Ala Gly Val Thr Asp Arg			
180	185	190	
Val Arg Gly Arg Leu Ala Leu Arg Ser Ser Phe Glu Phe Arg Asn Glu			
195	200	205	
Glu Ala Val Gly Gln Ser Glu Leu Ala Ser Leu Ala Ser Ser Met Thr			
210	215	220	
Val Thr Ala Pro Glu Gly Glu Ala Leu Glu Val Ala Arg Glu Ala Gly			
225	230	235	240
Leu Arg Ser Gly Ala Ser Ile Asn Leu Val Ser Ala Thr Thr Gly Glu			
245	250	255	
Gln Val Thr Val Ser Leu Arg Ala Pro Leu Gly Ile Gly Glu Tyr Thr			
260	265	270	
Ala Val Phe Ser Gly Phe Ile Ser Gly Ile Asp Ser Glu Leu Ala Val			
275	280	285	
Lys Ala Phe Leu Gly Lys Thr Thr Glu Ser Met Ser Val Ala Glu Thr			
290	295	300	
Glu Ala Arg Ile Leu Lys Ile Val Ser Leu Lys Asp Pro Val Asp Ala			
305	310	315	320
Met His Arg Leu Arg Leu Leu Ala Pro Ile Glu Thr Leu Val Tyr Arg			
325	330	335	
Gly Asp Gly Asp Ser Ala Asp Gln Ser Glu Gly Arg Pro Val Val Leu			
340	345	350	

Val Pro Lys Ala Ser Ser Ser Leu Val Asp Val Ile Asn Phe Leu Arg

355 360 365

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

370 375 380

Leu Gly Ala Thr Val Gln Leu Ile Gln Leu Leu Ala Ala Leu His Thr

385 390 395 400

Arg Lys Val Val His Gly Lys Leu Glu Pro Lys Ser Val Leu Leu Phe

405 410 415

Ser His Gly Leu Leu Tyr Leu Ser Asp Leu Gly Arg Ala Arg Arg His

420 425 430

Gly Glu Arg Phe Thr Thr Ser Arg Pro Ser Arg Tyr Gly Ala Pro Glu

435 440 445

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

450 455 460

Ser Leu Gly Ile Ile Leu Phe Glu Leu Trp Cys Gly Arg Leu Pro Phe

465 470 475 480

Asp Leu Gly Thr Pro Gly Val Asp Ser Ser Glu Lys Leu Glu Asn Ser

485 490 495

His Pro Ala Thr Leu Tyr Gln Thr Val Arg Asn Leu Asp Gln Arg Leu

500 505 510

Ser Phe Asp Val Cys Pro Ser Asp Met Pro Glu Ser Val Lys Thr Leu

515 520 525

Ile Arg Lys Phe Leu Thr Arg Arg Arg Trp Thr Arg Leu Val Pro Gln

530 535 540

Ala Ala Leu Arg Asp Ala Asn Phe Arg Arg Thr Met Gln Leu Leu Gln

545 550 555 560

Glu Thr Val Gln Gly Asn Gly Glu Thr Gln Leu

565 570

<210> 346

<211> 572

<212> PRT

<213> Toxoplasma gondii

<400> 346

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

1 5 10 15

Leu Pro Val Ala Ala Leu Ala Ala Ile Leu Leu Leu Gly Cys Met Tyr

20 25 30

Thr Arg Ala Ala Gly Thr Pro Asp Asp Ser Leu Phe Pro Leu Ser Glu

35 40 45

Asp Thr Ser Val Asp Pro Arg Glu Ser Phe Ser Ala Glu Asp Val Leu

50 55 60

Asn Ala Phe Val Ser Pro Glu Ser Val Glu Ser Leu Phe Ala Ser Ile

65 70 75 80

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

85 90 95

Pro Arg Asp Arg Asp Ser Ala Pro Glu Arg Arg Ser Asp Gly Gly Thr

100 105 110

Leu Arg Gly His Pro Glu Asp Ala Gly Glu Leu Leu Arg Leu Leu Leu

115 120 125

Ala Asp Ser Glu Asp Met Glu Leu Trp Lys Ala Asn Phe Phe Arg His

130 135 140

Leu Thr His Ser Met Arg His Ile Val Arg Asp Ser Val Leu Val Ser

145 150 155 160

Glu Lys Ala Phe Pro Ser Glu Gln Ala Asp Glu Ala Gly Arg Asp Pro

165 170 175

Gly Asp Leu Lys Lys Ala Leu Lys Glu Thr Gly Glu Asp Val Phe Trp

180 185 190

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

195 200 205

Lys Met Glu Lys Gln Ala Gly Lys Thr Gly Glu Gly Ala Gly His Thr

210 215 220

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

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

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

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

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

Gly Leu Pro Val Gly Gly His Ala Ile Lys Ile Ile Gly Trp Gly Thr

485 490 495

Glu Asn Gly Glu Glu Tyr Trp His Ala Val Asn Ser Trp Asn Thr Tyr

500 505 510

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

515 520 525

Asp Gly Glu Met Val Ala Gly Glu Ala Ala Trp Gln Glu Thr Glu Gly

530 535 540

Val Val Asn Gly Glu Glu Glu Leu Pro Gly Gln His Ala Ser Gly Ala

545 550 555 560

Arg Val Gly Ala His Ala Glu Glu Glu Arg Glu Met

565 570

<210> 347

<211> 537

<212> PRT

<213> Toxoplasma gondii

<400> 347

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

1 5 10 15

Leu Phe Ser Val Asp Cys Cys Pro Pro His Pro Ser Pro Ser Ser Val

20 25 30

Phe Gln Ser Asp Gly Lys His Glu Leu Pro Ala Ser Glu Ile Pro His

35 40 45

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

50 55 60

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

65 70 75 80

Thr Ser Ala Ala Ser Asp Thr Ser Ser Gln Ala Pro His Asp Val Pro

85 90 95

Val Phe Thr Asp Ser Leu Leu Ser Ser Ser Thr Ser Glu Trp Pro His

100 105 110

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

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

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

485 490 495
 Leu Pro Ile Asp Asn Arg Pro Gly Asp Gly Val His Phe Ile Thr Glu
 500 505 510
 Asp Thr Arg Leu Leu His Thr Pro Val Leu Arg Arg Ile Arg Thr Phe
 515 520 525
 Glu Pro Ile Ile Glu Ser Ser Val Asp

530 535

<210> 348

<211> 399

<212> PRT

<213> Toxoplasma gondii

<400> 348

Met Arg Thr Ser Val Ala Leu Phe Phe Ala Ala Leu Gly Ser Ile Ser

1 5 10 15
 Leu Pro Cys Thr Leu His Val Ser Leu Ala Ala Pro Met Gln Gly Thr
 20 25 30

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

275 280 285
 Ser Gly Ile Asp Ser Glu Leu Ala Val Lys Ala Phe Leu Gly Lys Thr
 290 295 300
 Thr Glu Ser Met Ser Val Ala Glu Thr Glu Ala Ser Ile Leu Lys Ile
 305 310 315 320
 Val Ser Leu Lys Asp Pro Val Asp Ala Met Arg Arg Leu Arg Leu Leu

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

385 390 395

<210> 349

<211> 96

<212> PRT

<213> Toxoplasma gondii

<400> 349

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

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

<210> 350

<211> 519

<212> PRT

<213> *Toxoplasma gondii*

<400> 350

Met Thr Asp Cys Pro Phe Ala Ala Ile Arg Gly Ser Ser Gly Arg Ile

1 5 10 15
Ser Arg Ser His Val Ala Phe Leu Val Ile Leu Ala Val Ser Val Thr

20 25 30
Ser Asn Pro Thr Leu Ala Phe His Arg Gly Ser Leu Gln Gly Thr Ala

35 40 45
Thr Arg Asp Asp Leu Pro Thr Gln Ala Gln Tyr Leu Ser Ala Ile Gly

50 55 60
Ala His Glu Thr Leu Val Arg Ala Gln Arg Arg Ala Ala Phe Gln Lys

65 70 75 80
Thr Pro Gly Lys Asn Ser Gly Arg Pro His Ser Leu Leu Gln Asp Val

85 90 95
Ala Glu Glu Arg Glu Asn Ser Ser Thr Ala Val Gly Ser Ile Pro His

100 105 110
Phe Ser Ala Leu Pro Glu Ser Glu Trp Asp Tyr Lys Gln His Gly Lys

115 120 125
Asp Trp Gly Gly Met Cys Ala Thr Gly Met Gln Gln Ser Pro Val Asp

130 135 140
Leu His Ile Glu Gly Leu Gln Glu Pro Glu Tyr Arg Asn Leu Thr Asn

145 150 155 160
Val Tyr Met Asn Ala Phe Ala Gly Thr Gln Pro Ser Arg Thr Leu Lys

165 170 175
Pro Trp Lys Arg Gly Asp Phe Phe Tyr Thr Tyr Pro His Gln Phe Thr

180 185 190
Lys Val Glu Val Tyr Lys Thr Ser Lys Val Phe Gln Val Arg Val Pro

195 200 205

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

450 455 460
 Ile Ala Asn Ser Leu Gly Phe Asp Thr Met Ala Lys Met Ser Lys Glu
 465 470 475 480
 Gly Ala Gln Met Phe Gln Gly Trp Phe Ser Ala Ala Gly Glu His Thr
 485 490 495
 Phe Gly His Ser Gly Ser Ala Leu Ala Phe Ala Thr Ala Ala Leu Val
 500 505 510
 Phe Leu Asn Thr Val Gly Ile
 515

<210> 351

<211> 176

<212> PRT

<213> Toxoplasma gondii

<400> 351

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

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

115 120 125
 Val Gly Glu Ser Ala Leu Cys Ser Leu Tyr Val Gln Arg Glu Thr Leu
 130 135 140

Ser Arg Thr Met Thr Arg Thr Lys Asp Val Gln Arg Asn Met Asp Glu
 145 150 155 160
 Ala Asp Thr Ile Val Thr Lys Met Ser Lys Trp Trp Asn Gly Ile Trp
 165 170 175

<210> 352

<211> 277

<212> PRT

<213> Toxoplasma gondii

<400> 352

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

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

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

180 185 190
 Thr Gly Asp Ala Ser Ala Phe Asp Asp Gln Ala Lys Lys Ile Val Arg
 195 200 205
 Leu Gly Ala Thr Val Gln Leu Ile Gln Leu Leu Ala Ala Leu His Thr
 210 215 220
 Arg Lys Val Val His Arg Met Leu Glu Pro Lys Ser Val Leu Leu Phe
 225 230 235 240
 Ser His Gly Leu Leu Tyr Leu Ser Asp Leu Gly Arg Ala Arg Arg His
 245 250 255

 Gly Glu Arg Phe Thr Thr Ser Arg Pro Ser Arg Ile Pro Gly Thr Leu
 260 265 270
 Leu Glu Gln Val Asp
 275
 <210> 353
 <211> 332
 <212> PRT
 <213> Toxoplasma gondii
 <400> 353
 Met Arg Thr Ser Val Ala Leu Phe Phe Ala Ala Leu Gly Ser Ile Ser
 1 5 10 15
 Leu Pro Cys Thr Leu His Val Ser Leu Ala Ala Pro Met Gln Gly Thr
 20 25 30

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

 Ser Ser Ser Ser Ile Arg Arg Gly Gly Asp Ser Asn Val Leu Leu Pro

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

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

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

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

<210> 354

<211> 264

<212> PRT

<213> Toxoplasma gondii

<400> 354

Met Phe Pro Arg Val Ala Leu Phe Pro Val Pro Thr Cys Asp Leu Phe
1 5 10 15

Leu Val Gly Arg Ser Arg Leu Ser Arg Ala Ala Lys Leu His Leu Thr
20 25 30

Arg Gln Leu Val Val Ser Val Ala Trp Leu His Arg His Gly Val Ala
35 40 45

His Asn Asp Leu Lys Leu Glu Asn Val Phe Pro Ser Glu Glu Gly Lys
50 55 60

Ala Val Ile Gly Asp Leu Gly Phe Gly Val Gln Ile Gly Thr Ser Ala
65 70 75 80

Arg Leu Lys Tyr Thr Ala Ala Tyr Leu Asp Pro His Ala Ala Glu Glu
85 90 95

Cys Leu Asn Asn Gln Val Glu Thr Val Ala Asn Glu Gly Thr Gly Ala
100 105 110

Trp Ala Leu Gly Thr Leu Val Phe Val Ile Trp Cys Arg Ser Tyr Pro
115 120 125

Val Val Ser Arg Glu Gln Ala Cys Leu Ser Thr Arg Asp Leu Arg Asp
130 135 140

Arg Leu Val Thr Met Ala Lys Thr Thr Lys Pro Thr Pro Ser Ser His
145 150 155 160

His Cys Gln Glu Leu Pro Ser Pro Val Lys Asp Leu Ile Ala Gly Phe
165 170 175

Leu Gln Trp Ser Arg Glu Ala Arg Arg Leu Pro Gly Asp Asp Val Asp
180 185 190

Glu Phe Leu Ala Ala Thr Leu Leu Leu Gln Ser Gln Lys Gln Arg Pro
195 200 205

Pro Gln Arg Val Cys Asp Thr Asp Asn Cys His Ile Gln Ile Thr Ala
210 215 220

Thr Val Ile Pro Lys Thr Asn His Trp Phe Thr Ile Leu Thr Thr Gly

225 230 235 240
 Lys Ser Gly Arg Pro Ile Asp Phe Leu Ile Tyr Glu Ile Gly Arg Gly
 245 250 255
 Leu Thr Gly Ile Arg Gly Gln Glu

260

<210> 355

<211> 122

<212> PRT

<213> Toxoplasma gondii

<400> 355

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

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

<210> 356

<211> 248

<212>

> PRT

<213> Toxoplasma gondii

<400> 356

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

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

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

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

 180 185 190
 Leu His Thr Arg Lys Val Val His Gly Lys Leu Glu Pro Lys Ser Val
 195 200 205
 Leu Leu Phe Ser His Gly Leu Leu Tyr Leu Ser Asp Leu Gly Arg Ala
 210 215 220
 Arg Arg Gln Gly Glu Arg Phe Thr Thr Ser Arg Pro Ser Arg Ile Pro
 225 230 235 240
 Gly Thr Leu Leu Glu Gln Val Asp
 245

<210> 357

<211> 489

<212> PRT

<213> Toxoplasma gondii

<400> 357

Met Ser Ile Leu Gly Lys His Thr Ala Thr Val Gly Asp Arg Tyr Lys

1 5 10 15

Val Arg Leu Thr Pro Glu Tyr Gly Pro Gly Gly Gly Tyr Gly His Cys

20 25 30

Arg Asp Tyr Leu Leu Gln Ser Glu Ser Cys Trp Arg Gly Asp Leu Thr

35 40 45

Ser Gly Val Arg Gly Val Leu Thr Lys Lys Gly Thr Arg Ala Arg Thr

50 55 60

Thr Lys Arg His Asp Leu Val Ala Val Thr Ser Gly Glu His Tyr Trp

65 70 75 80

Asn Gln Gly Leu Val Tyr His Glu Glu Gln Thr Ala Pro Pro Val Ala

85 90 95

Ala Ser Ser Ser Phe Met Gln Ser Thr Thr Ser Leu Ala Thr Pro Ala

100 105 110

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

115 120 125

Val Leu Lys Asn Arg Pro Pro Ala Glu Ala Gln Leu Ser Pro Arg Glu

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

His Arg Val Lys Val Gly Gly Ala Ser Ala Pro Gln Gln Leu Ala Ala

195 200 205

Lys Ile Asn Val Arg Ser Leu Gln Glu Leu Gln His Leu Ser Ser Ser

210 215 220
 Gln Lys Lys Thr Ala Leu Glu Asp Ile Gln Glu Arg Phe Leu Arg Glu
 225 230 235 240
 Glu Ser Ser Ala Arg Asn Ala Leu Gln His Val Thr Pro Glu Thr Ala

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

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

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

 435 440 445
 Leu Pro Pro Ala Val Gly His Leu Val Thr Ala Phe Leu Gln Trp Asn
 450 455 460

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

485

<210> 358

<211> 204

<212> PRT

<213> *Toxoplasma gondii*

<400> 358

Met Ser Ile Leu Gly Lys His Thr Ala Thr Val Gly Asp Arg Tyr Lys

1 5 10 15

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

20 25 30

Gln Leu Leu Gln Ala Val Ala Trp Leu His Ala Asn Gly Val Ala His

35 40 45

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

50 55 60

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

65 70 75 80

Ile Gln Phe Thr Ala Pro Tyr Leu Asp Pro Gln Thr Ala Glu Ala Val

85 90 95

Leu Gln Lys Lys Thr Lys Thr Thr Ala Ser Glu Glu Arg Asp Ala Trp

100 105 110

Ala Leu Ala Thr Leu Leu Phe Leu Leu Trp Cys Gly Ser Phe Pro Tyr

115 120 125

Val Ser Asp Glu Gln Ala Asp Leu Pro Thr Ser Asp Leu Leu Lys Leu

130 135 140

Leu Val Thr Leu Gly Lys Thr Glu Lys Pro Ala Pro Asn Phe His Leu

145 150 155 160

Cys Lys Asp Leu Pro Pro Ala Val Gly His Leu Val Thr Ala Phe Leu

165 170 175

Gln Trp Asn Ser Asp Asn Arg Ser Arg Pro Gly Asp Val Leu Asp Asp

180 185 190
 Phe Leu Ala Ala Thr Val Ser Glu Gly Ala Ser Ala

 195 200
 <210> 359
 <211> 568
 <212> PRT
 <213> *Toxoplasma gondii*
 <400> 359
 Met Arg Arg Leu Leu Leu Ser Pro Val Gly Phe Val Ile Val Leu Ala
 1 5 10 15
 Thr Leu Leu Glu Cys His Pro Pro Asp Arg Cys Val Ala His His Gly
 20 25 30
 Ser Ser Thr Asp Glu Ser Asn Val Trp Ser Pro Arg Gly Ala Gln Phe
 35 40 45

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

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

 Asn Ala Pro Ile Asp Leu Gln Gly Arg Arg Asp Ile Arg Asn Ile Val

180	185	190	
Arg Asn Arg Pro Pro Ala Asp Ser Asp Leu Ser Arg Ser Glu Ile Ala			
195	200	205	
Ala Lys Asn Gly Phe Glu Arg Arg Phe Val Arg Gly Leu Gln Leu Lys			
210	215	220	
Val Glu Ser Leu Phe Ser Gly Gly Val Phe Thr Leu Thr Gly Pro Ala			
225	230	235	240
Gln Phe Leu Gly Ile Gly Ser Thr Ala Ile Val Tyr Ser Leu Asn Lys			
245	250	255	
Val Gln Ala Asp Thr Ala Ser Ala Pro Glu Arg Val Ala Val Lys Ile			
260	265	270	
Ser Ile Asn Asn Leu Gln Arg Leu Arg Ser Leu Ser Val Phe Asp Arg			
275	280	285	
Gln Glu Leu Leu Asp Lys Thr Pro Glu Arg Phe Val Ser Ser Glu Gly			
290	295	300	
Ala Val Arg Asn Leu Leu Pro Gly Val Thr Pro Glu Thr Ala Leu Glu			
305	310	315	320
His Gly Ile Leu Leu Pro Leu Asp Ile Cys Arg Val Thr Asn Leu Pro			
325	330	335	
Ser Gly Phe Arg Ala Gly Pro Asp Tyr Lys Met Phe Pro Arg Val Ala			
340	345	350	
Leu Phe Pro Val Leu Thr Cys Asp Leu Phe Leu Val Gly Arg Ser Arg			
355	360	365	
Leu Ser Arg Ala Ala Lys Leu His Leu Thr Arg Gln Leu Val Val Ser			
370	375	380	
Val Ala Trp Leu His Arg His Gly Val Ala His Asn Asp Leu Lys Leu			
385	390	395	400
Glu Asn Val Phe Leu Ser Glu Glu Gly Lys Ala Val Ile Gly Asp Phe			
405	410	415	
Gly Phe Ala Ala Glu Val Gly Thr Ser Thr Lys Leu Arg Ser Thr Pro			
420	425	430	

Ala Phe Leu Asp Pro Gln Thr Ala Glu Glu Tyr Leu Gln Arg Lys Thr
435 440 445

Glu Thr Val Val Thr Glu Glu Arg Asp Ala Trp Ala Leu Gly Thr Ile
450 455 460

Ile Phe Val Ile Trp Cys Gly Ser Tyr Pro Phe Phe Ser Phe Glu Glu
465 470 475 480

Ala Val Leu Pro Pro Ala Val Leu Trp Gln Asn Val Val Phe Met Ser
485 490 495

Lys Thr Thr Arg Pro Ala Pro Pro Leu Gln His Cys Lys Gly Met Pro
500 505 510

Ser Pro Val Lys Ala Leu Ile Thr Gly Phe Leu Gln Trp Asn Ser Asp
515 520 525

Asp Arg Arg Arg Pro Arg Asp Val Val Glu Gly Phe Leu Ala Ala Thr
530 535 540

Ala Ser Glu Pro Ala Thr Ser Ser Ala Thr Ala Ala Glu Gly Ser Val
545 550 555 560

Arg Pro Arg Ala Ser Arg Ser Gln
565

<210> 360

<211> 541

<212> PRT

<213> Toxoplasma gondii

<400> 360

Met Lys Asn Thr Leu Leu Ser Pro Val Gly Phe Phe Thr Ala Leu Ala
1 5 10 15

Val Leu Ile Glu Cys His Leu Cys Asp Arg Cys Val Ala His His Gly
20 25 30

Ser Ser Thr Asp Gly Ser Gly Leu Arg Pro Pro Gln Glu Val Asp Ser
35 40 45

Ala Pro Arg Thr Pro Ser Ile Ala Val Lys Glu Leu Ala Thr Phe Pro
50 55 60

Gly Asp Asp Ile Gln Thr Ser Ser Gln Glu Leu Pro Gly Tyr Glu Leu

65	70	75	80
Trp Thr Arg Glu Gln Ser Gly Ala Ser Val Arg Val Gly Phe Pro Gln			
	85	90	95
Asn Ala Glu Ser Phe Leu Thr Gln Arg Glu Ala Arg Asp Glu Ile Ala			
	100	105	110
Asn Ala His Glu Leu Val Ala Val Thr Pro Glu Gly Asp Ala Trp Asn			
	115	120	125
His Ser Gly Val Val Pro Glu Glu Gln Thr Val Thr Pro Ala Ser Gly			
	130	135	140
Ser Phe Ile Gln Arg Gln Ala Ala His Ala Pro Pro Ser Thr Arg Leu			
145	150	155	160
Thr Pro Val Asp Arg Arg Gly Arg Ser His Thr Val Ser Ala Val Arg			
	165	170	175
Arg Arg Val Thr Val Glu Asp Val Met Arg Pro Asp Gln Ser Ala Ala			
	180	185	190
Met His Ala Val Leu Ser Ala Phe Gly Gly Gly Leu Val Leu Lys Ala			
	195	200	205
Lys Asn Lys Trp Gly Arg Thr Arg Tyr Thr Leu Gln Gly Pro Ala Thr			
	210	215	220
Phe Leu Gly Met Gly Ala Glu Gly Ile Val Val Arg Leu Asn Gln Val			
225	230	235	240
Lys Ser Asp Arg Glu Arg Ser Val Thr Pro Val Ala Val Lys Leu Cys			
	245	250	255
Leu Ile Arg Ala Ala Val Phe Ser Gly Leu Thr Trp Trp Arg Lys Arg			
	260	265	270
Arg Thr Arg Thr Glu Leu Met Lys Leu Phe Leu Ser Asn Glu Asn Ser			
	275	280	285
Val Lys Arg Ala Leu Pro Asp Leu Asp Pro Ala Glu Met Leu Glu His			
	290	295	300
Gly Leu Val Val Pro His His Ala Glu Leu Val Ser Gly Met Pro Thr			
305	310	315	320

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

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

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

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

<210> 361

<211> 199

<212> PRT

<213> Toxoplasma gondii

<400> 361

His Val Leu Arg Lys Leu His Leu Thr Arg Gln Leu Val Val Ser Val

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

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

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

<210> 362

<211> 697

<212> PRT

<213> Toxoplasma gondii

<400> 362

Met Arg Arg Ser Arg Ser Lys Tyr His Val Gly Thr Phe Val Thr Gly
1 5 10 15

Ser Ala Val Gln Arg Leu Thr Leu Val Gly Met Tyr Ser Ala Val Trp
20 25 30

Val Thr Ser Ala His Ser Ser Pro Val Asn Ser Ala Thr Val Ser Pro
35 40 45

Ser Phe Phe Phe Leu His Ser Lys Pro Pro His Gly Ser Pro Pro Asn

50 55 60

Glu Arg Thr Thr Gly Glu Ser Ser Gly Ser Asn Ala Ser Ile Glu Leu
65 70 75 80

Met Glu Met Gln Pro Thr Gln Pro Glu Ser Leu Ser Pro Thr Ala Met
85 90 95

Ala Ala Arg Arg Pro Asn Val Pro Pro Leu Pro Glu Ala Ser Gly Leu
100 105 110

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

115 120 125

Gly Asp Thr Gln Asp Ser Ala Gln Val Ser Thr Pro Ser Gly Thr Pro
130 135 140

Arg Val Gln Pro Ile Ser Ser Pro Lys Arg Glu Ala Leu Phe Arg Met
145 150 155 160

Ser Pro Pro Pro Val Pro Lys Arg Ser Leu Arg Arg Thr Leu Ser Gln
165 170 175

Tyr Phe Arg Ala Arg Lys His Ser Gly Val Pro Asn Pro Arg Ala Ser

180 185 190

Ala Gln Leu Pro Thr Ala Asp Arg Glu Gln Ala Val Asn Arg Pro His
195 200 205

Arg Ala Ser Arg Leu Met Lys Ser Ser Pro Ser Ser Ala Ser His Gln
210 215 220

Ala His Gly Ala Ala Pro His Arg Arg Arg Ala Ala Thr Ser Pro Gln
225 230 235 240

Pro Arg Thr Arg Arg Asp Pro Ala Gly Pro Val Gly Arg Thr Leu Arg

245 250 255

Asn Trp Ile Ser Asp Arg Leu Ser Arg Ala Tyr Arg His Val Arg Ser

260 265 270

Arg Leu Arg Thr Gly Tyr Ala Arg Leu Leu Arg Gln Leu His Ser Met

275 280 285

Thr Glu Lys Ile Pro Thr Pro Pro Val Gln Leu Pro Gly Gln Glu Cys

290 295 300

Val Asn Val Leu Gly Ala His Val Ala Arg Gln Val Ala Asp Trp Arg

305 310 315 320

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

325 330 335

Pro Arg Asp Lys Asp Ile Ser Phe Lys Ser Tyr Ile Ser Arg Lys Ser

340 345 350

Val Thr Leu Arg Met Gly Lys Val Leu Gly Gly Gly Ala Arg Ser Ile

355 360 365

Val Val Glu Val Thr Arg Val Asp Thr Gly Asp Arg Trp Ala Leu Lys

370 375 380

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

385 390 395 400

Pro Trp Asp Ala Ile Ser Glu Glu Ala His Ala Ile Lys Leu Leu Pro

405 410 415

His Thr Val Pro Ala Val Val Tyr Arg Asn Leu Arg Phe Leu Val Pro

420 425 430

Ala Asp Val Leu Ile Tyr Glu Gly Asp Gly Met Glu Lys Leu Trp Asn

435 440 445

Arg Arg Gly Thr Gly Ser Asn Phe Tyr Thr Thr Tyr Leu Leu Phe Pro

450 455 460

Ile Ala Gln Gly Ser Leu Leu Asp Ala Val Arg Ala Met Phe Arg Asp

465 470 475 480

Ala Arg Arg Gly Asn Ala Glu Val Ser Asp Gly Glu Ala Ala Arg Thr

485 490 495
Leu Ala Ala Asn Val Ser Phe Ser Ile Gln Ile Ile Arg Leu Thr Ala

500 505 510
Leu Leu His Ser His Gly Val Val His Gly Asp Phe Gln Thr Lys Ser

515 520 525
Phe Phe Leu Cys Gln Asp Gly Ser Leu Phe Leu Gly Arg Val Arg Ser

530 535 540
Leu Thr Arg Val Gly Ala Pro Tyr Arg Ser Pro Ser Ser Ala Thr Asp

545 550 555 560
Ser Pro Arg Cys Thr Pro Pro Glu Val Leu Ser Pro Pro Glu Asn Ala

565 570 575
Ala Phe Thr Phe Ser Leu Asn Ala Trp Glu Leu Gly Cys Ile Leu Tyr

580 585 590
Gln Leu Trp Cys Glu Gly Leu Pro Phe Gly Leu Ser Pro Thr Pro Glu

595 600 605
Thr Pro Gly Lys Ile Val Leu Pro Pro Val Ile Thr Ser Pro Tyr Leu

610 615 620
Gln Thr Lys Lys Arg Ser Gly Leu Ala Gly Thr Ser Thr Arg Pro Val

625 630 635 640
Lys His Leu Val Phe Thr Gly Cys Val Lys Asn Met Pro Val Glu Met

645 650 655
Arg Gln Leu Ile Arg Arg Leu Leu Gln Glu Asp Pro His Lys Arg Leu

660 665 670
Leu Pro Thr Glu Ile Leu Arg Asp Pro Val Phe Gln Lys Leu Glu Glu

675 680 685
Gln Ser Arg Pro Pro Asp Ala Gln Ala

690 695

<210> 363

<211> 114

<212> PRT

<213> Toxoplasma gondii

<400> 363

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

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

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<210> 364

<211> 494

<212> PRT

<213> *Toxoplasma gondii*

<400> 364

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

           50           55           60
Leu Ser Asp Thr Ala Arg Ala Pro Gly Asp Arg Ser Asn Ala Gln Asn
65           70           75           80

```

Arg Gly Glu Lys Ser Asp Val Asn Leu His Ala Ser Val Val Val Pro
85 90 95

Arg Glu Thr Asp Asn His Gly Glu Phe Ser Val Thr Leu Tyr Pro Pro
100 105 110

Arg Pro Ala Glu Glu Asp Lys Gln Ser Met Glu Gln Ser Glu Arg Pro
115 120 125

Glu Ser Glu Ala Val Leu Gln Ala Lys Asp Asp Asp Glu Val Ser Glu
130 135 140

Asp Asn Ala Val Leu Ser Glu Arg Gln Glu Trp Gln Arg Ile Glu Thr
145 150 155 160

Val Gly Arg Glu Trp Leu Lys Ser Gln Val Ala Ala Phe Val Pro Pro
165 170 175

Asp Val Thr Pro Trp Pro Asp Pro Asp Ser Ser Val Asp Arg Leu Phe
180 185 190

Ala Lys Lys Phe Pro Ser Gly Lys Leu Leu Ile Leu Glu Pro Asp Glu
195 200 205

Pro Gly Gly Thr Tyr Glu Val Leu Tyr Arg Gly Pro Val Leu Gly Arg
210 215 220

Gly Thr Arg Gly Ile Ala Phe Lys Gly Thr Met Val Ala Thr Gly Glu
225 230 235 240

His Phe Ala Val Lys Leu Gln Phe Val Arg Lys Ser Leu Phe Arg Arg
245 250 255

Arg Ser Ser Leu Leu Arg Asp Leu Val Lys Tyr Leu Gln Gln Glu Phe
260 265 270

Ala Val Arg Asn Met Leu Val Ala Ala Tyr Gly Glu Glu Asn Val Gln
275 280 285

Lys Lys Gly Met Val Leu Pro Leu Thr Val Arg Arg Arg His Ala Phe
290 295 300

Gly Asp Phe Ile Thr Thr Pro Phe Ser Phe Thr Met Phe Trp Asn Phe
305 310 315 320

Leu Val Phe Tyr Pro Leu Met Lys Cys Thr Leu Gly Asn Leu Leu Val

325 330 335
 Gly Pro His Trp Pro Arg Glu Ala Arg Leu Phe Val Ala Lys Arg Leu
 340 345 350
 Ile Glu Ile Ala Ala Ala Leu Gln Arg Ala Gly Val Leu His Arg Asp
 355 360 365
 Ile Phe Glu Ser Lys Ile Leu Leu Gln Glu Gly Ser Gly Asp Ile Phe

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

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

 <210> 365
 <211> 346
 <212> PRT
 <213> Toxoplasma gondii

 <400> 365
 Met Arg Phe Pro Val Ala Ser Leu Phe Ala Ala Gly Trp Leu Gly Leu
 1 5 10 15
 Ala Val Ser Ala Glu Glu Pro Thr Trp Glu Ser Leu Glu Glu Arg Gly
 20 25 30
 Arg Glu Leu Val Lys Gln His Val Ser Ala Val Ser Gly Tyr Thr His
 35 40 45

Leu Phe Glu Arg Glu Leu His Met Val Asn Ala Ala Thr Ala Val Leu
 50 55 60

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

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

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

 Ser Leu Phe Val Leu Ser Asp Ala Met Gly Val Gly Gly Ala Lys Gln
 260 265 270
 Asp Thr Val Arg Leu Gly Asn Ile Ala His Ala Ile Tyr Thr Gly Lys
 275 280 285
 Tyr Pro Ser Asp Asp Leu Asp Lys Cys Asn Asp Asn Pro Asp Phe Pro

290 295 300
 Lys Ala Asp Asp Thr Asp Val Asn Asp Val Val Ile Arg Ala Ala Ile
 305 310 315 320

Met Arg Leu Leu Cys Cys Gly Glu Cys Pro Met Gln Lys Pro Ala Asp
 325 330 335

Met Val Val Ala Ser Pro Leu Phe Ser Ser
 340 345

<210> 366

<211> 1781

<212> PRT

<213> Toxoplasma gondii

<400> 366

Met Thr Gly Gly Ala Ala Ala Pro Arg Ser Ser Ser Gly Ala Ser Arg
 1 5 10 15
 Thr Pro Leu Ser Leu Arg Phe Ser Leu Thr Leu Leu Cys Ser Leu Val
 20 25 30

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

Ala Lys Gly Gly Pro Glu Glu Ser Glu Met Gln Asp Gln Ser Thr Thr
 100 105 110
 Asp Val Asp Phe Glu Thr Thr Pro Pro Val Ala Arg Asp Ala Lys Thr
 115 120 125
 Gln Ser Lys Arg Asp Ala Thr Thr Arg Gly Lys Lys Gly Lys Arg Ser
 130 135 140
 Arg Arg Lys Arg Gly Glu Lys Ser Lys Lys Gly Asn Arg Glu Ala Gly

145						150						155						160	
Ala	Lys	Gly	Asp	Ser	Glu	Ala	Ser	Leu	Thr	Glu	Gly	Glu	Ser	Lys	Ala				
					165					170					175				
Asp	Ile	Gly	Gly	Glu	Thr	Thr	Ala	Gln	Val	Glu	Arg	Asp	Ala	Thr	Thr				
					180					185					190				
Lys	Gly	Lys	Lys	Ser	Lys	Arg	Arg	Arg	Ser	Arg	Ser	Arg	Arg	Lys	Arg				
					195					200					205				
Gly	Glu	Lys	Ser	Lys	Lys	Gly	Asn	Arg	Glu	Ala	Gly	Ala	Lys	Gly	Asp				
					210					215					220				
Ser	Glu	Ala	Ser	Leu	Thr	Glu	Gly	Glu	Ser	Lys	Ala	Asp	Ile	Gly	Gly				
225					230					235					240				
Glu	Thr	Thr	Ala	Gln	Val	Glu	Arg	Asp	Ala	Thr	Arg	Lys	Gly	Lys	Lys				
					245					250					255				
Ser	Lys	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Arg	Lys	Arg	Gly	Glu	Lys	Ser				
					260					265					270				
Lys	Lys	Gly	Asn	Arg	Glu	Ala	Glu	Ala	Lys	Gly	Asp	Ser	Glu	Ala	Ser				
					275					280					285				
Leu	Thr	Glu	Gly	Glu	Ser	Lys	Ala	Asp	Ile	Gly	Gly	Glu	Thr	Thr	Ala				
290					295					300									
Gln	Val	Glu	Arg	Glu	Ala	Thr	Arg	Lys	Gly	Lys	Lys	Ser	Lys	Arg	Arg				
305					310					315					320				
Arg	Ser	Arg	Ser	Arg	Arg	Lys	Arg	Gly	Glu	Lys	Ser	Lys	Lys	Gly	Asn				
					325					330					335				
Arg	Glu	Ala	Glu	Ala	Lys	Gly	Asp	Ser	Glu	Ala	Ser	Leu	Thr	Glu	Gly				
					340					345					350				
Glu	Ser	Lys	Ala	Asp	Ile	Gly	Gly	Glu	Thr	Thr	Ala	Gln	Val	Glu	Arg				
355					360					365									
Asp	Ala	Thr	Arg	Lys	Gly	Lys	Lys	Ser	Lys	Arg	Arg	Arg	Ser	Arg	Ser				
370					375					380									
Arg	Arg	Lys	Arg	Gly	Glu	Lys	Ser	Lys	Lys	Gly	Asn	Arg	Glu	Ala	Glu				
385					390					395					400				

Ala Lys Gly Asp Ser Glu Ala Ser Leu Thr Glu Gly Glu Ser Lys Ala
405 410 415

Asp Ile Gly Gly Glu Thr Thr Ala Gln Val Glu Arg Asp Ala Thr Arg
420 425 430

Lys Gly Lys Lys Ser Lys Arg Arg Arg Ser Arg Ser Arg Arg Lys Arg
435 440 445

Gly Glu Lys Ser Lys Lys Gly Asn Arg Glu Ala Gly Ala Lys Gly Asp
450 455 460

Ser Glu Ala Ser Leu Thr Glu Gly Glu Ser Lys Ala Asp Ile Gly Gly
465 470 475 480

Glu Thr Thr Ala Gln Val Glu Arg Asp Pro Thr Arg Lys Gly Lys Lys
485 490 495

Ser Lys Arg Ser Arg Ser Arg Ser Arg Arg Lys Arg Gly Glu Lys Ser
500 505 510

Lys Lys Gly Asn Arg Glu Ala Glu Ala Lys Gly Asp Ser Glu Ala Ser
515 520 525

Leu Thr Glu Gly Glu Ser Lys Ala Asp Ile Gly Gly Glu Thr Thr Ala
530 535 540

Gln Val Glu Arg Asp Ala Thr Thr Lys Gly Lys Lys Ser Lys Arg Ser
545 550 555 560

Arg Ser Lys Gly Lys Arg Gly Glu Lys Ser Lys Glu Ala Asp Leu Gln
565 570 575

Glu Gly Ala Lys Gly Asp Ser Glu Ala Ser Leu Thr Glu Gly Glu Ser
580 585 590

Lys Ala Asp Ile Gly Gly Glu Thr Thr Ala Gln Val Glu Arg Asp Ala
595 600 605

Thr Thr Lys Gly Lys Lys Ser Lys Arg Ser Arg Ser Lys Gly Lys Arg
610 615 620

Gly Glu Lys Thr Met Lys Arg Asp Thr Gln Leu Ala Gly Lys Gly Glu
625 630 635 640

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

645 650 655
 Ser Leu Thr Glu Arg Glu Ala Val Ala Lys Asp Pro Lys Glu Gly Asn
 660 665 670

 Ala Asp Ala Ile Val Gly Thr Asp Ser Ile Glu Ala Arg Val Ala Val
 675 680 685
 Ser Ala Glu Arg Thr Glu Glu Gly Gly Lys Pro Ala Glu Ala Val Ser
 690 695 700
 Ala Ala Asp Ala Ser Lys Ser Ala Glu Gln Gly Arg Gln Lys Ser Thr
 705 710 715 720
 Lys Arg Gly Lys Lys Arg His Arg Arg Asn Arg Lys Arg Ser Lys Ser
 725 730 735

 Lys Lys Ser His Thr Gly Ser Ser Ala Pro Thr Thr Ala Gly Val Ser
 740 745 750
 Ala Pro Thr Gly Ser Leu Pro Leu Ser Ser Glu Thr Pro Thr Ser Ala
 755 760 765
 Glu Lys Glu Ala Thr Glu Phe Leu Leu Ser Ser Gly Phe Pro Ala Ile
 770 775 780
 Ser Ala Val Leu Ala Ser Arg Gly Ser Lys Leu Asp Ala Ala Lys Lys
 785 790 795 800

 Ser Lys Gly Ala Pro Gly Ser Thr Ser Val Val Asp Ser Glu Ser Val
 805 810 815
 Val Ser Gly Arg Glu Arg Gln Thr His Asp Glu Phe Leu Pro Pro Val
 820 825 830
 Asp Val Ala Ser Val Leu Arg Arg Ala Asn Thr Gly Asp Glu Ser Leu
 835 840 845
 Phe Asp Pro Asp Glu Ala Asp Asn Thr Ser Ala Ala Thr Lys Ala Phe
 850 855 860

 Glu Val Thr Asp Asp Glu Pro Lys Ala Glu Lys Pro Ser Glu Thr Glu
 865 870 875 880
 Thr Gln Leu Gln Glu Leu Met Ala Thr Val Pro Gln Leu Asp Glu Leu
 885 890 895

Leu Gln Lys Leu Pro Lys Leu Glu Glu Leu Ala Thr Arg Val Pro Gln

900 905 910

Leu Glu Arg Leu Ser Glu Ser Glu Ala Gln Arg Glu Ala Ser Asn Glu

915 920 925

His Gly Arg His Ser Ala Glu Leu Arg Ala Thr Gly Pro Ser Leu Asp

930 935 940

Glu Pro Met Arg Gly Pro Arg Phe Gly Ala Leu Gln Ala Thr Glu Ser

945 950 955 960

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

965 970 975

Phe Pro Pro Arg Leu Ser Leu Leu Phe Ala Gln Pro Ala Ser Gly Ala

980 985 990

Thr Gln Lys Lys Ala Thr Val Gly Glu Gln Thr Ser Pro Ala Asp Ser

995 1000 1005

Pro Gln Thr Lys Gly Ala Leu Pro Pro Thr Ala Glu Leu Pro Lys

1010 1015 1020

Glu Arg Ala Ala Ala Asn Ser Asn Val Glu Thr Thr Ala Lys Ser

1025 1030 1035

Gln Gly Asp Ser Glu Ala Glu Lys Leu Leu Lys Glu Leu Arg Glu

1040 1045 1050

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

1055 1060 1065

Thr Arg Gly Glu Thr Glu Ser Asp Asn Ser Arg Thr Arg Pro Glu

1070 1075 1080

Ser Asp Ile Lys Tyr Arg Gly Met Ser Gly Ser Phe Ser Gly Ser

1085 1090 1095

Gly Pro Ala Ser Ser Arg His Met Lys His Arg Val Ser Ile Arg

1100 1105 1110

Gly Ser Phe Gly Glu Ala Asp Val Val Leu Leu His Gln Lys Pro

1115 1120 1125

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

1130	1135	1140
Thr Ala Asp Asn Ser Val Ser Gly Pro Arg Arg Arg Gly Phe Gly		
1145	1150	1155
Pro Val Pro Arg Ser Ile Phe Gly Ser Ala Phe Ser Asp Leu Glu		
1160	1165	1170
Ala Glu Leu Gln Gly Asp Val Ala Glu Phe Gly Asp Ala Ala Gly		
1175	1180	1185
Ile Glu Glu Ser Phe Gly Phe Phe Gly Glu Arg Arg Gly Gly Gly		
1190	1195	1200
Asp Arg Ser Arg Arg Ser Arg Glu Arg Arg Ser Glu Asp Arg Ser		
1205	1210	1215
Arg Arg Arg Arg Lys Gly Ser Lys Gly His Arg Glu Ala Gly Ser		
1220	1225	1230
Ser Ala Ala Thr Pro Gly Ser Arg His Leu Arg Gln Val Asp Arg		
1235	1240	1245
Arg Ser Gly Leu Ala Arg Ala Glu Asp Val Asp Pro Glu Glu Ser		
1250	1255	1260
Ser Glu Glu Ser Arg Gly Ser Arg Glu Glu His Ser Met Lys Lys		
1265	1270	1275
Leu Pro Ala Arg Glu Arg Ser Ser Arg Ser Ala Gly Pro Ser Leu		
1280	1285	1290
Ser Arg Arg Arg Ser Arg Leu Asp His Glu Leu Glu Gln Arg Arg		
1295	1300	1305
Ala Lys Glu Ala Met Glu Ala Ala Glu Thr Phe Asp Glu Arg Gly		
1310	1315	1320
Gly Tyr Gly Ser Gly Gly His Asn Trp Leu Thr Pro Gly Pro Pro		
1325	1330	1335
Leu Val Val Ser Gly Glu Ser Trp Pro Arg Arg Gly Leu Leu Tyr		
1340	1345	1350
Pro Glu Pro Ala Leu Leu Leu Glu Asp Ser Arg Ala Val Gln Met		
1355	1360	1365

Met Glu Asn Ala Ala Lys Glu Leu Ala His Ser Arg Gln Thr Pro		
1370	1375	1380
Val Leu Pro Gly Asp Arg Gly Arg Val Ala Ala Ala Gly Gly Ala		
1385	1390	1395
Phe Glu Arg Leu Phe Pro Arg Gly Ala Leu Phe Thr Leu Gln Pro		
1400	1405	1410
Thr His Gly Gln Pro Phe Glu Pro Lys Thr Leu Lys Arg Gly Arg		
1415	1420	1425
Phe Leu Lys Ala Gly Gly Gly Thr Leu Leu Phe Glu Val Trp Glu		
1430	1435	1440
Gly Arg Thr Arg Trp Ala Leu Arg Leu His Leu Thr Glu Leu Ser		
1445	1450	1455
Glu Arg Glu Arg Thr Gly Leu Val Ser Arg Phe Pro Val Asp Arg		
1460	1465	1470
Val Ser Gly Ala Gly Val Ser Ala Trp Gln Arg Thr Ala Asp Gly		
1475	1480	1485
Val Cys Ala Glu Ala Glu Glu Leu Glu Leu His Ala Val Arg Ile		
1490	1495	1500
Leu Met Gln Gln Asn Glu Gln Pro Arg Asp Leu Phe Cys Arg Glu		
1505	1510	1515
Arg Ile Ala Leu Pro Val Ala Val Gly Glu Val Ser Ser Leu Pro		
1520	1525	1530
Lys Val Thr Gln Leu Arg Asp Gly Glu His Val Thr Asn Ile Gly		
1535	1540	1545
Gly Leu Tyr Pro Leu Ala Ala Cys Asp Met Arg Glu Leu Ala Glu		
1550	1555	1560
Gln Tyr Val Met Pro Glu Glu Val Lys Leu Glu Ala Val Arg Gln		
1565	1570	1575
Met Val Ala Ala Val Gly Arg Leu His Ser Arg Gly Val Val His		
1580	1585	1590
Leu Asp Leu Lys Leu Glu His Phe Leu Leu Asp Asn His Gly Lys		

1595 1600 1605
Val Tyr Leu Gly Asp Leu Ser Thr Ser Glu Lys Ile Thr Gly Val
1610 1615 1620
Asn Val Glu Pro Thr Ser Cys Glu Phe Gly Ser Leu Glu Ser Leu
1625 1630 1635
Ser Pro Glu His Leu Ala Cys Trp Ala Arg Gln Gln Arg Lys Phe
1640 1645 1650

Thr Pro Ser Met Ala Thr Asp Ser Trp Ser Leu Gly Val Ala Ile
1655 1660 1665
Val Gln Leu Trp Cys Gly Glu Ala Pro Phe Arg Val Pro Asp Ala
1670 1675 1680
Leu Trp Ser Asn Gly Pro Val Ala Val Ala Gln Tyr Leu Asp Gln
1685 1690 1695
Leu Leu Arg Arg Thr Asp Gly Glu Ile Asp Phe Ser Gly Cys Pro
1700 1705 1710

Gly Gly Asp Ile Thr Asn Pro Glu Leu Lys Arg Ile Val Thr Gly
1715 1720 1725
Leu Leu Thr Tyr Asp Arg Val Lys Arg Trp Leu Pro Leu Asp Val
1730 1735 1740
Leu Phe Thr Ser Pro Leu Met Ile Asp Pro Ala Val Ala Arg Asn
1745 1750 1755
Ala Ser Ser Pro Ser Val Ser Pro Leu Thr Ser Gly Lys Arg Ser
1760 1765 1770

Ser Lys Asn Arg Lys Arg Asn Asn
1775 1780

<210> 367

<211> 538

<212> PRT

<213> Toxoplasma gondii

<400> 367

Met Ala Gly Pro Arg Ser Pro Leu Arg Phe Val Leu Leu Leu Ser Leu

1 5 10 15

Leu Ala Leu Lys Val Phe Val Asp Ser Pro Ser Val Leu Pro Ala Leu
 20 25 30
 Ala Gly Glu Ser Ala Ala Asp Leu Ser Thr Ser Ile Asp Asp Asp Asp
 35 40 45

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

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

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

 Glu Val Lys Lys Ala Cys Leu Ser Leu Asp Ala Glu Ile Ile Arg Lys
 245 250 255
 Leu Gly Pro Lys His Val Ala Gly Ser Thr Gly Ile Ile Val Ala Ile

260	265	270
Glu Arg Leu Ser Ala Pro Val Val Glu Asn Val Val Gly Arg Glu Ile		
275	280	285
Val Pro Arg Ala His Glu Glu Thr Phe Val Pro Leu Glu Lys Leu Ile		
290	295	300
Gln Glu Glu Glu Glu Ala Glu His Pro Glu Leu Val Gly Arg Tyr Pro		
305	310	315
Arg Val Pro Asp Val Gln Gln Lys Thr Ile Pro Ala Gly Ser Phe Leu		
325	330	335
Val Thr Ala Ile Asn Ile Gly Asp Ser Arg Ala Thr Leu Ile His Ser		
340	345	350
Asp Gly Gly Leu Thr Arg Leu Ser Lys Asp His Lys Pro Asn His Pro		
355	360	365
Thr Glu Ala Ser Arg Ile Glu Lys Ala Gly Gly Ser Val Glu Thr Phe		
370	375	380
Asp Val Pro Arg Val Asp Gly Val Leu Ala Leu Ser Arg Ala Phe Gly		
385	390	395
Asp Ser Asp Phe Lys Met Asn Pro Asn Leu Pro Pro Glu Glu Gln Lys		
405	410	415
Val Ile Ala Val Pro Asp Val Arg Gln Phe Tyr Ala Leu Ser Ser Asp		
420	425	430
Leu Leu Leu Leu Ala Cys Asp Gly Val Tyr Glu Pro Ser Gly Met Asp		
435	440	445
Trp Ala Tyr Val Arg Asp Leu Thr Val Ala Glu Met Gln Arg Ser Lys		
450	455	460
Gly Asp Leu Glu Glu Val Ala Ala Arg Val Met Asp Tyr Ala Tyr Asp		
465	470	475
Met Asn Ser Gln Asp Asn Ile Ser Val Met Leu Val Ala Phe His Asn		
485	490	495
Gln Glu Val Glu His Pro Thr Ala Val Tyr Lys Val Val Ser Gly Gln		
500	505	510

Gly Val Val Leu Ser Glu Thr Arg Arg Pro Ser Asp Ala Glu Asp Asp
515 520 525

Ser Val Glu Gly Asp Thr Val Ser Leu Phe
530 535

<210> 368
<211> 479
<212> PRT
<213> Toxoplasma gondii
<400> 368

Met Phe Ser Cys Glu Cys His Phe Cys Cys Ala Asn Pro Asn Lys Ser
1 5 10 15

Leu Pro Val Ile Glu Gln Val Thr Ala Tyr Thr Cys Ala Lys Ala Thr
20 25 30

Ala Ala Met Ala Ser Leu Arg Val Leu Ala Leu Ala Cys Leu Pro Leu
35 40 45

Phe Ala Val Leu His Ala Asp Ala Lys Thr Leu Leu Gly Lys Val Lys
50 55 60

Arg Ala Thr Gly Met Gly Val Gly Glu Gly Pro Ser Val Ala Lys Lys
65 70 75 80

Pro Lys Tyr Thr Ala Thr Val Pro Gly Phe Thr Pro Pro Ser Gly Asp
85 90 95

Gln Arg Met Asn Glu Phe Met Ala Val Asp Thr Ser Gly Glu Phe Met
100 105 110

Arg His Leu Tyr Ile Glu Glu Gly Arg Thr Val Cys Ala Ser Ala Thr
115 120 125

Ser Arg Asn Arg Arg Pro Thr Ser Glu Ser Pro His Ser Asp Asp Val
130 135 140

Val Val Val Glu Gly Met Leu Arg Gly Arg Pro Glu Thr Arg Val His
145 150 155 160

Ala Met Phe Asp Gly Phe Gln Gly Arg His Ser Ala Met Trp Leu Ala
165 170 175

Gln Asn Val Met Asn Tyr Leu Asn Asp Leu Arg Asp Val Asn Glu Glu

180	185	190	
Glu Ile Thr Arg Gln Phe Glu Arg Met Asp Gly Asp Leu Arg Ala Ala			
195	200	205	
Asn Leu Pro Gly Gly Ser Ser Ala Leu Ile Ile Phe Val Arg Tyr Glu			
210	215	220	
Lys Lys Pro Thr Glu Ala Arg Val Val Gly Arg Gln Ile Val Pro Glu			
225	230	235	240
Gly Ala Lys Glu Phe Thr Ser Val Ala Glu Ala Leu Gly Gly Pro Leu			
245	250	255	
Met Pro Val Val Ala Met Asn Phe Arg Arg Asp Pro Arg Ala Ala Lys			
260	265	270	
Gly Ile Tyr Thr Ile His Val Ala Ser Leu Gly Asn Ser Arg Cys Val			
275	280	285	
Leu Lys Ser Gly Arg Thr Ala Ile His Leu Ser Thr Pro His Thr Ala			
290	295	300	
Ser Ser His Lys Glu Arg His Arg Val Gln Ala Ala Gly Gly Val Phe			
305	310	315	320
Thr Thr Val Asn Gly Glu Leu Leu Leu Gly Gly Val Val Pro Met Thr			
325	330	335	
Arg Ala Phe Gly Ser Phe Asp Phe Lys Lys Gly Gly Gln Gly Lys Leu			
340	345	350	
Gln Gln Asp Leu Val Ser Ala Val Pro Asp Val Thr Thr Phe Phe Ala			
355	360	365	
Tyr Pro Gly Asp Asp Ile Val Ala Gly Thr Ala Gly Ala Phe Ala His			
370	375	380	
Phe Arg Ser His Ala Ala Ile Ala Ala Ala Ile Ala Leu Tyr Pro Val			
385	390	395	400
Ser Pro Glu Thr Val Leu Asp Ala Ala Lys Ala Met Val Val Asn Ala			
405	410	415	
Lys Arg Arg Lys Val Thr Lys Asn Ile Ser Thr Phe Val Arg His Leu			
420	425	430	

Pro Glu Ser Arg Thr Arg Ser Gln Lys Met Leu Glu Gly Thr Ser Gly
435 440 445
Glu Asn Gly Glu Glu Asp Phe Ser Ile Asp Arg Thr Asn Glu Leu Thr
450 455 460

Gln Ala Leu Gln Ala Gly Phe Phe Ser Phe Leu Leu Tyr Tyr Pro
465 470 475

<210> 369
<211> 320
<212> PRT
<213> Toxoplasma gondii
<400> 369

Met Thr Gly Gly Ala Ala Ala Pro Arg Ser Ser Ser Gly Ala Ser Arg
1 5 10 15
Thr Pro Leu Ser Leu Arg Phe Ser Leu Thr Leu Leu Cys Ser Leu Val
20 25 30
Ala Leu Leu Thr Leu Ser Val Ser Leu Ser Thr Pro Ala Ser His Thr
35 40 45
Tyr Val Phe Ala Val Val Ala Ala Asp Thr Gly Val Ser Ser Val Pro
50 55 60
Gly His Glu Arg Gly Ala Ser Lys Ala Gly Pro Asp Ala Ala Val Lys
65 70 75 80
Ser Lys Lys Arg Arg Glu Arg Ser Lys Lys Ser Asp Gly Asn Val Ser
85 90 95
Ala Lys Gly Gly Pro Glu Glu Ser Glu Met Gln Asp Gln Ser Thr Thr
100 105 110
Asp Val Asp Phe Glu Thr Thr Pro Pro Val Ala Arg Asp Ala Met Thr
115 120 125
Gln Ser Lys Arg Asp Ala Thr Thr Arg Gly Lys Lys Ser Lys Ser Lys
130 135 140
Arg Ser Arg Ser Arg Arg Lys Arg Gly Glu Lys Ser Lys Lys Gly Asn
145 150 155 160

Arg Glu Ala Gly Ala Lys Gly Asp Ser Glu Ala Ser Leu Thr Glu Gly

165 170 175

Glu Ser Lys Ala Asp Ile Gly Gly Glu Thr Thr Ala Gln Val Glu Arg

180 185 190

Asp Ala Thr Thr Lys Gly Lys Lys Ser Lys Arg Ser Arg Ser Arg Ser

195 200 205

Arg Arg Lys Arg Gly Glu Lys Ser Lys Lys Gly Asn Arg Glu Ala Gly

210 215 220

Ala Lys Gly Asp Ser Glu Ala Ser Leu Thr Glu Gly Glu Ser Lys Ala

225 230 235 240

Asp Ile Gly Gly Glu Thr Thr Ala Gln Val Glu Arg Asp Ala Thr Thr

245 250 255

Lys Gly Lys Lys Ser Lys Arg Arg Arg Ser Arg Ser Arg Arg Lys Arg

260 265 270

Gly Glu Lys Ser Lys Lys Gly Asn Arg Glu Ala Gly Ala Lys Gly Asp

275 280 285

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

290 295 300

Glu Thr Thr Ala Gln Val Glu Arg Asp Ala Thr Thr Lys Gly Lys Lys

305 310 315 320

<210> 370

<211> 1320

<212> PRT

<213> Toxoplasma gondii

<400> 370

Gly Ala Lys Gly Asp Ser Glu Ala Ser Leu Thr Glu Gly Glu Ser Lys

1 5 10 15

Ala Asp Ile Gly Gly Glu Thr Thr Ala Gln Val Glu Arg Asp Ala Thr

20 25 30

Thr Lys Gly Lys Asn Ser Lys Arg Ser Arg Ser Lys Gly Lys Arg Gly

35 40 45

Glu Lys Ser Lys Glu Ala Asp Leu Gln Ala Gly Ala Lys Gly Asp Ser
 50 55 60
 Glu Ala Ser Leu Thr Glu Gly Glu Ser Lys Ala Asp Ile Gly Gly Glu
 65 70 75 80
 Thr Thr Ala Gln Val Glu Arg Asp Ala Thr Thr Lys Gly Lys Lys Ser
 85 90 95

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

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

 Val Ala Val Ser Ala Glu Arg Thr Glu Glu Gly Gly Lys Pro Ala Glu
 225 230 235 240
 Ala Val Ser Val Ala Asp Ala Ser Lys Ser Ala Glu Gln Gly Arg Gln
 245 250 255
 Lys Ser Thr Lys Arg Gly Lys Lys Arg His Arg Arg Asn Arg Lys Arg
 260 265 270
 Ser Lys Ser Lys Lys Ser His Thr Gly Ser Ser Ala Pro Thr Thr Ala
 275 280 285

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

290	295	300	
Thr Ser Ala Glu Lys Glu Ala Thr Glu Phe Leu Leu Ser Ser Gly Phe			
305	310	315	320
Pro Ala Ile Ser Ala Val Leu Ala Ser Arg Gly Ser Lys Leu Asp Ala			
	325	330	335
Ala Lys Lys Ser Lys Gly Ala Pro Gly Ser Thr Ser Val Val Asp Ser			
	340	345	350
Glu Ser Val Val Ser Gly Arg Glu Arg Gln Thr His Asp Glu Phe Leu			
	355	360	365
Pro Pro Val Asp Val Ala Ser Val Leu Arg Arg Ala Asn Thr Gly Asp			
	370	375	380
Glu Ser Leu Phe Asp Pro Asp Glu Ala Asp Asn Thr Ser Ala Ala Thr			
385	390	395	400
Lys Ala Phe Glu Val Thr Asp Asp Glu Pro Lys Ala Glu Lys Pro Ser			
	405	410	415
Glu Thr Glu Thr Gln Leu Gln Glu Leu Met Ala Thr Val Pro Gln Leu			
	420	425	430
Asp Glu Leu Leu Gln Lys Leu Pro Lys Leu Glu Glu Leu Ala Thr Arg			
	435	440	445
Val Pro Gln Leu Glu Arg Leu Ser Glu Ser Glu Ala Gln Arg Glu Ala			
	450	455	460
Ser Asn Glu His Gly Arg His Ser Ala Glu Leu Arg Ala Thr Gly Pro			
465	470	475	480
Ser Leu Asp Glu Pro Met Arg Gly Pro Arg Phe Gly Ala Leu Gln Ala			
	485	490	495
Thr Glu Ser Lys Pro Val Pro Thr Ser Leu Ala Asn Val Leu Ile Ser			
	500	505	510
Ser Leu Val Phe Pro Pro Arg Leu Ser Leu Leu Phe Ala Gln Pro Ala			
	515	520	525
Ser Gly Ala Thr Gln Lys Lys Ala Thr Val Gly Glu Gln Thr Ser Pro			
	530	535	540

Ala	Asp	Ser	Pro	Gln	Thr	Lys	Gly	Ala	Leu	Pro	Pro	Thr	Ala	Glu	Leu
545						550				555					560
Pro	Lys	Glu	Arg	Ala	Ala	Ala	Asn	Ser	Asn	Val	Glu	Thr	Thr	Ala	Lys
				565					570						575
Ser	Gln	Gly	Asp	Ser	Glu	Ala	Glu	Lys	Leu	Leu	Lys	Glu	Leu	Arg	Glu
			580					585						590	
Leu	Glu	Lys	Gly	Met	Gln	Ser	Gln	Thr	Val	Gly	Asp	Ile	Ser	Ser	Thr
		595					600					605			
Arg	Gly	Glu	Thr	Glu	Ser	Asp	Asn	Ser	Arg	Thr	Arg	Pro	Glu	Ser	Asp
	610					615					620				
Ile	Lys	Tyr	Arg	Gly	Met	Ser	Gly	Ser	Phe	Ser	Gly	Ser	Gly	Pro	Ala
625					630				635						640
Ser	Ser	Arg	His	Met	Lys	His	Arg	Val	Ser	Ile	Arg	Gly	Ser	Phe	Gly
			645					650						655	
Glu	Ala	Asp	Val	Val	Leu	Leu	His	Gln	Lys	Pro	Gln	Arg	Gly	Asn	Glu
		660						665					670		
Thr	Ala	Glu	Arg	Thr	Ser	Ser	Phe	Ser	Ala	Thr	Ala	Asp	Asn	Ser	Val
	675						680					685			
Ser	Gly	Pro	Arg	Arg	Arg	Gly	Phe	Gly	Pro	Val	Pro	Arg	Ser	Ile	Phe
	690					695					700				
Gly	Ser	Ala	Phe	Ser	Asp	Leu	Glu	Ala	Glu	Leu	Gln	Gly	Asp	Val	Ala
705					710				715						720
Glu	Phe	Gly	Asp	Ala	Ala	Gly	Ile	Glu	Glu	Ser	Phe	Gly	Phe	Phe	Gly
			725					730					735		
Glu	Arg	Arg	Gly	Gly	Gly	Asp	Arg	Ser	Arg	Arg	Ser	Arg	Glu	Arg	Arg
		740						745				750			
Ser	Glu	Asp	Arg	Ser	Arg	Arg	Arg	Arg	Lys	Gly	Ser	Lys	Gly	His	Arg
		755					760					765			
Glu	Ala	Gly	Ser	Ser	Ala	Ala	Ala	Pro	Gly	Ser	Arg	His	Leu	Arg	Gln
	770					775					780				
Val	Asp	Arg	Arg	Ser	Gly	Leu	Ala	Arg	Ala	Glu	Asp	Val	Asp	Pro	Gly

785 790 795 800

Glu Ser Ser Glu Glu Ser Arg Gly Ser Arg Glu Glu His Ser Met Lys

805 810 815

Lys Leu Pro Ala Arg Glu Arg Ser Ser Arg Ser Ala Gly Pro Ser Leu

820 825 830

Ser Arg Arg Arg Ser Arg Leu Asp His Glu Leu Glu Gln Arg Arg Ala

835 840 845

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

850 855 860

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

865 870 875 880

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

885 890 895

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

900 905 910

Lys Glu Leu Ala His Ser Arg Gln Thr Pro Val Leu Pro Gly Asp Arg

915 920 925

Gly Arg Val Ala Ala Ala Gly Gly Ala Phe Glu Arg Leu Phe Pro Arg

930 935 940

Gly Ala Leu Phe Thr Leu Gln Pro Thr His Gly Gln Pro Phe Glu Pro

945 950 955 960

Lys Thr Leu Lys Arg Gly Arg Phe Leu Lys Ala Gly Gly Gly Thr Leu

965 970 975

Leu Phe Glu Val Trp Glu Gly Arg Thr Arg Trp Ala Leu Arg Leu His

980 985 990

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

995 1000 1005

Pro Val Asp Arg Val Ser Gly Ala Gly Val Ser Ala Trp Gln Arg

1010 1015 1020

Thr Ala Asp Gly Val Cys Ala Glu Ala Glu Glu Leu Glu Leu His

1025 1030 1035

Ala Val	Arg Ile Leu Met Gln	Gln Asn Glu Gln Pro	Arg Asp Leu
1040	1045	1050	
Phe Cys	Arg Glu Arg Ile Ala	Leu Pro Val Ala Val	Gly Glu Val
1055	1060	1065	
Ser Ser	Leu Pro Lys Val Thr	Gln Leu Arg Asp Gly	Glu His Val
1070	1075	1080	
Thr Asn	Ile Gly Gly Leu Tyr	Pro Leu Ala Ala Cys	Asp Met Arg
1085	1090	1095	
Glu Leu	Ala Glu Gln Tyr Val	Met Pro Glu Glu Val	Lys Leu Glu
1100	1105	1110	
Ala Val	Arg Gln Met Val Ala	Ala Val Gly Arg Leu	His Ser Arg
1115	1120	1125	
Gly Val	Val His Leu Asp Leu	Lys Leu Glu His Phe	Leu Leu Asp
1130	1135	1140	
Asn His	Gly Lys Val Tyr Leu	Gly Asp Leu Ser Thr	Ser Glu Lys
1145	1150	1155	
Ile Thr	Gly Val Asn Val Glu	Pro Thr Ser Cys Glu	Phe Gly Ser
1160	1165	1170	
Leu Glu	Ser Leu Ser Pro Glu	His Leu Ala Cys Trp	Ala Arg Gln
1175	1180	1185	
Gln Arg	Lys Phe Thr Pro Ser	Met Ala Thr Asp Ser	Trp Ser Leu
1190	1195	1200	
Gly Val	Ala Ile Val Gln Leu	Trp Cys Gly Glu Ala	Pro Phe Arg
1205	1210	1215	
Val Pro	Asp Ala Leu Trp Ser	Asn Gly Pro Val Ala	Val Ala Gln
1220	1225	1230	
Tyr Leu	Asp Gln Leu Leu Arg	Arg Thr Asp Gly Glu	Ile Asp Phe
1235	1240	1245	
Ser Gly	Cys Pro Gly Gly Asp	Ile Thr Asn Pro Glu	Leu Lys Arg
1250	1255	1260	
Ile Val	Thr Gly Leu Leu Thr	Tyr Asp Arg Val Lys	Arg Trp Leu

1265 1270 1275
 Pro Leu Asp Val Leu Phe Thr Ser Pro Leu Met Ile Asp Pro Ala
 1280 1285 1290

 Val Ala Arg Asn Ala Ser Ser Pro Ser Ile Ser Pro Leu Thr Pro
 1295 1300 1305
 Gly Lys Arg Ser Ser Lys Asn Arg Lys Arg Asn Asn
 1310 1315 1320
 <210> 371
 <211> 219
 <212> PRT
 <213> Toxoplasma gondii
 <400> 371
 Met Ala Ala Lys Asp Glu Tyr Tyr Asp Tyr Leu Tyr Lys Ile Val Leu
 1 5 10 15
 Ile Gly Asp Ser Gly Val Gly Lys Ser Asn Met Leu Ser Arg Phe Thr

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

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

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

<210> 372

<211> 332

<212> PRT

<213> *Toxoplasma gondii*

<400> 372

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

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

115 120 125
 Leu Ala Gln His Phe Arg Arg Leu Arg Val Leu Phe Gly Arg Leu Met
 130 135 140

Pro Arg Trp Gly Phe Gly Phe Gly Arg His Val Gly Arg Trp Trp Pro
145 150 155 160
Arg Arg Trp Pro Asp Pro Leu Phe Pro Cys Met Glu Pro Gly Asp Glu
165 170 175
Phe Ile Arg Ser Arg Leu Ser Gln Thr Glu Tyr Arg Thr Arg Phe Tyr
180 185 190
Arg Arg Gly Met Val Glu Gly Tyr Glu Val Glu Val Lys Ala Val Thr
195 200 205
Ala Ala Ile Trp Pro Gln Asn Thr Ala Arg Glu Val Ala Ser Leu Leu
210 215 220
Asp Arg Arg Lys Arg Thr Leu Arg Val Val Gly Ala Phe Gly Arg Ser
225 230 235 240
Val Arg Ser Val Leu Tyr Leu Ala Gln Asp Val Glu Ser Gln Glu Arg
245 250 255
Met Ala Ile Glu Val Phe Thr Leu Thr Ser Gly Asn Thr Val Ser Asp
260 265 270
Leu Ala Arg Val His Asp Asn Leu Phe Ala Met Thr Gly Leu Val Ser
275 280 285
Glu Ser Pro Gln Gln Ala Arg Asp Ile Cys Arg Leu Leu Leu Pro Thr
290 295 300
Asp Ala Val Thr Val Pro Thr Gln Pro Pro Phe Glu Glu Leu Asn Pro
305 310 315 320
Gly Gln Ser Asn Tyr Pro Val Ala Asn Tyr Ser Ser
325 330
<210> 373
<211> 222
<212> PRT
<213> Toxoplasma gondii
<400> 373
Met Phe Pro Arg Val Ala Leu Phe Pro Val Leu Thr Cys Asp Leu Phe
1 5 10 15
Leu Val Gly Arg Ser Arg Leu Ser Arg Ala Ala Lys Leu His Leu Thr

20 25 30
Arg Gln Leu Val Val Ser Val Ala Trp Leu His Arg His Gly Val Ala

35 40 45
His Asn Asp Leu Lys Pro Glu Asn Val Phe Leu Ser Glu Glu Gly Lys

50 55 60
Ala Val Ile Gly Asp Phe Gly Phe Ala Ala Glu Val Gly Thr Ser Thr

65 70 75 80
Glu Leu Arg Ser Thr Pro Ala Phe Leu Asp Pro Gln Thr Ala Glu Glu

85 90 95
Tyr Leu Gln Arg Lys Thr Glu Thr Val Val Thr Glu Glu Arg Asp Ala

100 105 110
Trp Ala Leu Gly Thr Ile Ile Phe Val Ile Trp Cys Gly Ser Tyr Pro

115 120 125
Phe Phe Ser Phe Glu Glu Ala Val Leu Pro Pro Ala Val Leu Trp Gln

130 135 140
Asn Val Val Phe Met Ser Lys Thr Thr Arg Pro Ala Pro Pro Leu Gln

145 150 155 160
His Cys Lys Gly Met Pro Ser Pro Val Lys Ala Leu Ile Thr Gly Phe

165 170 175
Leu Gln Trp Asn Ser Asp Asp Arg Arg Arg Pro Arg Asp Val Val Glu

180 185 190
Gly Phe Leu Ala Ala Thr Ala Ser Glu Pro Ala Thr Ser Ser Ala Thr

195 200 205
Ala Ala Glu Gly Ser Val Arg Pro Arg Ala Ser Arg Ser Gln

210 215 220
<210> 374

<211> 456
<212> PRT

<213> Toxoplasma gondii

<400> 374
Met Arg Arg Leu Leu Leu Ser Pro Val Gly Phe Val Ile Val Leu Ala

1	5	10	15
Thr	Leu	Leu	Glu
Cys	His	Pro	Pro
Asp	Arg	Cys	Val
Ala	His	His	Gly
20	25	30	
Ser	Ser	Thr	Asp
Glu	Ser	Asn	Val
Trp	Ser	Pro	Arg
Gly	Ala	Gln	Phe
35	40	45	
Val	Pro	Gly	Ala
Ser	Glu	Ala	Ala
Val	Lys	Asn	Gln
Val	Gly	Ile	Pro
50	55	60	
Asp	Ser	Ala	Leu
Leu	Trp	Pro	Ser
Gln	Asp	Ala	Thr
Glu	Thr	Gly	Leu
65	70	75	80
Arg	Pro	Thr	Glu
Gln	Val	Glu	Ala
Arg	Ser	Ser	Phe
Pro	Ala	Ala	Lys
85	90	95	
Gln	Tyr	Leu	Ser
Glu	Ala	Ala	Pro
Ala	Arg	Gly	Asp
Leu	Pro	Pro	Arg
100	105	110	
Ala	Thr	Gly	Leu
Leu	Arg	Arg	Arg
Gly	Ala	Arg	Val
Arg	Thr	Val	Lys
115	120	125	
Ala	His	Glu	Ile
Val	Val	Glu	Thr
Pro	Lys	Thr	Tyr
Gly	Trp	Asp	His
130	135	140	
Arg	Val	Val	Asp
Ser	Glu	Glu	Gln
Thr	Thr	Val	Pro
Val	Ala	Asp	Ser
145	150	155	160
Ser	Gly	Phe	Ile
Gln	Ile	Pro	Ser
Ser	Arg	Ala	Thr
Pro	Thr	Thr	Leu
165	170	175	
Asn	Ala	Pro	Ile
Asp	Leu	Gln	Gly
Arg	Arg	Asp	Ile
Arg	Asn	Ile	Val
180	185	190	
Arg	Asn	Arg	Pro
Pro	Ala	Asp	Ser
Asp	Leu	Ser	Pro
Ser	Glu	Ile	Ala
195	200	205	
Ala	Lys	Asn	Gly
Phe	Glu	Arg	Arg
Phe	Val	Gln	Gly
Leu	Gln	Leu	Lys
210	215	220	
Val	Glu	Ser	Leu
Phe	Ser	Gly	Gly
Val	Phe	Thr	Leu
Thr	Gly	Pro	Ala
225	230	235	240
Gln	Phe	Leu	Gly
Ile	Gly	Ser	Thr
Ala	Ile	Val	Tyr
Ser	Leu	Asn	Lys
245	250	255	

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

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

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

Glu Thr Val Val Thr Glu Glu Arg
450 455

<210> 375

<211> 351

<212> PRT

<213> Toxoplasma gondii

<400> 375

Val Arg Gly Leu Gln Leu Lys Val Glu Ser Leu Phe Ser Gly Gly Val

1	5	10	15
Phe Thr Leu Thr Gly Pro Ala Gln Phe Leu Gly Ile Gly Ser Thr Ala			
	20	25	30
Ile Val Tyr Ser Leu Asn Lys Val Gln Ala Asp Thr Ala Ser Ala Pro			
	35	40	45
Glu Arg Val Ala Val Lys Ile Ser Ile Asn Asn Leu Gln Arg Leu Arg			
	50	55	60
Ser Leu Ser Val Phe Asp Arg Gln Glu Leu Leu Asp Lys Thr Pro Glu			
65	70	75	80
Arg Phe Val Ser Ser Glu Gly Ala Val Arg Asn Leu Leu Pro Gly Val			
	85	90	95
Thr Pro Glu Thr Ala Leu Glu His Gly Ile Leu Leu Pro Leu Asp Ile			
	100	105	110
Cys Arg Val Thr Asn Leu Pro Ser Gly Phe Arg Ala Gly Pro Asp Tyr			
	115	120	125
Lys Met Phe Pro Arg Val Ala Leu Phe Pro Val Leu Thr Cys Asp Leu			
	130	135	140
Phe Leu Val Gly Arg Ser Arg Leu Ser Arg Ala Ala Lys Leu His Leu			
145	150	155	160
Thr Arg Gln Leu Val Val Ser Val Ala Trp Leu His Arg His Gly Val			
	165	170	175
Ala His Asn Asp Leu Lys Leu Glu Asn Val Phe Leu Ser Glu Glu Gly			
	180	185	190
Lys Ala Val Ile Gly Asp Phe Gly Phe Ala Ala Glu Val Gly Thr Ser			
	195	200	205
Thr Lys Leu Arg Ser Thr Pro Ala Phe Leu Asp Pro Gln Thr Ala Glu			
	210	215	220
Glu Tyr Leu Gln Arg Lys Thr Glu Thr Val Val Thr Glu Glu Arg Asp			
225	230	235	240
Ala Trp Ala Leu Gly Thr Ile Ile Phe Val Ile Trp Cys Gly Ser Tyr			
	245	250	255

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

Phe Leu Gln Trp Asn Ser Asp Asp Arg Arg Arg Pro Arg Asp Val Val
305 310 315 320
Glu Gly Phe Leu Ala Ala Thr Ala Ser Glu Pro Ala Thr Ser Ser Ala
325 330 335
Thr Ala Ala Glu Gly Ser Val Arg Pro Arg Ala Ser Arg Ser Gln
340 345 350

<210> 376

<211> 110

<212> PRT

<213> Toxoplasma gondii

<400> 376

Met Gln Ser Thr Thr Ser Leu Ala Thr Pro Ala Asp Leu Asn Ala Pro

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

65 70 75 80
Gly Trp Gly Ser Thr Ala Ile Val Phe Gly Leu His Arg Val Lys Ala
85 90 95
Gly Gly Ala Ser Ala Pro Gln Gln Leu Ala Ala Lys Ile Asn
100 105 110
<210> 377

<211> 354

<212> PRT

<213> Toxoplasma gondii

<400> 377

Gly Trp Asp His Arg Val Val Asp Ser Glu Lys Gln Thr Thr Ala Pro

1 5 10 15

Val Ala Asp Ser Ser Gly Phe Ile Gln Ile Pro Ser Ser Arg Ala Thr

20 25 30

Pro Thr Thr Leu Asn Ala Pro Ile Asp Leu Gln Gly Arg Arg Asp Ile

35 40 45

Arg Asn Ile Val Arg Asn Arg Pro Pro Ala Asp Ser Asp Leu Ser Arg

50 55 60

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

65 70 75 80

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

85 90 95

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

100 105 110

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

115 120 125

Ala Val Lys Ile Ser Ile Asn Asn Leu Gln Arg Leu Arg Ser Leu Ser

130 135 140

Val Phe Asp Arg Gln Glu Leu Leu Asp Lys Thr Pro Glu Arg Phe Val

145 150 155 160

Ser Ser Glu Gly Ala Val Arg Asn Leu Leu Pro Gly Val Thr Pro Glu

165 170 175

Thr Ala Leu Glu His Gly Ile Leu Leu Pro Leu Asp Ile Cys Arg Val

180 185 190

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

195 200 205

Pro Arg Val Ala Leu Phe Pro Val Leu Thr Cys Asp Leu Phe Leu Val

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

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

Ser Phe Glu Glu Ala Val Leu Pro Pro Ala Val Leu Trp Gln Asn Val
 340 345 350
 Val Phe

<210> 378

<211> 538

<212> PRT

<213> Toxoplasma gondii

<400> 378

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

35 40 45
 Thr Ala Glu Glu Arg Gly Ile Gly Asp Ile Ser Asp Tyr Pro His Ser
 50 55 60

Val	Val	Asp	Asp	Ala	Ala	Asp	Ile	Ser	Gly	Gly	Thr	Val	Pro	Glu	Gly
65				70				75				80			
Pro	Gly	Ser	Pro	Ala	Ser	Thr	Ser	Gly	Ser	Gly	Gly	Val	Phe	Asn	Arg
85				90				95							
Leu	Phe	Ser	Arg	Phe	Arg	Gln	Val	Ser	Gly	Ser	Thr	Gln	Gly	Arg	Gly
100				105				110							
Val	Ala	Asp	Glu	Pro	Gln	Gln	Gly	Pro	Arg	Pro	Ser	Leu	Arg	Glu	Arg
115				120				125							
Leu	Ala	Gln	His	Phe	Arg	Arg	Leu	Arg	Val	Leu	Phe	Gly	Arg	Leu	Met
130				135				140							
Pro	Arg	Trp	Gly	Phe	Gly	Phe	Gly	Arg	His	Val	Gly	Arg	Trp	Trp	Pro
145				150				155				160			
Arg	Arg	Trp	Pro	Asp	Pro	Leu	Phe	Pro	Cys	Met	Glu	Pro	Gly	Asp	Glu
165				170				175							
Phe	Ile	Arg	Ser	Arg	Leu	Ser	Gln	Thr	Glu	Tyr	Arg	Thr	Arg	Phe	Tyr
180				185				190							
Arg	Arg	Gly	Met	Val	Glu	Gly	Tyr	Glu	Val	Glu	Val	Lys	Ala	Val	Thr
195				200				205							
Ala	Ala	Ile	Trp	Pro	Gln	Asn	Thr	Ala	Arg	Glu	Val	Ala	Ser	Leu	Leu
210				215				220							
Asp	Arg	Arg	Lys	Arg	Thr	Leu	Arg	Val	Val	Gly	Ala	Phe	Gly	Arg	Ser
225				230				235				240			
Val	Arg	Ser	Val	Leu	Tyr	Leu	Ala	Gln	Asp	Val	Glu	Thr	Gln	Glu	Arg
245				250				255							
Met	Ala	Ile	Glu	Val	Phe	Thr	Leu	Thr	Ser	Gly	Asn	Thr	Val	Ser	Asp
260				265				270							
Leu	Ala	Arg	Val	His	Asp	Asn	Leu	Phe	Ala	Met	Thr	Gly	Leu	Leu	Ser
275				280				285							
Glu	Ser	Pro	Gln	Gln	Ala	Arg	Asp	Ile	Cys	Arg	Leu	Leu	Leu	Pro	Thr
290				295				300							
Asp	Ala	Val	Thr	Val	Pro	Ser	Gln	Pro	Pro	Phe	Glu	Glu	Leu	Asn	Pro

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

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

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

 485 490 495
 Val Glu Met Leu Val Arg His Phe Leu Asn Phe Asn Thr Arg Lys Arg
 500 505 510
 Leu Leu Pro Leu Thr Ala Met Gly Thr Pro Glu Phe Arg Gln Leu Gln
 515 520 525
 Leu Asp Ile Ser Thr Ser Leu Ser Ser Lys
 530 535
 <210> 379
 <211> 538
 <212> PRT

<213> Toxoplasma gondii

<400> 379

Met Ala Thr Asp Ala Arg Arg Leu Ala Thr Gly Leu Val Leu Leu Thr

1 5 10 15
Cys Leu Val Trp Arg Ala Gly Ala Phe Gln Pro Ser Pro Pro Thr Ala

20 25 30
Arg Ala Asn Glu Leu Thr Ser Gly Ile Pro Gly Glu Ala Pro Glu Asn

35 40 45
Thr Ala Glu Glu Arg Gly Ile Gly Asp Ile Ser Asp Tyr Pro His Ser

50 55 60
Val Val Asp Asp Ala Ala Asp Ile Ser Gly Gly Thr Val Pro Glu Gly

65 70 75 80
Pro Gly Ser Pro Ala Ser Thr Ser Gly Ser Gly Gly Val Phe Asn Arg

85 90 95
Leu Phe Ser Arg Phe Arg Gln Val Ser Gly Ser Thr Gln Gly Arg Gly

100 105 110
Val Ala Asp Glu Pro Gln Gln Gly Pro Arg Pro Ser Leu Arg Glu Arg

115 120 125
Leu Ala Gln His Phe Arg Arg Leu Arg Val Leu Phe Gly Arg Leu Met

130 135 140
Pro Arg Trp Gly Phe Gly Phe Gly Arg His Val Gly Arg Trp Trp Pro

145 150 155 160
Arg Arg Trp Pro Asp Pro Leu Phe Pro Cys Met Glu Pro Gly Asp Glu

165 170 175
Phe Ile Arg Tyr Leu Val Arg Ala Lys Lys Asp Arg Ile Gly Phe Tyr

180 185 190
Arg Arg Gly Met Val Glu Gly Tyr Glu Val Glu Val Lys Ala Val Thr

195 200 205
Ala Ala Ile Trp Pro Gln Asn Thr Ala Arg Glu Val Ala Ser Leu Leu

210 215 220
Asp Arg Arg Lys Arg Thr Leu Arg Val Val Gly Ala Phe Gly Arg Ser

225 230 235 240
 Val Arg Ser Val Leu Tyr Leu Ala Gln Asp Val Glu Thr Gln Glu His
 245 250 255
 Ile Ala Ala Glu Val Phe Thr Leu Thr Gly Glu Ser Arg Gly Leu Asp

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

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

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

 450 455 460
 Thr Pro Arg Met Lys Arg Ser Gly Arg Arg Pro Ser Met Arg Val Pro
 465 470 475 480

Gly Leu Asp Val Leu Ser Val Glu Ala Cys Thr Pro Met Pro Asp Ala
485 490 495
Val Glu Met Leu Val Arg His Phe Leu Asn Phe Asn Thr Arg Lys Arg
500 505 510
Leu Leu Pro Leu Thr Ala Met Gly Thr Pro Glu Phe Arg Gln Leu Gln
515 520 525
Leu Asp Ile Ser Thr Ser Leu Ser Ser Lys
530 535
<210> 380
<211> 525
<212> PRT
<213> Toxoplasma gondii
<400> 380
Met Ser Ser Ser Arg Leu Val Leu Val Ser Lys Met Val Asp Ser Cys
1 5 10 15
Ala Arg Leu Ala Cys Phe Cys Ile Gly Leu Phe Phe Cys Leu Ala Val
20 25 30
Trp Gln His Gln Ala Gly His Ala Tyr Ser Ala Thr His His His Ala
35 40 45
Val Asn Ser Asp Asn Lys Ser Phe Asn Asp Ser Ala Pro His Trp Thr
50 55 60
Leu Asn Gln Val Leu Arg Asp Gly Thr Val Gln Ser Glu Ser Pro Ser
65 70 75 80
Tyr Leu Gln His Ser Ser Leu Pro Ser Asn Ile Ser Pro Ala Leu Glu
85 90 95
Leu Ala Ala Leu Gly Gln Asp Pro Val Arg Arg Arg Pro Gln Pro Val
100 105 110
Gln Val Ala Arg Thr Gly Thr Thr Thr Thr Gly Arg Val Gln Leu Gly
115 120 125
Arg Gln Val Ala Arg Val Thr Pro Glu Glu Leu Ala Thr Met Val Glu
130 135 140
Pro Ser Leu Lys Asp Leu Leu Asn Arg Ser Thr Leu Pro Gln Thr Pro

145 150 155 160
 Phe Val Ile Glu Thr Leu Arg Val Phe Ala Thr Pro Glu Gly Asp Thr

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

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

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

 355 360 365
 Asn Val Leu Val Gly Arg Asp Gly Gln Leu Phe Leu Gly Gly Phe Gln
 370 375 380
 His Val Arg Ala Lys Asp Gly Gly Ile Ser Cys Gly Lys Ile Pro Ser
 385 390 395 400

Val Thr Phe Thr Asp Pro Arg Leu Ala His Cys Ala Val Asn Asn Pro
405 410 415
Gly Ser Tyr Ala Ala Val Asn Pro Ala Val Asp Ala Trp Met Ala Gly
420 425 430
Met Met Leu Leu Arg Trp Phe Cys Gly Asp Val Phe Phe Asn Arg Arg
435 440 445
Ser Ser Leu Ala Glu Pro Arg Gln Ala Val Gln Val Leu Ala Gln Leu
450 455 460
Gln Ala Asp Phe Ile Ala Ala Asn Asp Tyr Met Val Ser Phe Pro Ala
465 470 475 480
Phe Thr Gln Trp Asp Arg Cys Arg His His Val Asn Glu Arg Phe Gln
485 490 495
Phe Ile Ile Gln Ser Leu Leu Asp Val Asn Pro Tyr Lys Arg Gly Ala
500 505 510
Pro Ser Ala Gln Leu Thr Ala Tyr Phe Pro Val Thr Gly
515 520 525
<210> 381
<211> 568
<212> PRT
<213> Toxoplasma gondii
<400> 381
Met Arg Arg Leu Leu Leu Ser Pro Val Gly Phe Val Ile Val Leu Ala
1 5 10 15
Thr Leu Leu Glu Cys His Pro Pro Asp Arg Cys Val Ala His His Gly
20 25 30
Ser Ser Thr Asp Glu Ser Asn Val Trp Ser Pro Arg Gly Ala Gln Phe
35 40 45
Val Pro Gly Ala Ser Glu Ala Ala Val Lys Asn Gln Val Gly Ile Pro
50 55 60
Asp Ser Ala Leu Leu Trp Pro Ser Gln Asp Ala Thr Glu Thr Gly Leu
65 70 75 80

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

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

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

 Ser Val Arg Asn Leu Asn Ser Leu Arg Asp Ala Ser Ala Ser Glu Arg
 275 280 285
 Gln Gln Val Leu Asp Gln Ala Pro Glu Arg Phe Val Ser Ser Glu Gly
 290 295 300
 Ala Val Arg Asn Leu Leu Pro Gly Val Thr Pro Glu Thr Ala Leu Glu
 305 310 315 320
 Gln Gly Ile Leu Leu Pro Leu Asp Ile Cys Arg Val Thr Asn Met Pro

325	330	335
Ser Asn Phe Arg Ala Gly Pro Asp Trp Asn Val Phe Pro Arg Val Ala		
340	345	350
Leu Phe Pro Val Leu Thr Cys Asp Leu Phe Leu Val Val Glu Ser Gly		
355	360	365
Leu Ser Arg Ala Ala Lys Leu His Leu Thr Arg Gln Leu Val Val Ser		
370	375	380
Val Ala Trp Leu His Arg Asn Gly Val Ala His Asn Asp Leu Lys Leu		
385	390	395
		400
Glu Asn Val Phe Leu Ser Glu Glu Gly Lys Ala Val Ile Gly Asp Phe		
405	410	415
Gly Phe Ala Ala Glu Val Gly Thr Ser Thr Arg Leu Gln Ser Thr Pro		
420	425	430
Thr Phe Leu Asp Pro Gln Thr Ala Glu Glu Ser Leu Gln Arg Lys Thr		
435	440	445
Glu Thr Val Val Thr Glu Glu Arg Asp Ala Trp Ala Leu Gly Thr Met		
450	455	460
Ile Phe Leu Ile Trp Cys Gly Ser Tyr Pro Phe Phe Ser Phe Glu Glu		
465	470	475
		480
Ala Val Leu Pro Leu Ala Ala Leu Leu Gln Asn Val Val Phe Lys Ser		
485	490	495
Lys Thr Thr Arg Pro Ala Pro Pro Leu Gln His Cys Lys Gly Met Pro		
500	505	510
Ser Pro Val Lys Ala Leu Ile Thr Gly Phe Leu Gln Trp Asn Ser Asp		
515	520	525
Asp Arg Arg Arg Pro Arg Asp Val Val Glu Gly Phe Leu Ala Ala Thr		
530	535	540
Ala Ser Glu Pro Ala Thr Ser Ser Ala Thr Ala Ala Glu Gly Ser Val		
545	550	555
		560
Arg Pro Arg Ala Ser Arg Ser Gln		
565		

<210> 382

<211> 510

<212> PRT

<213> Toxoplasma gondii

<400> 382

Met Lys Asn Ser Leu Leu Ser Pro Val Gly Phe Phe Val Val Val Ala

1 5 10 15

Val Leu Ile Gly Cys Cys Pro Pro Gly Arg Cys Leu Ala His Tyr Gly

20 25 30

Ser Ser Ser Ile Asn Glu Ser Gln Trp Thr Asp Arg Glu Thr Gln Met

35 40 45

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

50 55 60

Arg Thr Ser Ser Arg Glu Met Asn Asp Thr Gly Ser Trp Ala Thr Glu

65 70 75 80

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

85 90 95

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

100 105 110

Leu Thr Lys Lys Gly Ala Arg Ala Arg Thr Thr Lys Arg His Glu Leu

115 120 125

Val Ser Val Thr Ser Glu Glu His Tyr Trp Asn Gln Gly Ile Ala Asp

130 135 140

His Lys Gly Gln Thr Ala Pro Pro Val Ala Ala Ser Ser Ser Phe Met

145 150 155 160

Gln Ser Pro Ser Ser Leu Ala Thr Pro Val Val Leu Asn Ala Pro Val

165 170 175

Asp Phe His Gly Gln Gly Asp Ile Thr Ala Ala Val Arg Ser Arg Pro

180 185 190

Leu Val Thr Ala Gly Leu Ser Arg His Gln Ile Glu Ala Lys Asn Asp

195 200 205

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

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

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

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

450				455				460							
Glu	Leu	Pro	Ser	Pro	Val	Lys	Asp	Leu	Ile	Ala	Gly	Phe	Leu	Gln	Trp
465				470				475				480			
Ser	Arg	Glu	Ala	Arg	Arg	Leu	Pro	Gly	Asp	Val	Val	Asp	Glu	Phe	Leu
485				490				495							
Ala	Ala	Thr	Val	Ser	Glu	Ala	Ala	Thr	Ser	Ser	Ala	Ser	Val		
500				505				510							
<210> 383															
<211> 552															
<212> PRT															
<213> Toxoplasma gondii															
<400> 383															
Met	Arg	Leu	Asp	Ala	Val	Tyr	Tyr	Leu	Ala	Gln	Met	Ala	Ser	His	Arg
1				5				10				15			
Ile	Pro	Arg	Cys	Gln	Ala	Thr	Phe	Arg	His	Phe	Ile	Cys	Trp	Phe	Leu
20				25				30							
Ile	Phe	Ala	Ala	Phe	Ala	Val	Ser	Asp	Phe	Ser	Asn	Val	His	Gly	Ser
35				40				45							
Phe	Leu	Pro	Asp	Pro	His	Phe	Leu	Cys	His	His	Arg	Thr	Leu	Arg	Phe
50				55				60							
Arg	Arg	Gly	Tyr	Val	Pro	Gln	Leu	Ser	Pro	Cys	Pro	His	Ala	Ser	Thr
65				70				75				80			
His	His	Val	Lys	Ser	Gly	Ser	Phe	Ser	Ser	Lys	Ile	Ser	Phe	Leu	Glu
85				90				95							
Glu	Ala	Ala	Gln	Pro	Pro	Ser	Pro	Ile	Ser	Ser	Pro	Glu	Ser	Lys	Thr
100				105				110							
Glu	Leu	Leu	Leu	Ser	Leu	Ser	Val	Gly	His	Tyr	Gly	Lys	Trp	Met	Thr
115				120				125							
Asp	Glu	Asp	Glu	Arg	Gly	Arg	Arg	Lys	Val	Ala	Ala	Ser	Val	Ser	Arg
130				135				140							
Leu	Leu	Arg	Ser	Glu	Arg	Pro	Lys	Ser	Ile	Ser	Asp	Arg	Val	Gln	Phe

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

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

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

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

 385 390 395 400

Leu Tyr Leu Ala Asp Phe Asp Ala Val Val Arg Glu Asn Asp Thr Ile
 405 410 415
 Gln Cys Asn Lys Lys Leu Ser Leu Leu Phe Ser Pro Pro Glu Val Leu
 420 425 430
 Arg Cys Phe Phe Asn Thr Pro Glu Glu Lys Ile Ala Leu Thr Gln Val
 435 440 445
 Val Asp Ser Trp Ser Leu Gly Met Ala Ala Trp Glu Val Leu Cys Met
 450 455 460
 Ser Glu Pro Phe Asp Gly Met Arg Phe Ser Glu Asp Asp Leu Tyr Asn
 465 470 475 480
 Met Lys Val Ile Ala Ala Leu Pro Glu Gly Gly Asp Asp Thr Arg Ala
 485 490 495
 Leu Asp Trp Asn Arg Cys Arg Gly Arg Pro Pro Ala Pro Leu Arg Lys
 500 505 510
 Ala Val Glu Cys Leu Leu Asp Arg Asn Ala Ala Thr Arg Cys Lys Ala
 515 520 525
 Leu Asp Leu Phe Lys Ser Ser Pro Leu Phe Ala Glu Glu Arg Pro Val
 530 535 540
 Pro Pro Glu Pro Ser Ser Ser Asp
 545 550
 <210> 384
 <211> 749
 <212> PRT
 <213> Toxoplasma gondii
 <400> 384
 Met Val His Gly Gln Met His Tyr Val Ser Trp Val Lys Asp Gly Cys
 1 5 10 15
 Arg Gln Phe Ala Pro Asp Asn Leu Gln Pro His Gly Leu Asp Leu Glu
 20 25 30
 Val Leu Arg Ser Phe Phe Ile Leu Gln Met Asn Pro His Ala Val Ala
 35 40 45
 Glu Ile Ala Pro Gly Asp Arg Ala Glu Trp Thr Arg Ala Thr Ile Tyr

50 55 60
 Arg Gln Cys Arg Ala Ala Ala Pro Ser Pro Gly Gly Ser Pro Val Ser
 65 70 75 80
 Thr Gly Ile Ser Ser Val Ser Asn Ser Arg Phe Pro Arg Ser Ile Leu

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

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

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

 275 280 285
 Pro Lys Ser Ser Pro Thr Thr Pro Ala Ala Ala Ser Pro Ser His Ala
 290 295 300

Ala Gly Gly Ala Arg Thr Gln Asn Thr Arg Gln Glu Ala Gly Ser Arg
305 310 315 320
Glu Gly Arg Thr Gln Arg Arg Leu Ala Gly Gln Glu Gly Ala Ala Arg
325 330 335
Lys Thr Gly Arg Pro Val Leu Thr Val His Thr Gly Gly Asn Ala Pro
340 345 350
Pro Val Val Thr Asp Ala Arg Phe Lys Met Pro Ser Thr Thr Leu Lys
355 360 365
Ser Leu Val Thr Pro Gln Asp Pro Gly Glu Trp Thr Ala Glu Lys Glu
370 375 380
Glu Phe Glu Arg Ser Tyr Pro Leu His Thr Pro Ile Gln Val Arg Ser
385 390 395 400
Thr Arg Thr Asn Glu Lys Phe Ser Val Gln Leu Glu Asp Val Leu Gly
405 410 415
Ala Gly Gly Tyr Gly Val Val Phe Ser Ala Arg Asp Leu Arg Thr Gly
420 425 430
Gln Gly Ile Ala Leu Lys Val Phe Arg Ile Arg Pro Asp Gln Arg Arg
435 440 445
Glu Glu Ser Lys Glu Asp Val Ile Leu Arg Arg Arg Val Gln Ser Glu
450 455 460
Leu Ala Ile Trp Glu Tyr Val Pro Arg Gly Ile Glu Pro Lys Gln Trp
465 470 475 480
Ser Glu Met Ser His Leu Val Ile Pro Phe Asp Val Ile Glu Val Val
485 490 495
Thr Pro Cys Ala Thr Pro Pro Met Asp Gln Thr Arg Tyr Ala Ser Glu
500 505 510
Trp Val Val Met Asp Leu Phe Ala Gly Asp Val Ala Arg Met Pro Lys
515 520 525
Ile Met Ala Ala Asp Pro Ser Val Lys Leu Glu Val Thr Glu Gln Val
530 535 540
Phe Leu Ala Asn Met Tyr Leu His Asp Met Gly Leu Val His Ser Asp

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

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

 660 665 670
 Ile Ser Ile Leu Ser Leu Leu Arg Thr Met Leu Thr Pro Asn Ala Ser
 675 680 685
 Arg Arg Pro Thr Leu Arg Glu Ile Tyr Lys Phe His Pro Val Phe Lys
 690 695 700
 Gln Arg Lys Ser Met Ile Leu Gln Lys Lys Thr Leu Val Ser Ile Leu
 705 710 715 720
 Lys Glu Val Asp His Lys Lys Gly Glu Asn Pro Gly Ala Gly Gly Gly

 725 730 735
 Ala Gln Ala Gly Ser Asp Ile Gly Ser Thr Glu Glu Asp
 740 745
 <210> 385
 <211> 611
 <212> PRT
 <213> Toxoplasma gondii
 <400> 385
 Met Asn Leu Leu Leu Leu Asn Glu Pro Ser Leu Arg Leu Pro Arg Ile
 1 5 10 15

Phe Thr Val Ser Leu Cys Ala Ile Leu Ser Trp Gly His Ala Ala Phe
 20 25 30

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

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

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

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

260	265	270
Asp Gly Phe Val Ala Glu Val Asp Lys Val Tyr Glu Glu Glu Val Glu		
275	280	285
Ala Arg Leu Ala Trp Glu Leu Arg Ile Trp Arg His Leu Pro Ser Ser		
290	295	300
Arg Ala Glu Gln Leu Ala Ala Glu Glu His Ile Leu Ile Pro Gly Ala		
305	310	315
Leu Leu Ser His Ser Gly Arg Gly Ser Pro Ser Ser Arg Arg Lys Asp		
325	330	335
Ala Ala Arg Phe Ser Arg Glu Leu Glu Gly Lys Trp Asn Asp Leu Leu		
340	345	350
Ser Glu Lys Val Phe Asn Val Phe Ile Trp Tyr Pro Ala Gly Tyr Arg		
355	360	365
Asp Thr Leu Glu Ser Ser Met Met His Ser Asp Gln Ile Thr Glu Pro		
370	375	380
Trp Phe Ser Ser Thr Pro Arg Asp Val Met Glu Ser Ile Thr Val Gln		
385	390	395
Met Ile Leu Ala Val Ala Asn Leu Asn Ser Tyr Gly Leu Val His Thr		
405	410	415
His Leu Arg Ser Ser Ser Phe Val Phe Thr Pro Glu Gly Ile Val Leu		
420	425	430
Leu Ser Asp Leu Asn Arg Val Val Arg Gln Gly Glu Phe Met Asp Cys		
435	440	445
Val Ala Asp Arg Glu Ala Ser Leu Asn Asp Leu Thr Ala Ser Pro Glu		
450	455	460
Glu Arg Val Cys Val His Glu His Gly Tyr Lys Gly Arg Asp Ala Lys		
465	470	475
Lys Lys Glu Glu Leu Val Gly Pro Leu Glu Ala His Pro Thr Val Asp		
485	490	495
Ala Trp Arg Leu Ala Val Ile Leu Tyr Lys Leu Trp Cys Leu Glu Ser		
500	505	510

Met Tyr Glu Arg Ser Ser Tyr His Gln Phe Val Ala Arg Gln Asp Leu
515 520 525
Gln Arg Val Pro Asp Ser Glu Ser Asn Ile Thr Phe Leu Arg Gln Asn
530 535 540

Pro Phe Pro Met Ser Ala Cys Arg Lys Asp Met Pro Ser Ser Leu Gln
545 550 555 560
Arg Leu Leu Arg Gln Met Phe Glu Pro Asp Pro Ala Asn Arg Ile Thr
565 570 575
Ser Ala Glu Ala Val Lys Asn Ser Ser Phe Phe His Asp Lys Lys Arg
580 585 590
Ala Val Leu Arg Lys Lys Gln Glu Arg Leu Ile Gln Lys Ser Gln Pro
595 600 605

Ala Asp Gly
610

<210> 386

<211> 548

<212> PRT

<213> Toxoplasma gondii

<400> 386

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

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

100 105 110
 Arg Glu Pro Lys Asp Met Phe Phe Thr Val Phe Ser Arg Leu Gly Gly

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

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

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

 305 310 315 320
 Ala Pro Phe Val Val Pro Asn Leu Phe Val Leu Met Pro Arg Pro Ala
 325 330 335
 Thr Ser Leu Ser Asp Leu Val Ser Phe Met Ser Thr Thr Lys Asn Ile
 340 345 350

Gly Gln Thr Leu Ala Val Arg Leu Ser Leu Thr Leu Gln Thr Ile Arg
355 360 365

Val Val Ala Gly Phe Asn Asn Arg Gly Phe Ile Asp Ala Asp Ile Arg

370 375 380

Pro Ala Ser Phe Phe Val Asn Ala Lys Gly Leu Val Phe Leu Gly Ile
385 390 395 400

Phe Thr Arg Thr Thr Ile Ala Lys Arg Gly Arg Arg Ala Ser Gly Arg
405 410 415

Arg Gln Phe Asp Val Ala Thr Ala Pro Glu Leu Val Phe Arg Glu Lys
420 425 430

Val Phe Phe Arg Arg Asp Glu Lys Thr Asn Ala Trp Ala Leu Gly Ile

435 440 445

Thr Leu Tyr Tyr Ile Trp Cys Asn Arg Phe Pro Phe Gly Ile Leu Asp
450 455 460

Gly Asp Ser Ala Pro Pro Pro Glu Leu Phe Gln Pro Val Pro Pro Glu
465 470 475 480

Phe Gly Val Cys Val His Asn Met Pro Asp Pro Val Lys Val Leu Val
485 490 495

Ala Glu Leu Leu Asp Arg Gln Arg Arg Ala Arg Pro Thr Ala Asn Thr

500 505 510

Ala Met Gln Arg Glu Ile Phe Arg His Leu Gln Asp Leu Leu Ser Ala
515 520 525

Ser Lys Leu Ser Ala Leu Pro Arg Thr Val Pro Val Val Ala Leu Leu
530 535 540

Lys Gly Ile Lys
545

<210> 387

<211> 535

<212> PRT

<213> Toxoplasma gondii

<400> 387

Met Ala Thr Arg Ser Phe Leu Phe Val Phe Leu Ala Leu Ser Ser Leu

1 5 10 15

Gly Gly Leu Cys Ser Glu Tyr Ala Thr Gln Arg Pro Leu Glu Pro Tyr

20 25 30

Arg Gly Glu Thr Glu Arg Pro Leu Pro Glu Arg Leu Gly Gln Lys Met

35 40 45

Tyr Ile Ser Val Val Gln His Lys Thr Leu Ser Phe Ser Arg Ser Ser

50 55 60

Gly Gly Pro Phe Arg Arg Gln Asn Pro Gln Thr Trp Pro Asn Phe Val

65 70 75 80

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

85 90 95

Ala Asp Ala Asp Glu Pro Thr Thr Ser Thr Gly Asn Arg Arg Asp Arg

100 105 110

Ala Phe Pro Leu Arg Ser Trp Leu Arg His Ala Ile Arg Arg Leu Gly

115 120 125

Val Gly Ala Asn Asn Arg Arg Gln Gly Val Gln His Lys Glu Val Leu

130 135 140

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

145 150 155 160

Gln Glu Ile Gly Arg Cys Arg Leu Gln Gln Arg Thr Asn Ala His Leu

165 170 175

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

180 185 190

Leu Leu Ser Asp Gly Gly Arg His Thr Arg Asn Ile Arg Tyr Asp Gly

195 200 205

Glu Ile Leu Gly Ser Gly Pro Trp Ser Leu Val Leu Arg Val Met Asp

210 215 220

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

225 230 235 240

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

245 250 255
Leu His His Arg Phe Thr Pro Pro Val Ser Pro His His Ala Leu Trp

260 265 270
Cys Leu Gln Leu Met Val Ala Ile Asp Leu Leu Lys Leu Pro Arg Ile

275 280 285
Pro Arg Phe Val Arg Glu Pro Ser Ser Arg Leu Thr Ile Ala Asn Arg

290 295 300
Phe Leu Leu Leu Pro Leu Ala Tyr Thr Asp Leu Leu Ala Val Leu Arg

305 310 315 320
Ala Leu Phe Thr Arg Gln Asp Val Ser Glu Ser Pro Gly Gly Phe Leu

325 330 335
Ala Arg Leu His Met Thr Ala Gln Val Val Lys Ala Leu Ala Ser Tyr

340 345 350
His Ser Gln Gly Phe Val His Gly Asp Leu Lys Pro Gln Lys Phe Leu

355 360 365
Val Met Ala Asn Gly Ser Leu Val Leu Gly Gly Phe Thr Glu Val Arg

370 375 380
Thr Pro Gly Ala Leu Arg Ser Gly Asp Val Phe Thr Glu Ser Tyr Leu

385 390 395 400
Pro Pro Glu His Leu Asp Arg Asn Ser Val Tyr Ser Phe Glu Ser Asp

405 410 415
Thr Trp Gln Leu Gly Leu Thr Ile Tyr Gln Ile Trp Cys Leu Leu Leu

420 425 430
Pro Phe Gly Leu Met Thr Pro Phe Val Ala Glu Gly Pro Glu Arg Arg

435 440 445
Val Phe Glu Glu Val Val Gln His Pro Gly Val Gln Pro Ser Phe Asn

450 455 460
Asp Pro Asp Cys Phe Ser Asn Val Pro Glu Tyr Ile Glu Met Met Val

465 470 475 480
His His Met Leu Gln Phe His Pro Glu Asp Arg Pro Arg Pro Ala Asp

485 490 495

Ile Leu Ile Ser Asp Asn Phe Gln Arg Leu Gln Asp His Ile Gln Arg
500 505 510
Leu Glu Arg Ser Gln Glu Glu Glu Glu Ser Val His Gly Ser Pro Ala
515 520 525
Gly Thr Leu Ser Arg Asn Pro
530 535
<210> 388
<211> 1122
<212> PRT
<213> Toxoplasma gondii
<400> 388
Met Ala Gly Tyr Gln Pro Ser Ala Ala Trp Pro Val Ala Ser Phe Pro
1 5 10 15
Ser Ala Ser Leu Pro Leu Thr Ser Phe Ser Ser Phe Val Ala Arg Val
20 25 30
Ala Arg Gln Phe Leu Leu Phe Cys Leu Ile Ser Ile Phe Ala Ser Ala
35 40 45
Trp Ser Val Leu Ala Thr Asp Ala Thr Gly Glu Glu Gly Glu Ala Val
50 55 60
Asp Asp Gly Ser Ala Asp Ala Ser Asn Asp Ala Glu Val Trp Leu Arg
65 70 75 80
Arg Gln Asp Tyr Ser Ser Ser Gly Leu His Ile Pro Gln Ala Ile Ala
85 90 95
Glu His Asp Arg Glu Gly Glu Ser Pro Leu Phe Asp Ser Glu Arg Ile
100 105 110
Thr Arg Thr Gln Ser Gln Gln Arg Trp Val Ser Glu Leu Gly Arg Gln
115 120 125
Pro Ser Gln Val Ser Glu Ser Leu Pro Tyr Gly Gly Met Lys Ala Gly
130 135 140
Ser Phe Gly Gly Tyr Glu Thr Phe Arg Pro Asp Lys Leu Glu Ala Val
145 150 155 160

Trp Asp Arg Gly Thr Ala Ala Thr Glu Leu His Arg Ser Gly Gly Ala

165 170 175

Arg Ala Ser Val Asn Pro Ala Ala Ala Ala Gly Ser Ala Gly Gly

180 185 190

Ser Thr Asp Val Tyr Arg Asp Glu Lys Gly Glu Gly Lys Arg Thr Glu

195 200 205

Arg Asp Gly Arg Asn Arg Glu Glu Ser Ala Arg Val Ser Arg Glu Gly

210 215 220

Glu Ile Gln Phe Ser Thr Gly Trp Glu Ala Glu Ala Asp Pro Glu Pro

225 230 235 240

Ala Trp Arg Val Glu Thr Arg Arg Ser Glu Gln Gly Asn Ala Ser Gln

245 250 255

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

260 265 270

Ala Thr Ala Ser Ser Arg Trp Gly Ala Ser Pro His Ser Asp Ala Ser

275 280 285

Leu Arg Pro Pro Gln Glu Ser Ser Trp Pro Ser Leu Leu Pro Pro Ala

290 295 300

Gly Arg Pro Gln Pro Pro Ala Pro Ser Pro Thr His Leu Pro Ser Leu

305 310 315 320

Leu Pro Gly Thr Pro Trp Pro Ser Thr Pro Phe Ala Leu Asp Pro Arg

325 330 335

Ala Arg Leu Leu Asn Tyr Arg Asn Glu Gly His Ala Leu Arg Asp Val

340 345 350

Tyr Asp Glu Glu Glu Gly Glu Leu Ser Asp Thr Glu Ser Leu His Arg

355 360 365

Ala His Arg Leu Ser Leu Glu Gly Pro Arg Tyr Gly Phe Arg Ala Gly

370 375 380

Ser Tyr Ala Pro Arg Arg Arg Glu Asn Asp Ala Gly Asp Leu Tyr Gly

385 390 395 400

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

405 410 415
Tyr Pro Asn Gln His Gly Glu Gly Leu Pro Asp Phe Ala Ser Ala Pro

420 425 430
Arg Thr Asn Val His Leu Pro Pro Gln Leu Gly Arg Ser Gly Val Asp

435 440 445
Pro Asp Gln Val Arg Ala Ala Gln Leu Arg Leu Ala Asn Leu Ala Gly

450 455 460
His Thr Gly His Thr Pro Gly Asp Gly Ser Ser Ser Tyr Gly Ala Ser

465 470 475 480
Arg Asp Glu Val Pro Ala Arg Arg Asp Gln Val Gln Gly Arg Gly Gly

485 490 495
Pro Ser Leu Leu Pro Gly Ala Leu Arg Ala Gly Phe Asp Pro Ser Ala

500 505 510
Gly Leu Val Ser Leu Gln Tyr Pro Gly Val Ser Ala Phe Arg Arg Pro

515 520 525
Gly Val Leu Gly Ala Ala Ser Ser Gln Gly Pro Ala Lys Ser Leu Leu

530 535 540
Val Glu Gly Ala Pro Gln Gln Arg Gln Phe Gly Ala Ser Gly Phe Ala

545 550 555 560
Gln Thr Pro Ser Leu Leu Ser Ser Ser Pro Phe Leu Asp Ala Phe Met

565 570 575
His Asn Arg Gly Gly Leu Asn Leu Gly Ala Gln Leu Phe Ala Thr Gln

580 585 590
Gln Val Leu Ser Gly Pro Ala Gly Met Trp Gly Ser Ala Gly Ser Ser

595 600 605
Glu Gly Glu Ala Asp Lys Trp Trp Arg Glu Gln Asp Gly Trp Val Trp

610 615 620
Pro Glu Leu Pro Ser Leu Ser Ala Thr Asp Leu Glu Ala Gly Val Lys

625 630 635 640
Asp Ile Ser Gly His Ala Gln Met Val Arg Val Glu Ala His Leu Val

645 650 655

Arg Ser Gln Val Asn Ala Gly Asn Ala Leu Gly Leu Tyr Ile His Gln
660 665 670

Gly Lys Arg Tyr Glu Leu Leu Asp Val Glu Gly Arg Leu Ala Pro Met
675 680 685

Thr Ala Ile Arg Gly Lys Val Leu Gly Phe Gly Ala Tyr Gly Val Val
690 695 700

Val Glu Leu Val Asp Val Ser Ala Ser Gly Ala His Arg Arg Ser Ser
705 710 715 720

Pro Ser Ser Thr Asp Ala Thr Ala Gly Glu Phe Gly Gly Thr Ala Val
725 730 735

Asn Ser Gly Ser Pro Ser Ala Ser Asn Ser Gly Asn Lys Val Ser Thr
740 745 750

Ser Gly Asn Lys Val Ser Ser Ser Gly Thr Thr Ala Ala Asn Val Glu
755 760 765

Ala Glu Pro Gly Gln Leu Ser Ser Ala Glu Arg Glu Gly Glu Pro Ala
770 775 780

Ala Lys Val Asp Gly Asp Ala Ala Ser Glu Ala Gly Gly Pro Pro Arg
785 790 795 800

Glu His Thr Glu Arg Ser Ser Arg Ile Pro Gly Lys Arg Ala Ser Gly
805 810 815

Ala Val Glu Lys Ser Gly Gly Ser Gly Ile Glu Pro Arg Gly Asp Ser
820 825 830

Ala Arg Val Ser Arg Ser Val Thr Tyr Ala Ala Lys Ile Met Tyr Trp
835 840 845

Ala Lys Ala Lys Thr Ser Ala Lys Pro Glu Glu Val Arg Gln Thr Leu
850 855 860

Glu Gly Phe Val His Glu Glu Leu Glu Ala Phe Lys Leu Leu Arg Glu
865 870 875 880

Thr Gly Ile Ser Asp Ser Asp Leu Phe Gln Lys His Gly Leu Val Val
885 890 895

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

900 905 910
 Ser Pro Ala Leu Phe Pro Asp Thr Pro Leu Phe Phe His Asn Gln Leu
 915 920 925
 Ile Met Phe Pro Ala Leu Lys Cys Ser Leu Asp Met Leu Ala Gln Asp

930 935 940
 Arg Phe Thr Arg Glu Gly Leu Arg Val Leu Val Arg Ser Leu Val Arg
 945 950 955 960
 Leu Val Ala Gly Leu His Ala Leu Gly Phe Ser His Asn Asp Val Lys
 965 970 975
 Pro Gln Asn Phe Leu Val Gly Gly Asp Gly Gly Leu Phe Leu Gly Asp
 980 985 990
 Phe Ala Tyr Leu Ala Pro Ile Asp Glu Val Gln Asp Cys Asn Lys Gly

995 1000 1005
 Phe Thr Val Asp Tyr Ser Ser Pro Glu Leu Met Ala Cys Ala Leu
 1010 1015 1020
 Lys Asn Gly Arg Met Ser Met Gly Pro Glu Arg Asp Ser Trp Ala
 1025 1030 1035
 Val Gly Val Ser Ala Tyr Arg Leu Ala Cys Arg Asn Arg Phe Pro
 1040 1045 1050
 Phe Leu Leu Asp Arg Lys Phe Asn Ala Lys Ser Asp Pro Arg Leu

1055 1060 1065
 Ile Ala Thr His Ile Ala Asn Leu Lys Glu Thr Asp Leu Glu Thr
 1070 1075 1080
 Ser Arg Cys Gly Thr Glu Asp Arg Val Val Met Ser Ile Val Leu
 1085 1090 1095
 Arg Leu Leu His Pro Asp Leu Ser Lys Arg Ala Thr Val Asp Gln
 1100 1105 1110
 Leu Val His Glu Pro Phe Phe Gln Asp
 1115 1120

<210> 389

<211> 435

<212> PRT

<213> *Toxoplasma gondii*

<400> 389

Met Leu Leu Ser Ile Ser Ala Gly Thr Gly Asp Thr Leu Ser Ser Arg

1 5 10 15

Ser Gln Leu Tyr Arg Glu Leu Gln Asn Gln Ala Met Asn Pro Ala Ala

20 25 30

Ala Ser Gln Arg Pro Asn Phe Ala Ala Gly Leu Gly Val Ile Leu Thr

35 40 45

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

50 55 60

Leu Leu Arg Thr Met Leu Thr Ala Arg Gly Arg Leu Ile Pro Pro Ser

65 70 75 80

Gly Gln Pro Ser Leu Ser Met Arg Leu Arg Pro Ile Gly Ile Gly Gly

85 90 95

Thr Glu Lys His Val Ser Phe Leu Gly Val Ala Gly Val His Glu Gly

100 105 110

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

115 120 125

Asp His Ile Tyr Trp Gln Pro Leu Phe Tyr Thr Asn Pro His Ser Glu

130 135 140

Lys Glu Ser Val Asp Pro Gln Phe Leu Lys His Gly Leu Val Gln Arg

145 150 155 160

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

165 170 175

Glu His Leu Cys Ser His Tyr Gly Val Met Phe Pro Gly Gly Thr Tyr

180 185 190

Val Leu Ala Ala Asp Asn Ala Pro Leu Gln Phe Asp Val Glu Ser Asp

195 200 205

Gln Ser Gly Ser Arg Ala Val Leu Asn Leu Phe Ile Gln Phe Ser Pro

210 215 220

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

225 230 235 240
 Leu Ala Ala Phe Leu Val Lys Gln Met Ile Leu Asn Thr Ala Met Leu

245 250 255
 His Ser Met Gly Val Val His Asn Gly Ile Ser Ser Ala Ala Phe Phe

260 265 270
 Leu Ser Gly Ser Glu Leu Thr Gly Thr Thr Pro Pro Ala Arg Leu Leu

275 280 285
 Tyr Leu Val Asn Phe Gly Ala Ala Arg Phe Tyr Thr Gly Lys Pro Glu

290 295 300
 Pro Phe Glu Glu Ala Gly His Val Met Tyr Tyr Asp Pro Glu Thr Ala

305 310 315 320
 Ser Val Phe Thr Lys Val Ala Ala Leu Arg Pro Asn Val Val Tyr Gly

325 330 335
 Gln Ala Arg Asp Ser Trp Ser Leu Gly Arg Val Met Phe Gln Leu Leu

340 345 350
 Cys Gly Gly Ser Gln His Pro Phe Gly His Leu Gly Pro Pro Ala Ser

355 360 365
 Pro Leu Val Thr Ala Lys Arg Ile Ser Met Leu Ala Arg Asp Arg Pro

370 375 380
 Ala Leu Arg Leu Ser Thr Cys Phe Pro Pro Thr Ser Ala Pro Glu Met

385 390 395 400
 Gln Asp Leu Met Ser Ile Met Ala Asn Phe Leu Lys Phe Asp Ala Asn

405 410 415
 Glu Arg Pro Thr Pro Leu Glu Ile Val Arg Arg Tyr Pro Gln Leu Phe

420 425 430
 Thr Pro Leu

435

<210> 390

<211> 975

<212> PRT

<213> Toxoplasma gondii

<400> 390

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

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

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

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

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

245 250 255

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

260 265 270

Ser Val Ala Pro Ala Ala Val Glu Asp Glu Glu Glu Val Glu Glu Val

275 280 285

Glu Ala Phe His Asp Pro Phe Ser Glu Asp Asp Val Ala Leu Leu Arg

290 295 300

Val Pro Asp Leu Leu Val Ser Gln Asn Ala Thr Ala Phe Arg Met Gln

305 310 315 320

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

325 330 335

Ala Val Gln Gly Ala Pro Ser Arg Ala Lys Lys Lys Arg Ala Pro Asp

340 345 350

Thr Ser Ala Ser Ala Ser Phe Ser Pro Pro Ala Ser His Ala Tyr Gly

355 360 365

Ser Leu Arg Trp Lys Asp Val Ser Phe Pro Ala Ser Ala Thr Val Thr

370 375 380

His Ile Pro Gly His Thr Gly Ser Phe Ala Glu Val Tyr Glu Pro Phe

385 390 395 400

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

405 410 415

Ser Leu Gly Leu Thr Gly Ala Tyr Gly Ala Phe Ala Ala Glu Gly Ala

420 425 430

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

435 440 445

Leu Ala Ser Pro Asp Gly Ala Ala Thr Leu Gly His Arg Ser Pro Ala

450 455 460

Arg Val Ser Arg His Arg Ser Ala Glu Arg Ser Arg Ser Ser Leu Arg

465 470 475 480

Ala Gly Gln Arg Ala Ala Gly Val Asp Gly Asn Ser Val Asp Pro Gln

485 490 495
Gln Gln Glu Ala Lys Gly Glu Glu Ala Ala Arg Arg Glu Leu Gln Arg

500 505 510
Asp Ala Asp His Val Glu Asn Ala Lys Gly Lys Glu Ala Glu Asn Glu

515 520 525
Ala Arg Pro Thr Ala Arg Ile Thr Arg Ser Val Val Gly Asn Ala Leu

530 535 540
Leu Thr Arg Glu Val Arg Glu Ser Ser Glu Asn Leu Ala Asn Leu Val

545 550 555 560
Asn Ala Leu Asp Ser Gly Gly Ser Pro Ala Gly Glu His Arg Gly Ala

565 570 575
Leu Gln Thr Glu Asp Lys Glu Gly Gly Ser Asn Val Pro Glu Ala Thr

580 585 590
Thr Pro Arg Leu Arg Leu Ala Asp Leu Pro Lys Val Leu Phe Ser Lys

595 600 605
Pro Ser Arg Ser Leu Val Lys Ala Ala Arg Ala Leu Glu Arg Ser Val

610 615 620
Ser Ser Lys Glu Lys Gln Lys Leu Ala Gly Ile Ile Pro Phe Asp Val

625 630 635 640
Pro Val Val Val Arg Ser Leu Ala Thr Gln Lys Arg Arg Thr Val Ile

645 650 655
Phe Asp Gly Val Leu Gly Ala Gly Gly Gln Gly Val Val Leu Leu Ala

660 665 670
Arg Asp Val Asp His Pro Gly Leu Glu Met Ala Val Lys Ile Phe Arg

675 680 685
Ile Lys Lys Lys Asn Arg Gly Ala Ser Ala Leu His Glu Ile Ala Arg

690 695 700
Leu Gln Arg Arg Leu Arg Trp Glu Thr Ala Ile Leu Lys His Ala Pro

705 710 715 720
Arg Asp Val Ser Ser Tyr Val Trp Ser Gln Leu Ala His Leu Val Met

725 730 735

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

740 745 750

Glu Met Arg Tyr Trp His Gln Trp Leu Ile Phe Glu Ser Phe Ala Gly

755 760 765

Asp Val Thr Arg Leu Lys Lys Leu His Ser Gly Ser Gly Gln Ala Arg

770 775 780

Leu Asp Ala Ser Lys Gln Ile Phe Met Ala Cys Met Arg Leu His Asp

785 790 795 800

Thr Gly Met Val His Ser Asp Ile Lys Leu Ala Asn Tyr Phe Ile Ser

805 810 815

Ser Glu Gly Arg Ile Phe Leu Gly Asp Tyr Ser Leu Ser Arg Pro Ile

820 825 830

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

835 840 845

Glu Asn Met Lys Cys Ile Arg Asp Gly Glu Lys Asn Leu Val Leu Ser

850 855 860

Ser Lys Lys Asp Thr Trp Ala Val Gly Val Ala Leu Tyr Lys Leu Trp

865 870 875 880

Cys Arg Asn Phe Phe Pro Phe Asp Leu Asp Ser Leu Ser Ser Glu His

885 890 895

Ala Val Asp Arg Val Ala Glu Val Ser Arg Asp Glu Leu Asn Phe Tyr

900 905 910

Pro Cys Ala Pro Asp Met Pro Val Ala Val Met Asp Leu Ile Gln Gln

915 920 925

Met Leu Asp Pro Asn Ile Glu Thr Arg Pro Thr Leu Arg Asp Leu Phe

930 935 940

Val Ser His Pro Val Phe Ser Gln Leu Arg Lys Val Thr Leu Gln Tyr

945 950 955 960

Thr Leu Ala Asp Phe Arg Glu Glu Gln Ala Asn Gln Lys Gly Ile

965 970 975

<210> 391

<211> 694

<212> PRT

<213> Toxoplasma gondii

<400> 391

Met Ala Glu Gln Lys Val Cys His Lys Lys Met Thr Gln Phe Ala Ala

1 5 10 15

Gln Ser Met Val Ser Ser Leu Ser Ser Pro Pro Arg Val Leu Arg Val

20 25 30

Ile Gln Leu Leu Leu Leu Gln Ile Thr Leu Val Thr Phe Ala Val Asp

35 40 45

Ala Gln Val Glu Pro Arg Arg Leu Leu Arg Gln Ala Arg Lys Pro Phe

50 55 60

Glu Ala His Leu Arg Gly Gln Asn Arg Phe Tyr Pro His Leu Glu Arg

65 70 75 80

Arg Asn Pro Pro Arg Gly Gln Gln Arg Tyr Val Pro Pro Arg Asn Gln

85 90 95

Gln Ile Leu Arg His Gly Gln Phe Ser Pro Asp Asp Gly Ala Met His

100 105 110

Phe Lys Pro Pro Ala Asn Arg Val Gln Ser Pro Tyr Asn Phe Val Lys

115 120 125

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

130 135 140

Lys Glu Arg Arg Gly Leu Ala Val Pro Val Asn Ser Arg Glu Glu Asp

145 150 155 160

Lys Leu Ile Asn Lys Arg Asp Gly Leu Arg Thr Phe Arg Lys Glu Arg

165 170 175

Asn Val Pro Thr Ser Ala Ser Ser Gln Pro Lys Glu Glu Trp Ala Asp

180 185 190

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

195 200 205

Gln Phe Ile Ala Arg Ala Val Met Ala Val Gln Gly Lys Gly Val Ser

210	215	220	
Pro Ser Phe Leu Thr Leu Gln Thr Leu Ser Gln His Ala Gly Gly Asp			
225	230	235	240
Glu Lys Arg Asn His Leu His Arg Arg Tyr Glu Glu Ala Glu Gly Glu			
	245	250	255
Ser Asp Glu Ser Val Ile Trp Asp Thr Ala Ala Leu Ile Gln Trp Met			
	260	265	270
Lys Pro Ser Arg Ser Tyr Asn Ile Arg Ala Thr Asp Ala Leu Gly Ile			
275	280	285	
Lys Asn Ala Ser Gly Ala Gln Gln Glu Ser Ser Trp Pro Leu Ser Thr			
290	295	300	
Ser Ser Phe Leu Glu Ile Ala Arg Lys Phe Asn Asn Trp Thr Arg Ala			
305	310	315	320
Ser Gly Phe Leu Asn Thr Val Arg Arg Phe Trp Pro Ser Gly Thr Val			
	325	330	335
Ala Lys Val Ala Asp Asp Ala Gly Leu Lys His Asn Ile Ile Trp His			
340	345	350	
Lys Leu Leu Gly Val Gly Gly Ile Gly Gly Val Leu Leu Leu Glu Asp			
355	360	365	
Lys Asp Glu Pro Val Gly Ser Pro Leu Lys Lys Phe Ala Gly Lys Ile			
370	375	380	
Leu Tyr Gln Leu Ser Asp Pro Ser Met Asn Leu Ser Gln Ser Lys Glu			
385	390	395	400
Tyr Phe Tyr Gln Ala Arg Asn Glu Glu Ile Gly Val Ala Ser Leu Phe			
	405	410	415
Lys His Ala Ala Leu Ser Leu His Asp Cys Pro Val Thr Ala Thr Asp			
420	425	430	
Arg Met Gln Phe Leu Phe Gln Arg Gly Phe Val Leu Pro Gln Lys Ala			
435	440	445	
Phe Trp Phe Glu Gly Thr Thr Gln Ile Pro Arg Phe Gln Asp Ile Val			
450	455	460	

Glu Ala Ser Pro Arg Val Val Gly Ser Pro Gly Gly Glu Ile Met Arg
465 470 475 480

Leu Asp Arg Tyr Ile Ile Ala Tyr Pro Ile Val Gly Pro Asp Leu Glu
485 490 495

Asp Leu Asp Pro Arg Lys Phe Ser Leu Ser Ala Val Thr Tyr Ile Ile
500 505 510

Tyr Lys Leu Thr Lys Leu Met Ala Thr Met Gln Glu Met Asn Leu Val
515 520 525

His Thr Asp Ile Lys Ala Glu Asn Phe Leu Ala Arg Asp Asp Gly Glu
530 535 540

Leu Phe Ala Ala Asp Leu Ser Met Ser Ile Lys Met Asp Pro Ala Thr
545 550 555 560

Leu Ile Pro Cys Leu Gln Gly Thr Met Leu Tyr Leu Asp Pro Asn Gly
565 570 575

Ala Glu Cys Ala Tyr Arg Arg Gly Tyr Gln Ser Pro Arg Ala Lys Arg
580 585 590

Asp Ala Tyr Ala Leu Gly Val Thr Phe Tyr Lys Leu Ile Cys His Asp
595 600 605

Gly Pro Phe His Leu Gly Arg Leu Glu Lys Glu Ala Met Glu Gln Thr
610 615 620

Lys Thr Cys Pro Gly Asn Asn Pro Leu Leu Leu Met Leu Ser Gly Ile
625 630 635 640

Ser Arg Phe Thr Arg Lys Asp Trp Val Glu Arg Lys Cys Pro Leu Ala
645 650 655

Asp Thr Ser Leu Leu Thr Ile Val Lys Leu Leu Leu Asp Pro Arg Glu
660 665 670

Asp Arg Arg Trp Thr Pro Leu Asp Leu Val Arg Lys Thr Ala Phe Phe
675 680 685

Asp Gln Ala Pro Gly Ile
690

<210> 392

<211> 489

<212> PRT

<213> Toxoplasma gondii

<400> 392

Met Ser Ile Leu Gly Lys His Thr Ala Thr Val Gly Asp Arg Tyr Lys

1 5 10 15

Val Arg Leu Thr Pro Glu Tyr Gly Pro Gly Gly Gly Tyr Gly His Cys

20 25 30

Arg Asp Tyr Leu Leu Gln Ser Glu Ser Cys Trp Arg Gly Asp Leu Thr

35 40 45

Ser Gly Val Arg Gly Val Leu Thr Lys Lys Gly Thr Arg Ala Arg Thr

50 55 60

Thr Lys Arg His Asp Leu Val Ala Val Thr Ser Gly Glu His Tyr Trp

65 70 75 80

Asn Gln Gly Leu Val Tyr His Glu Glu Gln Thr Ala Pro Pro Val Ala

85 90 95

Ala Ser Asn Ser Phe Met Gln Ser Thr Thr Ser Leu Ala Thr Pro Ala

100 105 110

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

115 120 125

Val Leu Lys Asn Arg Pro Pro Ala Glu Ala Gln Leu Ser Pro Arg Glu

130 135 140

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

145 150 155 160

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

165 170 175

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

180 185 190

His Arg Val Lys Val Gly Gly Ala Ser Ala Pro Gln Gln Leu Ala Ala

195 200 205

Lys Ile Asn Val Arg Ser Leu Gln Glu Leu Gln His Leu Ser Ser Ser

210	215	220	
Gln Lys Lys Thr Ala Leu Glu Asp Ile Gln Glu Arg Phe Leu Arg Glu			
225	230	235	240
Glu Ser Ser Ala Arg Asn Ala Leu Gln His Val Thr Pro Glu Thr Ala			
	245	250	255
Leu Glu His Gly Val Leu Phe Pro Val Asp Val Cys Arg Ile Ser Lys			
	260	265	270
Leu Phe Ser Gly Phe Cys Ala Gly Ile Ser Tyr Val Ile Leu Pro Val			
275	280	285	
Leu Ala Leu Phe Pro Val Phe Thr Cys Asp Leu Gln Gln Val Val Lys			
290	295	300	
Ser Gly Leu Ser Arg Ala Ala Lys Leu Tyr Ile Thr Arg Leu Leu Leu			
305	310	315	320
Gln Ala Val Ala Trp Leu His Ala Asn Gly Val Ala His Asn Asp Leu			
	325	330	335
Lys Leu Glu Asn Val Leu Leu Ser Ala Glu Gly Lys Ala Val Ile Ala			
340	345	350	
Asp Phe Gly Phe Ala Val Lys Leu Gly Thr Ala Ser Ala Ile Gln Phe			
355	360	365	
Thr Ala Pro Tyr Leu Asp Pro Gln Thr Ala Glu Ala Val Pro Gln Glu			
370	375	380	
Lys Thr Lys Thr Thr Ala Ser Glu Glu Arg Asp Ala Trp Ala Leu Ala			
385	390	395	400
Thr Leu Leu Phe Leu Leu Trp Cys Gly Ser Phe Pro Tyr Val Ser Asp			
	405	410	415
Glu Gln Ala Asp Leu Pro Thr Ser Asp Leu Leu Lys Leu Leu Val Thr			
420	425	430	
Leu Gly Lys Thr Glu Lys Pro Ala Pro Asn Phe His Leu Cys Lys Asp			
435	440	445	
Leu Pro Pro Ala Val Gly His Leu Val Thr Ala Phe Leu Gln Trp Asn			
450	455	460	

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

Ala Thr Val Ser Glu Gly Ala Ser Ala
485

<210> 393

<211> 470

<212> PRT

<213> Toxoplasma gondii

<400> 393

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

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

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

Val Lys Ala Gly Gln Pro Gly Ala Tyr Gly Ala Asp Gly Gly Thr His
180 185 190

Glu Lys Asn Met Arg Glu Lys Gly Glu Glu Ser Ala Pro Gln Cys Arg
195 200 205

Ser Ser Arg Trp His Leu Gly Glu Ser Gln Arg Glu His Ser Leu Ala
210 215 220

Ser Val Phe His Ser Val Met Val Ala Met Lys Ser Leu Pro Ala Thr
225 230 235 240

Phe Gln Arg Glu Trp Ser Leu Val Arg Lys Ile Tyr Arg Gln Ser Gly
245 250 255

Arg Val Lys His Ala Gln Arg Leu Glu Arg Ala Arg Glu Ala Lys Leu
260 265 270

Gln Lys Phe Gly Leu Ser Arg Arg Ala Ser Ser Arg Lys Pro Leu Pro
275 280 285

Ser Leu Val Ser Met Gln Gln Val Val Pro Thr Ala Glu Cys Ala Ser
290 295 300

Ala Leu Ile Lys Glu Val Arg Arg Asn Leu Glu Lys Ser Met Arg Asp
305 310 315 320

Phe Gln His Ala Ser Pro Ala Leu Ser Phe Arg Arg Glu Arg Leu Phe
325 330 335

Pro Pro Gly Arg Glu Phe Val Val Arg Ser Leu Ala Arg Asn Pro Pro
340 345 350

Phe Thr Thr Met Ala Leu Val Ala Gly Arg Leu Leu Gly Gly Gly Ser
355 360 365

Glu Ala Met Val Phe Ala Ala Glu Glu Ile Glu Leu Pro Glu Lys Arg
370 375 380

Asp Val Phe Ile Gly Ala Asp Asp Ala Ser Arg Glu Thr Ser Gly Glu
385 390 395 400

Tyr Leu Pro Arg Leu Leu Ala Ile Lys Ile Tyr Leu Cys Glu Ala Asn
405 410 415

Leu Leu Asp Gln Pro Val Lys Ala Ala Glu Glu Ala Glu Ala Val Glu

420 425 430
 Trp Leu Gln Met Ala Phe Trp Arg Leu Val Pro Ser Cys Val Asp Val
 435 440 445
 Leu Leu Ser Arg Gln Leu Gly Val Ala Ala Pro Ser Trp Arg Tyr Glu
 450 455 460
 Trp Arg Thr Glu Ser Thr
 465 470
 <210> 394
 <211> 531
 <212> PRT
 <213> Toxoplasma gondii
 <400> 394
 Met Arg Ala Gln Val Ala Leu Cys Leu Ser Leu Phe Leu Phe Ala Thr
 1 5 10 15

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

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

 Arg Arg Phe Arg His Thr Glu His Gly Pro Ile Pro Ala Val Asn Phe

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

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

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

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

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

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

Ala Gln Thr
530

<210> 395

<211> 632

<212> PRT

<213> Toxoplasma gondii

<400> 395

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

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

65					70				75				80			
Val	Glu	Pro	Thr	Ala	Gly	Arg	Asn	Lys	Arg	Ala	Leu	Ala	Thr	Ala	Ser	
				85				90				95				
Glu	Glu	Gln	Leu	Pro	Thr	Ser	His	Arg	Ser	Arg	Arg	Gly	Ala	Ala	Thr	
				100				105				110				
Ser	Ile	Leu	Ser	Gly	Leu	Arg	Ser	Val	Tyr	Asn	Ala	Ser	Ser	Arg	Pro	
				115				120				125				
Ala	Val	Asp	Ser	Arg	Asn	Arg	Ala	Lys	Asp	Pro	Asp	Arg	Phe	Val	Met	
				130				135				140				
Arg	Arg	Ala	Val	Val	His	Ser	Ile	Glu	Glu	Val	Thr	Glu	Arg	Ser	Asp	
				145				150				155				
160																
His	His	Asp	Leu	Arg	Gly	Glu	Asp	Ser	Ala	Gln	Thr	Asp	Ser	Val	Asn	
				165				170				175				
Ala	Pro	Asp	Asp	Glu	Leu	Val	Ser	Glu	Leu	Leu	His	Leu	Gly	Glu	Tyr	
				180				185				190				
Pro	His	His	Ile	Glu	Ser	Leu	Ser	Asp	Pro	Glu	Ala	Val	Lys	Ile	Leu	
				195				200				205				
Ala	His	Leu	Val	Ala	Thr	Thr	Asn	Thr	His	Asp	Ile	Val	Ser	Gln	Ser	
				210				215				220				
Arg	Lys	Lys	Lys	Leu	Val	Glu	Ala	Phe	Asn	Met	Tyr	Leu	Pro	Asp	Gly	
				225				230				235				
240																
Asp	Arg	Phe	Phe	Val	Glu	Ser	Leu	Ser	Asp	Ala	Ser	Glu	Ser	Lys	Glu	
				245				250				255				
Phe	Val	Arg	Gly	Pro	Leu	Leu	Gly	Val	Gly	Gly	Asn	Gly	Leu	Val	Phe	
				260				265				270				
Glu	Ala	Gln	Asp	Ser	Asp	Gly	His	Val	Tyr	Ala	Leu	Lys	Leu	Leu	Leu	
				275				280				285				
Val	Arg	Met	Ser	Thr	Phe	Leu	Glu	Ala	Val	Gly	Asp	Leu	Ser	His	Asp	
				290				295				300				
Ala	Trp	Arg	Arg	Glu	Glu	Asp	Trp	Ala	Phe	Ala	Arg	Ala	Leu	Arg	Lys	
				305				310				315				
												320				

Glu Met Lys Val Leu Arg Leu Phe Pro Pro Asp Lys Ser Pro Glu Gln
 325 330 335
 Leu Tyr Glu Glu Gly Phe Val Leu Pro Leu Phe Gln Gly Ile Leu Ala
 340 345 350
 Gly Lys Pro Arg Met Thr Pro Leu Thr Glu Glu Phe Gly Ala Thr Ser
 355 360 365
 Val Val Val Gly Phe His Lys Val Ala Cys Ser Val Gly Gln Leu Phe
 370 375 380
 Ser Ala His Arg Leu Pro Asp Gly Val Lys Leu Glu Leu Thr Lys Gln
 385 390 395 400
 Met Val Asp Arg Val Ala Arg Leu His Ser Tyr Gly Ile Leu His Gly
 405 410 415
 Asp Val Lys Trp Glu Asn Phe Phe Leu Asp Asp Asn Gly Arg Val Phe
 420 425 430
 Leu Gly Asp Phe Glu Gln Ala Gln Ser Leu Gly His Arg Arg Thr Gly
 435 440 445
 Pro Cys Gly Pro Arg Gly Gly Gly Thr Pro Ser Leu His Glu Pro Ala
 450 455 460
 Arg Ala Ala Cys Tyr Phe Ser Glu Pro Asp Arg Arg Leu Asp Leu Leu
 465 470 475 480
 Glu Ser Arg Asp Ser Trp Cys Leu Gly Val Val Ser Tyr Lys Leu Trp
 485 490 495
 Cys His Arg Leu Pro Phe Gly Leu His Leu Asn Arg Ala Asp Met Glu
 500 505 510
 Gly Phe Met Asn Gln Val Ala Thr Ile Glu Arg Asp Arg Leu Val Pro
 515 520 525
 Asp Phe Asp Asp Cys Arg Gly Ser Glu Gln Thr Pro Glu Asp Val Lys
 530 535 540
 Glu Leu Ile Ala Ala Leu Leu Tyr His Asp Arg Tyr Arg Arg Glu Thr
 545 550 555 560
 Pro Leu Ser Leu Ile Glu Lys Ser His Leu Phe Arg Arg Pro Pro Ser

565 570 575
 Glu Arg Asn Asp Val Ser Val Glu Leu Arg Ala His Glu Ser Asp Ala
 580 585 590
 Ala Asp Val Leu Arg Pro Ala Ala Pro Leu Pro Glu Glu Arg Leu His
 595 600 605
 Ala Pro Glu Thr Lys Phe Phe Lys Pro Arg Lys His Trp Trp Arg Ser
 610 615 620
 Tyr Leu Gln Ala Cys Ser Ile Gln
 625 630

<210> 396

<211> 746

<212> PRT

<213> Toxoplasma gondii

<400> 396

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

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

115 120 125
 Thr Thr Ser Glu Asp Pro Leu Ala Gly Arg Ala Phe Ser Glu Ser Leu
 130 135 140

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

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

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

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

 370 375 380
 Ile Lys Ala Val Pro Thr Ala Val Leu Ser Gly Ala Arg Lys Met Arg

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

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

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

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

 625 630 635 640

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

690 695 700
Arg Phe Thr Leu Glu Glu Ala Leu Gly His Ser Phe Phe Asp Gly Val
705 710 715 720
Asp Phe Glu Thr Leu Glu Gln Leu Lys His Pro Ala Pro Phe Pro Gly
725 730 735
Asp Phe Gln Asn Arg Ala Thr Phe Tyr Arg
740 745

<210> 397

<211> 553

<212> PRT

<213> Toxoplasma gondii

<400> 397

Met Met Phe Pro Ala Val Ala Ala Pro Arg Arg Arg Leu Pro Gly Glu

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

65 70 75 80
Phe Ala Glu Asn Ser Leu Ala Asn Arg Glu Pro Pro Glu Asp Ser Ala
85 90 95
Ala Arg Pro Ser Ser Arg Ser Gly Gly Ala Glu Arg Arg Arg Leu Asp

100	105	110	
Ser Leu Ile Pro Gly Phe Leu Lys Arg Arg Arg Ile Phe Lys Gln Leu			
115	120	125	
Arg Pro Val Asp Glu Phe Gln Leu Arg Glu Phe Gln Glu Ala Ser Ser			
130	135	140	
Lys Val Lys Ala Gln Phe Phe Ser Ala Gly His Ser Arg Val Thr Phe			
145	150	155	160
Val Asp Arg Pro Ser Ala Ala Leu Leu Ser Phe Leu His Leu Glu Glu			
165	170	175	
Glu Asp Val Pro Tyr Gly Val Val Ile Lys Ala Ile Pro Tyr Asp Ala			
180	185	190	
Phe Asp Phe Tyr Glu Ser Val Ala Glu Pro Tyr Ile His Arg Met Phe			
195	200	205	
Asp Asp Pro Arg Lys Phe Pro Tyr Val Val Pro Val Leu Ala Ala Leu			
210	215	220	
Arg Ser Thr Ser Lys Arg Val Leu Tyr Leu Val Leu Pro Leu Tyr Arg			
225	230	235	240
Glu Leu Pro Glu Thr Val Asp Glu Glu Ala Arg Ser Val Asp Phe Val			
245	250	255	
Leu Leu Leu Ala Glu Met Ala Met Ala Val Cys Gln Leu His Glu Arg			
260	265	270	
Asn Leu Ala His Arg Asp Leu Lys Glu Asp Asn Phe Leu Val Ser Pro			
275	280	285	
Glu Gly His Ile Val Val Ser Asp Leu Ala Thr Leu Asp Ile Thr Asp			
290	295	300	
Asn Lys Ser Phe Leu Ile Gly Thr Ser Gly Tyr Met Pro Pro Glu Thr			
305	310	315	320
Arg Ser Ser Tyr Leu Leu Arg Lys Gly Tyr Thr Arg Ser Arg Tyr Gly			
325	330	335	
Glu Lys Thr Asp Val Tyr Ser Leu Gly Val Ala Phe Arg His Leu Ala			
340	345	350	

Phe Met Leu Glu Gly Leu Gly Val Gln Val Pro His Arg Thr Gln Leu
 355 360 365
 Ala Lys Leu Ile Lys Lys Met Thr Ser Ala Asp Pro Glu Lys Arg Pro
 370 375 380
 Leu Ile Gly Glu Val Met Glu Asp Pro Phe Phe Ala Ser Val Asp Phe

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

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

 515 520 525
 Pro Gly Gln Arg Glu Glu Gln Arg Glu Gly Thr Gly Leu Glu Glu Gly
 530 535 540
 Phe Asn Lys Glu Asp Ala Gln Glu Ser
 545 550
 <210> 398
 <211> 640
 <212> PRT
 <213> Toxoplasma gondii
 <400> 398
 Met Pro Glu Gln Asp Leu Ala Ser Gly Phe Leu Leu Arg Phe Gln Asn

1 5 10 15
 Ala Arg Pro Val Cys Leu Ser Val Gly Ser Phe Val Ser Phe Arg Thr

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

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

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

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

Glu Arg Arg Leu Ala Val Arg Gly Asp Asp Ser Phe Ala Arg Gly His
 260 265 270
 Asn Arg Asp Arg Asp Ala Ser Asn Gly Arg Ser Ile Leu Arg Arg Ala
 275 280 285
 Pro Gly Trp Ala Lys Ile Ala Ala Leu Ala Thr Gly Leu Leu Val Ser
 290 295 300
 Ala Phe Gly Tyr Ser Ser Tyr Lys His Gly Gly Pro Arg Val Ala Leu
 305 310 315 320
 Arg Ile His Lys Leu His Leu Lys Arg Lys Leu Pro Ile Ser Trp Arg
 325 330 335
 Arg Tyr Leu Asn Asn Leu Pro Val Leu Asp Glu Arg Leu Phe Pro Glu
 340 345 350
 Phe Glu Asp Ile Leu Pro Trp Leu Arg Arg Gly Ala Arg Leu Val Lys
 355 360 365
 Arg Val Pro His Val Ser Glu Ala Leu Ala Asp Phe Ile Gly Leu Asp
 370 375 380
 Glu Glu Thr Arg Arg Thr Gly Ile Val Ile Lys Val Lys Ser Ser Thr
 385 390 395 400
 Asp Ala Glu Ala Arg Arg Leu Val Tyr Glu Val Asn Ala His Ala Asn
 405 410 415
 Met Val Pro Asp Asn Pro Phe Phe Leu Pro Ile Ile Gly Ala Tyr Gln
 420 425 430
 Gly Ala Ser Lys Arg Ala Val Tyr Met Ile Leu Pro Arg Ala Arg Ala
 435 440 445
 Asp Val Ala Asp Tyr Val Arg Ala Arg Pro Tyr Asp Val Asp Val Arg
 450 455 460
 Leu Ala Ala Ala Glu Met Val Tyr Ser Asn Tyr Ile Leu His Thr His
 465 470 475 480
 Gly Phe Leu His Arg Asp Ile Lys Ala His Asn Tyr Phe Val Thr Phe
 485 490 495
 Asp Gly His Val Val Leu Ala Asp Phe Glu Gly Val Gly Val Leu Gln

500 505 510
Gln Arg Thr Pro Val Val Gly Thr Arg Gly Tyr Phe Ala Pro Glu Leu
515 520 525
Ser Arg Ala Thr Asp His Thr Glu Lys Ser Asp Val Phe Ala Leu Gly

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

595 600 605
Pro Phe Arg Gly Asp Phe Ser Ile Asp Asp Pro Asp Ala Gly Gly Lys
610 615 620
Met Tyr Ile Pro Pro Ser Lys Glu Gln Asp His Glu Gln Glu Asn Glu
625 630 635 640

<210> 399

<211> 624

<212> PRT

<213> *Toxoplasma gondii*

<400> 399

Met Tyr Gln Leu Leu Arg Ile Arg Ser Leu Phe Ile Phe Val Ser Ile
1 5 10 15

Leu Val Leu Gln Thr Val Thr Val Ala Ala Leu Asp Asp Gly Ala Glu
20 25 30
Ser Leu Asp Pro Gln Pro Thr Ala Gly Glu Gly Ala Lys Glu Leu Gly
35 40 45
Asn Arg Thr Thr Ser Arg Arg Lys Asp Ala Val Ala Leu Lys Thr Asp
50 55 60
Gly Thr Leu Ser Glu Ala Glu Ala Lys Arg Pro Val Glu Glu Arg Ser

65	70	75	80
Pro Gln Ser Thr Tyr Asp Phe Ser Ser Ala Ala Ser Ala Phe Gln Lys			
	85	90	95
Trp Ala Asp Gly Met Thr Pro Lys Lys Lys Glu Pro Asp Asn Leu Leu			
	100	105	110
Val Val Lys Gly Asp Arg Lys Pro Lys Ala Pro Arg Ile Ala Glu Asp			
	115	120	125
Asn Gly Thr Asp Asp Ile Ala Val Asp Glu Gly Asn Glu Ile Glu Glu			
	130	135	140
Val Ile Leu Pro Pro Leu Thr Thr Phe Leu Glu Arg Glu His Tyr Ser			
145	150	155	160
Ala Val Ala Gln Met Leu Asn Gly Met His Glu Arg Tyr Glu His Tyr			
	165	170	175
Leu Ser Ala Thr Val Leu Glu Glu Thr Arg Ala Phe Leu Asp Lys Val			
	180	185	190
Lys Asp Leu Arg Ser Asn His Ile Glu Arg Phe Asn Lys Val Ile Gly			
	195	200	205
Asn Asn Glu Phe Ala Phe Leu Arg Pro Leu Arg Tyr Ser Arg Leu Pro			
	210	215	220
His Pro Ser Ser Asp Val Leu Arg Asn Leu His Pro Glu His Asn Ala			
225	230	235	240
Val Ala Glu Lys His Trp Lys Arg Ala Trp Gly Asn His Tyr Ala Ser			
	245	250	255
Gly Glu Val Leu Lys Ile Lys Arg Leu Asp Met Ile Asn Tyr Gly Tyr			
	260	265	270
Ala Ser Ala Thr Tyr Ala Val Lys Arg Ile Phe Pro Tyr Thr Leu Asp			
	275	280	285
Pro Asp Asp Arg Gln Ser Arg Thr Leu Asp Gln Asp Gly Ala Leu Lys			
	290	295	300
Val Phe Val Val Lys Arg Asn Arg Ile Glu Val Asp Leu Val Glu Glu			
305	310	315	320

Leu Leu Leu His Gln Thr Arg Ala Trp Arg Phe Phe Pro Pro Glu Arg
 325 330 335

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

Leu Lys Leu Val Asn Asp Asp Asp Glu Glu Ile Gly Gln Lys Glu Asp
 355 360 365

Arg Ile Asn Glu Leu Leu Gly Pro Lys Gly Asp Ile Leu Asn Ala Phe
 370 375 380

Leu Leu Tyr Pro Arg Ala Tyr Ala Cys Ser Leu Lys Phe Phe Leu Ile
 385 390 395 400

Ser Trp Gly Arg Thr Asp Leu Leu Ile Lys Thr Ala Pro Met Lys Ala
 405 410 415

Met Ile Ser Ile Ser Ile Gln Met Val Tyr Ala Val Ala Ser Leu Asn
 420 425 430

Ser Tyr Gly Leu Val His Gly His Ile Arg Pro Ser Ser Phe Val Met
 435 440 445

Thr Thr Asp Gly Lys Val Leu Leu Thr Asp Phe His Thr Val Val Glu
 450 455 460

Glu Gly Ser Lys Leu Ser Cys Ser His Lys Arg Val Arg Ala Met Ala
 465 470 475 480

Asp Leu Asn Ala Ser Pro Glu Glu Leu Glu Cys Ser His His Gly Pro
 485 490 495

Gly Gln Thr Phe Glu Ala Ser Phe Ala Leu Asp Ala Trp Arg Leu Gly
 500 505 510

Val Ser Leu Tyr Lys Leu Trp Cys Arg Glu Ser Trp Arg Glu Pro Lys
 515 520 525

Pro Gly Glu Thr Trp Thr Glu Arg Leu Thr Thr Arg Gln Val Ala Phe
 530 535 540

Val Lys Ala Gln Gln Arg Gly Arg Thr Ser Arg Ser Gly Leu Asp Leu
 545 550 555 560

Gln His Cys Arg Ala Asp Thr Pro Ser Phe Ile Leu Arg Leu Ile Gln

565 570 575
Gln Phe Leu Glu Pro Asn Pro Glu Thr Arg Leu Thr Pro Ile Asp Ala
580 585 590

Val Lys Gly Thr Ser Leu Phe Arg His Met Glu Arg Arg Leu Lys Val
595 600 605

Val Gln Asp Ile Arg Glu Thr Met Leu Arg Lys Arg Ser Glu Glu Leu
610 615 620

<210> 400

<211> 776

<212> PRT

<213> Toxoplasma gondii

<400> 400

Met Gly Arg Ala Ile Ser Phe Val Leu Leu Leu Ser Ala Leu Leu Pro
1 5 10 15

Glu Gly Arg Gly Ser Val Gly Ala Ala Ala Leu Gly Ser Leu Ser Leu

20 25 30
Ala Pro Thr Ala Thr Pro Gln Thr Leu Leu Glu Leu Ser Ala Ser Ser

35 40 45
Val Thr Pro Glu Glu Thr Gly Ala Ala Pro Leu Ala Thr Pro Gly Asp

50 55 60
Asp Ser Arg Lys Arg Lys Glu Asp Gln Ala Ala Gly Glu Leu Leu Leu

65 70 75 80
Ser Trp Leu Gln Val Ala Gly Thr Ser Pro Tyr Phe Pro Ala Ala Gly

85 90 95
Pro Gln Thr Arg Arg Pro Val Ala Ser Ser Tyr Gln Ser Arg Pro Arg

100 105 110
Asn Pro Ser His Gln Pro Pro Pro Arg Gly Arg Arg Gly Pro Val Arg

115 120 125
Arg Ser Pro Gln Pro Asp Ser Val Pro Tyr Asn Leu Arg Arg Arg Pro

130 135 140
Gln Ala Val Gly Val Gln Pro Gly Ser Ala Ala Thr Arg Gly Arg Leu

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

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

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

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

Ile Ser Ala Ala Ser Ala Ser Ser Ala Gln Ser Pro Glu Ser Gln Ala

405 410 415

Met Ser Glu Ser Ile Asp Arg Met Val Pro Pro Gln Ala Ser Tyr Ser

420 425 430

Val Ala Ala Pro Asp Gly Thr Val Arg Gln Phe Met Arg Gly Ala Phe

435 440 445

Leu Gly Ala Gly Ala Thr Gly Ile Val Thr Glu Leu Ile Glu Lys Thr

450 455 460

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

465 470 475 480

Met Glu Gly Ala Ser Pro Ala Ala Phe Gln Ala Ala Gln Gln Arg Leu

485 490 495

Gln Lys Glu Ser Asn Gly Asn Glu Leu Leu Arg Thr Thr Ala Ala Gln

500 505 510

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

515 520 525

Lys Leu Ser Ala Arg Ser Gly Asp Gly Asn Gln Leu Leu Gly Thr Asn

530 535 540

Leu Val Asp Pro Glu Tyr Thr Gly Leu Asp Gly His Gln Leu Met Val

545 550 555 560

Leu Ser Asp Phe Leu Leu Leu Pro Leu Met Gly Pro Arg Leu Asp Ser

565 570 575

Leu Pro His Thr Ala Leu Ser Asp Asn Ala Gln Lys Tyr Leu Phe His

580 585 590

Thr Leu Val Thr Val Val Gly Ser Leu His Lys Ser Gly Leu Val His

595 600 605

Gly Asn Ile Arg Thr Thr Asn Val Leu Ile Asn Lys Leu Thr Gly Glu

610 615 620

Ala Gly Leu Ala Asp Phe Ser Leu Leu Met Gln Thr Gly Ser Asp Val

625 630 635 640

Thr Asp Thr Met Ser Phe His Pro Thr Gln Ser Glu Pro Glu Arg Val

645 650 655
His Ser Leu Phe Gly Leu Gly Thr Gln Leu Pro Ala Ser Glu Asp Phe

660 665 670
Asp Ser Trp Asn Leu Gly Gln Leu Leu Phe Ser Leu Leu Cys Gly Phe

675 680 685
Asp Lys Leu Pro Trp Ala Leu Gly Gln Val Phe Ala Arg Phe Ser Ala

690 695 700
Glu Ser Pro Trp Glu Met Ala Ala Glu Lys Phe Tyr Arg Gln Phe Ile

705 710 715 720
Lys Glu Val Lys Arg Glu Lys Phe Asp Ala Phe Cys Pro Gly Met Thr

725 730 735
Gly Thr Lys Leu Gln Leu Ile Ser Ile Val Lys Leu Leu Leu Asp Pro

740 745 750
Thr His Glu Thr Arg Trp Thr Ala Arg Lys Leu Val Asp Glu His Pro

755 760 765
Phe Phe Gln Val Val Glu Asp Ala

770 775

<210> 401

<211> 541

<212> PRT

<213> Toxoplasma gondii

<400> 401

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

1 5 10 15
Val Leu Ile Glu Cys His Leu Ser Asp Arg Cys Val Ala His His Gly

20 25 30
Ser Ser Thr Asp Gly Ser Gly Leu Arg Pro Pro Gln Glu Val Asp Ser

35 40 45
Ala Pro Arg Thr Pro Ser Ile Ala Val Lys Glu Leu Ala Thr Phe Pro

50 55 60
Gly Asp Asp Ile Gln Thr Ser Ser Gln Glu Leu Pro Gly Tyr Glu Leu

65	70	75	80
Trp Thr Arg Glu Gln Ser Gly Ala Ser Val Arg Val Gly Phe Pro Gln			
	85	90	95
Asn Ala Glu Ser Phe Leu Thr Gln Arg Glu Ala Arg Asp Glu Ile Ala			
	100	105	110
Asn Ala His Glu Leu Val Ala Val Thr Pro Glu Gly Asp Ala Trp Asn			
	115	120	125
His Ser Gly Val Val Pro Glu Glu Gln Thr Val Thr Pro Ala Ser Gly			
	130	135	140
Ser Phe Ile Gln Arg Gln Ala Ala His Ala Pro Pro Ser Thr Arg Leu			
145	150	155	160
Thr Pro Val Asp Arg Arg Gly Arg Ser His Thr Val Ser Ala Val Arg			
	165	170	175
Arg Arg Val Thr Val Glu Asp Val Met Arg Pro Asp Gln Ser Ala Ala			
	180	185	190
Met His Ala Val Leu Ser Ala Phe Gly Gly Gly Leu Val Leu Lys Ala			
	195	200	205
Lys Asn Lys Trp Gly Arg Thr Arg Tyr Thr Leu Gln Gly Pro Ala Thr			
210	215	220	
Phe Leu Gly Met Gly Ala Glu Gly Ile Val Val Arg Leu Asn Gln Val			
225	230	235	240
Lys Ser Asp Arg Glu Arg Ser Val Thr Pro Val Ala Val Lys Leu Cys			
	245	250	255
Leu Ile Arg Ala Ala Val Phe Ser Gly Leu Thr Trp Trp Arg Lys Arg			
	260	265	270
Arg Thr Arg Thr Glu Leu Met Lys Leu Phe Leu Ser Asn Glu Asn Ser			
275	280	285	
Val Lys Arg Ala Leu Pro Asp Leu Asp Pro Ala Glu Met Leu Glu His			
290	295	300	
Gly Leu Val Val Pro His His Ala Glu Leu Val Ser Gly Met Pro Thr			
305	310	315	320

Trp Phe Ala Ala Gly Asp Ser Phe Phe Val Leu Pro Val Val Ser Val

325 330 335

Ser Pro Leu Phe Thr Cys Asp Leu Glu Thr Val Val Gln Asn Pro Leu

340 345 350

Thr Phe Trp Ala Lys Met Tyr Ile Thr Arg Gln Leu Leu Lys Ser Ile

355 360 365

Ala Trp Met His Gln Lys Gly Ile Ser His Asn Asp Leu Lys Leu Glu

370 375 380

Asn Val Leu Leu Ser Ala Asp Gly Arg Val Ala Ile Gly Asp Phe Gly

385 390 395 400

Phe Ser Ser Pro Phe Gly Ala Ser Leu Pro Ile Arg Gly Thr His Leu

405 410 415

Tyr Met Asp Pro Asp Ser Ser Glu Ala Phe Phe Glu Gln Arg Glu Asn

420 425 430

Glu Ile Thr Pro His Arg Asp Ala Trp Ala Thr Gly Val Leu Leu Phe

435 440 445

Tyr Leu Trp Cys Gly Val Phe Pro Phe Gly Leu Gln Asn Val Ala Asn

450 455 460

Ala Gly Pro Pro Gln Val Met Arg Val Thr Val Met His Ala Arg Thr

465 470 475 480

Thr Arg Pro Pro Pro Asn Phe Arg Leu Cys Arg Arg Ile Pro Arg Glu

485 490 495

Val Arg Asn Leu Val Thr Gly Phe Leu Gln Trp Asn Glu Glu Ala Arg

500 505 510

Arg Leu Pro Ser Asp Val Ala Asp Ala Phe Leu Ala Ala Thr Asp Asp

515 520 525

Gly Gly Arg Glu Ala Arg Arg Ile Arg Thr His Gln Phe

530 535 540

<210> 402

<211> 588

<212> PRT

<213> Toxoplasma gondii

<400> 402

Met Ser Lys Pro Phe Phe Pro Gln Val Trp Val Ser Cys Thr Gly Gly

1 5 10 15

Val Leu Asn Leu Arg Arg His Trp Leu Arg Val Gly Asn Met Ser Arg

20 25 30

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

35 40 45

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

50 55 60

Ala Pro His His Pro Cys Ile Gly Arg Pro Cys Asp Gln Val Ala Ser

65 70 75 80

Val Val Ala Val Pro Pro Ala Asn Asn Leu Gly Phe Lys Arg Glu Pro

85 90 95

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

100 105 110

Val Gly Gly Pro Pro Tyr Ala Gly Asp Gly Ser Pro Leu Leu Ala Ser

115 120 125

Arg Leu Asp Trp Gln Phe Leu Gln Gln Trp His Thr Asp Glu Asp Glu

130 135 140

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

145 150 155 160

Ser Gln Ile Leu Glu Asp Cys Asn Met Glu Met Val Leu Leu Leu Asp

165 170 175

Arg Val Phe Ser Arg Ser Pro Arg Ile Thr Leu Ser Ala Val Glu Pro

180 185 190

Arg Thr His Arg Arg Arg Thr Leu Lys Leu Lys Ile Arg Ser Val Ala

195 200 205

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

210 215 220

Trp Phe Phe Arg Leu Gly His Trp Leu Gly Ser Leu Gly Arg Gln Arg

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

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

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

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

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

 Asp Pro Glu Asn Arg Leu Asp Val Leu Ser Phe Tyr Met His Ser Asp
 545 550 555 560
 Phe Phe Asn Glu Gly Arg Asn Glu Ala Asn Arg Ser Pro Pro Gln Arg
 565 570 575
 Gly Ala Pro Ile Leu Pro Leu Arg Glu Ser Ile Val
 580 585
 <210> 403
 <211> 525
 <212> PRT
 <213> Toxoplasma gondii
 <400> 403
 Met Thr Pro Ser Thr Cys Cys Phe Gly Val Leu Phe Gln Ser Phe Arg
 1 5 10 15

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

 Arg Ile Ala Ser Leu Phe Gly Arg Gly Arg Gly Lys Gly Asp Glu Glu
 85 90 95
 Ala Ser Gly Asp Glu Gly Ala Ser Gly Gly Lys Glu Gln Pro Leu Gly

100	105	110
Pro Pro Ser Gly Ile Pro Arg Arg Arg Arg Phe Trp Gln Lys Glu His		
115	120	125
Val Glu Pro Glu Asp Ala Val Val Arg Ala Phe Arg Arg Phe Leu Lys		
130	135	140
Tyr Arg Val Leu Asp Val Glu Thr Ile Glu Gly Ala Pro Ser Gln Leu		
145	150	155
Asp Arg Ser Ser Trp Thr Pro Ser Pro Pro Phe Phe Gln Pro Gly Glu		
165	170	175
Gly Ser Ser Lys Ala Val Glu Tyr Phe Val Lys Gln Gln Thr Pro Ala		
180	185	190
Leu Thr Asp Glu Met His Lys Leu Leu Glu Val Val Asp Pro Val Met		
195	200	205
Pro Pro Gly Arg Pro Leu Gln Met Ser Ser Pro Ser Ser Lys Arg Thr		
210	215	220
Thr His Phe Glu Arg Gly Pro Met Leu Arg Thr Asp Phe Phe Ala Leu		
225	230	235
Thr Val Asp His Gln Pro Phe Asn Met Arg Ile Phe Pro Leu Pro Gly		
245	250	255
Gly Phe Glu Gly Glu Gln Lys Val Glu Gln Tyr Lys Lys Val Met Leu		
260	265	270
Asn Glu Gln Lys Val Leu Ser Ile Phe Gly Val Ala Asp Gly Lys Lys		
275	280	285
Val Ser Asn Ala Tyr His Cys Tyr Leu Pro Val Glu Glu Val Phe Phe		
290	295	300
Gly Lys Gly Gln Gln Val Ile Ser Leu Gly Pro Ser Leu Lys Met Pro		
305	310	315
Ser Val Val Phe Leu Tyr Pro Ser Ala Ser Ala Thr Leu Gly Gln Val		
325	330	335
Ala Glu Ala Ile Lys Leu Ala Ala Gln Gln Gln Gly Thr Ala Leu Val		
340	345	350

Ala Gln Ala Ala Gln Leu His Ile Thr Leu Gln Leu Ile Lys Leu Val
355 360 365

Ala Ile Thr Thr Ser Lys Gly Ile Leu Leu Arg Arg Leu Ser Leu Glu
370 375 380

Asn Phe Leu Leu Arg Gly Asp Gly Val Val Phe Leu Ser Gly Phe Ser
385 390 395 400

Glu Leu Val Asn Glu Lys Glu Ile Phe Tyr Glu Thr Glu Asp Gly Thr
405 410 415

Leu Val Thr Gln Pro Pro Thr Arg Thr Ser Arg Gly Arg Arg Phe Thr
420 425 430

Pro Ala Asp Asn Ser Cys Asp Leu Gly Leu Val Ile Phe Ser Leu Trp
435 440 445

Cys Asn Gly Ser Pro Pro Glu Arg Glu Pro Ser Gly Trp Val Asn Leu
450 455 460

Asp Phe Ser Ser Cys Glu Ser Glu Val Pro Val Leu Val Gln Gln Ile
465 470 475 480

Ile Cys Gly Leu Cys Arg Ala His Gly Tyr Pro Pro Gln Asn Ala Phe
485 490 495

Gln Thr Leu Gly Ser His Glu Phe Lys Gln Leu Arg Gln Leu Tyr Arg
500 505 510

Asp Val Glu Gln Arg Ala Glu Val His Leu Leu Val Glu
515 520 525

<210> 404

<211> 490

<212> PRT

<213> Toxoplasma gondii

<400> 404

Met Arg His Val Phe Asn Ser Ser Ala Trp Arg Val Asp Leu Ser Gly
1 5 10 15

Ser Ala Asn Val Gly Arg Val Ala Glu Glu Phe Asp Arg Gln Glu Gly
20 25 30

Pro Asp Ala Leu Ile Gly Gln Pro Thr His Ala Asp Asn Gln Glu Ser

35 40 45
 Leu Ser Asn Leu Cys His Thr Gln Asn Asp Thr Ser Thr Glu Pro Ala

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

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

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

 245 250 255
 Phe Ala Val Pro Leu Phe Cys Gly Arg Ile Arg Gly Leu Pro Asp Leu
 260 265 270
 Phe Asp Ile Gly Ser Arg Gly Ala Gly Cys Ser Ile Val Val Leu Tyr
 275 280 285

Lys Arg Leu Tyr Cys Ser Leu Ala Asp Leu Leu Ser Ala Cys Ala Ser
 290 295 300
 Leu Ser Tyr Gln Ala Arg Leu Phe Leu Thr Lys Gln Met Ile Glu Val

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

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

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

 <210> 405
 <211> 206
 <212> PRT
 <213> Toxoplasma gondii
 <400> 405

Met Asn Tyr Leu Gly Leu Cys Val Thr Arg Glu Lys Lys Gly Cys Thr

1 5 10 15

Thr Gly Asn Val Tyr Met Phe Thr Pro Leu Leu Gln Gly Asp Ile Arg

20 25 30

Arg Val Ala Val Gln His Pro Ser Gln Cys Ile Ser Gly Glu Leu Val

35 40 45

Leu Lys Glu Met Ala Ala Ser Leu Lys Val Leu His Asp Ala Gly Leu

50 55 60

Val His Gly Asp Val Lys Glu Gln Asn Phe Phe Val Gly Arg Asp Gly

65 70 75 80

His Val Val Ile Ala Asp Phe Gly Ala Leu Gly Tyr Pro Gly Cys Ser

85 90 95

Leu Glu Ala Gly Thr Leu Gly Tyr Ile Ala Pro Glu Arg Leu Val Asn

100 105 110

Asp Asn Ala Asn Ser Phe Ala Ser Asp Ile Trp Ala Leu Gly Val Thr

115 120 125

Phe Lys Asn Val Leu Thr Ala Leu Arg Ala Thr Val Arg Ala Asp Arg

130 135 140

Glu Val Leu Asp Gly Leu Ser Asn Arg Met Thr Ala Ser Asp Pro Ala

145 150 155 160

Ala Arg Pro Ser Val Asp Asp Val Leu Leu Asp Pro Cys Leu Ser Ala

165 170 175

Pro Pro Ser Leu Ala Ser His Asp Val Ala Pro Phe Thr Pro Asp Ala

180 185 190

Phe Gly Tyr Tyr Cys Leu Thr Gly Ala Thr Asn Thr Ser Asp

195 200 205

<210> 406

<211> 510

<212> PRT

<213> Toxoplasma gondii

<400> 406

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

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

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

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

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

Ala Ser Asp Ala Asp Glu Asp Ser Asp Asp Asp Asp Leu Pro
500 505 510

<210> 407
<211> 377
<212> PRT
<213> *Toxoplasma gondii*
<400> 407

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

195 200 205
 Ala Asn Met Val Ala Ala Leu Lys Ser Leu His Asn Leu Gly Leu Leu
 210 215 220
 His Arg Ser Ile Glu Leu Asn Ser Phe Ser Val Leu Pro Asp Gly Thr

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

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

 355 360 365
 Pro Phe Arg Tyr Lys Gln Asn Arg Leu
 370 375
 <210> 408
 <211> 159
 <212> PRT
 <213> Toxoplasma gondii
 <400> 408
 Met Asn Asp Thr Gly Ser Trp Ala Thr Glu Arg Ser Gly Ala Leu Pro
 1 5 10 15
 Arg Phe Arg Thr Thr Gly Glu Gln Leu Ser Glu Gly Ala Ser Val Arg
 20 25 30

Glu Asp Leu Ala Pro Gly Ile Arg Gly Val Leu Thr Lys Lys Gly Ala

35 40 45

Arg Ala Arg Thr Thr Lys Arg His Glu Leu Val Ser Val Thr Ser Glu

50 55 60

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

65 70 75 80

Pro Pro Val Ala Ala Ser Ser Ser Phe Met Gln Ser Pro Ser Ser Leu

85 90 95

Ala Thr Pro Val Val Leu Asn Ala Pro Val Asp Phe His Gly Gln Gly

100 105 110

Asp Ile Thr Ala Ala Val Arg Ser Arg Pro Leu Val Thr Ala Gly Leu

115 120 125

Ser Arg His Gln Ile Glu Ala Lys Asn Glu Phe Asp Arg Arg Phe Ala

130 135 140

Glu Gly Phe Gln Leu Thr Ala Glu Ser Ile Phe Thr Gly Glu Thr

145 150 155

<210> 409

<211> 1363

<212> PRT

<213> Toxoplasma gondii

<400> 409

Met Lys Gln Gly Thr Thr Arg Pro Arg Val Gly Leu Thr Gly Ala Val

1 5 10 15

Leu Leu Leu Val Val Trp Thr Val Ala Ile Leu Ile Asp Cys Ser Ser

20 25 30

Gly Ser Arg Val Leu Phe Asp Arg Arg Pro Ile Leu Ala Arg Leu Arg

35 40 45

Arg Ala Thr Ser Phe Val Asp Ser Thr Ser Gly Gln Asn Ala Ser Pro

50 55 60

Arg Pro Thr Lys Thr Asp Lys Ile Arg Lys Pro Arg Asn Asp Ser Arg

65 70 75 80

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

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

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

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

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

	325		330		335
Phe Val Phe Tyr Leu Pro Pro Gln Ala Lys Asn Trp Arg Ser Lys Pro					
	340		345		350
Leu Gln Phe Ile Ser Glu Met Leu Glu His Glu Gly Pro Thr Ser Leu					
	355		360		365
Ser Ser Lys Leu Lys Arg Glu Gly Leu Ile Thr Ser Leu Val Thr Asp					
	370		375		380
Tyr Trp Ser Pro Glu Leu Cys Thr Val Leu Gln Val Asn Val Arg Leu					
385		390		395	400
Thr Glu Gly Gly Arg Ser Lys Glu Ser Val Tyr Lys Ile Gly His Ala					
	405		410		415
Leu Phe Thr Phe Leu Arg Asn Leu Gly Val Ser Arg Pro Glu Arg Trp					
	420		425		430
Arg Val Thr Glu Met Ala Lys Ile Arg Gln Leu Gly Phe Thr Phe Ala					
	435		440		445
Asp Met Pro Asp Pro Tyr Ala Leu Thr Val Arg Ala Val Glu Gly Leu					
	450		455		460
Asn Tyr Tyr Thr Pro Glu Glu Val Ile Ala Gly Asp Arg Leu Ile Tyr					
465		470		475	480
His Phe Asp Pro Asp Ile Ile Gln Gln Tyr Val Gln Lys Phe Leu Val					
	485		490		495
Pro Asp Asn Val Arg Leu Phe Ile Phe Asp Lys Lys Leu Ala Ala Asp					
	500		505		510
Val Asp Arg Glu Glu Tyr Trp Phe Lys Ile Lys His Gly Val Glu Pro					
	515		520		525
Ile Met Asp Ser Val Phe Lys Lys Trp Lys Glu Ile Thr Ser Ala Pro					
	530		535		540
Ala Asn Thr Val Gln Ser Met Met Arg Met Glu Gly Met Ala Leu Pro					
545		550		555	560
Ala Pro Asn Arg Phe Leu Pro Asn Asn Val Ala Ile Leu Pro Arg Pro					
	565		570		575

Pro Gly Ser Gly Gln Gly Ala Glu Lys Ser Ala Phe Pro Glu Pro Leu
580 585 590

Val Phe Ala Gly Asp His Ile Cys Ala Asn Lys Cys Ala Val Phe His
595 600 605

Lys Gln Asp Thr Thr Phe His Ser Pro Lys Ala Val Val Glu Leu Gln
610 615 620

Ile Tyr Tyr Thr Gly Ser His Glu Asp Gly Val Arg Glu Arg Ile Leu
625 630 635 640

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

Ala Asp Thr His Arg Ala Gly Met Ser Leu Gly Leu Gly Ser Gly Val
660 665 670

Ala Val Gly Ser Thr Thr Leu Pro Thr Val Lys Arg Gln Arg Val Leu
675 680 685

Thr Leu Ser Ala Ala Gly Phe Ser Asp Lys Leu Asp Tyr Val Leu Arg
690 695 700

Ala Phe Ala Lys Ser Leu Ala Ala Thr Glu Gly Ala Ser Asp Glu Lys
705 710 715 720

Pro Ile Pro Ser Pro Met Glu Leu Gly Val Thr Met Ser His Gly Val
725 730 735

Arg His Leu Met His Ser Arg Val Thr Ala Pro Ser Asn Val Leu Ala
740 745 750

Ser Val Gln Ser Ser Arg Val Tyr Thr Thr Ala Val Arg Leu Pro Gly
755 760 765

Gly Gly Arg Ala Ala Arg Arg Thr Leu Thr His Asp Gln Ile Thr Thr
770 775 780

Met His Arg Lys Pro Ala Ser Met Asp Val Thr Leu Met Arg Thr Pro
785 790 795 800

Val Ser Ser Leu Gly Ile Arg Ile Val Gly Gly Arg Ala Glu Arg Glu
805 810 815

Ala Thr Pro Val Val Ala Gly Gly Gly Lys Pro Leu Leu Glu Lys Arg

820	825	830	
Phe Phe Arg Leu Ala Phe Asp Gln Leu Arg Thr Asp Leu Arg Val Ala			
835	840	845	
Thr Leu Asn Arg Thr Pro Leu Ala Gln Ala Asn Asp Ala Val Leu Glu			
850	855	860	
Leu Ile Met His Pro His Val Pro Val His Lys Met Tyr Ala Ala Leu			
865	870	875	880
Phe Glu Met Glu Lys Asn His Pro Thr Leu Asp Ala Ile Phe Glu Glu			
885	890	895	
Val Ala Asp Trp Gly Val Lys Leu Trp Asn Glu Ala Ala Val Glu Gly			
900	905	910	
Leu Val Gln Gly Asn Ile Thr Ser Glu Ser Ala Thr Gln Leu Val Gly			
915	920	925	
Asp Val Ile Ser Leu Leu Pro Leu Lys Asn Ile Val Ala Ala Asn Thr			
930	935	940	
Ile Ala Lys Pro Thr Ile Ser Ser Phe Ser Ser Leu Arg Arg Ala Ser			
945	950	955	960
Ser Val Ala Pro Gln Ser Ser Ser Lys Gln Asp Ser Val Pro Ser Ser			
965	970	975	
Asp Met Pro Thr Ser Thr Glu Thr Leu Ser Met Pro Ser Ser Ala Glu			
980	985	990	
Ser Gln Thr Pro Glu Ser Thr Asp Arg Ala Ser Phe Pro Met Glu Ser			
995	1000	1005	
Thr Thr Gly Pro Ala Pro Tyr Ser Val Glu Leu Ser Thr Gly Arg			
1010	1015	1020	
Thr Pro Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr Pro			
1025	1030	1035	
Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr Ser Asp Asp Leu Pro			
1040	1045	1050	
Thr Ser Ser Thr Pro Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr			
1055	1060	1065	

Pro Tyr Ser Asp Tyr Leu Pro Thr Ser Ser Thr Pro Tyr Pro Asp		
1070	1075	1080
Asp Leu Pro Thr Ser Ser Thr Pro Tyr Pro Asp Asp Leu Pro Thr		
1085	1090	1095
Ser Gly Thr Pro Tyr Pro Asp Asp Leu Pro Thr Arg Ser Thr Pro		
1100	1105	1110
Ala Ala Asp Asp Leu Pro Ala Ser Ser Thr Pro Tyr Pro Asp Asp		
1115	1120	1125
Leu Pro Thr Ser Gly Thr Pro Tyr Pro Asp Asp Phe Pro Thr Ser		
1130	1135	1140
Ser Thr Pro Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr		
1145	1150	1155
Pro Asp Asp Leu Pro Thr Arg Ser Thr Pro Ala Ala Asp Asp Leu		
1160	1165	1170
Pro Thr Ser Arg Thr Pro Tyr Pro Asp Asp Leu Pro Ile Arg Ser		
1175	1180	1185
Thr Pro Ser Pro Ile Val Leu Ser Ala Gly Arg Ala Pro Ser Val		
1190	1195	1200
Val Val Ser Pro Ile Glu Arg Thr Ser Ser Pro Ala Leu Leu Pro		
1205	1210	1215
Thr Glu Arg Thr Pro Leu Thr Glu Arg Ile Ala Gln Ala Leu Arg		
1220	1225	1230
Pro Val Gly Glu Ala Ala Ala Val Arg Arg Leu Leu Val Leu Arg		
1235	1240	1245
Arg Ser Ser Ile His Arg Met Pro Tyr Ser Pro Phe Gln Tyr Ser		
1250	1255	1260
Ser Thr Trp Phe His Pro Ser Ser Asn Ser Arg Arg Gln Met Met		
1265	1270	1275
Leu Arg Met Ala Leu Arg Arg Gln Leu Gly Ala Leu Thr Arg Gln		
1280	1285	1290
Ala Gln Pro Asp Thr Glu Gly Lys Pro Ser Thr Val Phe Val Phe		

1295 1300 1305
 Arg Arg Leu Ala Pro Met Pro Arg Arg Leu Asn Ile Glu Gln Gly
 1310 1315 1320

 Pro Ser Phe Leu Gln Arg Gln Gly Glu Tyr Ala Ala Ser Gly Ser
 1325 1330 1335
 Ala Pro His Ser Asp Cys Thr Asn Gly Ala Cys Ala Lys Gly Ala
 1340 1345 1350
 Cys Ser Gly Thr Gly Cys Gln Lys Arg Leu
 1355 1360
 <210> 410
 <211> 354
 <212> PRT
 <213> Toxoplasma gondii
 <400> 410
 Met Pro Arg Arg Leu Asn Ile Glu Gln Gly Pro Ser Phe Leu Gln Arg
 1 5 10 15

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

 Ser Asp His Pro Cys Thr Gly Asp Glu Cys Pro Val Pro Cys Arg Gly
 85 90 95
 Pro Gly Cys Ser Ala Pro Ala Ser His Pro Ser Pro Cys Thr Glu Ala
 100 105 110
 Glu Cys Gly Lys Asn Ser Cys Pro Gly Cys Lys Gln Glu Glu Glu Lys
 115 120 125
 Leu Val Gln Leu Arg Ser Ile Arg Lys Asn Leu Asn Pro Asn Asp Lys

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

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

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

 Asp Ile Asp Pro Glu Leu Leu Ser Asn Ile Thr Val Pro Asp Met Glu
 340 345 350
 Ser Asp

<210> 411

<211> 1645

<212> PRT

<213> *Toxoplasma gondii*

<400> 411

Met Lys Gln Gly Thr Thr Arg Pro Arg Val Gly Leu Thr Gly Ala Val

1 5 10 15

Leu Leu Leu Val Val Trp Thr Val Ala Ile Leu Ile Asp Cys Ser Ser

20 25 30

Gly Ser Arg Val Leu Phe Asp Arg Arg Pro Ile Leu Ala Arg Leu Arg

35 40 45

Arg Ala Thr Ser Phe Val Asp Ser Thr Ser Gly Gln Asn Ala Ser Pro

50 55 60

Arg Pro Thr Lys Thr Asp Lys Ile Arg Lys Pro Arg Asn Asp Ser Arg

65 70 75 80

Asn Tyr Arg Tyr Ile Glu Leu Pro Asn Glu Leu Arg Ala Leu Leu Val

85 90 95

Ser Asp Pro Glu Cys Asp Glu Ala Ala Ala Ser Met Arg Val Gly Val

100 105 110

Gly Ser Met Ser Asp Pro Pro Lys Ile Pro Gly Leu Ala His Phe Thr

115 120 125

Glu His Met Leu Phe Gln Gly Ser Lys Arg Phe Pro Gly Thr His Asp

130 135 140

Phe Phe Asp Phe Val His Asn His Gly Gly Tyr Thr Asn Ala Phe Thr

145 150 155 160

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

165 170 175

Glu Pro Gly Leu Asp Arg Leu Ala Asp Leu Phe Ser Ala Pro Leu Leu

180 185 190

Lys Ser Glu Asn Leu Leu Lys Glu Val Asn Ala Val His Ser Glu Tyr

195 200 205

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

210 215 220

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

225 230 235 240

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

245 250 255

Ala Met Arg Glu Phe His Asn Lys Trp Tyr Ser Ser Asn Leu Met Thr

260 265 270

Leu Ala Val Val Gly Arg Glu Ser Leu Asp Val Leu Glu Ser His Val

275 280 285

Arg Lys His Phe Gly Asn Val Pro Asn Gly Arg Val Thr Pro Pro Val

290 295 300

Phe Glu Glu Cys Ser Glu Ala Phe Ile Pro Leu Asp Pro Asn Glu Leu

305 310 315 320

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

325 330 335

Phe Val Phe Tyr Leu Pro Pro Gln Ala Lys Asn Trp Arg Ser Lys Pro

340 345 350

Leu Gln Phe Ile Ser Glu Met Leu Glu His Glu Gly Pro Thr Ser Leu

355 360 365

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

370 375 380

Tyr Trp Ser Pro Glu Leu Cys Thr Val Leu Gln Val Asn Val Arg Leu

385 390 395 400

Thr Glu Gly Gly Arg Ser Lys Glu Ser Val Tyr Lys Ile Gly His Ala

405 410 415

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

420 425 430

Arg Val Thr Glu Met Ala Lys Ile Arg Gln Leu Gly Phe Ala Phe Ala

435 440 445

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

450 455 460

Asn Tyr Tyr Thr Pro Glu Glu Val Ile Ala Gly Asp Arg Leu Ile Tyr

465 470 475 480
 His Phe Asp Pro Asp Ile Ile Gln Gln Tyr Val Gln Lys Phe Leu Val

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

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

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

 675 680 685
 Thr Leu Ser Ala Ala Gly Phe Ser Asp Lys Leu Asp Tyr Val Leu Arg
 690 695 700
 Ala Phe Ala Lys Ser Leu Ala Ala Thr Glu Gly Ala Ser Asp Glu Lys
 705 710 715 720

Pro Ile Pro Ser Pro Met Glu Leu Gly Val Thr Met Ser His Gly Val
725 730 735

Arg His Leu Met His Ser Arg Val Thr Ala Pro Ser Asn Val Leu Ala
740 745 750

Ser Val Gln Ser Ser Arg Val Tyr Thr Thr Ala Val Arg Leu Pro Gly
755 760 765

Gly Gly Arg Ala Ala Arg Arg Thr Leu Thr His Asp Gln Ile Thr Thr
770 775 780

Met His Arg Lys Pro Ala Ser Met Asp Val Thr Leu Met Arg Thr Pro
785 790 795 800

Val Ser Ser Leu Gly Ile Arg Ile Val Gly Gly Arg Ala Glu Arg Glu
805 810 815

Ala Thr Ser Val Val Ala Gly Gly Gly Lys Pro Leu Leu Glu Lys Arg
820 825 830

Phe Phe Arg Leu Ala Phe Asp Gln Leu Arg Thr Asp Leu Arg Val Ala
835 840 845

Thr Leu Asn Arg Thr Pro Leu Ala Gln Ala Asn Asp Ala Val Leu Glu
850 855 860

Leu Ile Met His Pro His Val Pro Val His Lys Met Tyr Ala Ala Leu
865 870 875 880

Phe Glu Met Glu Lys Asn His Pro Thr Leu Asp Ala Ile Phe Glu Glu
885 890 895

Val Ala Asp Trp Gly Val Lys Leu Trp Asn Glu Ala Ala Val Glu Gly
900 905 910

Leu Val Gln Gly Asn Ile Thr Ser Glu Ser Ala Thr Gln Leu Val Gly
915 920 925

Asp Val Ile Ser Leu Leu Pro Leu Lys Asn Ile Val Ala Ala Asn Thr
930 935 940

Ile Ala Lys Pro Thr Ile Ser Ser Phe Ser Ser Leu Arg Arg Ala Ser
945 950 955 960

Ser Val Ala Pro Gln Ser Ser Ser Lys Gln Asp Ser Val Pro Ser Ser

965	970	975
Asp Met Pro Thr Ser Thr Glu Thr Leu Ser Met Pro Ser Ser Ala Glu		
980	985	990
Ser Gln Thr Pro Glu Ser Thr Asp Arg Ala Ser Phe Pro Met Glu Ser		

995	1000	1005
Thr Thr Gly Pro Ala Pro Tyr Ser Val Glu Leu Ser Thr Gly Arg		
1010	1015	1020
Thr Pro Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr Pro		
1025	1030	1035
Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr Pro Asp Asp Leu Pro		
1040	1045	1050
Thr Ser Ser Thr Pro Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr		

1055	1060	1065
Pro Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr Pro Asp		
1070	1075	1080
Asp Leu Pro Thr Arg Ser Thr Pro Ala Ala Asp Asp Leu Pro Ala		
1085	1090	1095
Ser Ser Thr Pro Tyr Pro Asp Asp Leu Pro Thr Ser Gly Thr Pro		
1100	1105	1110
Tyr Pro Asp Asp Leu Pro Thr Ser Ser Thr Pro Tyr Pro Asp Asp		

1115	1120	1125
Leu Pro Thr Ser Ser Thr Pro Tyr Pro Asp Asp Leu Pro Thr Arg		
1130	1135	1140
Ser Thr Pro Ala Ala Asp Asp Leu Pro Thr Ser Arg Thr Pro Tyr		
1145	1150	1155
Pro Asp Asp Leu Pro Ile Arg Ser Thr Pro Ser Pro Ile Val Leu		
1160	1165	1170
Ser Ala Gly Arg Ala Pro Ser Val Val Val Ser Pro Ile Glu Arg		

1175	1180	1185
Thr Ser Ser Pro Ala Leu Leu Pro Thr Glu Arg Thr Pro Leu Thr		
1190	1195	1200

Glu Arg Ile Ala Gln Ala Leu Arg Pro Val Gly Glu Ala Ala Ala		
1205	1210	1215
Val Arg Arg Leu Leu Val Leu Arg Arg Ser Ser Ile His Arg Met		
1220	1225	1230
Pro Tyr Ser Pro Phe Gln Tyr Ser Ser Thr Trp Phe His Pro Ser		
1235	1240	1245
Ser Asn Ser Arg Arg Gln Met Met Leu Arg Met Ala Leu Arg Arg		
1250	1255	1260
Gln Leu Gly Ala Leu Thr Arg Gln Ala Gln Pro Asp Thr Glu Gly		
1265	1270	1275
Lys Pro Ser Thr Val Phe Val Phe Arg Arg Leu Ala Pro Met Pro		
1280	1285	1290
Arg Arg Leu Asn Ile Glu Gln Gly Pro Ser Phe Leu Gln Arg Gln		
1295	1300	1305
Gly Glu Tyr Ala Ala Ser Gly Ser Ala Pro His Ser Asp Cys Thr		
1310	1315	1320
Asn Gly Ala Cys Ala Lys Gly Ala Cys Ser Gly Thr Gly Cys Gln		
1325	1330	1335
Lys Thr Pro Val Lys Pro Ser Gly Gly Pro Cys Lys Gly Asp Ala		
1340	1345	1350
Cys Thr Gly Ser Ser Cys Asn Ser Leu Glu Cys Gln Arg Ser Ser		
1355	1360	1365
Ser Ser Lys Ser Asp His Pro Cys Thr Gly Asp Glu Cys Pro Val		
1370	1375	1380
Pro Cys Arg Gly Pro Gly Cys Ser Ala Pro Ala Ser His Pro Ser		
1385	1390	1395
Pro Cys Thr Glu Thr Glu Cys Gly Lys Asn Ser Cys Pro Gly Cys		
1400	1405	1410
Lys Gln Glu Glu Glu Lys Leu Val Gln Leu Arg Ser Ile Arg Lys		
1415	1420	1425
Asn Leu Asn Pro Asn Asp Lys Lys Asn Gln Ala Tyr Leu Leu Ile		

1430	1435	1440
Glu Val Gly Ala Leu Pro Asn Ile His Asp Arg Ala Val Leu Tyr		
1445	1450	1455
Met Val Ser Arg Trp Met Ser Gln Arg Phe Phe Asn Lys Leu Arg		
1460	1465	1470
Thr Glu Gln Gln Leu Gly Tyr Leu Thr Ala Met His Ser Ser Arg		

1475	1480	1485
Leu Glu Asp Arg Phe Tyr Tyr Arg Phe Phe Ile Thr Ser Thr Tyr		
1490	1495	1500
Asp Pro Ala Glu Val Ala Asp Arg Ile Val Glu Phe Ile Asn Ala		
1505	1510	1515
Glu Arg Ser Lys Ile Pro Thr Gln Glu Glu Phe Ala Thr Leu Lys		
1520	1525	1530
Gln Ala Ala Ile Asp Val Trp Lys Gln Lys Pro Lys Asn Ile Phe		

1535	1540	1545
Glu Glu Phe Arg Lys Asn Arg Arg Gln Val Val Leu Gly Asp Arg		
1550	1555	1560
Leu Phe Asp Ile Asn Glu Arg Met Val Ala Glu Leu Glu Arg Val		
1565	1570	1575
Thr Pro Glu Glu Ile Gln Ser Phe Lys Glu Lys Thr Met Phe Asn		
1580	1585	1590
Ala Pro Trp Leu Leu Met Glu Val Tyr Ser Gln Arg Glu Lys Pro		

1595	1600	1605
Gln Met Leu Pro Gln Ala Asn Gly Ala Ser Gly Glu Ser Lys Leu		
1610	1615	1620
Asp Pro Trp Val Asp Ile Asp Pro Glu Leu Leu Ser Asn Ile Thr		
1625	1630	1635
Val Pro Asp Met Glu Ser Asp		
1640	1645	

<210> 412

<211> 784

<212> PRT

<213> Toxoplasma gondii

<400> 412

Met Ala Arg Ser Ser Arg Ala Ala Pro Ser Gly Ala Phe Ala His Gly

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

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

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

195 200 205
Gly Ala Leu Leu Arg Arg Ile Trp Lys Glu His Gln Arg Val Gly Asp
210 215 220
Asp Met Arg Asp Leu Leu Arg Glu Tyr Ile Leu Ala Leu Glu Arg Glu

225 230 235 240
 Leu Tyr Thr Gln Gln Ala Glu Val Phe Gly Val Glu Gln Leu Lys Met
 245 250 255
 Asp Asp Val Ile His His Glu His Ser Ser Glu Ala Arg Lys Arg Glu

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

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

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

 450 455 460
 Lys Arg Thr His Gly His Pro Glu Lys Gln Leu His Phe Lys Arg Asn
 465 470 475 480

Gln Gly Ser Trp Lys His Asp Phe Arg Leu Pro Trp Glu Lys Glu Glu
485 490 495

Ala His Pro Trp Tyr Lys Gly Ser Ser Lys Pro Ser Arg Ala His Ser
500 505 510

His Arg Gln Ser Val Ser Val Tyr Ala Ser Pro Thr Glu Pro Val Glu
515 520 525

Asp His Glu Glu Asp Ser Ser Met Asn His Glu Asp Ser Ala Val Phe
530 535 540

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

Ala Ala Asp Asn Thr Pro Tyr Ala Lys Gln Lys Ser Phe Val Gln Arg
565 570 575

Ala Gln His Ser Val Gln Asp Ile Arg Glu His Arg Asp Val Asp Arg
580 585 590

Glu Asp Gly Val Glu Gly Glu Gln Pro Leu Ser Phe Leu Glu Thr Arg
595 600 605

Ser Ser Ala Glu Glu Gly Gly Gly Ser Asp Glu Met Arg Ser Glu Ser
610 615 620

Glu Gly Gln Gly Ser Ala Ala Asn Gly Thr Glu Gly Glu Ser Asp Lys
625 630 635 640

Ala Glu Glu Ala Gly Lys Thr Ala Gly Gly Ser Ala Glu Lys Asp Lys
645 650 655

Asp Ala Ser Glu Ala Glu Gly Ala Glu Glu Ala Ser Ser Glu Lys Thr
660 665 670

Asp Gly Gln Gly Gly Asn Asp Gln Pro Ser Glu Ser Glu Ser Ala Gly
675 680 685

Gly Ala Ala Thr His Gly Glu Ser Ser Thr Pro Glu Glu Gly Glu Gly
690 695 700

Ser Glu Lys Ala Glu Glu Lys Gly Gly His Asp Lys Pro Glu Glu Asn
705 710 715 720

Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly Gly His Asp Lys Pro Glu

725 730 735
 Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly Gly His Asp Lys
 740 745 750
 Pro Glu Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly Gly His
 755 760 765
 Asp Lys Pro Glu Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly

770 775 780

<210> 413

<211> 291

<212> PRT

<213> Toxoplasma gondii

<400> 413

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

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

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

Asp Lys Val Cys Val Arg Pro Arg Glu Leu Ala Asn Ala Met Leu Asn
165 170 175

Pro Asp Lys Pro Phe Tyr Ala Leu Gly Asp Gln Val Glu Ala Ser His
180 185 190

Cys Cys Phe Val Lys Cys Arg Pro Gly Ala Ser Phe Met Gly Ile Ser
195 200 205

Arg Val Ile Thr Cys His Glu Glu Gly Val Phe Asp Pro Gln Val Ala
210 215 220

Cys Ile Ala Lys Gly Thr Leu Ser Ser Gln Gln Gln Ala Phe Met Lys
225 230 235 240

Glu Val Gln Asp Tyr Ala Asp Val Val Glu Ala Ala Pro Glu Leu Ala
245 250 255

Ala Ala Gly Leu Glu Thr Gly Gly Ala Leu Ala Thr Ala Ser Thr Gln
260 265 270

Gly Val Ala Val Ala Ala Phe Ala Leu Ile Gly Val Ser Ala Ile Val
275 280 285

Lys Thr Phe
290

<210> 414

<211> 1158

<212> PRT

<213> Toxoplasma gondii

<400> 414

Met Ala Arg Ser Ser Arg Ala Ala Pro Ser Gly Ala Phe Ala His Gly

1 5 10 15
Val Ala Lys Ala Ser Phe Thr Trp Ile Ser Gly Met Lys Thr Pro Phe
20 25 30

Gly Cys Val Phe Phe Phe Cys Leu Ile Ala Leu Trp Gly Phe Ser Ala
35 40 45

Ala Leu Arg Thr Ser Asp Ile Gly Val Asp Ala Leu Ser Val Ser Ser
50 55 60

Arg Ala Ala Ala Asn Gly Ser Glu Gly Gly Val Ala Gln Ser Glu Gln

65 70 75 80

Glu Arg Ala Ser Asp Glu Gln Arg Asn Asp Ser Glu Ala His Asp Ser

85 90 95

Val Ala Ser Ser Glu Ser Ser Asp Ala Glu Arg Lys Asp Asp Pro Pro

100 105 110

Asp Asn Lys Ser Thr Ser Glu Thr Pro Glu Ala Lys Leu Ala Gly Arg

115 120 125

Asp Ala Ser Asn Pro Pro Ala Ser Ser Lys Ser Pro Thr Pro Ser Pro

130 135 140

Ala Pro Thr Pro Ala Val Ser Thr Ser Thr Thr Pro Ala Lys Ser Ser

145 150 155 160

Ala Asp Thr Ser Lys Asp Pro Lys Asn Lys Leu Ser Ser Ala Arg Lys

165 170 175

Glu Lys Arg Ile Gly Lys Lys Phe Lys Arg His Asp Glu Phe Leu Ala

180 185 190

Asp Ala Val Ile Asp Lys Leu Asp Ser Met Arg Ser Val Gln Val Ser

195 200 205

Gly Ala Leu Leu Arg Arg Ile Trp Lys Glu His Gln Arg Val Gly Asp

210 215 220

Asp Met Arg Asp Leu Leu Arg Glu Tyr Ile Leu Ala Leu Glu Arg Glu

225 230 235 240

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

245 250 255

Asp Asp Val Ile His His Glu His Ser Ser Glu Ala Arg Lys Arg Glu

260 265 270

Val Glu Leu Glu Met Gln Ala Leu Ala Glu Gln His Asn Phe Met Lys

275 280 285

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

290 295 300

Ala Leu Val Asn Arg Ile Glu Glu Leu Asp Lys Pro Ile Asp Ile Ile

305 310 315 320
 Asp Ala Ile Asp Lys Arg Ser Gly Ser Asp Val Leu His Cys Leu Lys

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

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

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

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

Ala Ala Asp Asn Thr Pro Tyr Ala Lys Gln Lys Ser Phe Val Gln Arg
565 570 575

Ala Gln His Ser Val Gln Asp Ile Arg Glu His Arg Asp Val Asp Arg
580 585 590

Glu Asp Gly Val Glu Gly Glu Gln Pro Leu Ser Phe Leu Glu Thr Arg
595 600 605

Ser Ser Ala Glu Glu Gly Gly Gly Ser Asp Glu Met Arg Ser Glu Ser
610 615 620

Glu Gly Gln Gly Ser Ala Ala Asn Gly Thr Glu Gly Glu Ser Asp Lys
625 630 635 640

Ala Glu Glu Ala Gly Lys Thr Ala Gly Gly Ser Ala Glu Lys Asp Lys
645 650 655

Asp Ala Ser Glu Ala Glu Gly Ala Glu Glu Ala Ser Ser Glu Lys Thr
660 665 670

Asp Gly Gln Gly Gly Asn Asp Gln Pro Ser Glu Ser Glu Ser Ala Gly
675 680 685

Gly Ala Ala Thr His Gly Glu Ser Ser Thr Pro Glu Glu Gly Glu Gly
690 695 700

Ser Glu Lys Ala Glu Glu Lys Gly Gly His Asp Lys Pro Glu Glu Asn
705 710 715 720

Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly Gly His Asp Lys Pro Glu
725 730 735

Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly Gly His Asp Lys
740 745 750

Pro Glu Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly Gly His
755 760 765

Asp Lys Pro Glu Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu Lys Gly
770 775 780

Gly His Asp Lys Pro Glu Glu Asn Asp Ser Ser Glu Lys Ala Glu Glu
785 790 795 800

Lys Gly Gly His Asp Lys Ser Glu Glu Asn Asp Ser Ser Glu Lys Ala

805	810	815	
Glu Glu Thr Gly Ser His Asp Lys Pro Glu Glu Asn Asp Ser Ser Glu			
820	825	830	
Lys Ala Glu Ala Thr Ser His Thr Arg Ser Glu Asp His Pro Arg Cys			
835	840	845	
Ile Glu Ile Met Asp Pro Gln Glu Cys Val Lys Thr Lys Asn Cys Phe			
850	855	860	
His Asp Asp Val Tyr Arg Gln Cys Phe Phe Asn Cys Thr Ala Ile Val			
865	870	875	880
Glu Ala Asp Lys Cys Lys Glu His Gln Asn Cys Arg Tyr Glu Thr Leu			
885	890	895	
Leu Pro Lys Asp Ala Cys Val Asn Gln Gly Tyr Gln Ser Val Ser Leu			
900	905	910	
Thr Lys Gln Ala Phe Glu Gly Ile Met Arg Gly Cys Glu Glu Phe Arg			
915	920	925	
Asp Lys Pro Ser Cys Asp Met Met Glu Lys Ala Thr Gln Arg Leu Lys			
930	935	940	
Glu Ser Gly Thr Pro Val Ile Tyr Asp Cys His Trp Leu Ser Glu Gly			
945	950	955	960
Pro Glu Val Ser Gly Glu Val Leu Ser Asp Gly Thr Gln Pro Gly Asp			
965	970	975	
Asn Glu Glu Lys Glu Val Gly Lys Glu Glu Ala Ala Gln Thr Gln Gly			
980	985	990	
Gly Arg Ser Ile Cys Val Asn Arg Leu Glu Ala Pro Thr Ala Glu Lys			
995	1000	1005	
Leu Leu Trp Gly Thr Ile Ile Ala Glu Lys Glu Arg Lys Leu Gln			
1010	1015	1020	
Glu Leu Gln Ile Ser Arg Asn Leu Thr Pro Asp Lys Val Cys Val			
1025	1030	1035	
Arg Pro Arg Glu Leu Ala Asn Ala Met Leu Asn Pro Asp Lys Pro			
1040	1045	1050	

Phe Tyr Ala Leu Gly Asp Gln Val Glu Val Lys Cys Arg Pro Gly
1055 1060 1065

Ala Ser Phe Met Gly Ile Ser Arg Val Ile Thr Cys His Glu Glu
1070 1075 1080

Gly Val Phe Asp Pro Gln Val Ala Cys Ile Ala Lys Gly Thr Leu
1085 1090 1095

Ser Ser Gln Gln Gln Ala Phe Met Lys Glu Val Gln Asp Tyr Ala
1100 1105 1110

Asp Val Val Glu Ala Ala Pro Glu Leu Ala Ala Ala Gly Leu Glu
1115 1120 1125

Thr Gly Gly Ala Leu Ala Thr Ala Ser Thr Gln Gly Val Ala Val
1130 1135 1140

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

1145 1150 1155

<210> 415

<211> 835

<212> PRT

<213> *Toxoplasma gondii*

<400> 415

Met Pro Glu Val Asn Cys Leu Gly Ala Glu Pro Ala Phe Cys Asn Pro

1 5 10 15

Ser Lys Cys Ile Phe Asn Leu Arg Leu Arg Gly Ala Ser Pro Leu Val

20 25 30

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

35 40 45

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

50 55 60

Ala Ile His His Leu Gly Asn Asn Arg Glu Gly Arg Arg Pro Glu Ser

65 70 75 80

Ser Ser Trp Gly Phe Ser Asp Gln Ser Pro Ser Ala Pro Arg Phe Ala

85 90 95

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

100	105	110	
Ser Pro Ser Ser Gly Gly Ile Trp Ala Gly Val Lys Lys Tyr Val Glu			
115	120	125	
Leu Gly Thr Ser Gly Glu Arg His Val Ala Gln Asp Asp Asn Glu Lys			
130	135	140	
Lys Thr Thr Asn Gly Asp Thr Ala Gln Gly Asp Met Pro Ser Gln Glu			
145	150	155	160
Gly Ala Thr Ala Ala Glu Ala Gln Pro Gln Glu Ala Lys Glu Ser Glu			
165	170	175	
Asp Ala Phe Ser His Glu Thr Thr Gly Lys Val Glu Thr Glu Thr Glu			
180	185	190	
Asn Lys Ser Glu Val Tyr Arg His Met Ala Gln Glu Glu Leu Arg Ser			
195	200	205	
Ala Arg Ala Asp Leu Val Lys Gln Thr Asn Gly Thr Pro Glu Glu Tyr			
210	215	220	
Glu Glu Thr Gly Ser Phe Pro Ser Leu Cys Gly Ser Trp Gln Thr Val			
225	230	235	240
Pro Ser Ser Pro His Phe Ser Ser Asn Lys Glu Phe Thr Arg Tyr Ser			
245	250	255	
Gln Gln Asn Ala Ser Leu Leu Glu Gly Glu Ser Asp Thr Ala Asp Pro			
260	265	270	
Leu Pro Tyr Pro Thr Cys Gln Trp Leu Pro Arg Arg Gly Ile His Ile			
275	280	285	
Ser Glu Arg Arg Thr Tyr Gly Phe Lys Pro Asn Val Val Ser Ile Glu			
290	295	300	
Arg Leu Glu Phe His Ser Glu Glu Gly Cys Leu Pro Lys His Leu Ala			
305	310	315	320
Lys Val Trp Arg Tyr Ser Gly Tyr Trp Asp Pro Gln Ser Ala Ala Lys			
325	330	335	
Asp Pro Gln Thr Lys Ser Glu Glu Ile Pro Ala Lys Leu Ser Trp Ser			
340	345	350	

Arg Val Asn Ile Lys Met Glu Val Asn Ala Leu Ser Arg Ser Gln His
355 360 365

Leu Ala Pro Pro Asp Ala Arg Ser Gly Glu Pro Thr Pro Val Glu Ala
370 375 380

Glu Cys Leu Gly Asp Gly Asp Arg Met Trp Ile Pro Pro Val Arg His
385 390 395 400

Met His Leu Asp Leu Arg Asp Thr Cys Thr Arg Pro His Gly Asn Phe
405 410 415

Leu Tyr Ser Gln Pro Val Pro Pro Glu Phe Ile Ile Thr Pro Gln Glu
420 425 430

Ile Pro Val Ser His Glu Val Leu Ala His Arg Leu Lys Arg Arg Leu
435 440 445

Arg Ala Arg Met Ser Ile Leu Gln Arg Lys His Thr Asn Ser Pro Asp
450 455 460

Val Pro Arg Asp Val Ser Leu Lys Ser Glu Ala Glu Glu Ala Ile Ala
465 470 475 480

Ser Lys Trp Thr Asp Ala Val Asp Gln Arg Phe Ala Thr Arg Trp Arg
485 490 495

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

His Leu Leu Arg Glu Ser Cys Leu Val Pro Pro Pro Leu Ala Gly Pro
515 520 525

Thr Pro Pro Glu His His Lys Asp Lys Gly Asp Gly Lys Lys Glu His
530 535 540

Glu Ser Gln Cys Tyr Ile Pro Ser Val Arg His Ser Leu Thr Arg Glu
545 550 555 560

Asn Gly Ile Asp Tyr Leu Asp Val Pro Leu Phe Pro Phe Thr Glu Asp
565 570 575

Ala Glu His Val Arg Leu Arg Lys Val Gly Gly Cys Asn Pro His Leu
580 585 590

Gln Val Asp Leu Arg Gln Asn Lys Asp Ala Ser Lys Leu Ala Glu Glu

595 600 605
 Gln Glu Arg His Ser Ala Asp Glu Glu Leu Ala Ser Val Ala Val Thr
 610 615 620

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

 Gln Gln Asp Ala Ala Lys Leu Gly Ser Gln Asp Glu Ala Thr Ile Lys
 690 695 700
 Pro Val Ala Gln Gln Asp Ile Pro Val Glu Lys Ala Thr Ser Thr Asp
 705 710 715 720
 Ala Thr Glu Ser Val Glu Thr Pro Val Glu Lys Ile Gly Glu Asn Ser
 725 730 735
 Gln Glu Glu Pro Ala Ala Val Glu Gln Pro Ser Ser Val Glu Gly Gln
 740 745 750

 Thr Glu Pro Asp Gln Gln Pro Ser Asp Glu Glu Ala Gln Lys Asp Gly
 755 760 765
 Ala Glu Asn Glu Thr Pro Glu Ser Thr Gly Glu Thr Ala Glu Thr Pro
 770 775 780
 Ala Ala Glu Ile Pro Glu Gln Glu Ala Glu Ser Ala Ala Pro Ala Val
 785 790 795 800
 Asp Ala Ser Ser Ser Asp Ala Ala Gly Pro Ala Ala Thr Glu Ala Pro
 805 810 815

 Asp Gln Glu Thr Gly Glu Ala Asn Glu Glu Ala Ser Ser Ala Thr Glu
 820 825 830
 Asp Ser Ser
 835

<210> 416

<211> 1479

<212> PRT

<213> *Toxoplasma gondii*

<400> 416

Met Thr Lys Arg Ala Gly Leu Pro Leu Gly Arg Ala Phe Leu Val Leu

1 5 10 15

Ile Leu Leu Ser Ala Ala Asp Ser Leu Phe Phe Ser Ser Phe Pro Arg

20 25 30

Ser Ala Leu Gln Leu Phe Ser Ser Val Leu Phe Thr Asp Ala Ala Glu

35 40 45

Pro Asp Ser Asp Ala Thr Pro Gly Leu Arg Pro Gln Pro Ser Pro Arg

50 55 60

Thr Phe Arg Pro Thr Gly Tyr Gln Arg Ile Glu Val Lys Thr Val Asp

65 70 75 80

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

85 90 95

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

100 105 110

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

115 120 125

Ser Trp Ser Trp Ser Gly Thr Pro Pro Glu Val Gln Thr Thr Gly Gly

130 135 140

Ser Gln Ile Ser Phe Gly Trp Val Pro Asp Thr Glu Thr Pro Ser Leu

145 150 155 160

Pro Glu Arg Asn Leu Leu Gln Leu Lys Arg Met Leu Arg Asp Glu Gly

165 170 175

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

180 185 190

Ala Val Leu His Asn Leu Arg Gln Leu Pro Val Asn Phe Arg Glu Val

195 200 205

Leu His Glu Glu Tyr Glu Ser Arg Ser Asn Pro Ala Lys Met Tyr Glu

210 215 220
 Val Ala Asn Ser Tyr Val Gln Gln Arg Gly Ser Asp Ala Ala Arg Trp

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

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

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

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

Gly Gln Lys His Trp Tyr Gln Thr Gly Gly Ala Arg Lys His Lys Asn
 465 470 475 480
 Arg Asp Met Leu Pro Leu His Arg Gln Leu Cys Asp Ala Leu Glu Leu

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

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

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

 675 680 685
 Lys Leu Arg Lys Lys Ile Pro Glu Asn Asp Pro Tyr Ala Leu Arg Ala
 690 695 700
 Ala Ile Phe Leu Ala Leu Asn Ser Arg Thr Phe Cys Ala Gln Pro Thr

705 710 715 720
 Ser Phe Leu Ser Ser Phe Arg Thr Phe Leu Thr Asn Gln Tyr His Lys
 725 730 735
 Leu Ser Gln Gly Arg Asn Leu Pro Arg Ser Gln Arg Ser Leu Met Ala

 740 745 750
 Phe Met Arg Thr Gly Gln Val Lys Phe Phe Gln Glu Trp Cys Ser Phe
 755 760 765
 Asp Pro Leu Ala Val Asn Ala Leu Phe Leu Phe Arg Phe Ala Val Ser
 770 775 780
 Gly Thr Asp Pro Ala Ala Leu His Asp Arg Gln His Thr Arg Val Ser
 785 790 795 800
 Arg Asn Lys Lys Thr Met Arg Ile Leu Asn Ser Lys Trp Thr Pro Ala

 805 810 815
 Val Leu Lys Lys Leu Met Arg Lys Val Asn His Lys His Met Ala Arg
 820 825 830
 Glu Ala Lys Ala Leu Leu Leu Arg Ser Leu Asp Pro Thr Val Leu Ser
 835 840 845
 Ser Ile Val Thr Ala Phe Asp Phe Ile Thr His Thr Gln Ala Asn Leu
 850 855 860
 Glu Val Asn Gln Asn Ala Phe Met Tyr His Glu Val Arg Ala Arg Glu

 865 870 875 880
 Val Ser Arg Gln Ser Ala Ala Glu Lys Gly Ser His Arg Leu His Glu
 885 890 895
 Arg Gly Leu Val Arg Glu Thr Asp Asp Met Ile Lys Arg Trp Ala Glu
 900 905 910
 His Gly Ile Pro Gly Asp Ile Lys Arg Arg Leu Ala Arg Gly Glu Lys
 915 920 925
 Leu Pro Glu Gly Met Ser Phe Gly Gly Ile Pro Ile Pro Asn Leu Thr

 930 935 940
 Asn Trp Asp Ala Gln Leu Asn Ser Lys Trp Leu Glu Ala Tyr Asn Ala
 945 950 955 960

Tyr Leu Arg His Pro Tyr Gly Arg Ala Ala Leu Asn Ala Arg Asp Pro
 965 970 975
 Val Ala Leu Leu Val Lys Asp Ser Arg Asp Arg Leu Gln Ala Glu Ala
 980 985 990
 Glu Gly Thr Ile Phe Leu Gly Arg Ile Ala Lys Arg Val His Gln Ser
 995 1000 1005
 Lys Asn Leu Leu Arg Arg Ala Gly Arg Ala Leu Lys Thr Phe Phe
 1010 1015 1020
 Leu Ser Leu Leu Arg Glu Asn Glu Arg Ser Glu Tyr Ala Val Trp
 1025 1030 1035
 Phe Gly Val Lys Val Asp Met Arg Gln Val Ile Gln Thr Cys Arg
 1040 1045 1050
 Gln Ile Asn Ser Val Ala Glu Val Val Lys Asn Asp Arg Leu Tyr
 1055 1060 1065
 Asp Phe Ile Thr Asp Gly Trp Met Glu Leu Val Lys Asp Val Val
 1070 1075 1080
 Ala Gly Tyr Thr Lys Ala Ser Val Arg Val Pro Gly Phe Asp Thr
 1085 1090 1095
 Ile Ser Ala Ala Asn Glu Gln Leu Arg Lys Glu Gly Val Ala Ala
 1100 1105 1110
 Ala Thr Ala Arg Asn Gln Gly Phe Leu Ser Ile His Tyr Asp Tyr
 1115 1120 1125
 Ala Asn Leu Pro Glu Glu Glu Arg Lys Lys Glu Phe Gln Arg Ser
 1130 1135 1140
 Met Cys Met Glu Gln Cys Glu Ala Leu Trp Lys Leu Val Met Ala
 1145 1150 1155
 Phe Val Met Pro Asn Leu Gln Asn Pro Lys Lys Leu Lys Gly Tyr
 1160 1165 1170
 Glu Lys Asp Phe Ser Gly Ala Lys Glu Ile Glu Lys Leu Asn Ser
 1175 1180 1185
 Pro His His Val Asn Ala Phe Arg Phe Ser Leu Ser Val Gln Ile

1190	1195	1200
Asp Phe Phe Asp Asn Met Leu	Asp Lys Thr Ser Lys	Lys Asn Leu
1205	1210	1215
Lys Ala Met Lys Phe Gly Ala	Ser Thr Trp Phe Thr	Tyr Ala Met
1220	1225	1230
Lys Leu Ala Gly Gln Val Asn	Ser Glu Met Gly Asn	Pro Asn Leu
1235	1240	1245
Gly Thr Ala Leu Tyr Met Gln	Ala Ala Tyr Tyr Gly	Asn Tyr Ile
1250	1255	1260
Arg Lys Trp Met Glu Gln Arg	Arg Lys Ser Arg Lys	Gln Ala Ile
1265	1270	1275
Ile Gly Val Leu Thr Leu Gly	Met Met Gly Leu Tyr	Ala Leu Leu
1280	1285	1290
Asn Val Ala Asp Ile Val Gln	His Met Glu Asp Ile	Gly Gly Ala
1295	1300	1305
Pro Pro Val Ser Cys Val Thr	Asn Glu Ile Leu Gly	Val Thr Cys
1310	1315	1320
Ala Pro Gln Ala Ile Ala Lys	Ala Thr Thr Ser Ala	Ala Arg Val
1325	1330	1335
Ala Thr Gln Asp Phe Leu Lys	Val Gly Leu Phe Ala	Gly Met Ala
1340	1345	1350
Pro Tyr Leu Met Leu Pro Met	Ala Val Val Ser Val	Trp Asn Ile
1355	1360	1365
Leu Lys Ser Glu Ile Lys Val	Leu Leu Gln Phe Glu	Met Ala Leu
1370	1375	1380
Lys His Thr Phe Thr Arg Leu	Lys Arg Trp Leu Ala	Ala Pro Phe
1385	1390	1395
Lys Asn Trp Trp Ala Lys Arg	Gly Arg Leu Lys Asp	Ala Leu Phe
1400	1405	1410
Arg Arg Ala Ser Gln Thr Tyr	Arg Lys Thr Glu Gln	Glu Thr Lys
1415	1420	1425

Gln Pro Pro Arg Pro Arg Asn Leu His Asn Pro Ser Ser Trp Gly
 1430 1435 1440
 Asp Thr Glu Leu Asp Ser Leu Gly Val Pro Pro Glu Pro Phe Val
 1445 1450 1455
 Gln Asp Phe Glu Ile Lys Tyr Thr Thr Pro Val Phe Pro Met Ser
 1460 1465 1470
 Ala Pro Leu Ile Lys Ala
 1475

<210> 417

<211> 1958

<212> PRT

<213> Toxoplasma gondii

<400> 417

Met Thr Thr Ser Pro Arg Val Ala Lys Trp Ala Leu Arg Val Leu Ala
 1 5 10 15
 Leu Val Phe Leu His His Val Thr Val Cys Thr Val Cys Glu Ala Lys
 20 25 30
 Ala Leu His Val Ile Arg Pro His Arg Asn Phe Ala Gly Leu Asp Val
 35 40 45
 Gln Gln Ser Ser Val Ala Asp Leu Gln Asp Glu Gly Lys Gly Ile Ser
 50 55 60
 Phe Ala Gln Thr Tyr Arg Glu Arg Asp Ile Trp Phe Gly Met Leu Tyr
 65 70 75 80
 Phe Glu Tyr Val Ile Thr Ala Ser Thr Thr Met Thr Leu Ala Phe Lys
 85 90 95
 Ser Met Ala Lys Tyr Ile Tyr Thr Ala Pro Phe Leu Thr Lys Leu Phe
 100 105 110
 Ala Ser Asn Arg Trp Leu Lys Tyr Ser Thr Leu Asp Phe Pro Gln Lys
 115 120 125
 Gln Gln Ile Ile Arg Lys Ile Ala Arg Arg Ala Ser Ser Lys Ser Leu
 130 135 140
 Phe Ser Arg Ala Leu Pro Gly Asp Arg Val Ala Asp Leu Phe Ala Asp

145 150 155 160
 Met Tyr Leu Arg Arg Val Thr Ser Arg Leu Ser Arg Thr Pro Gly Phe
 165 170 175
 Arg Lys Pro Gln Tyr Leu Lys Met Lys Glu Asp Leu Thr Gln Leu Ile

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

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

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

 370 375 380
 Arg Arg Gly Gly Ala Val Glu Ser Gly Val Leu Ala Gly Gln Gly Val
 385 390 395 400

Trp Thr Leu Ser Asp Gly Leu Phe Val Gly Leu Lys Asp Phe Gly Gln
405 410 415
Leu Phe Arg Ala Tyr Phe Glu Arg Tyr Val Asn Leu Thr Ser Ala Ile
420 425 430
His Thr Tyr Cys Ala Lys Gln Thr Thr Asn Phe Phe Thr Glu Thr Glu
435 440 445
Leu Asp Glu Phe Tyr Asn Gly Glu Asn Val Asp Arg Ile Pro Pro Arg
450 455 460
Glu Arg Leu Leu Ala Trp Cys Asp Lys Asn Lys Ser Tyr Leu Ala Ile
465 470 475 480
Ile Glu Lys Asp Phe Ile Gly Leu Ala Thr Asn Phe Leu Asn His Met
485 490 495
Ile Lys Cys Leu Lys Met Asp Phe Lys Tyr Phe Glu Gly Tyr Leu Ala
500 505 510
Asn Ile Met Ser Ile Phe Tyr Glu Met Thr Phe Ala Thr Leu Glu Ser
515 520 525
Asp Ile Val Ser Ala Ile Asn Ala Asn Gln Gly Arg Ala Pro His Thr
530 535 540
Leu Glu Leu Glu Ala Ile Leu Lys Arg Arg Gln Gln Ala Asn Asn Pro
545 550 555 560
Pro Lys Glu Ala Glu Met Pro Arg Thr Met Phe Arg Lys Pro Trp Met
565 570 575
Arg Ala Ala Ile Arg Lys Leu Ala His Gly Tyr Phe Ser Ser Ala Ala
580 585 590
Gly Phe Ala Leu Lys Thr Leu Leu Gln Gln Ile Lys Pro Ala Asn Ala
595 600 605
Glu Lys Leu Leu Asp Lys Ala Phe Thr Arg Val Lys Glu Gly Ser Lys
610 615 620
Leu Ile Arg Ser Ser Leu Thr Val Ile Leu Gly Arg Phe Phe Asn Ser
625 630 635 640
Gln Ala Leu Ile Val Arg Ala His Asp Gln Thr Val Arg Met Arg Met

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

690 695 700
Arg Asp Leu Leu Leu Ser Gln Val Ile Glu Thr Asp Pro Ala Lys Asp
705 710 715 720
Ser Ile Asp Pro Thr Glu Phe Phe Ala Glu Trp Glu Ala Trp Leu Gln
725 730 735
Ala Lys Gly Tyr Lys Pro His Gln Lys Gly Lys Glu Tyr Leu Leu Phe
740 745 750
Ala Glu Asp Ile Asn Gln Lys Ala Asn Ile Ile Ala Phe Val Glu Ala

755 760 765
Leu Arg His Thr Leu Arg Asp Arg Leu Arg Phe Gly Arg Phe Asp Gln
770 775 780
Glu Gly Ala Asp Asn Leu Arg Leu Phe Asp Val Asn Gly Arg Ser Ala
785 790 795 800
Ile Phe Arg Pro Arg Asp Pro Gln Ser Met Trp Asp Arg Ile Lys Glu
805 810 815
Val Arg Pro Asp Pro Leu Asp Ala Pro Ala Thr Phe Glu Val Leu Asp

820 825 830
Tyr Asn Glu Gly Ile Leu Arg Phe Ser Ser Lys Pro Gly Ile Pro Phe
835 840 845
Glu Gly Arg Leu Glu Tyr Ala Asp Asp Arg Arg Glu Leu Arg Ser Ile
850 855 860
Gln Gln Asp Pro Gln Ala Ile Lys Glu Leu Leu Val Ser Gln Ile Met
865 870 875 880
Gln Ile Lys Pro Arg Leu Ser Ala Glu Met Thr Ala Thr Leu Met Met

885 890 895

Val Leu His Arg Tyr Thr Thr Ser Phe His Arg His Ser Phe Ala Thr
900 905 910

Phe Leu Gln Asn Leu Ser Pro Lys Met Phe Phe Asp Gly Val Leu Ala
915 920 925

Phe Ala Asp Gln His Gln Gln Gln Ala Glu Ala Thr Leu His Leu Asp
930 935 940

Arg Arg Leu Tyr Ser Phe Pro Met Thr Phe Gln Thr Phe Lys Asp Ile

945 950 955 960

Val Phe Asn Ser Leu Asn Thr Met Val Leu Arg Met His Ser Leu Asp
965 970 975

Thr Ala Asp Ser Leu Ser Val Phe Leu Val Gly Leu Val His Tyr Ala
980 985 990

Tyr Gln Lys Ile Gln Lys Asn Arg Thr Gly Arg Thr Leu Val Met Gln
995 1000 1005

His Phe Leu Arg Gly Leu Val His Val Met Arg Ser Val Asp Ala

1010 1015 1020

Glu Arg Phe Arg Glu Asp Phe Pro Glu Cys Gln Phe Leu Ile Glu
1025 1030 1035

Pro Asn Gly Thr Ile Asp Glu Val Val Ala Ile Lys Cys Ala Leu
1040 1045 1050

Tyr Arg Phe Val Lys Leu Arg Ser Leu Glu Leu Pro Arg Ala Ile
1055 1060 1065

Ala Pro Asp Val Glu Glu Ser Arg Met Thr Glu Ala Arg Ala Arg

1070 1075 1080

Thr Tyr Leu Asn Gly Phe Val Glu Tyr Leu Asp Arg Leu Arg Ser
1085 1090 1095

Glu Arg Thr Ser Trp Ala Ser Phe Leu Asn Phe Lys Gly Phe Leu
1100 1105 1110

Glu Thr Ala Glu Leu Tyr Arg Glu Thr Val Gly Ala Tyr Ser Tyr
1115 1120 1125

Glu Glu Leu Glu Arg Gln Ile Lys Thr Glu Pro Ile Thr Asp Leu

1130	1135	1140
Asp Val Leu Glu Gln Leu Arg	Ala Leu Met Asp Pro	Ser Leu Gly
1145	1150	1155
Arg Ile Val Ala Pro Lys Lys	Asp Glu Gly Thr Ala	Gln Val Ile
1160	1165	1170
Arg Lys Ile Trp Gly Asn Leu	Gly Glu Phe Ser Ser	Gly Thr Arg
1175	1180	1185
Gln Arg Val Arg Ser Ala Leu	Ser Gln Met Arg Ser	Arg Leu Val

1190	1195	1200
Ser Val Met Gly Ser Thr Thr	Leu Pro Lys Ala Met	Arg Leu Phe
1205	1210	1215
Asn Val Met Asn Ser Ser Gln	Phe Phe Gly Ala Leu	Glu Phe Ala
1220	1225	1230
Glu Phe Arg Ala Phe Pro Asp	Thr Arg Thr Pro Pro	Glu Asp Ile
1235	1240	1245
Leu Lys Ala Ser Asp Leu Ala	Leu Phe Gly Arg Val	Leu Leu Val

1250	1255	1260
Leu Glu Thr Thr Pro Leu Tyr	Leu Asp Asn Pro Lys	Gln Met Ser
1265	1270	1275
Asp Ile Val Met Gln Met Arg	Ser Ile Pro Phe Ile	Ser Pro Glu
1280	1285	1290
Cys Gln Glu Leu Phe Arg Glu	Ile Glu Glu Met Val	Arg His Met
1295	1300	1305
Ser His Glu Asp Val Arg Val	Ala Val Gly Trp Leu	Leu Thr Phe

1310	1315	1320
Asn Ile Gly Lys Gly Leu Thr	Gly Ser Thr Val Ala	Leu Gly Leu
1325	1330	1335
Leu Ala Leu Ala Gly Val Pro	Phe Ala Asn Ser Gln	Ile Ser His
1340	1345	1350
Gln Asp Lys Ile Gly Ile Leu	Arg Thr Leu Asp Ala	Asp Thr Leu
1355	1360	1365

Arg Phe Ile Lys Lys His Leu Leu Met Pro Met Val Phe Arg His

1370 1375 1380

Met Ala Ser Leu Ser Asp Gly Glu Ala Met Asn Leu Leu Arg Phe

1385 1390 1395

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

1400 1405 1410

Tyr Leu Pro Leu Ser Glu Pro Val Asn Val Val Asp Ala Val Asp

1415 1420 1425

Lys Leu Ile Ala Ser Lys Ala Ile Asp Ala Val Gln Gln His Leu

1430 1435 1440

Gly Gln Val Arg Gln Leu Pro Gly Glu Ala Ser His Asp Ala Val

1445 1450 1455

Cys Arg Thr Met Ile Asn Asn Ile Lys Val Glu Leu Gly Leu Ser

1460 1465 1470

Thr Glu Asp Ala Met Lys Phe Trp Thr Arg Ser His Met Phe Phe

1475 1480 1485

Asp Lys Arg Leu Pro Ala Ala Cys Ile Leu Leu Ile His Leu Lys

1490 1495 1500

Ala Met Arg Glu Gln Asn Ile Arg Glu Thr Thr Val Ala Ala Leu

1505 1510 1515

Val Asp Met Leu Tyr Tyr Asn Gly Thr Ala Leu Asn Asp His Leu

1520 1525 1530

Ala Phe Ile Ala Lys Lys Gly Ala Asn Glu Leu Glu Arg Gln Lys

1535 1540 1545

Gln Ile Asp Arg Val Gly Ser Leu Leu Thr Met Val Tyr Val Ala

1550 1555 1560

Val Val Ser Gly Ser Leu Gln Val Asp Ala Ser Phe Met Gly Tyr

1565 1570 1575

Ser Gly Glu Thr Lys Asn Leu Thr Phe His Ser Arg Arg Ser Ser

1580 1585 1590

Arg Gly Thr Glu Val Pro Leu Leu Thr Ala Cys Ile Gln Ala Thr

1595	1600	1605
Thr His Ile Met Gly Pro Pro	Lys Glu Lys Pro Glu	Ile Phe Gln
1610	1615	1620
Ala Ser Leu Ser Ser Tyr Phe	Leu Gly Glu Trp Phe	Arg Phe Val
1625	1630	1635
Glu Thr Ser Arg Leu Glu Glu	Tyr Ala Ala Ala Tyr	Arg Arg Gly
1640	1645	1650
Gly Gly Phe Gln Asn Ile Ser	Arg Glu Thr Leu Lys	Asn Ile Ser
1655	1660	1665
Ser Val Tyr Asn Tyr Tyr Asp	Ile Gly Asp Tyr Phe	Ile Ser Ile
1670	1675	1680
Arg Gln Arg Ser Leu Tyr Pro	Gln Asn Glu Ile Val	Lys Thr Ala
1685	1690	1695
Ser Met Ala Leu Ile Gln Asp	Glu Ala Thr Ile Asp	Asp Tyr Gly
1700	1705	1710
Met Ala Met Leu Thr Val Asp	Met Gly His Arg Val	Arg Lys Ala
1715	1720	1725
Lys Ile Lys Cys Tyr Glu Asp	Ala Leu Lys Asp Tyr	Val Glu Tyr
1730	1735	1740
Val Asp Lys Ser Arg Ser Ala	Gln Glu Met Phe Lys	Ile Asp Cys
1745	1750	1755
Val His Asn Tyr Phe Ile Asp	Met Gly Ser Leu Gly	Tyr Ser Ala
1760	1765	1770
Ala Ser Ile Thr Pro Glu Gln	Lys Asp Gln Ile Ile	Ala Ser Leu
1775	1780	1785
Asp Arg Val Phe Ala Gly Lys	Cys Glu Asp Met Tyr	Thr Ala Leu
1790	1795	1800
Ile Gly Ser Gln Pro Asp Ile	His Lys Leu Lys Gln	Gln Ala Trp
1805	1810	1815
Ala Phe Ala Thr Leu Ala His	Asn Ser Leu Asn Ser	Ala Thr Arg
1820	1825	1830

Leu Gly Ser Ile Val Asn Met Leu His Asn Leu Ile Thr Asp Ile

1835 1840 1845

Ala Ala Gly Thr Pro Trp Asn Asn Val Val Asp Gly Ile Ala Ala

1850 1855 1860

Glu Arg Ala Asn Lys Ile Trp Glu Arg Leu Gly Asp Val Ser His

1865 1870 1875

Arg Thr Pro Ile Tyr Thr Ala Ile Asp Arg Pro Tyr Leu Phe Asn

1880 1885 1890

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

1895 1900 1905

Lys Ala His Lys Leu Arg Met Pro Lys Met Leu Leu Met Lys Arg

1910 1915 1920

Ala Ala Val Leu Lys Glu Leu Pro Phe Lys Lys Lys Thr Thr Pro

1925 1930 1935

Pro Gly Met Thr Glu Tyr Lys Glu Arg Ala Ala Ala Leu Lys Asp

1940 1945 1950

Ala Phe Phe Ala Pro

1955

<210> 418

<211> 984

<212> PRT

<213> Toxoplasma gondii

<400> 418

Met Ala Ile Lys Asn Thr Leu Thr Gly Ser Gly Leu Leu Val Leu Leu

1 5 10 15

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

20 25 30

Pro Arg Met Tyr Pro Asn Met Asn Glu Arg Pro Leu Ser Ala Glu Ser

35 40 45

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

50 55 60

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

65 70 75 80

Asn Asn Ser Lys Val Glu Ser Ile Ile Ala Gly Ser Asp Thr Thr Pro

85 90 95

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

100 105 110

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

115 120 125

Gln Pro Pro Thr Ala Ala Pro Arg Thr Ser Arg Ser Val Asp Thr Gly

130 135 140

Ser Gly Ser Asp Ala Ser Thr Glu Gln Gln Ala Gly Gly Gln Lys Val

145 150 155 160

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

165 170 175

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

180 185 190

Thr Asn Glu Gly Gly Gly Thr Ser Glu Gly Pro Gln Val Pro Gln Ser

195 200 205

Gly Ile Pro Pro Arg Thr Gly Arg Arg Arg Ala Lys Ala Arg Asn Arg

210 215 220

Lys Arg His Pro Thr Pro Ala Ser Arg Glu Ser Ser Ser Glu Asp Glu

225 230 235 240

Asn Gln Pro Pro Thr Thr Ala Ser Arg Pro Ser Asn Gly Glu Gly Glu

245 250 255

Ser Gln Pro Pro Thr Ala Ala Pro Arg Thr Ser Arg Ser Val Asp Thr

260 265 270

Gly Ser Gly Ser Asp Ala Ser Thr Glu Gln Gln Ala Gly Gly Gln Lys

275 280 285

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

290 295 300

Glu Leu Arg Gln Thr Gln Glu Gly Glu Glu Ser Ala Pro Gln Pro Ala

305 310 315 320
 Asp Val Thr Trp Phe Ser Met Ser Val Pro Met Gly Val Val Asp Arg

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

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

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

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

Arg Lys Lys Thr Glu Arg Gly Lys Leu Glu Asp Asp Gln Ala Leu Val
 565 570 575
 Ala Leu Cys Ser Ala Ala Gly Ala Phe Val Asp Ala Trp Gln His Gln
 580 585 590
 Gln Gln Ala Leu Ile Leu Glu Asp Pro Gly Thr Pro Lys Ala His Ala
 595 600 605
 Gln Leu Ile Glu Arg Leu Arg Asn Ala Gly Lys Tyr Phe Met Lys Ser
 610 615 620
 Tyr Asp Glu Thr Thr Gly Glu Ser Asp His Gln Gln Trp Lys Lys Asn
 625 630 635 640
 Lys Ala Glu Val Ser Lys Leu Gly Lys Ser Ala Leu Met Lys Ser Cys
 645 650 655
 Val Lys Tyr Ile Lys Ala Ser Gly Asp Val Ala Thr Arg Pro Phe Asp
 660 665 670
 Ser Gly Thr Ala Lys Tyr Pro Ser Arg Ser Leu Tyr Gly Gly Ile Ala
 675 680 685
 Asn Thr Leu Glu Thr Pro Phe Ala Asp Ser Glu Ala Val Ala Lys Ala
 690 695 700
 Val His Asp Tyr Ala Lys Glu His Lys Lys Pro Glu Lys Leu Val Gly
 705 710 715 720
 Leu Cys Gly Ala Leu Gln Ile Ser Gly Tyr Phe Lys Lys Cys Phe Ser
 725 730 735
 Asp Ala Gly Arg Leu Ser Ser Val Ser Phe Phe His Gln His Val Asp
 740 745 750
 Gly Ala Ser Val Leu Val Arg Thr Leu Ala Arg Glu Arg Pro Ile Gly
 755 760 765
 Arg His Ala Leu Ser Gln Ala Ile Cys Asp Pro Asn Ile Ser Ala Gln
 770 775 780
 Tyr Phe Glu Gly Ala Phe Arg Leu Phe Ser Ser Thr Val Ser Gln Glu
 785 790 795 800
 Trp Glu Lys Glu Asn Leu Phe Ala Gln Leu Ala Ser Trp Thr Gly Lys

805 810 815
 Glu Met Val Leu Ala Pro Ser Leu Glu Glu Gln Ala Ala Val Pro Pro
 820 825 830
 Ala Gln Pro Ala Tyr Glu Thr Val Tyr Gly Asp Glu Glu Asp Arg Ile

835 840 845
 Tyr Arg Ile His Val Ser Gly Arg His Ser Ser Pro Gln Glu Val Leu
 850 855 860
 Tyr Val Gly Gly Ile Pro Ser Thr Val Lys Pro Gln Gln Val His Val
 865 870 875 880
 Leu Gly Pro Thr Val Ser Asp Glu Ser Arg Arg Val Ile His Pro Val
 885 890 895
 Arg His Arg Ser Arg Thr Ala Pro Ser Ser Glu Ala Ala Ser Ala Ala

900 905 910
 Ala Glu Ser Ser Asp Glu Asp Pro Leu Pro Ala Glu Asn Ala Thr Ala
 915 920 925
 Phe Leu Gly Val Thr Pro Gln Glu Glu Glu Ser Asp Ala Tyr Lys His
 930 935 940
 Thr Leu Asp Phe Asp Ala Val Ser Pro Arg Lys Asn Lys Asn Lys Glu
 945 950 955 960
 Asn Arg Ile Ser Ala Pro Leu Lys Gln Ser Asp Thr Leu Ile Glu Glu

965 970 975
 Ser Thr Ser Lys Thr Ser Glu Leu
 980

<210> 419

<211> 1702

<212> PRT

<213> Toxoplasma gondii

<400> 419

Met Ala Glu Phe Thr Trp Arg Pro Leu Leu Met Ser Leu Pro Lys Met
 1 5 10 15
 Ile Ala Phe Phe His Ile Leu Leu Phe Ser Gly Ala Leu Ala Ala Ala
 20 25 30

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

35 40 45

Asn Glu Arg Lys Asp Leu Tyr Ala Arg Asp Thr Gln Pro Thr Ala Arg

50 55 60

Thr Gly Ile Asp Ile Gly Val Ser Phe Thr Gln Gln Ala Ser Gly Asn

65 70 75 80

Ala Arg Thr Phe Glu Ile Arg Gln His Gly Ser Gly Pro Pro Arg Pro

85 90 95

Ala Pro Arg Arg Ala Ala Ala Val Ala Asp Asp Ile Phe Gly Ser Glu

100 105 110

Asp Phe Ser Pro Pro Pro Met Asn Val Ala Gly Ala Pro Leu Arg Asp

115 120 125

Met Gly Val His Phe Leu Glu Cys Gln Ala Thr Asp Gly Lys Ile Glu

130 135 140

Cys Thr Gly Gln Gly Ala Gly Ala Arg Pro Pro Phe Phe Arg Gly Gly

145 150 155 160

Val Asp Pro Thr Glu Ile His Glu Ile Val Gln Ser Arg Thr Val Gly

165 170 175

Pro Ala Asp Tyr Asp Glu Glu Arg Pro Glu Gln Thr Pro Asp Tyr Leu

180 185 190

Ser Pro Thr Asp Val Val Thr Leu Gln Arg Phe Val Ser Ser Ala Asn

195 200 205

Ala Ser Asn Ser Pro Leu Leu Glu Asp Pro Val Gln Val Cys Leu Ser

210 215 220

Arg Arg Lys Pro Thr Tyr Thr Cys His Leu Leu His Glu Phe Ala Ala

225 230 235 240

Thr Ser Val Ile Val Glu Glu Ser Gly Asn Leu Val Cys Glu Asp Lys

245 250 255

Ala Pro Leu Thr Val Ala Glu Lys Arg Lys Ile Asn Asp Ala Val Lys

260 265 270

Ala Gly Arg Thr Pro Gln Ala Thr Gly Gly Gln Ser Ser Arg Pro Pro

275 280 285
Asn Pro Thr Val Ser Pro Ser Lys Ala Gly Ala Ala Pro Gln Asn Ala

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

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

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

485 490 495
Ala Ile Glu Thr Leu Thr Pro Gln Met Val Ala Asn Ala Leu Leu Glu
500 505 510
Leu Ser Gly Ile Glu Glu Leu Ile Asn His Thr Ala Arg Val Lys Ser
515 520 525

Arg Leu Ala Ala Arg Gly Gln Asp Ser Pro Ala Asn Val Arg Lys Glu
 530 535 540
 Ile Val Gln Glu Ser Phe Arg Gln Leu Lys Val Glu Leu Phe Gln Glu

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

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

 675 680 685
 Ala Ala Pro Ala Pro Ser Phe Tyr Gly Ile Thr Thr Ser Gly Cys Arg
 690 695 700
 Asn Val Asn Asp Ile Met Lys Ser Lys Phe Phe Asp Met Tyr Leu His
 705 710 715 720
 Gln Ser Gly Phe Met Lys Leu Gln Arg His Gly Asn Asp Asn Ser Arg
 725 730 735
 Gln Arg Phe Met His Arg Val Thr Leu Leu Gln Asn Asp Gly Ile Leu

 740 745 750
 Pro Gln Leu Pro Leu Glu Ala Asp Tyr Glu Leu Met Glu Leu Asn Ala
 755 760 765
 Ala Met Gln Lys Asn Phe Val Ala Ala Asn Lys Ser Ile Phe Ser Arg

770 775 780
 Arg Ala Ala Arg His Ser Lys Tyr Gly Tyr Leu Asp Leu Cys Asp Val
 785 790 795 800
 Ala Cys Tyr Gln Lys Ile Asp Arg Leu His Asn Asp Val Met Thr Asn

 805 810 815
 Val Phe Phe Ser Leu Asp Thr Thr Leu Met Lys Ile Val Ala Lys Val
 820 825 830
 His Arg Ser Tyr Gly Ile Ala Lys Ala Phe Phe Gln Leu Gly Ala Arg
 835 840 845
 Gln Gln His Ile Ala Asp Pro Asn Leu Gly Met Trp Ala Arg Arg Leu
 850 855 860
 Phe Val His Trp Ala Ser His Asn Glu Val Lys Gln Met Gln Gly Gln

 865 870 875 880
 Lys Val Val Lys Val Asn Tyr Glu Asn Leu Arg His Gly Glu Phe Thr
 885 890 895
 Leu Asp Thr Val Arg Met Arg Asp Ala Leu Val Arg Tyr Thr Asn Met
 900 905 910
 Leu Lys Ala Asp Pro Ile Thr Arg Asp Leu Met Ser Leu Val Ile His
 915 920 925
 Thr Trp Ile His Ile Arg Gly Val Arg Asn Ala Ala Met Gly Phe Lys

 930 935 940
 Asn Ser Gln Lys Leu Asn Glu Ser Met Asn Ala Ser Ala Ile Gly Ala
 945 950 955 960
 Val Phe Ala Lys Leu Trp Tyr Glu Ser Asp Ile Ser Val Val Ala Pro
 965 970 975
 His Gln Glu Leu Lys Pro Phe Gly Ala Pro Leu Ala Ser Met Ala Leu
 980 985 990
 Gln Ile Gly Phe Phe Leu His Thr Val Val Glu Glu Tyr Lys Met Ser

 995 1000 1005
 Leu Leu Glu Lys Ala Gly Ala Gln Ile Lys Ser Trp Phe Val Gly
 1010 1015 1020

Met Phe	Gln Lys Asn Lys Arg	Arg Thr Val Pro Arg	Thr Trp Lys
1025	1030	1035	
Ala Val	Val Ala Ala Thr Asn	Arg Ala Pro Lys Val	Asn Leu Lys
1040	1045	1050	
Ala Tyr	Gln Gly Ala Leu Leu	Val Ile Lys Thr Leu	Ala Lys Met
1055	1060	1065	
Phe Arg	Glu Arg Phe Leu Tyr	Arg Phe Tyr Met Gln	Gly Gln Gly
1070	1075	1080	
Ser Lys	Val Asp Phe Asn Thr	Pro Thr Leu Leu Ile	His Ala Leu
1085	1090	1095	
Val Ala	Ser Trp Met Asp Pro	Ser Leu Asp Arg Leu	Glu Leu Ser
1100	1105	1110	
Ser Arg	Thr Ile Pro Asn Ala	Lys Lys Leu Phe Trp	Tyr Tyr Val
1115	1120	1125	
Trp Val	Asn Glu Asn Gly Pro	Ser Asn Ala Ala Thr	Arg Ile Val
1130	1135	1140	
Leu Thr	Gly Cys Lys Lys Tyr	Thr Phe Leu Leu Pro	Gly Val Val
1145	1150	1155	
Arg Ser	Val Thr Ser Ser Thr	Ser Glu Val Val Glu	Ala Gly Ser
1160	1165	1170	
Asn Ile	Leu Lys Ile Asp Lys	Ile Ile Leu Lys Arg	Ser Ser Leu
1175	1180	1185	
Glu Ala	Tyr Met Asn His Leu	Gln Ala Thr Tyr Asp	Asp Pro Leu
1190	1195	1200	
Thr Ile	Val Gln Val Ala Leu	Asp Leu Ala Ala Arg	Cys Glu Gly
1205	1210	1215	
Tyr Ser	Ala Ala Lys Asp Gln	Pro Ala Gln Ala Met	Arg Gly Pro
1220	1225	1230	
Ala Arg	Val Arg Arg Ala Thr	Gly Glu Ser Thr Thr	Phe Thr Ile
1235	1240	1245	
Arg Gly	Gly Gly Val Gln Gly	Gly Thr Met Ser Phe	Val Glu Ala

1250	1255	1260
Glu Ala Asp Asp Glu Arg Lys	Glu Asp Ser Glu Asp	Asn Thr Val
1265	1270	1275
Asp Leu Ser Glu Gln Asp Gln	Asp Ser Ser Phe Val	Gln Leu Lys
1280	1285	1290
Lys Leu Phe Asn Arg Arg Gly	Ser Ser Ala Ala Gly	Gln Ala Val

1295	1300	1305
Gln Thr Asp Ala Gln Pro Leu	Pro Lys Ala Val Gln	Thr Asp Ala
1310	1315	1320
Gln Pro Leu Pro Lys Val Arg	Arg Gly Gly Pro Asp	Val Asp Ala
1325	1330	1335
Ser Ala Val Ile Leu Gly Ser	Arg Phe Met Leu Asp	Leu Trp Cys
1340	1345	1350
Ser Lys Tyr Arg Lys Met Leu	Val Glu Lys Leu Ser	Gly Ile Ser

1355	1360	1365
Thr Lys Asp Ala Thr Val Met	Gln Gln Glu Ile Ser	Lys Val Phe
1370	1375	1380
Ser Ala Val Ser Ser Ile Lys	Ile Ala Ile Pro Asp	Tyr Lys Asp
1385	1390	1395
Leu Trp Asp Phe Ser Leu Arg	Cys Asp Trp Met Asp	Gly Tyr Pro
1400	1405	1410
Asp Ala Glu Lys Met Arg Ala	Ala Arg Ala Glu Met	Val Thr Tyr

1415	1420	1425
Ala Met Ala Lys Ala Ser Thr	Gly Lys Arg Leu Lys	Arg Met Leu
1430	1435	1440
Gln Lys Val Arg Ser Trp Ile	Arg Lys Lys Ala Phe	Ala Ala Ala
1445	1450	1455
Arg Lys Leu Lys Ser Leu Lys	Asn Arg Ile Ser Thr	Ala Phe Gly
1460	1465	1470
Arg Gly Lys Pro Pro Lys Ala	Lys Val Pro Asp Trp	Ala Val Val

1475	1480	1485
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Asn	Ala	Gly	Met	Gly	Met	Trp	Thr	Gly	Lys	Val	Phe	Ser	Thr	His
1490						1495					1500			
Leu	Thr	Phe	Asn	Glu	Asp	Glu	Met	Ser	Cys	Asn	Gly	Pro	His	Glu
1505						1510					1515			
Pro	Ile	Arg	Val	Met	Ser	Trp	Lys	Gln	Asn	His	Phe	Thr	Thr	Phe
1520						1525					1530			
Ala	Ser	Ser	Ser	Thr	Asn	Ala	Glu	Arg	Asn	Tyr	Val	Leu	Val	Lys
1535						1540					1545			
Lys	Gly	Asp	Asp	Ser	His	Cys	Trp	Ala	Thr	Arg	Glu	Ala	Leu	Val
1550						1555					1560			
His	Lys	Gly	Trp	Ser	Gly	Ile	Pro	Val	Tyr	Gln	Tyr	Ala	Glu	Pro
1565						1570					1575			
Ala	Gly	Phe	Trp	Leu	Gln	Glu	Val	Ser	Pro	Ser	Asn	Gln	Pro	Phe
1580						1585					1590			
Val	Val	Asn	Trp	Asp	Gly	Tyr	Leu	Thr	Thr	Ser	Asp	Asn	Leu	Thr
1595						1600					1605			
Leu	Gln	Asp	Ile	Asp	Ile	Asn	Ala	Ser	Ser	Asp	Ser	Leu	Lys	Ser
1610						1615					1620			
His	Ala	Val	Met	Arg	Ile	Val	Asp	Ser	Asn	Gly	Lys	Thr	Ile	Tyr
1625						1630					1635			
Gln	Gly	Pro	Pro	Thr	Gly	Val	Val	Gln	Thr	Gln	Gly	Gly	Val	Val
1640						1645					1650			
Thr	Leu	Gly	Ser	Ile	Arg	Asn	Leu	Val	Ser	Gly	Val	His	Ser	Thr
1655						1660					1665			
Gly	Asp	Ser	Val	Glu	Val	Arg	Val	Thr	Ala	Ser	Gly	Pro	Gln	Leu
1670						1675					1680			
Thr	Ser	Val	Ala	Asp	Leu	Asp	Thr	Gln	Phe	Lys	Glu	Ile	Pro	Asp
1685						1690					1695			
Leu	Val	Leu	Arg											
1700														

<210> 420

<211> 1738

<212> PRT

<213> *Toxoplasma gondii*

<400> 420

Met Gly Gly Arg Ala Thr Thr Ser Gly Ala Arg Ser Leu Ala Leu Pro

1 5 10 15
Leu Leu Ala Leu Phe Lys Pro Ser Phe Val Leu Leu Phe Phe Leu Ser

20 25 30
Ser Ala Val Ser Ser Gly Leu Ala Gly Ser Arg Ile Ala Asp Gly Val

35 40 45
Leu Leu Pro Ala Gly Gln Asp Arg Ser Arg Ser Ala Pro Pro Gln Ile
50 55 60

Lys Pro Gly Val Gly His Phe Gly Glu Gly Ser His Gly Leu Asn Ile

65 70 75 80
Ser Arg Thr Phe Leu Ala Asn Ser Ala Ser Thr Ser Leu His Ser Ser

85 90 95
Ser Thr Gly Pro Ser Arg Ser Ala Ala Ala Arg Leu Ser Ser Val His

100 105 110
Ser Val Ala Pro Ser Ser Thr Pro Leu Ser Pro Ser Ser Leu Leu Arg

115 120 125
Gly Ser Lys Ala Ser Arg Ser Ala Phe Pro Ser Phe Ser Ser Leu Arg

130 135 140
Lys Glu Lys Leu Ser Thr Ser Ser Ala Glu Lys Gln Gly Ile Val Asp

145 150 155 160
Asn Ser Phe Glu Asp Glu Gly Leu Glu Gly Arg Ala Arg Lys Pro Arg

165 170 175
Ala Pro Pro Ala Val Asp Glu Ser Leu Ile Asp Leu Ser Gly His Ser

180 185 190
Asp Thr Pro Glu Met Ser Pro Ser Ala Gly Val Asn Asp Val Leu Ala

195 200 205
Pro Ala Arg Ile Leu Asn Pro Lys Gln Phe Ala Arg Gln Leu Val Ala

210 215 220

Lys Val His Thr Ala Phe Val Gln Arg Asp Gln Arg Ile Ala Glu Asp
 225 230 235 240
 Gln Lys Asp Gly Lys Glu Asn Val Glu Lys Glu Arg Arg His Gly Ser
 245 250 255
 Ser Ala Leu Leu Gly Val Asp Glu Gln Leu Lys Gln Ala Asp His Gly

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

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

 385 390 395 400
 Glu Lys Glu Asp Thr Thr Glu Lys Glu Glu Lys Ser Glu Asn Gly Asp
 405 410 415
 Thr Ser Glu Arg Gly Asp Lys Ser Glu Asn Gly Asp Thr Ser Glu Lys
 420 425 430
 Glu Asp Gln Ser Gly Lys Gly Asp Thr Ser Gln Gln Gly Asp Lys Ser
 435 440 445
 Glu Lys Glu Glu Lys Ser Glu Ala Ala Asp Lys Ser Glu Ala Asp Thr

 450 455 460
 Ser Lys Asn Ser Ser Ser Ala Lys Ala Gly Val Ser Glu Lys Phe Lys

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

 515 520 525
 Lys Ala His Glu Lys His Arg Glu Gly Glu Ala Leu Pro Glu Pro Arg
 530 535 540
 Asp Ser Glu Lys Glu Ser Glu Ser Lys Ala Glu Ala Ala Ala Ser His
 545 550 555 560
 Asn Glu Pro Gly Asn Glu Gly Asp Glu Ala Pro Gly Asp Ser Gly Asp
 565 570 575
 Gln Glu Arg Gln Ala Gly Gly Asp Ser Val Pro Ser His Pro Gly Asp

 580 585 590
 Asn Ala Val Asn Glu Ser Arg Ser Gly Asp Asn Arg Gly Glu Ala Gly
 595 600 605
 Glu Thr Arg Glu Ala Glu Asn Asp Ala Ala Val Gly His Ser Asp Glu
 610 615 620
 Thr Gly Thr Gly Glu Thr Pro Ser Ala Glu Gly His His Gly Glu Glu
 625 630 635 640
 Ser Gly Ala Glu Thr Ala Val Pro Ser Asp Pro Arg Glu Glu Met Gly

 645 650 655
 Arg Ala Glu Ala Arg Ser Ala Asn Ser Pro Glu Glu Asn Thr Ala Glu
 660 665 670
 Ala Thr Gly Gly Gly Ala Ser Pro Tyr Arg Glu Glu Ala Glu Thr Ile
 675 680 685
 Val Gln Pro Tyr Thr Asp Ala Arg Gln Gly Gly Asn Asn Asp Ala Ser
 690 695 700
 Ala Ala Ser Pro Val Ala Arg His Asp Tyr Thr Glu Gly Ser Gln Ala

 705 710 715 720

Ser Pro Ala Ser Arg Pro Asp Asp Asn Ala Arg Ala Thr Gly Ser Asp
 725 730 735
 Ser Ser Pro Val Tyr Arg Glu His Ala Trp Ser Gly Glu Ala Pro Ala
 740 745 750
 Gly Glu Gly Gln Gln Glu Tyr Thr Gly Gly Ala Gly Tyr Ala Ala Pro
 755 760 765
 Val Ser His His Asp Gln Thr Glu Ala Ser Pro Ala Arg Ser Val Thr
 770 775 780
 Thr Pro Glu Trp Ser Ala Gln Ala Thr Gly Ser Glu Pro Gln Pro Gly
 785 790 795 800
 Glu Asp Thr Ala Arg Asp Gln Asp His Val Asp Asn Ala Ser Ala Asp
 805 810 815
 Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys Ser Glu Gly Ser
 820 825 830
 Pro Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly Ser Glu Pro Gln
 835 840 845
 Pro Gly Glu Asp Thr Ala Arg Asp Gln Asp His Val Asp Asn Ala Ser
 850 855 860
 Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys Ser Glu
 865 870 875 880
 Gly Ser Pro Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly Ser Glu
 885 890 895
 Pro Gln Pro Gly Glu Asp Thr Ala Arg Asp Gln Asp His Val Asp Asn
 900 905 910
 Ala Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys
 915 920 925
 Ser Glu Gly Ser Pro Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly
 930 935 940
 Ser Glu Pro Gln Pro Gly Glu Gly Thr Ala Arg Asp Gln Glu His Val
 945 950 955 960
 Asp Asn Ala Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu

965	970	975
Ala Lys Ser Glu Gly Ser Pro Glu Asn Asn Ala Gln Glu Thr His Glu		
980	985	990
Thr Gly Ser Glu Pro Gln Pro Gly Glu Gly Thr Ala Arg Asp Gln Asp		
995	1000	1005
His Val Asp Asn Ala Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu		
1010	1015	1020
Gly Asn Glu Ala Lys Ser Glu Gly Ser Pro Glu Asn Asn Ala Gln		
1025	1030	1035
Glu Thr His Glu Thr Gly Ser Glu Pro Gln Pro Gly Glu Gly Thr		
1040	1045	1050
Ala Arg Asp Gln Asp His Val Asp Asn Ala Ser Ala Asp Arg Gln		
1055	1060	1065
Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys Ser Glu Gly Ser Pro		
1070	1075	1080
Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly Ser Glu Pro Gln		
1085	1090	1095
Pro Gly Glu Gly Thr Ala Arg Asp Gln Asp His Val Asp Asn Ala		
1100	1105	1110
Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys		
1115	1120	1125
Ser Val Thr Gly Pro Asp Gly Gly Ala Gln Ala Asn Gly Gly Glu		
1130	1135	1140
Ser Ala Ile Thr Gln His Lys Gln Ala Ser Ala Gly Asp Ser Glu		
1145	1150	1155
Gly Arg Gln Asp Tyr Arg Asn Gly Ala Gly Tyr Ala Ser Pro Val		
1160	1165	1170
Ala Arg His Asp His Ala Glu Ala Ser Leu Val Arg Ser Ala Thr		
1175	1180	1185
Thr Leu Glu Gly Arg Ala Gln Asn Thr Gly Thr Pro Ala Ser Ala		
1190	1195	1200

Gln Arg Glu Glu Thr Lys Pro Arg Pro Ala Ala Val Glu Asp Val

1205 1210 1215

Ser Lys Asn Lys Glu Pro Glu Ile Glu Glu Glu Pro Ile His Leu

1220 1225 1230

Gln His Thr Gly Thr Asn Ala Asn Ile Gly His Thr Asn Ala Thr

1235 1240 1245

Ser Ala Asn His Gln Pro Thr Thr Glu Ala Glu Gly Gly Ser Ala

1250 1255 1260

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1265 1270 1275

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Ala Gly Gly Ser Ala

1280 1285 1290

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1295 1300 1305

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1310 1315 1320

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1325 1330 1335

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1340 1345 1350

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1355 1360 1365

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1370 1375 1380

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1385 1390 1395

Arg Glu Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1400 1405 1410

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1415 1420 1425

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1430 1435 1440
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1445 1450 1455
 Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1460 1465 1470
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1475 1480 1485
 Arg Val Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1490 1495 1500
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1505 1510 1515
 Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1520 1525 1530
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1535 1540 1545
 Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1550 1555 1560
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1565 1570 1575
 Arg Ala Pro Arg Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1580 1585 1590
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1595 1600 1605
 Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1610 1615 1620
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1625 1630 1635
 Arg Glu Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1640 1645 1650
 Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1655 1660 1665

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1670 1675 1680

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1685 1690 1695

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala

1700 1705 1710

Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

1715 1720 1725

Arg Ala Pro Gly Glu Gly Gly His Glu Ala

1730 1735

<210> 421

<211> 733

<212> PRT

<213> Toxoplasma gondii

<400> 421

Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala Asp Ala His His Gly

1 5 10 15

Gly Asp Glu Gln Lys Glu Gly Glu His Glu Arg Ala Pro Gly Glu Gly

20 25 30

Gly His Glu Ala Glu Gly Gly Ser Ala Asp Ala His His Gly Gly Asp

35 40 45

Glu Gln Lys Glu Gly Glu His Glu Arg Ala Pro Gly Glu Gly Gly His

50 55 60

Glu Ala Glu Gly Gly Ser Ala Asp Ala His His Gly Gly Asp Glu Gln

65 70 75 80

Lys Glu Gly Glu His Glu Arg Ala Pro Gly Glu Gly Gly His Glu Ala

85 90 95

Glu Gly Gly Ser Ala Asp Ala His His Gly Gly Asp Glu Gln Lys Glu

100 105 110

Gly Glu His Glu Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly

115 120 125

Gly Ser Ala Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu

130 135 140

His Glu Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser

145 150 155 160

Ala Asp Ala His His Gly Gly Asp Glu Gln Lys Glu Gly Glu His Glu

165 170 175

Arg Ala Pro Gly Glu Gly Gly His Glu Ala Glu Gly Gly Ser Ala Asp

180 185 190

Ser His His Gly Gly Asp Glu Gln Lys Glu Arg Gly Gly Glu Gly Ser

195 200 205

Ala Glu Glu Gln Glu Arg Gly Ser Gly Gly Ala Trp Glu Ala Ala Val

210 215 220

His Pro His Glu Gln Gly Arg Val Thr Glu Ala Glu Gly Glu Ser Ser

225 230 235 240

Arg Val Glu Glu Glu His Glu Ala Gly Gly Ala Pro Val His Ala His

245 250 255

Leu Gly Asn Glu Gly Gly Asn Glu Val Gly Leu Ser Leu Gly Asp Gln

260 265 270

Lys Gln Gly Ser Gly Gly Glu Ser Ser Ser Ser Gln Ala Gly His Ala

275 280 285

Lys Thr Glu Glu Arg Lys Ser Gly Tyr Ser His His Gly Pro Glu Thr

290 295 300

Glu Glu Asp Thr Ala Phe Ser His Ser Gly Gly Gly Thr Gly Asp Glu

305 310 315 320

Arg Glu Thr Arg Arg Ser Asn Ser Glu Gln Arg Lys Glu Arg Thr Glu

325 330 335

Glu Gly Gly Ala Arg Asp Gln Pro Gln Asn Glu Lys Lys Thr Glu Glu

340 345 350

Gln His Ala Gln Lys Gln Glu Glu Gln Tyr Lys Arg Asp Ile Ala Leu

355 360 365

Ser Lys His Gln Glu Ala Glu Glu Asn Arg Arg His Ala Asp Val Leu

370 375 380
 Leu Gln His His His Leu Gly Gln Gly Gly Pro Arg Gly Arg Thr Ala

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

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

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

 580 585 590
 Arg Gly Lys His Tyr Gln Met Phe Ala Ser Pro Pro Asp His Pro Leu
 595 600 605
 Pro Gln Pro Leu Leu Ile Gln Gly Ser Asn Leu His Ala Cys Leu Arg
 610 615 620

Leu Leu Pro Val His Gln Ala Thr Arg Cys Ser Pro Glu Ser Ala Glu
 625 630 635 640
 Thr Val Glu Ala Ala Leu Lys Asp Thr Gln Ala Val Ala Gln Gln Pro

 645 650 655
 Pro Pro His Val Leu Glu Gln Ala Val Leu Phe Glu Asn Ile Gln Val
 660 665 670
 Pro Met Pro Gly Ser Tyr Lys Leu Cys Met Leu Gln Tyr Trp Arg Pro
 675 680 685
 Pro Asp Ser Lys Pro Thr Asp Asn Val Phe Ile Met Gly Ile Asp Glu
 690 695 700
 Ile Gly Thr Leu Asp Val Leu Gln Gln Pro Asp Ala Glu Thr Leu Lys

 705 710 715 720
 His Val Gln Gly Leu His Lys Lys Asp Ser Gln Met His
 725 730

 <210> 422
 <211> 2265
 <212> PRT
 <213> Toxoplasma gondii
 <400> 422

 Met Gly Gly Arg Ala Thr Thr Ser Gly Ala Arg Ser Leu Ala Leu Pro
 1 5 10 15
 Leu Leu Ala Leu Phe Lys Pro Ser Phe Val Leu Leu Phe Phe Leu Ser
 20 25 30

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

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

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

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

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

340	345	350
Ala Glu Gly Ser Ser Gln Glu Asp Asp Asp Met Val Gly Ser Asn Glu		
355	360	365
Glu Thr Gly Ser Lys Ser Lys Ser Glu Gly Gly Asp Ala Ser Glu Lys		
370	375	380
Glu Glu Lys Ser Glu Lys Gly Asp Thr Ser Glu Arg Gly Asp Lys Ser		
385	390	395
Glu Lys Glu Asp Thr Thr Glu Lys Glu Glu Lys Ser Glu Asn Gly Asp		
405	410	415
Thr Ser Glu Arg Gly Asp Lys Ser Glu Asn Gly Asp Thr Ser Glu Lys		
420	425	430
Glu Asp Gln Ser Gly Lys Gly Asp Thr Ser Gln Gln Gly Asp Lys Ser		
435	440	445
Glu Lys Glu Glu Lys Ser Glu Ala Ala Asp Lys Ser Glu Ala Asp Thr		
450	455	460
Ser Lys Asn Ser Ser Ser Ala Lys Ala Gly Val Ser Glu Lys Phe Lys		
465	470	475
Ser Ala Ala Gln Pro Arg Ser His Leu Val His Ile Thr Thr Gly Tyr		
485	490	495
Leu Pro Lys Ile Arg Ala Tyr Arg Ala Thr Val Asn Pro Ser His Ser		
500	505	510
Arg Arg Arg Lys Lys Lys Lys Glu Gly Gly Ser Glu Asp Thr Glu Ser		
515	520	525
Lys Ala His Glu Lys His Arg Glu Gly Glu Ala Leu Pro Glu Pro Arg		
530	535	540
Asp Ser Glu Lys Glu Ser Glu Ser Lys Ala Glu Ala Ala Ala Ser His		
545	550	555
Asn Glu Pro Gly Asn Glu Gly Asp Glu Ala Pro Gly Asp Ser Gly Asp		
565	570	575
Gln Glu Arg Gln Ala Gly Gly Asp Ser Val Pro Ser His Pro Gly Asp		
580	585	590

Asn Ala Val Asn Glu Ser Arg Ser Gly Asp Asn Arg Gly Glu Ala Gly
 595 600 605

 Glu Thr Arg Glu Ala Glu Asn Asp Ala Ala Val Gly His Ser Glu Asp
 610 615 620
 Thr Gly Thr Gly Glu Thr Pro Ser Ala Glu Gly His His Gly Glu Glu
 625 630 635 640
 Ser Gly Ala Glu Thr Val Val Pro Ser Asp Pro Arg Glu Glu Met Gly
 645 650 655
 Met Ala Glu Ala Arg Ser Ala Asn Ser Pro Glu Glu Asn Thr Ala Glu
 660 665 670

 Ala Thr Gly Gly Gly Ala Ser Pro Tyr Arg Glu Glu Ala Glu Thr Ile
 675 680 685
 Val Gln Pro Tyr Thr Asp Ala Arg Gln Gly Gly Asn Asn Asp Ala Ser
 690 695 700
 Ala Ala Ser Pro Val Ala Arg His Asp Tyr Thr Glu Gly Ser Gln Ala
 705 710 715 720
 Ser Pro Ala Ser Arg Pro Asp Asp Asn Ala Arg Ala Thr Gly Ser Asp
 725 730 735

 Ser Ser Pro Val Tyr Arg Glu His Ala Trp Ser Gly Glu Ala Pro Ala
 740 745 750
 Gly Glu Gly Gln Gln Glu Tyr Thr Gly Gly Ala Gly Tyr Ala Ala Pro
 755 760 765
 Val Ser His His Asp Gln Thr Glu Ala Ser Pro Ala Arg Ser Val Thr
 770 775 780
 Thr Pro Glu Trp Ser Ala Gln Ala Thr Gly Ser Glu Pro Gln Pro Gly
 785 790 795 800

 Glu Gly Thr Ala Arg Asp Gln Glu His Val Asp Asn Ala Ser Ala Asp
 805 810 815
 Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys Ser Glu Gly Ser
 820 825 830
 Pro Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly Ser Glu Pro Gln

835	840	845
Pro Gly Glu Gly Thr Ala Arg Asp Gln Glu His Val Asp Asn Ala Ser		
850	855	860
Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys Ser Glu		
865	870	875 880
Gly Ser Pro Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly Ser Glu		
885	890	895
Pro Gln Pro Gly Glu Gly Thr Ala Arg Asp Gln Asp His Val Asp Asn		
900	905	910
Ala Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys		
915	920	925
Ser Glu Gly Ser Pro Glu Asn Asn Ala Gln Glu Thr His Glu Thr Gly		
930	935	940
Ser Glu Pro Gln Pro Gly Glu Gly Thr Ala Arg Asp Gln Glu His Val		
945	950	955 960
Asp Asn Ala Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu Gly Asn Glu		
965	970	975
Ala Lys Ser Glu Gly Ser Pro Glu Asn Asn Ala Gln Glu Thr His Glu		
980	985	990
Thr Gly Ser Glu Pro Gln Pro Gly Glu Gly Thr Ala Arg Asp Gln Glu		
995	1000	1005
His Val Asp Asn Ala Ser Ala Asp Arg Gln Asn Ala Glu Ala Glu		
1010	1015	1020
Gly Asn Glu Ala Lys Ser Glu Gly Ser Pro Glu Asn Asn Ala Gln		
1025	1030	1035
Glu Thr His Glu Thr Gly Ser Glu Pro Gln Pro Gly Glu Gly Thr		
1040	1045	1050
Ala Arg Asp Gln Asp His Val Asp Asn Ala Ser Ala Asp Arg Gln		
1055	1060	1065
Asn Ala Glu Ala Glu Gly Asn Glu Ala Lys Ser Val Thr Gly Pro		
1070	1075	1080

Asp Gly	Gly Ala Gln Ala Asn	Gly Gly Glu Ser Ala	Val Thr Gln
1085	1090	1095	
His Lys	Gln Ala Ser Ala Gly	Asp Ser Glu Gly Arg	Gln Asp Tyr
1100	1105	1110	
Arg Asn	Gly Ala Gly Tyr Ala	Ser Pro Val Ala Arg	His Asp His
1115	1120	1125	
Ala Glu	Ala Ser Leu Ala Arg	Ser Ala Thr Thr Leu	Glu Gly Arg
1130	1135	1140	
Ala Gln	Asn Thr Gly Thr Pro	Ala Ser Ala Gln Arg	Glu Glu Thr
1145	1150	1155	
Lys Pro	Arg Pro Ala Ala Val	Glu Asp Val Ser Lys	Asn Lys Glu
1160	1165	1170	
Pro Glu	Ile Glu Glu Glu Pro	Ile His Leu Gln His	Thr Gly Thr
1175	1180	1185	
Asn Ala	Asn Ile Gly His Thr	Asn Ala Thr Ser Ala	Asn His Gln
1190	1195	1200	
Pro Thr	Thr Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1205	1210	1215	
Gly Asp	Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1220	1225	1230	
Gly Gly	His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1235	1240	1245	
Gly Asp	Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1250	1255	1260	
Gly Gly	His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1265	1270	1275	
Gly Asp	Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1280	1285	1290	
Gly Gly	His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1295	1300	1305	
Gly Asp	Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Ser Glu

1310	1315	1320
Gly Gly His Glu Ala Glu Ser	Gly Ser Ala Asp Ala	His His Gly
1325	1330	1335
Gly Asp Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1340	1345	1350
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1355	1360	1365
Gly Asp Glu Gln Lys Glu Gly	Glu His Ala Arg Ala	Pro Gly Glu
1370	1375	1380
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1385	1390	1395
Gly Asp Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1400	1405	1410
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1415	1420	1425
Gly Asp Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1430	1435	1440
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1445	1450	1455
Gly Asp Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1460	1465	1470
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1475	1480	1485
Gly Asp Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1490	1495	1500
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1505	1510	1515
Gly Asp Glu Gln Lys Glu Gly	Glu His Glu Arg Ala	Pro Gly Glu
1520	1525	1530
Gly Gly His Glu Ala Glu Gly	Gly Ser Ala Asp Ala	His His Gly
1535	1540	1545

Gly Asp	Glu Gln Lys	Glu Gly	Glu His	Glu Arg	Ala	Pro Gly	Glu
1550		1555			1560		
Gly Gly	His Glu	Ala Glu	Gly Gly	Gly Ser	Ala Asp	Ala	His His Gly
1565		1570			1575		
Gly Asp	Glu Gln Lys	Glu Gly	Glu His	Glu Arg	Ala	Pro Gly	Glu
1580		1585			1590		
Gly Gly	His Glu	Ala Glu	Gly Gly	Gly Ser	Ala Asp	Ala	His His Gly
1595		1600			1605		
Gly Asp	Glu Gln Lys	Glu Gly	Glu His	Glu Arg	Ala	Pro Gly	Glu
1610		1615			1620		
Gly Gly	His Glu	Ala Glu	Gly Gly	Gly Ser	Ala Asp	Ala	His His Gly
1625		1630			1635		
Gly Asp	Glu Gln Lys	Glu Gly	Glu His	Glu Arg	Ala	Pro Gly	Glu
1640		1645			1650		
Gly Gly	His Glu	Ala Glu	Gly Gly	Gly Ser	Ala Asp	Ala	His His Gly
1655		1660			1665		
Gly Asp	Glu Gln Lys	Glu Gly	Glu His	Glu Arg	Ala	Pro Gly	Glu
1670		1675			1680		
Gly Gly	His Glu	Ala Glu	Gly Gly	Gly Ser	Ala Asp	Ala	His His Gly
1685		1690			1695		
Gly Asp	Glu Gln Lys	Glu Gly	Glu His	Glu Arg	Ala	Pro Gly	Glu
1700		1705			1710		
Gly Gly	His Glu	Ala Glu	Gly Gly	Gly Ser	Ala Asp	Ala	His His Gly
1715		1720			1725		
Gly Asp	Glu Gln Lys	Glu Arg	Gly Gly	Glu Gly	Ser	Ala Glu	Glu
1730		1735			1740		
Gln Glu	Arg Gly	Ser Gly	Val	Ala Trp	Glu Ala	Ala	Val His Pro
1745		1750			1755		
His Glu	Gln Gly	Arg Val	Thr	Glu Ala	Glu Gly	Glu	Ser Ser Arg
1760		1765			1770		
Val Glu	Glu Glu	His Glu	Ala	Gly Gly	Ala Pro	Val	His Ala His

1775	1780	1785
Leu Gly Asn Glu Gly Gly Asn	Glu Val Gly Leu Ser	Leu Gly Asp
1790	1795	1800
Gln Lys Gln Gly Ser Gly Gly	Glu Ser Ser Ser Ser	Gln Ala Gly
1805	1810	1815
His Ala Lys Thr Glu Glu Arg	Lys Ser Gly Tyr Ser	His His Gly
1820	1825	1830
Pro Glu Thr Glu Glu Asp Thr	Ala Phe Ser His Ser	Gly Gly Gly
1835	1840	1845
Thr Gly Asp Glu Arg Glu Thr	Arg Arg Ser Asn Ser	Glu Gln Arg
1850	1855	1860
Lys Glu Arg Thr Glu Glu Gly	Gly Ala Arg Asp Gln	Pro Gln Asn
1865	1870	1875
Glu Lys Lys Thr Glu Glu Gln	His Ala Gln Lys Gln	Glu Glu Gln
1880	1885	1890
His Lys Arg Asp Ile Ala Leu	Ser Lys His Gln Glu	Ala Glu Glu
1895	1900	1905
Asn Arg Arg His Ala Asp Val	Leu Leu Gln His His	His Leu Gly
1910	1915	1920
Gln Gly Gly Pro Arg Gly Arg	Thr Ala Val Thr Ser	His Ser His
1925	1930	1935
Met His Val Gln Asp Val Thr	Gln His His Gln Leu	Gln Glu Ala
1940	1945	1950
Thr Gln Met Ala Gly Lys Leu	Thr Arg His Leu Gln	Ile Gln Asn
1955	1960	1965
Ser Leu Lys Leu Arg Glu Met	Phe Leu Lys Arg Lys	Glu Val Gly
1970	1975	1980
His Leu Asn Leu Leu Lys His	Phe Gln Asp Leu Met	Gln Ala Val
1985	1990	1995
Val Ser Arg Ile Tyr Ser Lys	Leu Lys Gly Ala Lys	Arg Ser Leu
2000	2005	2010

Lys Arg Met Tyr Ser His Ser	Arg Ser Ile Ile Lys	Arg Phe Leu
2015	2020	2025
His Glu Thr Asp His Lys Val	Val Arg Pro Glu Glu	Leu Pro Ser
2030	2035	2040
Ala Val Leu Thr Pro Pro Asp	Glu Gly Asn Val Leu	Gly Lys Thr
2045	2050	2055
Thr Asn Gly Ile Val Met Asp	Cys Pro Thr Asp Cys	Asn Pro Ala
2060	2065	2070
Ala Cys Asp Asn Lys Pro Val	Glu Pro Ala Gln Cys	Phe Lys Tyr
2075	2080	2085
Glu Ala Val Ala Gly Gly Gly	Gly Phe Arg Arg Cys	Glu Pro Phe
2090	2095	2100
Ala Asp Pro Leu Thr Ala Thr	Cys Gly Lys Gly Phe	Thr Arg Cys
2105	2110	2115
Ala Met Ala Ala Pro Thr Arg	Gly Lys His Tyr Gln	Met Phe Ala
2120	2125	2130
Ser Pro Pro Asp His Pro Leu	Pro Gln Pro Leu Leu	Ile Gln Gly
2135	2140	2145
Ser Asn Leu His Ala Cys Leu	Arg Leu Leu Pro Val	His Gln Ala
2150	2155	2160
Thr Arg Cys Ser Pro Glu Ser	Ala Glu Thr Val Glu	Ala Ala Leu
2165	2170	2175
Lys Asp Thr Gln Ala Val Ala	Gln Gln Pro Pro Pro	His Val Leu
2180	2185	2190
Glu Gln Ala Val Leu Phe Glu	Asn Ile Gln Val Pro	Met Pro Gly
2195	2200	2205
Ser Tyr Lys Leu Cys Met Leu	Gln Tyr Trp Arg Pro	Pro Asp Ser
2210	2215	2220
Lys Pro Thr Asp Asn Val Phe	Ile Met Gly Ile Asp	Glu Ile Gly
2225	2230	2235
Thr Leu Asp Val Leu Gln Gln	Pro Asp Ala Glu Thr	Leu Lys His

2240 2245 2250

Val Gln Gly Leu His Lys Lys Asp Ser Gln Met His

2255 2260 2265

<210> 423

<211> 2980

<212> PRT

<213> Toxoplasma gondii

<400> 423

Met Val Ala Thr Thr Leu His Ser Leu Pro Ser Arg Tyr Leu Tyr Thr

1 5 10 15

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

20 25 30

Ser Pro Asp Gly Leu Pro Glu Ala Pro Asp Arg Pro Gln Asn Ala Glu

35 40 45

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

50 55 60

Ala Gly Lys Ser Glu Glu Phe Ala Phe Thr Ala Glu Tyr Phe Pro Pro

65 70 75 80

Thr Glu Ser Ser Lys Asn Glu Asp Gly Ala Gln Gln Ser Phe Val Glu

85 90 95

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

100 105 110

Asp Val Arg Ser Glu Val Gln Leu Arg Val Thr Thr Gln Gln Met Glu

115 120 125

Arg Gly Leu Leu Ala Glu Ile Val Val Leu Gln Glu Gly Gln Met Val

130 135 140

Ser Gly Phe Arg Ala Ser Leu Gln Thr Lys Glu Gln Ala Ala Leu Leu

145 150 155 160

His Arg Leu Ala Asp Leu Thr Asn Asp Pro Asn Ile His Phe Arg Val

165 170 175

Glu Trp Arg Gly Arg Gly Asp Gly Thr Gly Gly Leu Tyr Ile Arg Thr

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

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

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

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

 420 425 430

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

675 680 685
 Gly Glu Leu Leu Lys Ser Lys Pro Gln Lys Pro Val Thr Ala Thr Val
 690 695 700
 Gln Phe Gly Asp Asp Leu Pro Gly Leu Leu Tyr Asp Phe His Lys Pro
 705 710 715 720
 Phe Gln Lys Lys Lys Val Pro Thr Val Val Tyr Pro Phe Leu Gln Gly
 725 730 735
 Gln Gly Gln Gly Ser Arg Asp Ala Leu Asn Gly Gly Val Leu Gly Glu

 740 745 750
 Glu Tyr Tyr His Arg Pro Arg Lys Thr Lys Ile Thr Met Arg Pro Glu
 755 760 765
 Ile Pro Ile Leu Asn Thr His Asp Thr Phe Val Asp Gly Ser Gly Pro
 770 775 780
 His Pro Asn Val Pro His Phe Val Ile Pro Leu Thr Ala Gly Pro Gln
 785 790 795 800
 Gln His Leu Ala Pro Leu Lys Ala Leu Arg Gln Trp Leu Arg Lys Glu

 805 810 815
 Tyr Pro Gly Ser Gln Leu Pro Phe Lys Leu Asp Arg Met Ser Asp Glu
 820 825 830
 Asp Leu Leu Gly Ile Ala Asp His Leu Val Phe Arg Phe Pro Asp Gly
 835 840 845
 Thr Glu Ala Thr Leu Arg Ser Ile Phe Gly Pro Glu Val Phe Ser Pro
 850 855 860
 Asn Trp Ala Thr Met Asn Pro Asp Ala Tyr Gln Lys Leu Met Asp Val

 865 870 875 880
 Leu Thr Arg Pro Lys Lys Val Tyr Leu Ala Lys Asn Phe Arg Ile Val
 885 890 895
 Val Thr Asp Val Asp Gly Gln Gln Ile Pro Phe Asp Ile Gln Ile Glu
 900 905 910
 Pro Gly Asp Thr Trp Ala Lys Thr Leu Asp Asp Phe Phe Lys Ala His
 915 920 925

Pro Asn Leu Lys Pro Ala Asn Val Lys Leu Val Leu Tyr Asp Asp Lys

930

935

940

Asp Thr Ala Leu Arg Gln Phe Asp Ile Asn Leu Asp Met Tyr Ala Ser

945

950

955

960

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

965

970

975

Thr Leu Glu Thr Pro Ala Pro Ile Val Ser Cys Tyr Gln Ala Asp Pro

980

985

990

Ala Arg Pro Gly Gln Cys Leu Ala Val Asp Met Lys Arg Ile Phe Cys

995

1000

1005

Gly Arg Val Asn Pro Ala Lys Met Val Ser Arg Ala Trp Asn Glu

1010

1015

1020

Glu Cys Thr Ala Ala Trp Ile Ala Arg Ala Asp Leu Gly Glu Val

1025

1030

1035

Glu Asp Arg Tyr Leu Met Gly Pro Asp Asp Val Arg Ala Arg Ser

1040

1045

1050

Ile Arg Asp Leu Leu Thr Ser Ala Lys Asn Ala Leu Lys Gln Arg

1055

1060

1065

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

1070

1075

1080

Thr Glu Ser Glu Glu Leu Asn Arg Lys Met Arg Glu Arg Thr Glu

1085

1090

1095

Leu Ala Met Lys Ser Gly Lys Thr Leu Glu Asp Leu Asp Arg Leu

1100

1105

1110

Arg His Leu Lys Phe Glu Ile Arg Thr Leu Gln Arg Gln Gly Glu

1115

1120

1125

Leu Gln Trp Ala Lys Leu Val Gly Ala Thr Ile Thr Thr Thr Glu

1130

1135

1140

Lys Gly Lys Pro Ala Glu Arg His Ile Arg Leu Asp Pro Lys Lys

1145

1150

1155

Phe Phe Leu Asn Asp Lys Leu Trp Lys Val Phe Lys Glu Leu Ala

1160 1165 1170
Ala Gln Val Pro Gly Leu Lys Phe Glu Asn Val Phe Asn Phe Ser

1175 1180 1185
Phe Glu Val Met Asn Lys Glu Ala Arg Glu Gln Trp Lys Lys Glu

1190 1195 1200
Gln Thr Thr Val Thr Lys Glu Ala Lys Lys Gln Met Arg Ser Gln

1205 1210 1215
Lys Thr Val Val Asp Val Ile Phe Val Gly Pro Asp Gly Ser Ala

1220 1225 1230
Leu Phe Arg Asp Ile Gly Val Glu Leu Arg Gln Leu Ser Asp Glu

1235 1240 1245
Ala Leu Gly Arg Leu Ser Lys Gly Asp Lys Arg Gly Leu Ile Asn

1250 1255 1260
Gln Leu Ala Lys Arg Tyr Asp Ile Pro Arg Gln Tyr Phe Ile Arg

1265 1270 1275
Arg Gly Gly Phe Pro Ser Ala Ala Val Asn Gly Thr Lys Trp Val

1280 1285 1290
Ile Thr Ala Met Leu Gly Leu Val Gly Gly Ala Gly Lys Lys Gly

1295 1300 1305
Leu Ala Ser Leu Leu Lys Asp Pro His Ala Phe Val Thr His Leu

1310 1315 1320
Gln Ser Ala Gly Gly Phe Ser Pro Thr Asp Thr Val Lys Leu Val

1325 1330 1335
Phe Asp Asn Gly Ser Val Leu Asp Val Pro Leu Ser Gln Leu Pro

1340 1345 1350
Asp Gln Asp Leu Gly Ser Leu Ala Glu Ile Tyr Phe Pro Trp Lys

1355 1360 1365
Lys Thr Ala Gly Gln Ala Gln Glu Glu Lys Lys Lys Ala Val Glu

1370 1375 1380
Ser Lys Val Ala Glu Gly Ser Gly Ile Met Arg Lys Leu Glu Val

1385 1390 1395

Thr Val Met Gln Pro Ser Leu Trp Pro Glu Val Phe Gly Ala Trp		
1400	1405	1410
Leu Ser Asp Leu His Glu Met Asp Leu Phe Asp Asp Gly Pro Ile		
1415	1420	1425
Leu Leu Gln Val Arg Pro Glu Gly Ala Gln Lys Gly Gln Val Ile		
1430	1435	1440
Arg Cys Ser Val Lys Thr Leu Gly Glu Leu Tyr Gln Ala Leu Asn		
1445	1450	1455
Lys Pro Glu Ile Ile Arg Ser Lys Cys Pro Gly Met Ala Asp Leu		
1460	1465	1470
Lys Lys Pro Phe Thr Phe Glu Leu Ser Ile Arg Thr Pro Ala Glu		
1475	1480	1485
Gln Tyr Tyr Lys Leu Tyr Asn Arg Ser Arg Ser Pro Glu Asp Gln		
1490	1495	1500
Arg Arg Thr Ala Ala Val Leu Leu Lys Leu Lys Asp His Ile Arg		
1505	1510	1515
Asn Leu Pro Asp Asp Gly Gln Val Ile Phe Glu Tyr Arg Lys Ile		
1520	1525	1530
Lys Arg Thr Leu Thr Pro Gln Glu Leu Gln Gln Leu Lys Ala Leu		
1535	1540	1545
Ile Glu Gly Leu Gln Pro Asn Glu Asn Thr Asp Asp Val Leu Thr		
1550	1555	1560
Lys Ile Leu Arg Leu Leu Gly Ile Ser Asp Gln Asp Ile Ala Lys		
1565	1570	1575
Ser Gly Arg Leu Arg Phe Gly Ile Lys Gln Ala Pro Thr Ser Ser		
1580	1585	1590
Glu Gln Gln Met Leu Arg Glu Gly Ser Ile Thr Ala Val Val Glu		
1595	1600	1605
Asp Phe Gln Gly Gly Arg Arg Lys Ala Thr Val Arg Ile Ser Ile		
1610	1615	1620
Pro Glu Glu Glu Pro Leu Arg Leu Gly Ala Ser Ala Gln Asn Tyr		

1625	1630	1635
Gln Val His Met Ser Leu Phe	Ser Lys Asn Ala Gln	His Leu Asn
1640	1645	1650
Thr Pro Cys Gly Ser Lys Ser	Gly Ala Glu Val Ala	Lys Ala Thr

1655	1660	1665
Trp Gly Gln Leu Cys Arg Trp	Cys Asn Leu Lys Leu	Ala Asp Leu
1670	1675	1680
Pro Gly Leu Gly His Pro Thr	Leu Tyr Ile Arg Ile	Ile Ser Asn
1685	1690	1695
Glu Lys Thr Gln Thr Val Arg	Gly Gly Gln Pro Val	Thr Thr Asn
1700	1705	1710
Val Asp Gly His Pro Val Val	Tyr Asp Ile Arg Met	Pro Gly Asp

1715	1720	1725
Pro Arg Ser Ala Ser Gly Met	Pro Lys Ser Val Phe	Trp Asn Leu
1730	1735	1740
Val Glu Arg Pro Gly Ser Asn	Glu Leu Gly Pro Val	Trp His Gln
1745	1750	1755
Ser Ile Pro Lys Ala Asp Gly	Gly Leu Arg Lys Asp	Tyr Ser Tyr
1760	1765	1770
Phe Asp Pro Asn Pro Gly Ala	Trp Asp Pro Thr Leu	Phe Gly Pro

1775	1780	1785
Ser Ser Gly Thr Phe Pro Gln	Asn Thr Arg Ala Gly	Ile Asp Ile
1790	1795	1800
Val Thr Asn Pro Glu Ala Met	Glu Thr Gly Asp Ala	Tyr Ala Pro
1805	1810	1815
Pro Ile Arg Phe Gly Phe Gly	Phe Arg Asn Trp Asn	Asp Arg Asp
1820	1825	1830
Ala Val Lys Pro Gln Phe Asn	Asn Met Val Ser Gly	Ile Ala Pro

1835	1840	1845
Gln Glu Arg Asp Leu Tyr Lys	Val Tyr Ile Gln Ile	Pro Lys Gly
1850	1855	1860

Asp Gly	Asn Tyr	Tyr Pro	Cys Ser	Gly Val	Asp Ile	Asn Leu	Phe
1865			1870		1875		
Met Gln	Leu Thr	Lys Glu	Gln Ile	Ala Arg	Ala Cys	Gly Ile	His
1880			1885		1890		
Pro Ser	Leu Leu	Glu Ala	Pro Phe	Gly Val	Tyr Leu	Leu Lys	Glu
1895			1900		1905		
Thr Pro	Thr Tyr	Ala Arg	Ala Gln	Pro Ser	Phe Pro	Leu Phe	Phe
1910			1915		1920		
Val Asp	Gly Glu	Gly Gln	Glu His	Pro Ser	Leu Gly	His Trp	Thr
1925			1930		1935		
Asp Ala	Pro Ala	Lys Phe	Phe Ser	Pro His	Leu Arg	Gly Ala	Ser
1940			1945		1950		
Pro Asn	Ser Leu	Ile Gln	Leu Glu	Phe Ala	Pro Gly	Val Thr	Cys
1955			1960		1965		
Asn Leu	Thr Gln	Gln Glu	Leu Met	Ser Leu	His Thr	Trp Glu	Ala
1970			1975		1980		
Leu Leu	Lys Arg	Cys Asn	Ile Asp	Ala Gly	Lys Glu	Arg Pro	Ala
1985			1990		1995		
Thr Ile	Thr Thr	Arg Ile	Val Pro	Met Phe	Ser Thr	Pro Asn	Val
2000			2005		2010		
Thr Val	Lys Val	Pro Asn	Glu Leu	Leu Leu	Gln Pro	Leu Leu	Arg Gln
2015			2020		2025		
His Arg	Gly Ile	Ser Pro	Asp Gln	Leu Phe	Arg Gln	Lys Pro	Leu
2030			2035		2040		
Glu Glu	Val Val	Ala Leu	Leu Leu	Leu Ser	Asn Ala	His Leu	Gly Leu
2045			2050		2055		
Tyr His	Val Gly	Leu Lys	Tyr Ile	Asp Gly	Thr Asp	Gln Pro	Tyr
2060			2065		2070		
Ser Glu	Cys Pro	Glu His	Leu Arg	Gln Leu	Pro Pro	Ser Gln	Ile
2075			2080		2085		
Pro Gly	Leu Gln	His Ile	Tyr Ile	Val Pro	Ala Ser	Glu Gly	Glu

2090	2095	2100
Gly Asp Phe Pro Gly Val	Phe Arg Gly Gly Thr	Leu Gly Asp Met
2105	2110	2115
Met Lys Gly Met Asn Leu Ser	Pro Gln Thr Thr Tyr	Gly Asp Phe
2120	2125	2130
Val Arg Thr Val Lys Lys Lys	Ile Asn Ser Pro Glu	Gly Leu Thr
2135	2140	2145
Ile Pro Gly Val Arg Gln His	Val Gly Gly Ser Gly	Arg Pro Ala
2150	2155	2160
Gln Gln Ile Ile Asp Phe Asp	Phe Ala Gly Pro Glu	Ser Pro Pro
2165	2170	2175
Gly Ala Ala Gly Lys Pro Gly	Trp Glu Ala Thr Trp	Arg Pro Ala
2180	2185	2190
Thr Val Gly Ala Phe Pro Asp	Asn Met Pro Ile Gly	Asp Ile Asp
2195	2200	2205
Arg Glu Met His His Pro Phe	Leu Val Phe Thr Thr	Gly His Pro
2210	2215	2220
Pro Lys Tyr Asp Leu Asn Gly	Leu Ala Ala Tyr Gly	Gly Gln Pro
2225	2230	2235
Phe Arg Glu Glu Thr Thr His	Leu Asp Ala Ser Leu	Arg Asn Leu
2240	2245	2250
Val Glu Trp Met Lys Asp Ser	Leu Gly Ile Ser Asp	Pro Asn Gly
2255	2260	2265
Ile Leu Ala Glu Ile Val Ile	Asp Thr Ile Arg Cys	Pro Phe Pro
2270	2275	2280
Leu Ser Ala Ala Gln Leu Ile	Ser Ala Thr Ile Gly	His Leu Leu
2285	2290	2295
His His Cys Gln Val Asn Asp	Leu Glu Met Ser His	Ser Ile Tyr
2300	2305	2310
Val Thr Pro Thr Pro Val Pro	Gly Tyr Thr Ala Thr	Pro Lys Arg
2315	2320	2325

Asn Gly	Pro Gln Ile Val Ile	Asn Gly His Asn Tyr	Gly Ala Pro
2330	2335	2340	
Gly Thr	Ala Pro Arg Asp Phe	Gly Gln Leu Phe Asn	Leu Pro Gly
2345	2350	2355	
Arg Pro	Gly Ala Arg Pro Leu	Asn Gln Asp Leu Glu	Val Ser Phe
2360	2365	2370	
Ser Pro	Leu Pro Gly Lys Pro	Pro Val Arg Gly Val	Leu Pro Gly
2375	2380	2385	
Asp Val	Leu Pro Leu Leu Gln	Ser Ile Ser Asp Lys	His Gly Gln
2390	2395	2400	
Pro Gly	Val Ala Val Val Leu	Asn Phe Leu Arg Gln	Leu His Ala
2405	2410	2415	
Leu Ala	Glu Leu Pro Pro Gly	Ala Thr Leu Asn Ile	Asp Thr Lys
2420	2425	2430	
Leu Ile	Pro Ser Gln Ser Pro	Gln Gln Leu Tyr Ala	Pro Asp Gln
2435	2440	2445	
Val Pro	Gln Pro Gly Pro Trp	Ile Ala Gly Pro Thr	Gly Gly Gly
2450	2455	2460	
Arg Phe	Pro Gly Gly Gly Val	Val Val Asn Glu Ser	Gly Gly Arg
2465	2470	2475	
Arg Gly	Pro Gly Gly Ser Ala	Ala Val Lys Phe Met	Pro Ser Thr
2480	2485	2490	
Leu Arg	Leu Pro Leu Leu Arg	Gln Pro Ser Val Glu	Leu Pro Arg
2495	2500	2505	
Asn Ser	Met Leu Arg Gly Ser	Ile Gly Gly Val Gly	Gly Leu Pro
2510	2515	2520	
Arg Thr	Glu Phe Val Val Pro	Ile Leu Pro Ser Gln	Lys Ser Met
2525	2530	2535	
Pro Ile	Glu Gln Val Leu Lys	Phe Phe Gly Ile Ala	Pro Ala Ala
2540	2545	2550	
Val Gln	Thr Leu Asp Val Gln	Glu Lys Pro Glu Gln	Gly Ala Ile

2555	2560	2565
Leu Ile Glu Ser Gly Thr Val	Thr Phe Val Pro Leu	Lys Gly Pro
2570	2575	2580
Thr Phe Thr Val Ser Met Lys	Lys Ile Asn Ala Thr	Asp Lys Asn
2585	2590	2595
Thr Leu Ala Thr Leu Leu Lys	Ala Ala Gly Arg Ser	Ile Ile Asp
2600	2605	2610
Leu Val Gly Ala Ser Asp Gly	Thr Gln Pro Leu Val	Leu Lys Ile
2615	2620	2625
Val Val Asp His Gly Ala Val	Ser Pro Thr Lys Val	Thr Thr Pro
2630	2635	2640
Val Gly Thr Pro Ser His Ala	Arg Ser Ala Met Glu	Gly Leu Thr
2645	2650	2655
Ile Trp Asn Leu Leu Pro Pro	Leu Ile Asp Val His	Ser Val Lys
2660	2665	2670
Thr Ile Thr Ile Arg Val Gln	Ala Ala Lys Ala Phe	Gln Gln Ala
2675	2680	2685
Ala Lys Ala Ala Ala Ala Ala	Glu Gly Thr Glu Gly	Asp Ser Ala
2690	2695	2700
Gly Glu Pro Leu Ser Arg Pro	Lys Asn Val Glu Pro	Ala Val Arg
2705	2710	2715
Thr Lys Phe Lys Asn Lys Ile	Pro Glu Leu Pro Ala	Ala Phe Lys
2720	2725	2730
Pro Arg Gln Arg Thr Val Ser	Glu Ile Asn Gly Ala	Pro Asn Pro
2735	2740	2745
Lys Leu Val Ile Phe Val Glu	Gln Asp Gly Gln Lys	Thr Ile Arg
2750	2755	2760
Phe Thr Phe Pro Ser Arg Val	Asn Asp Val Val Ile	Gly Gln Ser
2765	2770	2775
Thr Val Ser Val Val Leu Asp	Ala Leu Leu Pro Asn	Pro Gly Thr
2780	2785	2790

Trp His Arg Thr Phe Trp Gly Ala Leu Ser Pro Asp Gly Thr Ser

2795 2800 2805

Cys Lys Pro Thr Met Glu Phe Gln Tyr Pro His Trp Leu Gln Thr

2810 2815 2820

Lys Met Ala Glu Leu Pro Val Pro Asn His Ser Ser Cys Leu Leu

2825 2830 2835

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

2840 2845 2850

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

2855 2860 2865

Gln Gly Lys Gln Arg Ile Pro Ile Phe Glu Glu Gln Val Asp Pro

2870 2875 2880

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

2885 2890 2895

Ile Pro Lys Thr Gln Leu Asp Thr Ile Leu Gln Cys Ser Ser Thr

2900 2905 2910

Asn Ile Asp Ala Pro Gly Glu Cys Pro Ser Asp Ser Ser Thr Thr

2915 2920 2925

Val Asp Pro Glu Thr Val Ile Pro Asp Ala Val Ala Thr Gln Ser

2930 2935 2940

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

2945 2950 2955

Phe Leu Gln Val Leu Trp Arg Arg Gln Arg Arg Arg Asn Ser Ile

2960 2965 2970

Gln Lys Arg Ile Thr Ser His

2975 2980

<210> 424

<211> 422

<212> PRT

<213> Toxoplasma gondii

<400> 424

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

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

305 310 315 320
 Pro Cys Pro His Ala Glu Glu His Asn Ala Thr Asn Gly Ser Asn Ser
 325 330 335
 Ala Glu Ala Ala Ser Glu Asp Ser Asn Pro His Glu Ala Val Lys His
 340 345 350
 Thr Asp Ala His Gly Gln Thr Gln Ala Ser Asp Gln Ala Gln Gly His
 355 360 365
 Asp Gln Glu Glu Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn

370 375 380
 Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser
 385 390 395 400
 Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Gln Arg
 405 410 415
 Ser Ser Asp Ala Ser Gln

420

<210> 425

<211> 1159

<212> PRT

<213> Toxoplasma gondii

<400> 425

Thr Asp Gly His Glu Lys Thr Asn Glu Val Arg Ala Asp Gln Lys Gly

1 5 10 15
 Gly Glu Gly Ala Ser Thr Thr Gln His Glu Glu Gly Gln Glu Thr Glu
 20 25 30

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

275 280 285
 Glu Asn Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser
 290 295 300
 Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn Ala Gln Glu Pro Lys Gln
 305 310 315 320
 Ala Glu Glu Arg Glu Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu

 325 330 335
 Glu Asn Ala Gln Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser
 340 345 350
 Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln
 355 360 365
 Gly Glu Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu
 370 375 380
 Glu Asn Ala Gln Val Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser

 385 390 395 400
 Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln
 405 410 415
 Gly Glu Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu
 420 425 430
 Glu Asn Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser
 435 440 445
 Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln

 450 455 460
 Gly Glu Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Gly
 465 470 475 480
 Glu Asn Ala Glu Glu Pro Lys Gln Thr Glu Glu Pro Glu Glu Ala Ser
 485 490 495
 Gln Ser Thr His Ser Pro Ala Glu Glu Gln Ser Pro Glu Gln Ala Gln
 500 505 510
 Gly Gln Glu Arg Glu Asn Ala Ser Gln Pro Ser Glu Ser Pro Ala Glu

 515 520 525

Glu Ser Thr Pro Glu Gln Ala Glu Glu Lys Gly Thr Glu Ala Ala Glu
 530 535 540
 Glu Pro Ala Gln Glu Gln Pro Ala Glu Thr Gln Glu Gly Ser Asp Ala
 545 550 555 560
 Glu Ala Asp Ala Glu Gly Gly Ser Gly Ala Asn Gly Glu Ala Gln Pro
 565 570 575
 Gln Glu Glu Ser Gly Glu Asn Lys Asp Val Pro Ala Ala Asp Gln Glu
 580 585 590
 Ala Pro Gly Leu Asp Glu Gln Gly Arg Asp Glu Val Gly Thr Gly Ala
 595 600 605
 Pro Glu Ala Ala Ala Ala Ser Ala Ala Gly Ala Ser His Glu Asn Glu
 610 615 620
 Ala His Gly Ala Asp Gln Gln Asp Asp Ser Val Glu Ser Ala Gly Pro
 625 630 635 640
 Ala Ala Asp Glu Gln Gln Lys Asp Ala Thr Gly Glu Val Gly Glu Leu
 645 650 655
 His Gly Ala Glu Thr Gln Thr Pro Gln Leu Ala Ala Glu Ala Glu Thr
 660 665 670
 Ala Gly Ala Glu Gln Glu Ala Gly Arg Ala Asp Ser Val Ser Asp Gly
 675 680 685
 Cys Tyr Val Thr Arg Arg Gln Glu Val Glu Ala Glu Ala Lys Lys Leu
 690 695 700
 Leu Glu Val Cys Glu Arg Asn Asp Asn Phe Thr Lys Val Asp Gln Gln
 705 710 715 720
 Phe Cys Asp Glu Leu Phe Lys Arg Ile Asp Gly Pro Phe Thr Val Gly
 725 730 735
 Glu Val Ser Ala Phe Leu Arg Ala Ala Asp Thr Ala Asn Asn Ile Ser
 740 745 750
 Arg Asn Phe Arg Phe Cys Arg Ala Thr Pro Thr Ser Ser Pro Pro Arg
 755 760 765
 Val Arg Asp Gly Asp Ser Val Ile His Ala Ala Ile Ala Ala Ser Lys

770 775 780
 Pro Arg Val Val Glu Ile Leu Leu Gln Tyr Gly Ala Phe Pro Asn Ile
 785 790 795 800
 Glu Ala Phe Pro Arg Ser Pro Asp Ala Ala Asn Arg Met Gly Met Arg
 805 810 815
 Pro Leu His Tyr Val Ala Arg Tyr Pro Thr Leu Glu Asn Tyr Glu Ser
 820 825 830
 Leu Phe Leu Leu Leu Lys Tyr Gly Ser Pro Val Asn Val Arg Asp Val

 835 840 845
 Gly Gly Arg Thr Pro Leu Met Ile Ala Ala Arg Ser Ser His Pro Phe
 850 855 860
 Ser Lys Leu Phe Ala Arg Ala Leu Ile Asp Arg Asn Ala Asp Val Thr
 865 870 875 880
 Ala Arg Asp Lys Ala Gly Leu Ser Ala Leu His Tyr Ala Ala Ala Ser
 885 890 895
 Asn Ser Cys Lys Leu Val Lys Leu Leu Ile Asn Arg Gly Ala Asp Val

 900 905 910
 Met Ser Gln Asp Ile Arg Gly Asn Thr Pro Leu His Tyr Ala Ala Ala
 915 920 925
 Phe Asn Ala Asp Lys Ser Met Asn Thr Leu Leu Asn Leu Ala Gly Asn
 930 935 940
 Ala Ile Lys Val Asn Val Pro Asn Lys Asn Gly Lys Ala Pro Ile His
 945 950 955 960
 Leu Ala Ala Ala Pro Ser Ser Phe Asp Val Val Pro Ala Lys Ile Val

 965 970 975
 Pro Ala Leu Ser Leu Glu Leu Leu Leu Glu Lys His Ala Asp Pro Val
 980 985 990
 Ala Arg Asp Ala His Gly Asn Thr Pro Leu Met Asp Ala Val Leu Gly
 995 1000 1005
 Gly Tyr Leu Glu Ile Ala Lys Arg Leu Leu Gln Ile Ala Arg Val
 1010 1015 1020

Pro Leu His Asp Lys Asn Met Asp Gly Lys Thr Ala Leu Asp Leu

1025 1030 1035

Ala Gln Glu Ala Ala Glu Arg Thr Gly Asp Asp Val Leu Ala Tyr

1040 1045 1050

Leu Thr Ala Val Ser Ser Lys Pro Ser Cys Pro Phe Ile Pro Arg

1055 1060 1065

Val Ala Asn Ser Ile His Val Leu Ser Asp Thr Gln Phe Gly Ser

1070 1075 1080

Leu Met Arg Val Gly Asp Thr Val Thr Tyr Glu Cys His His Gly

1085 1090 1095

Phe Arg Leu Leu Gly His Ala Thr Leu Thr Cys Met Ser Arg Asp

1100 1105 1110

Gly Ser Pro Glu Phe Ile Pro Asp Pro Pro Val Cys Ile Pro Met

1115 1120 1125

Glu Gln Gly Ala Ala Ser Ser Leu Tyr Ser Ala Pro Leu Gly Leu

1130 1135 1140

Ala Thr Ala Leu Leu Val Tyr Leu Ile Pro Phe Phe Leu Thr Gln

1145 1150 1155

Phe

<210> 426

<211> 1493

<212> PRT

<213> Toxoplasma gondii

<400> 426

Met Leu Ser Val Phe Pro Glu Ser Ala Arg Lys Met Glu Ser Val Asn

1 5 10 15

Arg Pro Arg Phe Pro Pro Phe Phe Cys Pro Pro Ser Leu Gly Val Ser

20 25 30

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

35 40 45

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

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

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

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

290	295	300
Ser Ser Ala Pro Ala Gln Ser His Glu Thr Pro Val Ala Glu His Ala		
305	310	315 320
Pro Cys Pro His Ala Glu Glu His Asn Ala Thr Asn Gly Ser Asn Ser		
	325	330 335
Ala Glu Ala Ala Ser Glu Asp Ser Asn Pro His Glu Ala Val Lys His		
	340	345 350
Thr Asp Ala His Gly Gln Thr Gln Ala Ser Asp Gln Ala Gln Gly His		
355	360	365
Asp Gln Glu Glu Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn		
370	375	380
Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser		
385	390	395 400
Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Ala Glu		
	405	410 415
Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn		
	420	425 430
Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser		
435	440	445
Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Ala Glu		
450	455	460
Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn		
465	470	475 480
Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser		
	485	490 495
Ser Gln Thr Pro Ala Glu Glu Asn Ala Gln Glu Pro Lys Gln Ala Glu		
500	505	510
Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn		
515	520	525
Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser		
530	535	540

Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Ala Glu
545 550 555 560

Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn
565 570 575

Thr Glu Glu Pro Lys Gln Ala Glu Glu Arg Ala Asn Ala Ser Gln Ser
580 585 590

Ser Glu Thr Pro Ala Glu Glu Asn Ala Gln Glu Pro Lys Gln Gly Glu
595 600 605

Glu Gln Ala Asn Ala Ser Gln Ser Ser Ala Thr Pro Ala Glu Glu Asn
610 615 620

Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser
625 630 635 640

Ser Glu Thr Pro Ala Glu Glu Asn Ala Gln Glu Pro Lys Gln Ala Glu
645 650 655

Glu Arg Glu Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn
660 665 670

Ala Gln Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser
675 680 685

Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Gly Glu
690 695 700

Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn
705 710 715 720

Ala Gln Val Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser
725 730 735

Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Gly Glu
740 745 750

Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Glu Glu Asn
755 760 765

Ala Glu Glu Pro Lys Gln Ala Glu Glu Gln Ala Asn Ala Ser Gln Ser
770 775 780

Ser Glu Thr Pro Ala Glu Glu Asn Ala Glu Glu Pro Lys Gln Gly Glu

785 790 795 800
Glu Gln Ala Asn Ala Ser Gln Ser Ser Glu Thr Pro Ala Gly Glu Asn

 805 810 815

Ala	Glu	Glu	Pro	Lys	Gln	Thr	Glu	Glu	Pro	Glu	Glu	Ala	Ser	Gln	Ser		
820						825						830					
Thr	His	Ser	Pro	Ala	Glu	Glu	Gln	Ser	Pro	Glu	Gln	Ala	Gln	Gly	Gln		
835						840						845					
Glu	Arg	Glu	Asn	Ala	Ser	Gln	Pro	Ser	Glu	Ser	Pro	Ala	Glu	Glu	Ser		
850						855						860					
Thr	Pro	Glu	Gln	Ala	Glu	Glu	Lys	Gly	Thr	Glu	Ala	Ala	Glu	Glu	Pro		
865						870						875				880	

Ala	Gln	Glu	Gln	Pro	Ala	Glu	Thr	Gln	Glu	Gly	Ser	Asp	Ala	Glu	Ala
885							890				895				
Asp	Ala	Glu	Gly	Gly	Ser	Gly	Ala	Asn	Gly	Glu	Ala	Gln	Pro	Gln	Glu
900							905				910				
Glu	Ser	Gly	Glu	Asn	Lys	Asp	Val	Pro	Ala	Ala	Asp	Gln	Glu	Ala	Pro
915							920				925				
Gly	Leu	Asp	Glu	Gln	Gly	Arg	Asp	Glu	Val	Gly	Thr	Gly	Ala	Pro	Glu
930							935				940				

Ala Ala Ala Ala Ser Ala Ala Gly Ala Ser His Glu Asn Glu Ala His
945 950 955 960

Gly Ala Asp Gln Gln Asp Asp Ser Val Glu Ser Ala Gly Pro Ala Ala
965 970 975

Asp Glu Gln Gln Lys Asp Ala Thr Gly Glu Val Gly Glu Leu His Gly
980 985 990

Ala Glu Thr Gln Thr Pro Gln Leu Ala Ala Glu Ala Glu Thr Ala Gly
995 1000 1005

Ala	Glu	Gln	Glu	Ala	Gly	Arg	Ala	Asp	Ser	Val	Ser	Asp	Gly	Cys
1010						1015			1020					
Tyr	Val	Thr	Arg	Arg	Gln	Glu	Val	Glu	Ala	Glu	Ala	Lys	Lys	Leu
1025						1030			1035					

Leu Glu	Val Cys Glu Arg Asn	Asp Asn Phe Thr Lys	Val Asp Gln
1040	1045	1050	
Gln Phe	Cys Asp Glu Leu Phe	Lys Arg Ile Asp Gly	Pro Phe Thr
1055	1060	1065	
Val Gly	Glu Val Ser Ala Phe	Leu Arg Ala Ala Asp	Thr Ala Asn
1070	1075	1080	
Asn Ile	Ser Arg Asn Phe Arg	Phe Cys Arg Ala Thr	Pro Thr Ser
1085	1090	1095	
Ser Pro	Pro Arg Val Arg Asp	Gly Asp Ser Val Ile	His Ala Ala
1100	1105	1110	
Ile Ala	Ala Ser Lys Pro Arg	Val Val Glu Ile Leu	Leu Gln Tyr
1115	1120	1125	
Gly Ala	Phe Pro Asn Ile Glu	Ala Phe Pro Arg Ser	Pro Asp Ala
1130	1135	1140	
Ala Asn	Arg Met Gly Met Arg	Pro Leu His Tyr Val	Ala Arg Tyr
1145	1150	1155	
Pro Thr	Leu Glu Asn Tyr Glu	Ser Leu Phe Leu Leu	Leu Lys Tyr
1160	1165	1170	
Gly Ser	Pro Val Asn Val Arg	Asp Val Gly Gly Arg	Thr Pro Leu
1175	1180	1185	
Met Ile	Ala Ala Arg Ser Ser	His Pro Phe Ser Lys	Leu Phe Ala
1190	1195	1200	
Arg Ala	Leu Ile Asp Arg Asn	Ala Asp Val Thr Ala	Arg Asp Lys
1205	1210	1215	
Ala Gly	Leu Ser Ala Leu His	Tyr Ala Ala Ala Ser	Asn Ser Cys
1220	1225	1230	
Lys Leu	Val Lys Leu Leu Ile	Asn Arg Gly Ala Asp	Val Met Ser
1235	1240	1245	
Gln Asp	Ile Arg Gly Asn Thr	Pro Leu His Tyr Ala	Ala Ala Phe
1250	1255	1260	
Asn Ala	Asp Lys Ser Met Asn	Thr Leu Leu Asn Leu	Ala Gly Asn

1265	1270	1275
Ala Ile Lys Val Asn Val Pro	Asn Lys Asn Gly Lys	Ala Pro Ile
1280	1285	1290
His Leu Ala Ala Ala Pro Ser	Ser Phe Asp Val Val	Pro Ala Lys
1295	1300	1305
Ile Val Pro Ala Leu Ser Leu	Glu Leu Leu Leu Glu	Lys His Ala
1310	1315	1320
Asp Pro Val Ala Arg Asp Ala	His Gly Asn Thr Pro	Leu Met Asp
1325	1330	1335
Ala Val Leu Gly Gly Tyr Leu	Glu Ile Ala Lys Arg	Leu Leu Gln
1340	1345	1350
Ile Ala Arg Val Pro Leu His	Asp Lys Asn Met Asp	Gly Lys Thr
1355	1360	1365
Ala Leu Asp Leu Ala Gln Glu	Ala Ala Glu Arg Thr	Gly Asp Asp
1370	1375	1380
Val Leu Ala Tyr Leu Thr Ala	Val Ser Ser Lys Pro	Ser Cys Pro
1385	1390	1395
Phe Ile Pro Arg Val Ala Asn	Ser Ile His Val Leu	Ser Asp Thr
1400	1405	1410
Gln Phe Gly Ser Leu Met Arg	Val Gly Asp Thr Val	Thr Tyr Glu
1415	1420	1425
Cys His His Gly Phe Arg Leu	Leu Gly His Ala Thr	Leu Thr Cys
1430	1435	1440
Met Ser Arg Asp Gly Ser Pro	Glu Phe Ile Pro Asp	Pro Pro Val
1445	1450	1455
Cys Ile Pro Met Glu Gln Gly	Ala Ala Ser Ser Leu	Tyr Ser Ala
1460	1465	1470
Pro Leu Gly Leu Ala Thr Ala	Leu Leu Val Tyr Leu	Ile Pro Phe
1475	1480	1485
Phe Leu Thr Gln Phe		
1490		

<210> 427

<211> 1167

<212> PRT

<213> *Toxoplasma gondii*

<400> 427

Met Ser Ser Asn Leu Ala Phe Leu Ser Leu Ser Leu Ala Glu Ser Thr

1 5 10 15

Ala Ser Leu Gly Lys Ser Leu Glu Glu Thr Arg Thr Arg Leu Thr Glu

20 25 30

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

35 40 45

Met His Gln Thr Ala Thr Gly Pro Gly Leu Ser Val Glu Gly Lys Gln

50 55 60

Thr Glu Gln Met Ser Arg Lys Ser Ala Glu Asp Thr Arg Ala Ser Ser

65 70 75 80

Leu Ser Ser Asp Pro Asp Asp Gly Arg Ala Ala Gln Leu Ala Gly Gln

85 90 95

Lys Gly His Val Thr Pro Cys Ile Ala Gly Leu Ile Ala Thr Ser Asn

100 105 110

Pro Phe Leu Phe Thr His Met Leu Ala Leu Gly Ala Ala Tyr Leu Gly

115 120 125

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

130 135 140

Gly Thr Arg Thr Leu Leu Ser Thr Leu Ser Pro Leu Asp Thr Pro Arg

145 150 155 160

Leu Leu Asp Ser Met Ala Ala Ala Asp Arg Leu Ser Pro Lys Arg Ser

165 170 175

Ile Leu Ser Arg Phe Ser Arg Arg Lys Arg Ser Leu Asp Ala Pro Ala

180 185 190

Pro Glu Pro Ser Gly Trp Asp Gln Lys Arg Lys Ser Arg Leu Pro Leu

195 200 205

Gly Ser Leu Arg Leu Val Leu Asp Ile Leu Asp Arg His Leu Glu Ala

210 215 220
 Leu Thr Thr Tyr Val Gln Gln Gln Ile Glu Ile Phe Arg Gln Ala Gly
 225 230 235 240

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

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

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

 Thr Pro His Arg Glu Gly Ile Leu Ser Pro Val Asp Phe Ile Arg Glu
 435 440 445
 Ala Phe Ala Gly Glu Arg Ser Tyr Ala Met Ser Thr Ala Arg Leu Lys
 450 455 460

Pro Leu Leu Ser Asp Asp Leu Val Ile Leu Gly Val Pro Lys Gly Phe
 465 470 475 480
 Ser Phe Leu Trp Leu Phe Glu Phe Leu Leu Glu Glu Asp Ser Pro Asn
 485 490 495

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

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

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

Gly Met Ser Asp Asn Leu Tyr Thr Leu Val Glu Asp Thr Ile Lys Asn
 690 695 700
 Leu Gln Asp Gly Ser Ser Arg Asp Asp Thr Ile Phe Phe Gly Arg Ile

705	710	715	720
Ala Arg Gly Ala Arg Glu Ser Val Gly Gln Lys Met Trp Arg Gly Val			
	725	730	735
Lys Thr Phe Phe Leu Asp Leu Val Arg Asp Val Pro Gly Ser Asp His			
	740	745	750
Ala Val Trp Phe Gly Val Gly Phe Asn Phe Pro Arg Ile Phe Gln Ile			
	755	760	765
Leu Arg Lys Met Lys Glu Ile Ala Leu His Ala Ala Gly Asp Gln Gly			
	770	775	780
Ser Ala Ile Leu Leu Asp Glu Ala Phe Val Glu Leu Val Gln Glu Thr			
785	790	795	800
Val Ala Val Arg Ala Gln Thr Tyr Arg Arg Gln Pro Pro Thr Thr Leu			
	805	810	815
Arg Asn Ile Gly Val Ile Gly Leu Arg Pro Asp Tyr Ala Asn Leu Asp			
	820	825	830
Thr Glu Gln Arg Ser Met Glu Tyr Gln Leu Ser Met Cys Ala Asp His			
	835	840	845
Cys Val Ser Leu Trp Val Gln Ile Leu Gly Phe Ile Tyr Pro Tyr Val			
	850	855	860
Leu Asn Pro Ser Leu Leu Thr Asp Tyr Glu Lys Ser Phe Gly Thr Gly			
865	870	875	880
His Ala Ile Lys Lys Leu Asp Asp Pro Ser Tyr Val Asn Ser Phe Arg			
	885	890	895
Tyr Ile Phe Ala Asn Asp Ala Ser Leu Asn Phe Phe Glu His Asn Thr			
	900	905	910
Pro Gln Asp Thr Arg Lys Ala Leu Val Ser Leu Lys Ser Gly Gln Ala			
	915	920	925
Phe Met Tyr Ala Asn Met Met Arg Phe Ala Gly Ile Ala Phe Glu Gln			
	930	935	940
Leu Ser Met Pro Tyr Leu Ala Val Ser Leu Gln Arg Gln Ala Pro Phe			
945	950	955	960

Met Gly Gln Met Val Lys Asp Trp Val Ala Lys Arg Ser Arg Ser Arg
 965 970 975
 Lys Leu Ala Ile Val Ser Val Leu Ser Leu Gly Leu Ile Phe Ala Tyr
 980 985 990
 Thr Leu Leu Ser Ala Leu Asp Ile Ala Gln Phe Leu Thr Asp Ser Gly
 995 1000 1005

Met Lys Ala Ile Glu Asp Cys Ser Trp Asn Pro Ile Met Gln Gln
 1010 1015 1020
 Met Ala Cys Val Val Val Ala Gly Ser Gly Ser Leu Val Ala Pro
 1025 1030 1035
 Thr Phe Ala Ala Leu Ser Asp Val Phe Lys Val Gly Leu Tyr Ser
 1040 1045 1050
 Gly Ile Gly Ser Thr Leu Ile Ala Ala Ser Val Val Gly Asn Ala
 1055 1060 1065

Tyr Met Ile Ile Arg Ser Gln Ser Arg Thr Ile Leu Arg Thr Glu
 1070 1075 1080
 Met Ala Ile Lys Asn Val Ala Val Lys Leu Trp Lys Gln Met Arg
 1085 1090 1095
 Lys Tyr Phe Ser Trp Val Thr Arg Phe Thr Lys Arg Arg Lys Ala
 1100 1105 1110
 Ile Leu Ser Thr Met Met Ala Arg Ala Thr Ala Leu Ala Lys Asn
 1115 1120 1125

Lys Lys Pro Arg Ser Glu Thr Ala Ala Thr Met Thr Arg Ser Gly
 1130 1135 1140
 Asp Ser Val Met Asp Met Leu Leu Gln Gly Val Ser Pro Ala Thr
 1145 1150 1155
 Pro Gln Arg Ala Gln Asp Gly Ser Arg
 1160 1165

<210> 428

<211> 218

<212> PRT

<213> Toxoplasma gondii

<400> 428

Gln Gln Thr Arg His Ile Leu Pro Phe Gly Ser Leu Phe Pro Gly Gly
1 5 10 15

Ile Leu Gly Lys Ile Met Gln Lys Leu Met Arg Ser Tyr Ile Met Phe
20 25 30

Phe His Pro Val Leu Ala Asn Phe Lys Gly Leu Leu Ala Leu Phe Leu
35 40 45

Gly Val Leu Cys Lys Val Arg Leu Pro Gln Leu Ile Asn Ala Val Phe
50 55 60

Gly Ala Ile Phe Arg Ala Lys Arg Arg Ala Gly Arg Tyr Ile His Lys
65 70 75 80

Phe Phe Phe Lys Thr Ile Ser Leu Arg Lys Asp Ile Thr Gly Lys Ile
85 90 95

Leu Val Asp Asp Leu Val Arg Gly Ser Gly Ala Val Met Ile Thr Leu
100 105 110

Leu Phe Gln Leu His Gly Val Asp Ile Asp Ala Ile Ser Arg Arg Gly
115 120 125

Gly Ala Val Glu Ser Gly Val Leu Ala Gly Gln Gly Val Trp Thr Leu
130 135 140

Ser Asp Gly Leu Phe Val Gly Leu Lys Asp Phe Gly Gln Leu Phe Arg
145 150 155 160

Ala Tyr Phe Glu Arg Tyr Val Asn Leu Thr Ser Ala Ile His Thr Tyr
165 170 175

Cys Ala Lys Gln Thr Thr Asn Phe Phe Thr Glu Thr Glu Leu Asp Glu
180 185 190

Phe Tyr Asn Gly Glu Asn Val Asp Arg Ile Pro Pro Arg Glu Arg Leu
195 200 205

Leu Ala Trp Leu Gln Ile Pro Met Ala Ala
210 215

<210> 429

<211> 446

<212> PRT

<213> *Toxoplasma gondii*

<400> 429

Met Ala Cys Arg Gln Leu Leu Cys Ser Val Gln Asn Leu Leu Phe Tyr

1 5 10 15

Phe Leu Pro Asp Ile Tyr Cys Thr Asp Phe Asp Thr Met Glu Gln Arg

20 25 30

Leu Pro Ile Ile Leu Leu Val Leu Ser Val Phe Phe Ser Ser Thr Pro

35 40 45

Ser Ala Ala Leu Ser Ser His Asn Gly Val Pro Ala Tyr Pro Ser Tyr

50 55 60

Ala Gln Ala Ser Leu Ser Ser Asn Gly Glu Pro Arg His Arg Gly Ile

65 70 75 80

Arg Gly Ser Phe Leu Met Pro Val Lys Pro His Ala Asn Ala Asp Asp

85 90 95

Phe Ala Ser Asp Asp Asn Tyr Glu Thr Leu Pro Ser Phe Val Glu Ala

100 105 110

Pro Val Arg Asp Pro Arg Gln Val Pro Gly Arg Gly Glu Ala Ala Leu

115 120 125

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

130 135 140

Ala Glu Gly Glu Gly Thr Ser Thr Asn Glu Ser Ala Ser Glu Asn Ser

145 150 155 160

Glu Asp Asp Thr Phe His Asp Ala Leu Gln Glu Leu Pro Glu Asp Gly

165 170 175

Leu Glu Val Pro Pro Pro Asn Ala Gln Glu Leu Pro Pro Pro Asn Ser

180 185 190

Gln Glu Leu Pro Pro Pro Asn Ser Gln Glu Leu Pro Pro Pro Asn Ser

195 200 205

Gln Glu Leu Pro Pro Pro Asn Ala Gln Glu Leu Leu Pro Pro Thr Glu

210 215 220

Gln Asp Leu Pro Pro Pro Thr Glu Gln Glu Leu Pro Pro Pro Val Gly

225	230							235							240												
Glu	Gly	Gln	Gly	Leu	Gln	Val	Pro	Gly	Glu	His	Gly	Pro	Gln	Gly	Pro	Gln	Gly	Pro									
				245								250								255							
Pro	Asp	Asp	Asp	Gln	Gln	Leu	Leu	Leu	Glu	Pro	Thr	Glu	Glu	Gln	Gln												
				260								265								270							
Glu	Gly	Pro	Gln	Glu	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Thr	Gln	Gly											
				275								280								285							
Glu	Gln	Pro	Glu	Gly	Gln	Gln	Pro	Gln	Gly	Pro	Val	Arg	Gln	Asn	Phe												
				290								295								300							
Phe	Arg	Arg	Ala	Leu	Gly	Ala	Ala	Arg	Ser	Arg	Phe	Gly	Gly	Ala	Arg												
305								310								315								320			
Arg	His	Val	Ser	Gly	Val	Phe	Arg	Arg	Val	Arg	Gly	Gly	Leu	Asn	Arg												
				325								330								335							
Ile	Val	Gly	Gly	Val	Arg	Ser	Gly	Phe	Arg	Arg	Ala	Arg	Glu	Gly	Val												
				340								345								350							
Val	Gly	Gly	Val	Arg	Arg	Leu	Thr	Ser	Ala	Ala	Ser	Gln	Gly	Leu	Arg												
				355								360								365							
Arg	Ala	Gly	Glu	Gly	Leu	Arg	Arg	Gly	Phe	Thr	Arg	Val	Arg	Gly	Ala												
370								375								380											
Leu	Arg	Gly	Arg	Gly	Arg	Ala	Ala	Asp	Gly	Ala	Ser	Ser	Val	Arg	Glu												
385								390								395								400			
Arg	Phe	Gly	Ala	Ala	Ser	Gly	Arg	Val	Arg	Asp	Ala	Phe	Ser	Ala	Gly												
				405								410								415							
Leu	Thr	Arg	Leu	Arg	Arg	Arg	Gly	Arg	Thr	Ser	Gly	Glu	Glu	Gly	Arg												
				420								425								430							
Pro	Leu	Leu	Gly	Glu	Gly	Arg	Glu	Gln	Asp	Asp	Gly	Ser	Gln														
435								440								445											
<210>	430																										
<211>	586																										
<212>	PRT																										
<213>	Toxoplasma gondii																										

<400> 430

Met Gly Arg Pro Arg Trp Pro Leu Pro Ser Met Phe Phe Leu Ser Leu
1 5 10 15

Leu Cys Val Ser Glu Lys Arg Phe Ser Val Ser Gly Leu His Leu Arg
20 25 30

Phe Arg Glu Ser Pro Gln Trp Asp Ser Leu Leu Pro Leu Gln Asp Arg

35 40 45
Arg Ala Val Gln Pro Ser Ser Arg Trp Asp Ser Ser Leu Thr Leu Glu

50 55 60

Ala His Ala Pro Gln Arg Ile Asp Thr Ser Asp Ala Gly Asp Asp Asp
65 70 75 80

Leu Phe Leu Asp Ala Thr Gln Gln Val Tyr Arg Gly Asp Pro Val Leu
85 90 95

Glu Thr Ser Ser Leu Pro Pro Ala Ala Leu Pro Val Arg Pro Val Ser

100 105 110
Ser Lys Thr Glu Asp Gly Phe Ser Gly Ser Arg Glu Glu Glu Ser Asp

115 120 125

Gly Gly Val Pro Thr Gly Ser Asp Gln Gly Glu Val Trp Arg Ser Ser
130 135 140

Ser Leu Val Asp Val Ser Ser Pro Gly Asp Arg Gly Gly Glu Glu Gln
145 150 155 160

Glu Ser Ser Ala Gln Ala Lys Gly Glu Ala Asp Thr Lys Asp Glu Ala

165 170 175
Glu Lys Ser Glu Asp Gln Ser Gln Ser Ser Thr Ala Asp Pro Asn Thr

180 185 190

Pro Thr Ala Gln Gly Thr Asp Ala Ser Glu Ser Gly Glu Asp Ser Gly
195 200 205

Ser Asp Thr Met Gly Asp Ser Glu Val Thr Asp Ile Pro Val Asp Pro
210 215 220

Leu Asn Ser Gly Pro Glu Thr Ala Ser Ser Gly Glu Thr Gly Gln Arg

225 230 235 240

Ile Gly Ala Glu Ser Gly Ala Gln Pro Ser Ala Glu Ala Ser Gln Asp
245 250 255

Ser Ala Ala Ala Ser Glu Thr Ile Pro Ala Ala Asp Ala Thr Ser Pro
260 265 270

Thr Asp Leu Pro Gly Thr Leu Ala Gly Ala Thr Val Ala Asp Asp Ser
275 280 285

Arg Gln Glu Ala Thr Thr Asp Gly Leu Glu Lys Ser Pro Gly Glu Pro
290 295 300

Lys Glu Val Asp Val Phe Asn Pro Pro Leu Ala Thr Lys Ser Asp Val
305 310 315 320

Ala Pro Leu Ser Val Ser Thr Ile Arg Ala Gln Ala Ala Pro Asp Thr
325 330 335

Glu Ala Asn Ile Gly Ala Glu Val Ala Thr Gly Asn Glu Gly Ala Pro
340 345 350

Glu Val Glu Glu Ala Thr Glu Asp Val Ala Gly Thr Gly Ala Asp Met
355 360 365

Ser Thr Gly Thr Asp Ala Ala Thr Glu Asp Val Ala Gly Thr Gly Ala
370 375 380

Asp Met Ser Ile Gly Thr Asp Ala Ala Thr Glu Asp Val Ala Gly Thr
385 390 395 400

Gly Ala Asp Met Ile Pro Gly Ala Glu Pro Gly Thr Glu Asn Glu Ala
405 410 415

Ser Thr Gly Ala Glu Gly Ala Thr Glu Ala Asp Glu Gln Val Pro Leu
420 425 430

Lys Thr Glu Ala Gln Gly Ser Ala Gly Ser Ser Pro Thr Gln Gly His
435 440 445

Ala Ser His Ser Val Glu Glu Thr Gly Arg Phe Ser Val Ile Pro Phe
450 455 460

Glu Phe Gly Ser Ser Pro Arg Leu Arg Arg Trp Thr Thr Gln Phe Leu
465 470 475 480

Ile Arg Gly Lys Asp Leu Phe Asn Leu Met Gln Lys Ser Asn Ile Ala

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

545 550 555 560
 Thr Ala Ser Pro Glu Glu Ala Ala Arg Glu Ala Ala Glu Ala Ile Gly
 565 570 575

Thr Pro Val Ser Thr Glu Asp Ala Pro Asn
 580 585

<210> 431

<211> 236

<212> PRT

<213> Toxoplasma gondii

<400> 431

Met Ala Arg Val Leu Pro Cys Val Phe Leu Val Ala Tyr Leu Ser Cys
 1 5 10 15
 Phe Leu Leu Ala Gly Glu Leu Thr His Thr Thr Ala Leu Ser Val Ala

20 25 30
 Pro Lys Ala Gln Leu Phe Ser Thr Asp Glu Gly Pro Val Ser Glu Ser
 35 40 45

Ala Ser Lys Leu Asp Ala Glu Leu Glu Glu Lys Ala Ile Gln Glu Ala
 50 55 60

Lys Glu Ala Gln Glu Asp Glu Val Asp Asp Ile Pro Thr Asp Arg Asn
 65 70 75 80

Ala Pro Pro Thr Asn Gly Asp Pro Thr Asp Gln Pro Asp Val Gln Leu

85 90 95
 Asn Ala Val Asp Ile Asp Gly Phe Pro Thr Pro Glu Val Pro Leu Pro
 100 105 110

Val Glu Leu Asp Ala Glu Lys Leu Gln Glu Asp Glu Phe Asn Arg Glu
115 120 125
Glu Glu Ala Asp Asn Thr Val Pro Asn Ile Leu Val Gly Pro Ala Gln
130 135 140
Thr Pro Glu Pro Val Ala Ile Pro Val Thr Ser Leu Leu Ala Pro Ala
145 150 155 160
Pro Gly Thr Val Thr Thr Ala Ser Pro Gln Glu Gly Val Glu Ala Lys
165 170 175
Glu Glu Pro Pro Ala Ala Thr Gly Val Pro Ser Ala Pro Ser Ser Pro
180 185 190
Ala Arg Arg Arg Ala Phe Phe Arg Ser Arg Gly Thr Arg Thr Ile Thr
195 200 205
Val Asn Val Arg His Phe Phe Pro Asn Gly Val Pro Ile Val Val Val
210 215 220
Arg Pro Gln Arg Arg Ser Phe Leu Leu Arg Arg Phe
225 230 235
<210> 432
<211> 400
<212> PRT
<213> Toxoplasma gondii
<400> 432
Met Lys Arg Thr Glu Leu Cys Ile Ala Ala Leu Val Ala Val Gly Ala
1 5 10 15
Phe Ala Phe Thr Ser Pro Asn Ala Val Ala Lys Ser Phe Glu Arg Ser
20 25 30
Leu Gly His Leu Asp Ala Ser Ser Phe Leu Ser Ser Pro Leu Asn Ser
35 40 45
Asp Val Glu Leu Gly Arg Ser Thr Phe Pro Ala Gln Ser Leu Ser Phe
50 55 60
Thr Glu Gly Thr Asn Glu Thr Asn Pro Pro Thr Ser Arg Pro Pro Gly
65 70 75 80
Trp Lys Tyr Glu Gly Ser Asp Leu Gln Arg Arg Val Ala Ala Arg Arg

85

90

95

Glu Glu His Lys Lys Arg Gln Glu Glu Trp Glu Gln Arg Lys Ala Ser

100

105

110

Arg Arg Ser Ala Leu Thr Pro Ser Ala Pro Asp Pro Asp Gly Asp Gly

115

120

125

Asp Pro Ala Thr Ser Phe Pro Ser Gln Arg Arg Leu Leu Asp Arg Cys

130

135

140

Leu Gln Gln Phe Arg Glu Gln Leu Val Asp Leu Glu Asn Leu Cys Lys

145

150

155

160

Gly Ser Pro Glu Pro Asp Asp Cys Arg Ser Thr Val Gln Glu Ile Leu

165

170

175

Gly Lys Gln Ser Phe Gly Ala Leu His Thr Thr Val Ile Ser Phe Ser

180

185

190

Ile Phe Val Asn Arg Asp Pro Arg Arg Leu Ser Phe Pro Val Leu Asp

195

200

205

Ala Thr Asp Leu Arg Leu Thr Val Lys Leu Lys His Leu Leu Asp Arg

210

215

220

Ile Pro Gly Cys Ala Ala Leu Ser Leu Pro Val Tyr Ile Gly Leu Val

225

230

235

240

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

245

250

255

Cys Ser Glu Asp Phe Gly Arg Ser Ala Arg Glu Glu Pro Ser Arg Ala

260

265

270

Gly Arg Ala Ala Ala Val Ile Arg Phe Met Gly Leu Thr Pro Glu

275

280

285

Arg Gln Thr Phe Tyr Gln Pro Phe Met Phe Val Thr Thr Gln Ala Ala

290

295

300

Met Leu Leu Ser Met Val Leu Lys His Pro Phe Leu Ser Ile Leu Val

305

310

315

320

Asn Met Ala Cys Val Ala Gly Ser Leu Cys Arg Lys Gly Ile Arg Glu

325

330

335

Val Leu Leu Arg Ala Leu Arg Glu Ala Asp Phe Leu Thr Glu Asp Val
340 345 350

Pro Leu Asp Ser Ala Pro Gln Glu Leu Val Asp His Leu Lys Val Tyr
355 360 365

Leu Lys Leu Leu Phe Leu Arg Lys Tyr Arg Arg Leu Arg Arg Gln Ala
370 375 380

Ala Asn Val Ala Ala Gln Val Val Tyr Ala Asn Ser Leu Arg Leu Leu
385 390 395 400

<210> 433

<211> 1061

<212> PRT

<213> *Toxoplasma gondii*

<400> 433

Met Tyr Ser Ser Pro Gln Ser Glu Glu Ala Ser Leu Val Asn Ser Arg

1 5 10 15
Gly Ile Arg Asp Glu Ser Gly Pro Asn Gly Phe Ser Ile Gly Ser Ala
20 25 30

Thr Asp Thr Ala Leu Lys Ala Gly Ser Pro Thr Gly Lys Ser Trp Lys
35 40 45

Gln Leu Ser Leu Asn Leu Gly Arg Arg Val Trp Asp Ala Leu Asp Pro
50 55 60

Thr Trp Ser Cys Ala Glu Lys Arg Arg Arg Leu Asp Pro Glu Thr Leu

65 70 75 80
Arg Lys Leu Lys Ser Thr Tyr Trp Leu Ser Arg Ile Val Phe Leu Arg
85 90 95

Ala Leu Gly Phe Val Tyr Phe Phe Ala Phe Leu Ile Ala Phe Asn Gln
100 105 110

Ser Gln Gly Leu Ile Gly Ser Asp Gly Ile Leu Pro Ala Ser Asp Tyr
115 120 125

Val Ala Met Val Lys Asp Ser Phe Ala Asp Ala Glu Ala Trp Gln Arg

130 135 140

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

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

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

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

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

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

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

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

Gly Tyr Ile Gly Lys Glu Arg Tyr Glu Leu Ile Ile Gln Gly Thr Asn

645 650 655

Ala Ser Ser Pro Thr Gln Thr Leu Tyr Trp Gln Asn Tyr Glu Phe Lys

660 665 670

Cys Lys Pro Gly Asp Leu Tyr Arg Arg Pro Cys Trp Ala Ala Pro Tyr

675 680 685

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

690 695 700

Glu Thr Val Lys Asp Met His Pro Trp Leu Ser Asn Phe Leu Ser Arg

705 710 715 720

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

725 730 735

Phe Gln Asn Ser Asp Pro Pro Thr Ala Leu Arg Val Leu Arg Ile Gln

740 745 750

Tyr Arg Phe Thr Lys Gly Pro Val Phe Gly Gly Gly Pro Trp Trp Glu

755 760 765

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

770 775 780

Gly Ala Ala Ala His Leu Arg Lys Gln Leu Leu Ile Leu Arg Arg Arg

785 790 795 800

Glu Glu Lys Gln Arg Leu Glu Gln Arg Arg Lys Glu Glu Ala Glu Ile

805 810 815

Arg Arg Lys Glu Glu Glu Ala Phe Lys Arg Arg Arg Glu Arg Ala Met

820 825 830

Lys Glu Glu Glu Arg Arg Lys Arg Glu Ala Glu Glu Ala Glu Lys Arg

835 840 845

Arg Ile Ala Glu Gln Ala Arg Gln Ala Glu Asp Glu Lys Arg Ile Arg

850 855 860

Glu Gln Ala Glu Ala Ala Arg Lys Ala Glu Glu Glu Ala Val Arg Lys

865 870 875 880

Gln Ile Glu Glu Glu Lys Lys Arg His Glu Glu Glu Glu Lys Glu Arg

885 890 895
 Gln Ala Glu Glu Glu Arg Glu Arg Arg Glu Gln Gln Glu Glu Glu Glu

 900 905 910
 Lys Arg Arg Ala Glu Asp Glu Lys Arg Arg Lys Glu Lys Glu Gln Ala
 915 920 925
 Thr Leu Leu Ala Arg Gln Arg Ser Glu Glu Ala Leu Lys Glu Ala Glu
 930 935 940
 Lys Lys Ala Arg Lys Asp Ala Glu Glu Glu Glu Arg Lys Arg Lys Glu
 945 950 955 960
 Asp Ala Leu Gln Glu Glu Lys Arg Gln Lys Glu Glu Lys Glu Ala Glu

 965 970 975
 Glu Lys Arg Arg Lys Gln Ala Glu Ala Arg Arg Glu Ala Ala Arg Ala
 980 985 990
 Ala Ala Glu Lys Glu Ser Glu Lys Ala Arg Gln Leu Gln Glu Gln Glu
 995 1000 1005
 Ala Lys Arg Lys Ala Leu Glu Glu Gln Glu Arg Arg Lys Ala Arg
 1010 1015 1020
 Glu Arg Gln Arg Ser Ala Ser Ser Gln Val Ala Val Tyr Thr Ala

 1025 1030 1035
 Gln Pro His Asp Gly Gly Gly Val Pro Leu Arg His Ala Pro Leu
 1040 1045 1050
 Leu Thr Arg Lys Lys Gln Ala Leu
 1055 1060
 <210> 434
 <211> 333
 <212> PRT
 <213> Toxoplasma gondii
 <400> 434
 Met Leu Lys Thr Thr Pro Ala Phe Phe Leu Phe Leu Thr Trp Met Phe
 1 5 10 15
 Pro Arg Cys Asp Gly Phe Val Leu Thr His Lys Asn Gly Thr Thr Asp

20	25	30	
Ala Tyr Asp Ser Ala Val Leu Ser Phe Leu Leu Thr Thr Glu Gly Val			
35	40	45	
Arg Glu Gly Ala Ala Lys Ser Ser Gly Thr Glu Ile Pro Ser Thr Leu			
50	55	60	
Ala Cys Pro Ser Ser Ser Pro Leu Lys Thr Ala Lys Asp Lys His Asp			
65	70	75	80
Ala Ser Leu Leu Gly Leu Val Ser Ser Val Pro Asp Ser Ser Ile Leu			
85	90	95	
Lys Pro Glu Phe Val Gly Ala Gly Ala Ala Leu Val Ala Val Thr Arg			
100	105	110	
Ser Val Lys Trp Thr Gln Leu Lys Gln Ser Leu Lys Ala Leu Val Asp			
115	120	125	
Thr Gly Val Lys Cys Lys Val Asn Cys Lys His Asn Asn Lys Lys Leu			
130	135	140	
Ser Lys Asn Thr Asp Phe Lys Asp Gln Gln Glu Phe Pro Gln Thr Ser			
145	150	155	160
Ala Arg Ile Leu Pro Thr Ser Asp Arg Glu Pro Leu Ile Ala Gly Pro			
165	170	175	
Gln Lys Val Thr Glu Glu Asp Leu Gln Val Leu Leu Phe Glu Ile Ala			
180	185	190	
His Asp Cys Lys Met Ser Ala Pro Gln Ala Ala Ile Thr Lys Pro Leu			
195	200	205	
Thr Ile Leu Leu Ala Gly Ile Pro Gly Ala His Ile Ser Lys Arg Pro			
210	215	220	
Phe Glu Ala Ala Ile Pro His Phe Ile Leu Gln Lys Glu Asp Thr Val			
225	230	235	240
Asp Leu Leu Leu Thr Val Asp Arg Ser Trp Cys Gly Lys Gly Leu Ser			
245	250	255	
His Leu Val Arg Tyr His Val Gly Tyr Met Ser Phe Asn Leu Glu Val			
260	265	270	

Asn Gly Arg Arg Leu Ala Asp Asp Asp Thr Phe Glu Asp Asp Arg Leu

275 280 285
Tyr Arg Gln Val Val Leu Thr Thr Lys Phe Thr Ala Lys Ser Leu Gly

290 295 300
Gly Thr Leu Lys Gln Val Arg Ser Leu Thr Asp Ile His Lys Lys Thr

305 310 315 320
Gly Lys His Gly Glu Asn Arg Pro His Ser Ser Pro Phe

325 330
<210> 435

<211> 707

<212> PRT

<213> Toxoplasma gondii

<400> 435

Met Lys Val Thr Thr Lys Gly Leu Ala Phe Ala Leu Ala Leu Leu Phe
1 5 10 15

Cys Thr Arg Cys Ala Thr Ala Arg Tyr Met Ser Phe Glu Glu Ala Gln
20 25 30

Lys Ala Ser Glu Ala Ala Lys Arg Gln Ile Ala Thr Leu Pro Ser Pro
35 40 45

Asp Ser Thr Leu Ser Asn Pro Gly Ser Lys His Arg Asn Arg Gly Gly
50 55 60

Ser Pro Ala Ala Gly Gln Pro Ser Gln Ser Thr Leu Gln Pro Glu Gln
65 70 75 80

Ala Ala Ala Glu Val Gly Leu Gly Ala Gly Gly Ser Thr Gln Gly Gln
85 90 95

Gly Arg Thr Gly Gly Ser Ala Gly Ala Arg Glu Glu Arg Arg Ser Pro
100 105 110

Ser Pro Gln Ser Ala Tyr Pro Ala Thr Ser Ser Ala Ser Leu Arg Gly
115 120 125

Tyr Gln Thr Gln Leu Ser Pro Ser His Leu Pro Pro Arg Ser Ser Gly
130 135 140

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

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

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

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

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

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

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

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

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

Leu Ser Asp Phe Ser Ala Lys Asp Cys Asn Glu Ser Asp Pro Ala Val
645 650 655
Met Gly Ile Val Ala Gln Phe Leu Asn Pro Asn Pro Glu Glu Arg Pro
660 665 670
Glu Leu Pro Lys Phe Val Ser Ser Tyr Thr Phe Phe Arg Gln Ala Pro
675 680 685
Gly Val Thr Ser His Leu Thr Arg Ile Pro Thr Thr Glu Leu Ser Ser
690 695 700

His Arg Met

705

<210> 436

<211> 608

<212> PRT

<213> *Toxoplasma gondii*

<400> 436

Met Glu Leu Val Leu Cys Phe Val Ile Ile Thr Ile Ser Gly Val Ile
1 5 10 15
Arg Glu Ser Ser Ala Leu Leu Leu Arg Ser Pro Thr Ser Asn Asp Val
20 25 30
Phe Gly Glu Leu Val Ala Ser Ala Glu Arg Ala Gln Pro Leu Ala Thr
35 40 45
Arg Leu Thr Lys Arg Ile Ser Arg Leu Asn Phe Asn Asp Arg Glu Asp
50 55 60
Asp Phe Trp Glu Asp His Gly Asp Ala Ser Trp Asn Asn Ser Tyr Thr
65 70 75 80
Leu Val Asn Gly Arg Thr Thr Leu Gly Ser Glu Asn Arg Arg Arg Pro
85 90 95
Ala Ser His Ser Leu Ile Glu Arg Pro Tyr Tyr Arg Asp Gly Arg Leu
100 105 110
Ser Pro Val Leu Gly Val Gln Glu Arg Arg Gly Arg Ser Val His Ser
115 120 125
Tyr His Glu Glu Pro Val Ser Phe Phe Asp Gln Arg Ala Phe Asp Glu

130 135 140
 Tyr Thr Phe Arg Arg Arg Ser Gln Leu His Arg Gln Arg Ala Arg Ala
 145 150 155 160
 Gly Leu Arg Ser Arg Ile Lys Gln Asn Val Arg Arg Leu Trp Arg Ser
 165 170 175
 Ala Arg Gly Ala Val Gly Gly Trp Gly Arg Arg Val Arg Arg Lys Ile

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

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

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

 370 375 380

Ala Leu Phe Pro Lys Ala Gln Gly Asp Leu Glu Glu Ala Val Val Leu
385 390 395 400
Leu Ala Asp Met Asp Arg Thr Asn Ala Tyr Asn Ile Arg Met Ser Cys
405 410 415
Thr Ile Gln Met Val Lys Leu Leu Ala Arg Phe His Ala Phe Glu Leu
420 425 430
Val His Gly Asp Val Lys Leu Gln Asn Phe Leu Val Asp Lys Ser Gly
435 440 445
Leu Leu Leu Leu Ser Asp Phe Thr Gln Ile Leu Arg Thr Asn Glu Arg
450 455 460
Arg Tyr Pro Pro Val Val Thr Val Ile Tyr Met Ser Pro Glu Ile Ala
465 470 475 480
Thr Cys Met Ile Thr Arg Leu Arg Asn Ala Ile Pro Tyr Thr Pro Gln
485 490 495
Ile Asp Ser Trp Met Leu Gly Ile Ser Leu Tyr Arg Leu Trp Cys Gly
500 505 510
Asn Phe Pro Phe Gly Met Thr Leu Asp Ala Thr Ala Leu Gln Val Ala
515 520 525
Gly Ile Val Ile Arg Ser Ser Ala Ser Ser Leu Asp Phe Ala Ser Cys
530 535 540
His Asp Ile Pro Glu Gln Phe Arg Glu Met Ile Val Gly Phe Leu Arg
545 550 555 560
Lys Thr Pro Gly Val Arg Leu Ser Pro Gln Gln Ala Leu Glu Gln Phe
565 570 575
Ser Leu Leu Asn Trp Lys Gly Pro Ser Pro Ala Ser Asp Thr Ala Ser
580 585 590
Glu Ser Glu Pro Val Ser Thr Glu Glu Ala Ala Leu Leu Gln Lys Glu
595 600 605
<210> 437
<211> 554
<212> PRT
<213> Toxoplasma gondii

<400> 437

Met Phe Ser Val Gln Arg Pro Pro Leu Thr Arg Thr Val Val Arg Met
1 5 10 15

Gly Leu Ala Thr Leu Leu Pro Lys Thr Ala Cys Leu Ala Val Leu Asn
20 25 30

Val Ala Leu Val Phe Leu Leu Phe Gln Val Gln Asp Gly Thr Gly Ile
35 40 45

Thr Leu Asp Pro Ser Lys Leu Asp Ser Lys Pro Thr Ser Leu Asp Ser
50 55 60

Gln Gln His Val Ala Asp Lys Arg Trp Pro Ala Thr Val Gly His Tyr
65 70 75 80

Lys Tyr Leu Ala Gly Ala Thr Glu Ser Thr Arg Asp Val Ser Leu Leu
85 90 95

Glu Glu Arg Ala Gln His Arg Val Asn Ala Gln Glu Thr Asn Gln Arg
100 105 110

Arg Thr Ile Phe Gln Arg Leu Leu Asn Leu Leu Arg Arg Arg Glu Arg
115 120 125

Asp Gly Glu Val Ser Gly Ser Ala Ala Asp Ser Ser Ser Arg Pro Arg
130 135 140

Leu Ser Val Arg Gln Arg Leu Ala Gln Leu Trp Arg Lys Ala Lys Ser
145 150 155 160

Phe Phe Thr Arg Gly Ile Pro Arg Tyr Phe Ser Gln Gly Arg Asn Arg
165 170 175

Leu Arg Ser Leu Arg Ala Gln Arg Arg Arg Ser Glu Leu Phe Phe Glu
180 185 190

Lys Ala Asp Ser Gly Cys Val Ile Gly Lys Arg Ile Leu Ala His Met
195 200 205

Gln Glu Gln Ile Gly Gln Pro Gln Ala Leu Gly Asn Ser Glu Arg Leu
210 215 220

Asp Arg Ile Leu Thr Val Ala Ala Trp Pro Pro Asp Val Pro Glu Arg
225 230 235 240

Phe Val Ser Val Thr Thr Gly Glu Thr Arg Thr Leu Val Arg Gly Ala
 245 250 255
 Pro Leu Gly Ser Gly Gly Phe Ala Thr Val Tyr Glu Ala Thr Asp Val
 260 265 270

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

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

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

 Asp Ala Trp Gln Leu Gly Ile Thr Leu Tyr Cys Ile Trp Cys Lys Glu
 465 470 475 480
 Arg Pro Thr Pro Ala Asp Gly Ile Trp Asp Tyr Leu His Phe Ala Asp

485 490 495
 Cys Pro Ser Thr Pro Glu Leu Val Gln Asp Leu Ile Arg Asn Leu Leu
 500 505 510
 Asn Arg Glu Pro Gln Lys Arg Met Leu Pro Leu Gln Ala Leu Glu Thr
 515 520 525

 Ala Ala Phe Asn Glu Met Asp Ser Val Val Lys Arg Ala Ala Gln Asn
 530 535 540
 Phe Glu Gln Gln Glu His Leu His Thr Glu
 545 550
 <210> 438
 <211> 433
 <212> PRT
 <213> Toxoplasma gondii
 <400> 438
 Met Glu Asn Cys Ala Ser Val Arg Ser Ser Ser Cys Leu Ile Trp Leu
 1 5 10 15
 Ala Ala Ala Phe Phe Val Ser Ala Leu Gly His Val Gln Gln Gly Ala
 20 25 30

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

 Asn Ser His Thr Glu Thr Pro Thr Gln Ser Pro Ser Ala Phe Arg Arg
 100 105 110
 Leu Leu Arg Arg Leu Arg Phe Trp Arg Arg Gly Arg Thr Gly Gly Ser
 115 120 125
 Asp Gly Gly Gly Glu Pro Pro Gln Thr Pro Arg Pro Ser Leu Pro Thr
 130 135 140

Arg Leu Phe Gln His Leu Arg Arg Ala Ala Ala Ala Ile Pro Ala Ala
145 150 155 160

Ala Ser Arg Phe Phe Gly Arg Phe Arg Arg Gly Arg Leu Pro Val Phe
165 170 175

Pro Pro Asp Glu Phe Pro Glu Asp Val Asp Thr Asn Pro Ile Tyr Phe
180 185 190

Arg Gly Thr Asp Pro Gly Asp Val Val Ile Glu Glu Leu Phe Asn Arg
195 200 205

Ile Pro Gln Ala Asn Val Arg Thr Thr Ser Glu Tyr Met Gln Ser Ala
210 215 220

Ala Asp Ser Leu Val Ser Thr Ser Leu Trp Asn Thr Gly Gln Pro Phe
225 230 235 240

Arg Val Glu Ser Glu Leu Gly Glu Arg Pro Arg Thr Leu Val Arg Gly
245 250 255

Thr Val Leu Gly Gln Glu Asp Pro Tyr Ala Tyr Leu Glu Ala Thr Asp
260 265 270

Gln Glu Thr Gly Glu Ser Phe Glu Val His Val Pro Tyr Phe Thr Glu
275 280 285

Arg Pro Pro Ser Asn Ala Ile Lys Gln Met Lys Glu Glu Val Leu Arg
290 295 300

Leu Arg Leu Leu Arg Gly Ile Lys Asn Gln Lys Gln Ala Lys Val His
305 310 315 320

Leu Arg Phe Ile Phe Pro Phe Asp Leu Val Lys Asp Pro Gln Lys Lys
325 330 335

Lys Met Ile Arg Val Arg Leu Asp Glu Arg Asp Met Trp Val Leu Ser
340 345 350

Arg Phe Phe Leu Tyr Pro Arg Met Gln Ser Asn Leu Gln Thr Phe Gly
355 360 365

Glu Val Leu Leu Ser His Ser Ser Thr His Lys Ser Leu Val His His
370 375 380

Ala Arg Leu Gln Leu Thr Leu Gln Val Ile Arg Leu Leu Ala Ser Leu

385 390 395 400
His His Tyr Gly Leu Val His Thr Tyr Leu Arg Pro Val Asp Ile Val
405 410 415

Leu Asp Gln Arg Gly Gly Val Phe Leu Thr Gly Phe Glu His Leu Val
420 425 430
Arg

<210> 439

<211> 382

<212> PRT

<213> Toxoplasma gondii

<220><221> misc_feature

<222> (127)..(127)

<223> Xaa can be any naturally occurring amino acid

<400> 439

Met Gly His Pro Thr Ser Phe Gly Gln Pro Ser Cys Leu Val Trp Leu
1 5 10 15
Ala Ala Ala Phe Leu Val Leu Gly Leu Cys Leu Val Gln Gln Gly Ala

20 25 30
Gly Arg Gln Arg Pro His Gln Trp Lys Ser Ser Glu Ala Ala Leu Ser
35 40 45

Val Ser Pro Ala Gly Asp Ile Val Asp Lys Tyr Ser Arg Asp Ser Thr
50 55 60

Glu Gly Glu Asn Thr Val Ser Glu Gly Glu Ala Glu Gly Ser Arg Gly
65 70 75 80
Gly Ser Trp Leu Glu Gln Glu Gly Val Glu Leu Arg Ser Pro Ser Gln

85 90 95
Asp Ser Gln Thr Gly Thr Ser Thr Ala Ser Pro Thr Gly Phe Arg Arg
100 105 110

Leu Leu Lys Arg Leu Arg Phe Trp Arg Arg Gly Ser Thr Arg Xaa Asn
115 120 125

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

130 135 140
 Lys Pro Leu Val Gln Lys Ala Lys Ser Arg Asn Glu Val Gly Trp Val

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

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

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

 340 345 350
 Met Glu Glu Gln Leu Ser Ala Ala Ser Arg Leu Tyr Ser Gly Asp Gly
 355 360 365
 Thr Leu Thr Gly Gly Asp Asp Asp Met Pro Pro Leu Glu Thr
 370 375 380

<210> 440

<211> 461

<212> PRT

<213> *Toxoplasma gondii*

<400> 440

Met Ser Gly Gly Arg Val Pro Arg Val Pro Ala Ser Ser Thr Thr Thr

1 5 10 15

Ser Ala Ser Glu Gly Ile Phe Arg Arg Leu Val Arg Arg Leu Arg Arg

20 25 30

Gly Arg Gly Thr Ala Asp Gly Ala Gly Val Ala Asp Glu Thr His Gln

35 40 45

Glu Pro Arg Pro Pro Leu Arg Lys Arg Leu Ala Gln His Phe Arg Arg

50 55 60

Leu Arg Gly Phe Phe Gly Arg Leu Thr Pro Arg Trp Leu Ser Gly Leu

65 70 75 80

Gly Arg Arg Ala Gln Arg Trp Trp Arg Gly Arg Gln Arg Pro Leu Leu

85 90 95

Asp Pro Ser Phe His Gly Leu Glu Ala Gly Asp Ser Phe Met Arg Asp

100 105 110

Leu Leu Lys Arg Glu Lys Glu Leu Ile Gly Tyr Cys Arg Glu Glu Ala

115 120 125

Leu Lys Glu Pro Ala Ala Met Val Glu Ala Val Thr Ala Thr Val Trp

130 135 140

Pro Gln Asn Ala Glu Thr Thr Val Asp Ser Leu Leu Ser Gln Gly Glu

145 150 155 160

Arg Lys Leu Lys Leu Val Gln Pro Leu Arg Val Gly Asp Arg Ser Val

165 170 175

Val Phe Leu Val Arg Asp Val Glu Arg Leu Glu Tyr Phe Ala Leu Lys

180 185 190

Val Phe Thr Met Gly Ala Glu Asn Ser Arg Ser Glu Leu Glu Arg Leu

195 200 205

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

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

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

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

<210>

441

<211> 549

<212> PRT

<213> *Toxoplasma gondii*

<400> 441

Met Ala Thr Lys Leu Ala Arg Leu Ala Thr Trp Leu Val Leu Val Gly

1 5 10 15

Cys Leu Leu Trp Arg Ala Gly Ala Val Gln Leu Ser Pro Pro Asn Ser

20 25 30

Arg Thr Asn Asp Leu Ala Ser Gly Thr Pro His Val Ala Arg Gly Asp

35 40 45

Thr Glu Ala Gln Ser Gly Thr Gly Asp Asp Ser Asp Phe Pro Gln Ala

50 55 60

Val Ala Glu Glu Val Ala Asp Met Ser Gly Gly Arg Val Pro Arg Val

65 70 75 80

Pro Ala Ser Ser Thr Thr Thr Ser Ala Ser Glu Gly Ile Phe Arg Arg

85 90 95

Leu Val Arg Arg Leu Arg Arg Gly Arg Gly Thr Ala Asp Gly Ala Gly

100 105 110

Val Ala Asp Glu Thr His Gln Glu Pro Arg Pro Pro Leu Arg Lys Arg

115 120 125

Leu Ala Gln His Phe Arg Arg Leu Arg Gly Phe Phe Gly Arg Leu Thr

130 135 140

Pro Arg Trp Leu Ser Gly Leu Gly Arg Arg Ala Gln Arg Trp Trp Arg

145 150 155 160

Gly Arg Gln Arg Pro Leu Leu Asp Pro Ser Phe His Gly Leu Glu Ala

165 170 175

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

180 185 190

Gly Tyr Cys Arg Glu Glu Ala Leu Lys Glu Pro Ala Ala Met Val Glu

195 200 205

Ala Val Thr Ala Thr Val Trp Pro Gln Asn Ala Glu Thr Thr Val Asp
210 215 220

Ser Leu Leu Ser Gln Gly Glu Arg Lys Leu Lys Leu Val Gln Pro Leu
225 230 235 240

Arg Val Gly Asp Arg Ser Val Val Phe Leu Val Arg Asp Val Glu Arg
245 250 255

Leu Glu Tyr Phe Ala Leu Lys Val Phe Thr Met Gly Ala Glu Asn Ser
260 265 270

Arg Ser Glu Leu Glu Arg Leu His Glu Ala Thr Phe Ala Ala Ala Arg
275 280 285

Leu Leu Gly Glu Ser Pro Glu Glu Ala Arg Asp Arg Arg Arg Leu Leu
290 295 300

Leu Pro Ser Asp Val Val Ala Val Gln Ser Gln Pro Pro Phe Ala Gln
305 310 315 320

Leu Ser Pro Gly Gln Ser Asp Tyr Ala Val Ala Asn Tyr Leu Leu Leu
325 330 335

Met Pro Ala Ala Ser Val Asp Leu Glu Leu Leu Phe Ser Thr Leu Asn
340 345 350

Phe Val Tyr Val Phe Arg Gly Gly Glu Gly Ile Leu Ala Arg His Ile
355 360 365

Leu Thr Ala Gln Leu Ile Arg Leu Ala Ala Asn Leu Gln Ser Lys Gly
370 375 380

Leu Val His Gly Arg Phe Thr Pro Asp Asn Leu Phe Leu Met Pro Tyr
385 390 395 400

Gly Pro Val Met Leu Gly Asp Val Ser Ala Leu Trp Lys Val Gly Thr
405 410 415

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

Leu Asn Ala Asn Thr Ala Thr Phe Thr His Ala Leu Asn Ala Trp Gln
435 440 445

Leu Gly Leu Ser Ile Tyr Arg Val Trp Cys Leu Val Leu Pro Phe Gly

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

500 505 510
 Arg Arg Leu Leu Pro Leu Glu Ala Met Glu Thr Pro Glu Phe Leu Gln
 515 520 525
 Leu Gln Asn Glu Ile Ser Arg Arg Leu Ser Thr Gly Gln Pro Thr Ala
 530 535 540

Ala Pro Ser Val Ala

545

<210> 442

<211> 549

<212> PRT

<213> Toxoplasma gondii

<400> 442

Met Ala Thr Lys Leu Ala Arg Leu Ala Thr Trp Leu Val Leu Val Gly

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

65 70 75 80
 Pro Ala Ser Ser Thr Thr Thr Ser Ala Ser Glu Gly Ile Phe Arg Arg
 85 90 95
 Leu Val Arg Arg Leu Arg Arg Gly Arg Gly Thr Ala Asp Gly Ala Gly
 100 105 110

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

355 360 365
Leu Thr Ala Gln Leu Ile Arg Leu Ala Ala Asn Leu Gln Ser Lys Gly

370 375 380
Leu Val His Gly Arg Phe Thr Pro Glu Asn Leu Phe Ile Met Pro Asp

385 390 395 400
Gly Arg Leu Met Met Gly Asp Val Ser Thr Leu Arg Lys Val Gly Thr

405 410 415
Arg Gly Pro Ala Ser Ser Val Pro Val Thr Tyr Ala Pro Arg Glu Phe

420 425 430
Leu Asn Ala Asn Thr Ala Thr Phe Thr His Ala Leu Asn Ala Trp Gln

435 440 445
Leu Gly Leu Ser Ile Tyr Arg Val Trp Cys Leu Val Leu Pro Phe Gly

450 455 460
Leu Val Thr Pro Gly Ile Lys Arg Thr Trp Lys Arg Pro Ser Leu Arg

465 470 475 480
Val Pro Gly Thr Asp Ser Leu Leu Phe Asp Ser Cys Ile Pro Val Pro

485 490 495
Asp Phe Val Gln Thr Leu Thr Arg Arg Phe Leu Asn Phe Asp Arg Arg

500 505 510
Arg Arg Leu Leu Pro Leu Glu Ala Met Glu Thr Pro Glu Phe Leu Gln

515 520 525
Leu Gln Asn Glu Ile Ser Ser Ser Leu Ser Thr Gly Gln Pro Thr Ala

530 535 540
Ala Pro Ser Val Ala

545

<210> 443

<211> 480

<212> PRT

<213> Toxoplasma gondii

<400> 443

Met Arg Ser Ser Val Gly Gln Ser Arg Leu Pro Leu Lys Phe Phe Leu

1 5 10 15

Ala Pro Phe Ser Val Lys Asn Ser Val Phe Ala Leu Phe Phe Val Phe

20 25 30

Ala Leu Val Cys Val Ser Gly Leu Ser Trp Glu Asp Ala Glu Asp Gly

35 40 45

Ala Ala Trp Asp Ser Val Ser Asn Asp Ser Asp Asp Ser Phe Ala Lys

50 55 60

Gly Ser Asp Phe Gly Glu Val Lys Leu Gly Ser Ala Gly Gln Arg Gln

65 70 75 80

Leu Leu Ser Gln Leu Gln Asn Glu Leu Gly Gly Glu Phe Glu Asp Ala

85 90 95

Asp Val Ser Met Leu Gln Arg Asp His Gly Ile His Gly Glu Glu Ala

100 105 110

Gly Leu Phe Arg Lys Ala Val Pro Gly Leu Asp Asp Pro Ala Glu Asp

115 120 125

Asp Glu Ala Asp Gly Glu Ser Ala Ser Asp Glu Ala Glu Ala Asp Ser

130 135 140

Asp Val Leu Ala Asp Asp Glu Glu Gly Thr Ser Leu Ile Glu Asn Ala

145 150 155 160

Ser Glu Glu Asp Thr Asp Asn Ser Glu Ala Asp Ser Gln Gln Glu Asp

165 170 175

Asp Ser Val Gly Glu Asp Ser Phe Leu Gln Gln Glu Gly Glu Asp Ser

180 185 190

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

195 200 205

Tyr Leu Glu Glu Asp Asn Thr Val Asp Asp Ser Ala Ala Glu Asp Tyr

210 215 220

Ala Pro Ala Ser Phe Val Gln Ile Gly Ser Gly Glu Arg Lys Ile Arg

225 230 235 240

Ala His Met His Leu Asp Ser Arg Gln Val Ala Pro Glu Arg Phe Ala

245 250 255

His Ala Phe Asn Gln Asp His Val Arg Leu Leu Asp Gln Thr Ala Val

260 265 270
Glu Asp Glu Leu Leu Asp Glu Ala Ala Pro Gly Gly Gly Ala Ser Ala

275 280 285
Val Val Ser Pro Ile Asp Glu Asn Pro Ala Glu Met Glu Ser Thr Ile

290 295 300
Ser Glu Gly Glu Ala Gly Ser Ala Val Ala Ala Pro Glu Gln Gly Ile

305 310 315 320
Gln Pro Glu Ala Glu Phe Ala Thr Ala Ser Glu Glu Pro Arg Pro Leu

325 330 335
Glu Pro Val Asp Pro Glu Met Ala Ala Gln Gln Pro Gln Leu Pro Gln

340 345 350
Glu Ala Met Pro Thr Glu Asn Ala Asp Leu Leu Gly Asn Gln Pro Arg

355 360 365
Met Arg Asn Ala Leu Glu Pro Ser Ala Lys Val Leu Glu Pro Glu Thr

370 375 380
Leu Glu Gly Ser Pro Ala Leu Val Pro Pro Ala Glu Thr Glu Glu Gly

385 390 395 400
Thr Ala Ala Gln Ile Ala Glu Glu Met Ser Lys Gln Asp Gln Gly Met

405 410 415
Gln Glu Ala Arg Pro Gln Glu Val Leu Thr Arg His Thr Trp Gln Asp

420 425 430
Met Glu Arg Thr Glu Asp Leu Arg Lys Asn Asp Val Pro Ala Ala Val

435 440 445
Ala Asn Ser Gly Ser Gln Ile Ile Thr Ala Ala Ser Ser Val Ala Leu

450 455 460
Ala Gly Leu Leu Val Ala Gly Gln Leu Leu Phe Ser Val Gly Met Tyr

465 470 475 480

<210> 444

<211> 91

<212> PRT

<213> Toxoplasma gondii

<400> 444

Met Gly His Pro Thr Ser Phe Gly Gln Pro Ser Cys Leu Val Trp Leu

1 5 10 15

Ala Ala Ala Phe Leu Val Leu Gly Leu Cys Leu Val Gln Gln Gly Ala

20 25 30

Gly Ile Gln Arg Pro His Gln Trp Lys Ser Ser Glu Ala Ala Leu Ser

35 40 45

Val Ser Pro Ala Gly Asp Ile Val Asp Lys Tyr Ser His Asp Ser Thr

50 55 60

Glu Gly Glu Asn Thr Val Ser Glu Gly Glu Ala Glu Gly Ser Arg Gly

65 70 75 80

Gly Ser Trp Leu Glu Gln Glu Gly Val Glu Leu

85 90

<210> 445

<211> 575

<212> PRT

<213> Toxoplasma gondii

<400> 445

Met Gly His Pro Thr Ser Phe Gly Gln Pro Ser Cys Leu Val Trp Leu

1 5 10 15

Ala Ala Ala Phe Leu Val Leu Gly Leu Cys Leu Val Gln Gln Gly Ala

20 25 30

Gly Ile Gln Arg Pro His Gln Trp Lys Ser Ser Glu Ala Ala Leu Ser

35 40 45

Val Ser Pro Ala Gly Asp Ile Val Asp Lys Tyr Ser His Asp Ser Thr

50 55 60

Glu Gly Glu Asn Thr Val Ser Glu Gly Glu Ala Glu Gly Ser Arg Gly

65 70 75 80

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

85 90 95

Asp Ser Gln Thr Gly Thr Ser Thr Ala Ser Pro Thr Gly Phe Arg Arg

100 105 110

Phe Leu Arg His Leu Arg Phe Trp Arg Arg Gly Ser Thr Arg Gly Ser
 115 120 125
 Asp Asp Ala Ala Glu Val Ser Arg Arg Thr Arg Val Pro Leu His Thr
 130 135 140

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

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

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

 Gly Lys Pro Leu Val Gln Lys Ala Lys Ser His Asn Glu Val Gly Trp
 340 345 350
 Val Ile Asn Leu Leu Leu Leu Leu Pro Ala Ile Glu Ile Asp Met Gly

355 360 365
 Arg Phe Val Glu Glu Leu Tyr Glu Leu Pro Thr Glu Asp Arg Pro Leu
 370 375 380
 Ala Asp Ala Ala Arg Leu Tyr Leu Thr Val Gln Ala Val Arg Leu Val
 385 390 395 400

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

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

Glu Ala Arg Leu Leu Ala Leu Gln Ala Thr Glu Thr Pro Glu Tyr Arg
 530 535 540
 Glu Met Glu Glu Gln Leu Ser Ala Ala Ser Arg Leu Tyr Ser Gly Asp
 545 550 555 560
 Gly Thr Leu Thr Gly Gly Asp Asp Asp Met Pro Pro Pro Glu Thr
 565 570 575

<210> 446

<211> 587

<212> PRT

<213> Toxoplasma gondii

<400> 446

Met Pro Lys Ile Leu Ala Arg Thr Val Asp Ala Leu Val Thr Cys Glu

1 5 10 15

Arg Leu Phe Cys Val Leu His Ile Cys Asn Met Glu Asn Cys Ala Ser

20 25 30

Val Arg Ser Ser Ser Cys Leu Ile Trp Leu Ala Ala Ala Phe Phe Val

35 40 45

Ser Ala Leu Gly His Val Gln Gln Gly Ala Gly Val Val Arg Pro Arg

50 55 60

His Trp Gln Asn Ser Glu Ala Ala Val Ser Val Arg Pro Pro Gly Gly

65 70 75 80

Ala Ser Pro Arg His Phe His Ser Pro Ile Glu Pro Val Ala Phe Ile

85 90 95

Asp Gly Glu His Val Glu Asp Lys His Gly Gly Ser Trp Leu Glu Gln

100 105 110

Glu Ala Ala Glu Glu Val Thr Pro Leu Leu Asn Ser His Thr Glu Thr

115 120 125

Pro Thr Gln Ser Pro Ser Ala Phe Arg Arg Leu Leu Arg Arg Leu Arg

130 135 140

Phe Trp Arg Arg Gly Arg Thr Gly Gly Ser Asp Gly Gly Gly Glu Pro

145 150 155 160

Pro Gln Thr Pro Arg Pro Ser Leu Pro Thr Arg Leu Phe Gln His Leu

165 170 175

Arg Arg Ala Ala Ala Ile Pro Ala Ala Ala Ser Arg Phe Phe Arg

180 185 190

Arg Phe Arg Arg Val Gln Glu Pro Val Phe Pro Pro Asp Glu Phe Pro

195 200 205

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

210 215 220

Asp Val Val Ile Glu Glu Leu Phe Asn Arg Ile Pro Glu Thr Ser Val

225 230 235 240

Trp Asn Glu Asn Glu Arg Val Leu Ser Asn Ala Asn His Leu Val Ser

245 250 255
Thr Ala Leu Trp Arg Asn Glu Gln Ser Phe Arg Val Glu Ser Glu Leu

260 265 270
Gly Glu Arg Pro Arg Thr Leu Val Arg Gly Pro Val Leu Arg Asp Asp

275 280 285
Gly Ser Tyr Ile Cys Leu Glu Ala Thr Asp Gln Glu Thr Gly Glu Pro

290 295 300
Leu Glu Val His Val Pro Tyr Phe Thr Glu Arg Pro Pro Ser Asn Ala

305 310 315 320
Ile Lys Gln Leu Ser Glu Gln Val Leu Arg Leu Arg Leu Leu Arg Gly

325 330 335
Ile Lys Asn Gln Arg Gln Ala Lys Ala Tyr Leu Arg Phe Ile Phe Pro

340 345 350
Ile Asp Leu Val Lys Asp Pro Lys Lys Arg Lys Met Ile Arg Val Arg

355 360 365
Leu Asp Glu Arg Asp Met Trp Val Leu Ser Arg Phe Phe Leu Tyr Pro

370 375 380
Arg Met Gln Ser Asn Leu His Ile Leu Gly Asp Val Leu Leu Ser His

385 390 395 400
Ser Ser Thr His Lys Ser Leu Val His His Ala Arg Leu Gln Leu Thr

405 410 415
Leu Gln Leu Ile Arg Leu Ala Ala Ser Leu Gln His Tyr Gly Leu Val

420 425 430
His Ala Asp Phe Gln Val Arg Asn Ile Leu Leu Asp Gln Arg Gly Gly

435 440 445
Val Phe Leu Thr Gly Phe Glu His Leu Val Arg Asp Gly Ala Ser Ala

450 455 460
Val Ser Pro Ile Gly Arg Gly Phe Ala Pro Pro Glu Thr Thr Ala Glu

465 470 475 480
Arg Met Leu Pro Tyr Arg Gln His His Pro Thr Leu Met Thr Phe Pro

485 490 495

Phe Asp Thr Trp Thr Leu Gly Leu Ala Ile Tyr Trp Ile Trp Cys Ala
500 505 510
Asp Leu Pro Asn Thr Glu Asp Ala Glu Leu Gly Gly Ile Glu Trp Ile
515 520 525
Tyr Arg Arg Cys Lys Asn Ile Pro Gln Pro Val Arg Ala Leu Leu Glu
530 535 540
Gly Phe Leu Arg Tyr Ser Lys Glu Asp Arg Leu Leu Pro Leu Gln Ala
545 550 555 560
Met Glu Thr Ser Glu Tyr Glu Gln Leu Arg Thr Glu Leu Ser Ala Val
565 570 575
Leu Pro Leu Tyr Gln Thr Asp Gly Glu Pro Ala
580 585

<210> 447

<211> 575

<212> PRT

<213> Toxoplasma gondii

<400> 447

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

Thr Gln Ser Pro Ser Ala Phe Arg Arg Leu Thr Arg Arg Leu Arg Phe

115 120 125

Trp Arg Arg Gly Val Thr Gly Gly Ser Asp Ala Gly Glu Glu Ala Pro

130 135 140

Gln Thr Pro Arg Pro Ser Leu Arg Thr Arg Ile Leu Gln Tyr Leu Arg

145 150 155 160

Arg Val Gly Thr Phe Phe Arg Arg Asp Ile Pro Ala Ala Ala Leu Arg

165 170 175

Phe Phe Arg Arg Phe Arg Arg Val Arg Gln Pro Val Phe Pro Pro Asp

180 185 190

Glu Phe Pro Glu Asp Val Asp Thr Asn Pro Ile Tyr Phe Arg Gly Thr

195 200 205

Asp Pro Gly Asp Val Val Ile Glu Glu Leu Phe Asn Arg Ile Pro Gln

210 215 220

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

225 230 235 240

Leu Val Ser Thr Ser Leu Trp Asn Thr Gly Gln Pro Phe Arg Val Glu

245 250 255

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

260 265 270

Gly Gln Glu Asp Pro Tyr Ala Tyr Leu Glu Ala Thr Asp Gln Glu Thr

275 280 285

Gly Glu Ser Phe Glu Val His Val Pro Tyr Phe Thr Glu Arg Pro Pro

290 295 300

Ser Asn Ala Ile Lys Gln Met Lys Glu Glu Val Leu Arg Leu Arg Leu

305 310 315 320

Leu Arg Gly Ile Lys Asn Gln Lys Gln Ala Lys Val His Leu Arg Phe

325 330 335

Ile Phe Pro Phe Asp Leu Val Lys Asp Pro Gln Lys Lys Lys Met Ile

340 345 350

Arg Val Arg Leu Asp Glu Arg Asp Met Trp Val Leu Ser Arg Phe Phe

355 360 365
Leu Tyr Pro Arg Met Gln Ser Asn Leu Gln Thr Phe Gly Glu Val Leu

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

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

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

565 570 575

<210> 448

<211> 353

<212> PRT

<213> Toxoplasma gondii

<400> 448

Met Thr His Pro Asn Pro Leu Gln Thr Arg Phe Ser Arg Ser Ala Ser
1 5 10 15

Leu Val Ser Arg Met Pro Leu Val Arg Leu Phe Phe Thr Ile Ala Ala
20 25 30

Pro Leu Leu Phe Ser Pro Ser Pro Cys Pro Phe Leu Pro Leu Lys Thr
35 40 45

His Cys Leu Ala Ile Gln Leu Gly Lys Pro Gln Gly Ser Pro Pro Ala
50 55 60

Ser Gln Lys Glu Ala Ile Arg Asp Thr Gly Val Ser His Gln Lys Gly
65 70 75 80

Glu Pro Ser Asp Ser Ser Ser Glu Pro Lys Pro Gln Gly Thr Val Ala
85 90 95

Glu Thr Pro Gly Ala Ala Ser Ala Ala Ala Ala Glu Val Gly Arg Pro
100 105 110

Ser Arg Ser Ser Ala Gly Pro Gly Lys Lys Lys Arg Gly Pro Ser Leu
115 120 125

Phe Thr Glu Glu Thr Met Gly Pro Ser Lys Arg His Pro Cys Leu Lys
130 135 140

Thr Leu Ala Ala Ala Val Glu Arg Phe Gln Ala Gln His Leu Thr Gly
145 150 155 160

Arg Asp Ala Ala Lys Ala Phe Val Asp Ala Ile Gln Glu Cys Gly Ile
165 170 175

Gln Val Val Ala Ser Asp Tyr Asp Arg Thr Ala Ile Ser Val His Ser
180 185 190

Gly Gly Ser Ala Arg Arg Asp Asp Leu Ser Val Leu Gly Ala Leu Thr
195 200 205

Pro Asp Phe Lys Leu Leu Gly Glu Glu Leu Thr Arg Arg Asn Ile Pro
210 215 220

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

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

Glu Asp Lys Ile Leu Leu Leu Asp Asp Asp Arg Ala Asn Cys Val Asn
305 310 315 320
Phe Cys Arg Ser Gly Gly Ala Ala Ile His Val Ser Gly His Glu Gly
325 330 335
Phe Asp Phe Gly Ala Val Arg Val Val Val Lys Pro Ser Leu Ile Met
340 345 350

Gln

<210> 449

<211> 102

<212> PRT

<213> Toxoplasma gondii

<400> 449

Met Gly His Pro Thr Ser Phe Gly Gln Pro Ser Cys Leu Val Trp Leu

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

85 90 95
 Asp Ser Gln Ala Gly Ser
 100
 <210> 450
 <211> 1010
 <212> PRT
 <213> Toxoplasma gondii
 <400> 450
 Met Lys Pro Pro Arg Glu Thr Ser Arg Gly Gly Met Glu Gly Lys Val
 1 5 10 15
 Gly Phe Gly Ala Ser Ile Arg Asp Arg Trp Phe Phe Gln Asn Phe Ser
 20 25 30
 Asp Gly Leu Ser Asn Gly Glu Lys Ser Trp Trp Arg Arg Ser Val Val
 35 40 45
 His Phe Leu Gln Met Ala Asp Pro Thr Trp Ser Cys Arg Glu Thr Arg
 50 55 60
 Arg Ala Leu Glu Pro Gly Met Leu Glu Lys Met Lys Ser Thr Tyr Trp
 65 70 75 80
 Leu Thr Arg Ile Val Phe Ile Arg Ala Leu Ser Phe Val Tyr Phe Val
 85 90 95
 Ala Phe Leu Val Ala Phe Asn Gln Ala Gln Gly Leu Ile Gly Ser Asp
 100 105 110
 Gly Ile Leu Pro Ala Gln Thr His Ala Asp Ser Ile Arg Glu Val Leu
 115 120 125
 Ala Glu Glu Asp Thr Trp Thr Lys Ile Lys Ala Phe Pro Ser Leu Phe
 130 135 140
 Leu Phe Leu Pro Ala Asn Asp Phe Trp Ile His Cys Leu Pro Phe Leu
 145 150 155 160
 Gly Ile Leu Val Ser Leu Val Thr Gly Val Leu Gly Gly Ser Asn Gly
 165 170 175
 Phe Val Met Leu Phe Leu Trp Ile Leu Tyr Gln Ser Val Asn Ser Ile
 180 185 190

Gly Gln Glu Trp Tyr Ala Phe Gly Trp Glu Ser Glu Leu Leu Glu Ile
195 200 205

Gly Phe Leu Ser Ile Trp Leu Cys Pro Phe Trp Ser Phe Ser Arg Leu
210 215 220

Pro Ala Ser Trp Pro Thr Pro Lys Ile Cys Val Trp Gly Asn Arg Trp
225 230 235 240

Leu Leu Phe Arg Leu Met Leu Gly Ala Gly Leu Ile Lys Leu Arg Asn
245 250 255

Asp Asn Leu Trp Thr Asp Leu Thr Ala Leu Asp Tyr His Tyr Glu Thr
260 265 270

Met Pro Ile Pro Asn Pro Phe Ser Trp Tyr Met His Asn Gln Ser His
275 280 285

Thr Ala His Ala Phe Gln Val Ile Val Asn His Val Val Glu Cys Val
290 295 300

Phe Pro Phe Leu Leu Leu Ile Pro Phe Arg Gln Cys Arg Leu Val Gly
305 310 315 320

Gly Val Thr Gln Ile Leu Phe Gln Gly Ala Ile Ile Phe Ser Gly Asn
325 330 335

Phe Ser Phe Leu Asn His Leu Ser Ile Leu Pro Ala Leu Met Thr Leu
340 345 350

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

Leu Gln Pro Leu Leu Gln Gly Cys Leu Gly Ala Trp Ser Leu Pro Lys
370 375 380

His Gln Ala Trp Pro Val Asp Ser Cys Ser Glu His Thr Asn Glu His
385 390 395 400

Gln Gly Val Gly Ser Val Lys Asp Pro Glu Ala Ala Ala Leu Leu Asn
405 410 415

Asp Gly Gly Ser Gln Leu Glu Trp Ser Val Asp Thr Asp Asp Asp Ser
420 425 430

Asn Gln Ala Ser Ala Arg Thr Cys Cys Cys Trp Tyr Ser Pro Arg Ile

435 440 445
 Leu Gln Phe Phe Arg Ser Ile Pro Arg Thr Ile Phe Pro Ser Arg Ala
 450 455 460
 Arg Asn Arg Met Lys Arg Asp Met Glu Glu Ser Trp Lys Ser Met Leu

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

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

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

 660 665 670
 Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu Met Trp
 675 680 685

Phe Val Pro Met Asp Ile Pro Glu Ile Val Gly Val Arg His Pro Trp
 690 695 700
 Phe Pro Arg Phe Leu Gly Lys Leu Leu Gln Asn Ser Pro Ser Val Thr
 705 710 715 720
 Gly Leu Leu Ala Asp Asn Pro Phe Lys Asn Lys Asp Pro Pro Thr Ala
 725 730 735
 Val Arg Val Leu Lys Thr Leu Tyr Arg Phe Thr Lys Arg Pro Phe Trp
 740 745 750
 Gly Ser Gly Pro Trp Trp Glu Ile Val Pro Asn Thr Thr Ser Val Phe
 755 760 765
 Val Ala Pro Gly Asp Val Pro Asp Ala Asp Gln His Leu Glu Gln Met
 770 775 780
 Ile Val Leu Lys Arg Val Gln Glu Gln Lys Ala Gln Glu Glu Leu Leu
 785 790 795 800
 Arg Lys Glu Leu Lys Glu Glu Gln Arg Lys Ala Arg Glu Arg Ala Glu
 805 810 815
 Ala Glu Lys Met Val Ala Glu Glu Glu Arg Lys Lys Leu Leu Glu Gln
 820 825 830
 Arg Thr Gln Glu Glu Leu Glu Thr Lys Arg Arg Ile Gln Glu Glu Lys
 835 840 845
 Glu Leu Arg Glu Lys Gln Ala Glu Glu Met Arg Lys Gln Glu Glu Glu
 850 855 860
 Gln Arg Lys Lys Gln Glu Ala Glu Glu Lys Ala Arg Ala Ala Ala Glu
 865 870 875 880
 Glu Ala Arg Lys Arg Lys Glu Val Glu Ile Ala Arg Ala Gln Glu Glu
 885 890 895
 Gln Glu Ala Glu Arg Gln Arg Glu Ala Ala Glu Glu Glu Lys Arg Lys
 900 905 910
 Lys Glu Ala Gln Arg Thr Ala Glu Glu Glu Ala Ala Lys Leu Arg Lys
 915 920 925
 Glu Glu Ala Arg Lys Arg Asp Glu Glu Ala Ala Lys Leu Ala Glu Gln

930 935 940
 Arg Glu Ser Leu Arg Arg Lys Glu Gln Lys Glu Lys Gln Ala Met Leu
 945 950 955 960
 Ala Lys Lys Arg Ala Glu Ala Ala Glu Lys Glu Gln Glu Arg Asn Ser
 965 970 975
 Gln Leu Ser Asp Gln Ser Arg Ala Ser Ala Asp Gly Gly Val Pro Leu

 980 985 990
 Arg Ala Ala Ala Leu Phe Asn Arg Lys Lys Ala Ala Ile Phe Arg Leu
 995 1000 1005
 Asn Gln
 1010
 <210> 451
 <211> 1063
 <212> PRT
 <213> Toxoplasma gondii
 <400> 451
 Met Leu Arg His Phe Gly Gly Gly Phe Met Pro Trp Arg His Leu Asp
 1 5 10 15
 Ile Ser Ser Leu His Trp Val Asp Ser Ala Arg Phe Gly Ser His Cys
 20 25 30

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

 Phe Lys Glu Trp Leu Lys His His Cys Ser Leu Ser Lys Lys Asp His
 100 105 110
 Ala Leu Thr Ala Glu Asp Leu Lys Val Met Glu Gly Thr Tyr Trp Leu
 115 120 125

Ala Arg Ile Val Phe Phe Arg Thr Leu Gly Phe Val Tyr Phe Thr Ala
130 135 140

Phe Leu Ile Ala His Met Gln Gly Pro Gly Leu Phe Gly Gln Asp Gly
145 150 155 160

Leu Leu Arg Leu Glu Asp Thr Pro Pro Cys Lys Ser Ser Gly Gln Asp
165 170 175

Ser Arg Glu Leu Trp Thr Arg Phe Ala Ala Glu Pro Ser Leu Phe His
180 185 190

Phe Phe Ser Cys Thr Asp Ala Ser Leu Leu Phe Ile Thr Ser Ser Gly
195 200 205

Leu Val Leu Ser Ala Val Leu Ile Leu Thr Gly Gly Val Thr Val Pro
210 215 220

Val Leu Leu Trp Leu Trp Leu Ser Tyr Met Thr Ile Gln Ala Ala Gly
225 230 235 240

Gln Arg Phe Tyr Thr Phe Thr Trp Asp Thr Leu Leu Leu Glu Val Gly
245 250 255

Phe Trp Ala Met Pro Leu Thr Leu Val Cys Phe Leu Arg Pro Phe Leu
260 265 270

Pro Leu Thr Ser Ala Pro Ser Pro Ser Asn Thr Thr Pro Asp Gly Pro
275 280 285

Gly Ala Arg Pro Ser Thr Leu Lys Ser Ala Thr Met Ser Gln Ser Ala
290 295 300

Gly Gly Gly Gly Val Ser Gly Ala Gln Leu Asp Pro Gly His Pro Lys
305 310 315 320

Glu Gly Ala Asp Gly Arg Gly Ser Thr Ser Ala Ala Ala Glu Leu Ser
325 330 335

Ser Thr Asp Gly Val Arg Glu Asn Pro Ser Gly Pro Glu Ser Asp Ser
340 345 350

Ser Ser Ser Gly Lys Arg Ser Thr Leu Arg Gly Gln Gln Met Leu Arg
355 360 365

Trp Pro Arg Ala Ala Leu Gln Leu Leu Leu Arg Cys Cys His Ser Leu

370	375	380	
Val Ser Pro Gly Ala Pro Phe Leu Pro Pro Thr Trp Pro Thr Pro Trp			
385	390	395	400
Ile Ser Val Trp Gly Tyr Arg Trp Leu Leu Phe Arg Leu Met Leu Gly			
405	410	415	
Ala Gly Leu Ile Lys Leu Arg Ala Asp Thr Ala Trp Thr Asn Leu Thr			
420	425	430	
Ala Met Gln Trp His Tyr Glu Thr Gln Pro Leu Pro Asn Pro Val Ala			
435	440	445	
Trp Phe Val His Met Leu Pro Met Ser Met His Lys Phe Glu Val Leu			
450	455	460	
Met Asn His Phe Ala Glu Leu Val Leu Pro Phe Ala Val Leu Ser Pro			
465	470	475	480
Trp Arg Gln Leu Arg Leu Phe Ser Gly Cys Phe Gln Leu Leu Phe Gln			
485	490	495	
Val Ala Ile Ile Ile Thr Gly Asn Leu Ala Phe Ile Asn Trp Leu Thr			
500	505	510	
Ile Val Phe Ile Val Phe Leu Phe Asp Asp Arg Phe Leu Met Trp Leu			
515	520	525	
Phe Pro Thr Ser Thr Leu Asn Lys Leu Arg Pro Leu Leu Gln Gly Cys			
530	535	540	
Pro Gly Asn Trp Ser Phe Pro Ser Ser Asp Ser Val Thr Lys Asp Thr			
545	550	555	560
Ser Thr Ser Val Ser Lys Ser Glu Ser Glu Lys Ser Pro Arg Glu Pro			
565	570	575	
Gln Ala Cys Ser Glu Gln Arg Pro Leu Leu Arg Asn Asp Val Lys Leu			
580	585	590	
Arg Glu Thr Ser Glu Ala Glu Glu Ala His Cys Pro Pro Ser Ser Ser			
595	600	605	
Ser Ala Thr Thr Ala Ala Val Ser Arg Ala Leu Pro Trp Arg Leu Leu			
610	615	620	

Thr Gly Pro Lys Trp Thr Gly Arg Ala Leu Arg Arg Met Leu Ala Thr
 625 630 635 640
 Trp Gly Cys Trp Arg Ile Pro Leu Phe Leu Phe Ile Ala Ala Val Leu
 645 650 655
 Val Thr Ser Asp Gly Ile Leu Leu Leu Leu Leu Gly Lys Ala Ala Thr
 660 665 670

 Ala Pro Ser Leu Ser Thr Thr Leu Val Trp Glu Ser Ala Gly Leu Leu
 675 680 685
 Leu Leu Ile Leu Thr Ser Val Val Ala Leu Gly Gly Leu Ala Gly Ala
 690 695 700
 Ala Gly Val Pro Trp Ser Leu Leu Gly Ala Ala Val Ser Ala Phe Ser
 705 710 715 720
 Pro Arg Phe Thr Val Glu Asn Gln His Pro Leu Thr Asn Leu Ala Ser
 725 730 735

 Val Glu Arg Ser Glu Thr Ala Glu Asn Ala Ser Leu Pro Thr His Pro
 740 745 750
 Gln Asp Ser Glu Arg Arg Gly Thr Val Leu Arg Arg Pro Arg Gln Thr
 755 760 765
 Glu Glu Asp Val Gly Gly His Glu Gly Gly Val Val Glu Ser Arg Arg
 770 775 780
 Gln Ser Lys Ser Val Val Asp Ala Asp Glu Gly Arg Asp Glu Ala Lys
 785 790 795 800

 Leu Leu Trp Lys Arg Thr Gln Asp Val Gly Ala Leu Ala Phe Glu Val
 805 810 815
 Leu Val Ala Gly Val Val Leu Ala Asn Leu Leu Phe Met His Phe His
 820 825 830
 Leu Gly Pro Thr Phe Ala Gly Leu Asp Leu Leu Thr Gly Leu Leu Cys
 835 840 845
 Val Leu Leu Phe Ala Phe Ala His Arg His Cys Ser Asn Ser Phe Leu
 850 855 860

 Val Leu Arg Val Met Thr Glu Val Gly Leu Leu Ile Val Leu Val Trp

865 870 875 880
 Arg Ser Ile Pro Val Val Glu Asn Leu Leu Ser Pro His Gln Ile Met
 885 890 895
 Asn Asp Thr Tyr Asp Ser Phe Arg Leu Val Asn Ser Tyr Gly Leu Phe
 900 905 910
 Gly Phe Met Thr Lys Gln Arg Glu Glu Leu Val Ile Gln Gly Thr Tyr
 915 920 925

 Glu Pro Asp Pro Pro Ser Ala Pro Ala Asn Pro Ala Trp Gln Thr Tyr
 930 935 940
 Glu Phe Tyr Cys Lys Pro Gly Asp Ile Asp Arg Arg Pro Cys Phe Val
 945 950 955 960
 Ser Pro Tyr Tyr Tyr Arg Leu Asp Trp Leu Met Trp Phe Ala Ala Phe
 965 970 975
 Asn Ala Asp Leu Gln Ala Pro Tyr Trp Leu Leu Arg Leu Val Lys Lys
 980 985 990

 Met Leu Ala Asn Asp Pro Lys Thr Ser Ala Leu Leu Ala His Asn Pro
 995 1000 1005
 Phe Arg Gly Lys Arg Pro Pro Thr Phe Ile Arg Ile Leu Arg Tyr
 1010 1015 1020
 Asp Tyr His Phe Ala Tyr Lys Gly Lys Glu Gln Asp Met Tyr Glu
 1025 1030 1035
 Gln Gly Lys Trp Trp Gln Arg Lys Tyr Leu Ser Glu Phe Leu Pro
 1040 1045 1050

 Pro Val Ser Ala Ala Leu Phe Arg Lys Ile
 1055 1060
 <210> 452
 <211> 1254
 <212> PRT
 <213> Toxoplasma gondii
 <400> 452
 Met Gly Trp Val Pro Pro Cys Ala Ala Pro Ala His Ser Gln Ala Ala
 1 5 10 15

Ala Asn Leu Arg Val Glu Ser Leu Gly Ser Arg Ser Phe Pro Asp Gly
20 25 30

Ser Thr Lys Lys Arg Arg Arg Glu Glu Arg Thr Asp Arg Phe Arg Asn
35 40 45

Leu His Phe Arg Thr Leu Leu Tyr Ser Cys Ser Ser Phe Ser Cys Ser
50 55 60

Arg Asn Ala Pro Ala Asn Gly His Lys Thr Ser Ser Pro Gly His Pro
65 70 75 80

Glu Glu Ser Leu Arg Pro Thr Pro Leu Phe Val Lys Arg Ala Arg Phe
85 90 95

Cys Phe Tyr Leu Leu Phe Leu Phe Ser Val Leu Ala Ser Asn Phe Phe
100 105 110

Ser His Arg Ala Asp Glu Cys Thr Arg Phe Cys Asn Val Phe Ala Gln
115 120 125

Ala Leu His Val Lys Leu Asp Asn Pro Glu Leu Ser Arg Gln Thr Leu
130 135 140

Pro Ala Ser Leu Arg Trp Gln Gln Val Lys Thr Lys Asn Gly Glu Glu
145 150 155 160

Val Asn Ala Ala Glu Ser Ala Ser Trp Lys Gly Phe Ala Asp Val Gln
165 170 175

Leu Ala Pro Phe Arg Pro Asp Glu Lys Pro Ser Arg Glu Arg Thr Val
180 185 190

His Glu His Arg Asp Thr Val His Gly Leu Ser Gly Arg Asp Thr Leu
195 200 205

Gly Ile Asp Ser Phe Arg Gly Thr Asp Leu Arg Gly Asn Arg Leu Phe
210 215 220

Val Arg Leu Pro Arg Pro Ala Leu His Ser Pro Phe Leu Phe Pro Ser
225 230 235 240

Phe Ser Phe Pro Ala Ala Thr Gln Pro Ala Glu Ser Ser Val Phe Phe
245 250 255

Gly Ala Asp Gly Ile Pro Ser Phe Ser Glu Ile His Ser Glu Gln Ser

260 265 270
 Glu Asp Ala Glu Glu Pro Glu Ser Gln Asp Ser Ser Ser Ser Arg Asn
 275 280 285
 Gln Asp Glu Ala Pro Lys Pro Thr Glu His Ala Ser Gln Glu Lys Ala
 290 295 300

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

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

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

 Ala Ala Gly Lys Glu Asp Ser Ala Pro Thr Thr Glu Lys Pro Leu Ser
 500 505 510

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

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

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

 Val Phe Gly Asp Val Met Pro Pro Leu Arg Asp Ser Asp Thr Val Leu
 690 695 700
 Glu Asn Val Ser Pro Met Leu Glu Val Leu Phe Glu Glu Leu Phe Phe
 705 710 715 720
 Val Ser Val Ile Leu Leu Val Trp Tyr Val Val Phe Val Ile Leu Phe
 725 730 735
 Gln Cys Met Ile Arg Gln Ile Ile Glu Trp Met Arg Lys Ile Asp Glu
 740 745 750

 Glu Glu Asp Ile Pro Leu Ile Ala Arg Asp Ala Glu Thr Gln Ser His

755	760	765	
Arg Trp Cys Gly Ala Val	Leu Gly Arg Ser Ala Leu	Asp Lys Ala Asn	
770	775	780	
Phe Ile Ala His Arg Tyr	Glu Phe Thr Asp Asn Val	Gln Ser Met Ser	
785	790	795	800
Ile Pro Gly Val Asp Pro	Ser Gly Tyr Tyr Phe Met	Glu Tyr Leu Arg	
805	810	815	
Ala Ser Leu Leu Lys Met	Ala Ile Glu Met Ile Arg	Leu Pro Asn Ser	
820	825	830	
Thr Leu Phe Phe Leu Met	Ile Met Asp Ile Cys Leu	Arg Pro Thr Phe	
835	840	845	
Ser Phe Arg Leu Gly Gln	Glu Val Gly Leu Ile Ser	Gly Leu Ser Ala	
850	855	860	
Thr Cys Leu Val Gly Met	Leu Leu Val Trp Ala Tyr	Thr Ala Arg Ile	
865	870	875	880
Glu Lys Gln Leu Leu Pro	Arg His Val Pro His Tyr	Leu Val Met Arg	
885	890	895	
Tyr His Met Glu Val Gly	Gly Asp Thr Ser Ser Glu	Tyr Leu Lys Glu	
900	905	910	
Phe Ala Pro Pro Tyr Lys	Leu Gln Lys Gln Lys Asn	Ala Trp Pro Gly	
915	920	925	
Val Cys Ser Thr Phe Leu	Arg Gly Thr Thr Leu Pro	Asn Lys His Gln	
930	935	940	
Gln Leu Phe Cys Phe Trp	Ala Asn Gly Pro Asn Ile	Val Leu Arg Ala	
945	950	955	960
Val Glu Ala Ser Phe Phe	Cys Gln Leu Leu Val Leu	Ala Trp Trp Val	
965	970	975	
Gln Leu Phe Arg Ser His	Pro Ala Thr Trp Leu Asn	Phe Cys Trp Trp	
980	985	990	
Gly Asn Val Val Val Val	Leu Cys Ala Gly Ser Gln	Phe Ala Leu Leu	
995	1000	1005	

Lys Ser Val Val Tyr Thr Val	Leu Leu Ala Leu Asn	Ser Gly Met
1010	1015	1020
Leu Val Asp Pro Glu Leu Leu	Glu Lys Val Trp Asp	Leu Gln Arg
1025	1030	1035
Ala Glu Asn Val Arg Arg Thr	Ala Glu Leu Ile Asp	Ala Leu Arg
1040	1045	1050
Val Gln Ser Thr Leu Phe Ala	Ile Ser Glu Gly Gly	Asp Met Phe
1055	1060	1065
Trp Arg Gln Leu Leu Ile Arg	Ser Lys Gly Ala Ser	Arg Gln Ala
1070	1075	1080
Gln Glu Gln Arg Leu Ser Leu	Trp Ala Ala Leu Asp	Glu Glu His
1085	1090	1095
Gln Gly Glu Ile Ser Arg Ala	Lys Ile Phe Lys Phe	Leu Thr Ser
1100	1105	1110
Gln Gly Leu Pro Ile Lys Ser	Glu Ser Gly Val Asn	Asp Phe Leu
1115	1120	1125
His Val Phe Asp Arg Asn His	Lys Gly Gly Val Asn	Glu Asp Glu
1130	1135	1140
Phe Phe Val Met Val Met Val	Val Lys Gln Met Leu	Met Glu Pro
1145	1150	1155
Leu Asp Arg Asp Ala Val Arg	Glu Leu Phe Glu Gly	Arg Tyr Gly
1160	1165	1170
Ile Pro Trp Thr Ser Pro Val	Gly Ile Asp Leu Ala	Asn Leu Ser
1175	1180	1185
Lys Ile Leu Ala Glu Leu Arg	Leu Thr Leu Ser Glu	Gly Lys Lys
1190	1195	1200
Arg Tyr Leu Leu Asp Phe Ile	Gly Gly Lys Arg Gly	Thr Thr Ala
1205	1210	1215
Val Ser Pro Asp His Phe Val	Ser Gln Leu Gln Ala	Met Glu Glu
1220	1225	1230
Gln Ala Leu Asn Pro Ile Gln	Ser Glu Ser Leu Arg	Gly Pro Pro

1235 1240 1245

Ile Pro Gly Glu Arg Val

1250

<210> 453

<211> 1257

<212> PRT

<213> Toxoplasma gondii

<400> 453

Met Val Ser Leu Cys Leu Pro Ser Pro Leu Leu Gly Leu Gln Gly Pro

1 5 10 15

Cys Pro Ser Arg Lys Lys Pro Thr Arg Ser Asn Gly Lys Leu Gln Ser

20 25 30

Gln Pro Cys Ala Arg Trp Lys Pro Val Asp Leu Thr Thr Pro Gln Ser

35 40 45

Arg Leu Leu Cys His Ser Leu Pro Thr Val Pro Ser Ser Ile Ser Pro

50 55 60

Ser Gln Ser Ser Ala Ser Ser Arg Leu Ser Val Asn Pro Ser Cys Leu

65 70 75 80

Ala Phe Ser Pro Ala Val Cys Phe Leu Asp Ala Asn Arg Arg Ala Ser

85 90 95

Trp Ser Pro Cys Phe Ser Leu Lys Cys Ser Phe Arg Asn Ser Arg Arg

100 105 110

Pro Phe Leu Cys Met Ala Leu Cys Ile Val His Leu Trp Leu Phe Ser

115 120 125

Ala Leu Ser Phe Arg Glu Ile Val Tyr Val Ser Asp Ser Ala His His

130 135 140

Asn Lys Ala Asn Pro Thr Cys Leu Ser Ser Trp Ser Leu Ala Ala Pro

145 150 155 160

Val Asp Ala Arg Gln Pro Val Asn Ala Ala Leu Thr Lys Glu Ala Gln

165 170 175

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

180	185	190	
Gly Arg Gly Ser Gly Phe Ser Leu Lys Thr Gly Asp Ala Phe Lys Asp			
195	200	205	
Val Ala Pro Asp Asp Ser Gly Val Ala Leu Leu Ser His Glu Ser Gln			
210	215	220	
Gln Ser Ser Ala Ala His Glu Leu Asn Met His His Asp Ile Gln Pro			
225	230	235	240
Asp Pro Ser Ser Thr Glu Phe Ser Asn Gly Arg Ser Ala Pro Val Ser			
245	250	255	
Phe Leu Leu Ser Arg Ala Phe His Leu Ser Arg Gln Pro Gly His Leu			
260	265	270	
Ser Leu His Asp Ser Leu Ser Arg Leu Ser Leu Phe Pro Ser Lys Gly			
275	280	285	
Ser Ser Ile Ser Phe Ser Ser Met Ser Ser Pro Ser Leu Ser Ala Leu			
290	295	300	
Pro Ser Ser Ser Ala Asp Ser Pro Leu Ser Ser Gly Leu Thr Pro Pro			
305	310	315	320
Leu Ser Leu Ser Thr Glu Ser Val Pro Ala Ala Glu Glu Ser Pro Ser			
325	330	335	
Ser Gly Ala Ser Ser Ser Ser Pro Cys Glu Phe Ser Pro Ser Arg			
340	345	350	
Asp Phe Ala Phe Leu Glu Ala Gly Gln Ala Thr Ser Gly Lys Asn Ser			
355	360	365	
Leu Pro Arg Ala Cys Ala Tyr Ala Gly Cys Lys Ala Gly Phe Phe Thr			
370	375	380	
Pro Arg Pro Ala Asn Asp Pro Asn Thr Cys Tyr Thr Leu Ser Glu Cys			
385	390	395	400
Ser Gln Cys Arg Val His Pro Glu Ser His Ala Asp Leu Cys Ser Gln			
405	410	415	
Val Glu Glu Arg Asn Gly Leu Leu Leu Leu Met Lys Ser Ser Leu Gly			
420	425	430	

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

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

 Gln Ala Gln Glu Val Arg His Gly Gln Arg Thr Ala Gly Glu Thr Ala
 565 570 575
 Thr Gly Phe Ala Ala Ser Leu Ser Pro Leu Pro Phe Ser Ser Ala Ser
 580 585 590
 Gly Ala Ser Phe Asp Leu Ser Val Ser Ser Ala Pro Ser His Ser Gln
 595 600 605
 Ser Pro Phe Ser Phe Leu Gly Glu Lys Val Ser Ser Trp Asp Asn Glu
 610 615 620

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

675	680	685
Ser Leu Leu Gly Asp Val Gly Arg Cys Ala Thr Asp Ser Lys Asn Tyr		
690	695	700
Met Arg Leu Gln Ile Thr Val Ala Leu Gln Pro Arg Arg Phe Arg Met		
705	710	715
Ser Val Ala Lys Ala Lys Lys Leu Met Gly Leu Arg Ala Arg Lys Pro		
725	730	735
Ile Pro Arg Ser Phe His Glu Gly Asp Glu Gly Glu Asp Gly Gly Tyr		
740	745	750
Asp Asp Ala Asp Gly Gly Tyr Asp Asp Glu Gln Gly Phe Leu Glu Leu		
755	760	765
Glu Asn Glu Arg Arg Glu Gly Arg Pro Val Gln Gly Asp Gly Thr Gly		
770	775	780
Glu Leu Gly Thr Glu Ser Arg Glu Gln Glu Gly Asn Trp His Glu Leu		
785	790	795
Ser Gly Leu Thr Glu Gly Arg Asp Thr Ser Glu Asp Ala Arg Glu Arg		
805	810	815
Gln Arg Gly Lys Asp Arg Gly Glu Asn Gly Arg His Thr Gly Val Val		
820	825	830
Ser Leu Ser Asp Thr Ala Ala Glu Leu Gly Tyr Glu Gly Lys Ser Glu		
835	840	845
Pro Asp Leu Gln Asp Gly Arg Glu Gln Asp Leu Lys Phe Arg Phe Ser		
850	855	860
Ser Thr Arg Val Ala Asp Leu Glu Gly Glu Ala Asn Gln Pro Leu Ser		
865	870	875
Phe Val Gln Val Glu Asp Asp Asp Tyr Gly Asp Asp Glu Asp Asp Asp		
885	890	895
Gly Glu Gly Arg Gly Leu Gly Lys Lys Met Lys Gly Phe Phe Gly Gly		
900	905	910
Val Lys Arg Val Phe Ser Arg Lys Lys His Gly Glu Asp Asp Asp Glu		
915	920	925

Glu Gly Gly Tyr Asp Asp Asp Asn Pro Pro Asp Asp Glu Gly Glu Ala
930 935 940

Ser Pro Ser Lys Lys Gly Lys Arg Arg Gly Ser Phe Met Asn Lys Val
945 950 955 960

Arg Gly Leu Val Ser Ser Lys Ser Pro Gln Glu Lys Arg Phe Lys Lys
965 970 975

Glu Thr Lys Lys Ala Arg Arg Gly Ile Lys Arg Val Ser Arg Val Ala
980 985 990

Val Asp Ile Ala Phe His Ser Pro Ala Val Lys Lys Cys Arg Lys Ser
995 1000 1005

Leu Ser Trp Ser Ala Thr Phe Pro Ala Ala Lys Ile Leu Gln Thr
1010 1015 1020

Ser Phe Phe Ile Leu Ala Arg Gln Gly Glu Val Gly Gly Gln Leu
1025 1030 1035

Ser Ala Phe Ile Asn Ser Gly Phe Ser Val Thr Leu Lys Cys Lys
1040 1045 1050

Met Lys Gly Gly Cys Met Met Asn Glu Val Pro Val Ser Cys Ala
1055 1060 1065

Leu Val Ser Cys Val Lys Ala Lys His Val Ser Thr Glu Ala Leu
1070 1075 1080

Glu Glu Gly Lys Lys Arg Ala Ala Ala Leu Ala Glu His Asn Leu
1085 1090 1095

Lys Leu Ala Gln Thr Ser Leu Val Met Ser Pro Ala Asp Arg Ala
1100 1105 1110

Ala Arg Ala Ala Glu Tyr Glu Arg Lys Ile Gln Glu Lys Gln Gln
1115 1120 1125

Glu Ile Glu Ala Gly Asn Leu Thr Gln Gln Gln Met Leu Thr Ala
1130 1135 1140

Gln Gln Gln Gln Phe Leu Leu Gln Gln Gln Leu Ala Ala Ile Ser
1145 1150 1155

Ser Ser Gln Ser Pro Leu Asp Pro Met Gln Ala Lys Leu Leu Ala

1160	1165	1170
Ala Val Gln Gly Gly Glu Asp	Ala Ser Ser Ser Thr	Ser Gly Val
1175	1180	1185
Thr Met Gln Glu Ala Ser Ser	Gly Val Thr Asp Ser	His Thr Gln
1190	1195	1200
Arg Leu Ile Gln His Met Ile	Ala Phe Asp Ser Arg	Arg Gly Gly
1205	1210	1215
Arg Gly Ser Arg Met Ser Gly	Gly Ala Ile Ala Ala	Leu Val Ile
1220	1225	1230
Leu Gly Leu Leu Gly Ile Leu	Val Gly Gly Ile Ala	Val Phe Lys
1235	1240	1245
Tyr Arg Gly Gly Arg Arg Arg	Arg Arg	
1250	1255	
<210> 454		
<211> 1490		
<212> PRT		
<213> Toxoplasma gondii		
<400> 454		
Met Arg Ile Phe His Leu Leu Leu Leu Gly Trp Ala Val Cys Leu Ala		
1 5 10 15		
Leu Gly Leu Arg Val Asp Leu Ala Ala Ala Glu Thr Glu Thr Asp Gly		
20 25 30		
Phe Gly Arg Arg Arg Arg Lys Lys Glu Gln Glu His Tyr Gly Asp Asn		
35 40 45		
Ile Glu Met Thr Thr Leu Pro Thr Lys Lys Gly Gly Thr Ala Pro Ala		
50 55 60		
Val Pro Ser Ser Pro Ala Glu Ala Ala Lys Trp Pro Phe Asn Ser Ser		
65 70 75 80		
Cys Met Tyr Ser Glu Val Glu Ile Tyr Arg Pro Gly Ile Lys Glu Tyr		
85 90 95		
Leu His Ala Arg Thr Tyr Asp Pro Leu Ala Pro Ile Ala Gly Asn Gln		

100	105	110	
Gln Glu Asn Leu Lys Ala Leu Gln Glu Leu Leu Thr Ala Asp Phe Met			
115	120	125	
Thr Gln Gly Val Ala Ser Val Leu Leu Ala Val Glu Gln Val Ala Gly			
130	135	140	
Phe Val Asp Phe Gln Gln Pro Pro Leu Ser Glu Gly Arg Leu Phe Cys			
145	150	155	160
Ser Glu Ala Lys Asp Glu Leu Cys His Arg Ile Arg Asp Ala Leu Arg			
165	170	175	
Ser Gly Gln Pro Cys Lys Val Ile Ala Pro Val Leu Asn Cys Ser Gln			
180	185	190	
Leu Asn Lys Lys Asp Met Glu Ala Phe Leu Glu Ala Phe Glu Ala Glu			
195	200	205	
Ala Ala Ile Leu Pro Ser Ser Pro Asp Asn Glu Cys Gly Lys Ala Tyr			
210	215	220	
Ala Glu Ala Val Ser Leu Tyr His Leu Val Ile Val Asp Thr Pro Leu			
225	230	235	240
Ser Phe Ser Glu Thr Pro Met Glu Ser Glu Glu Met Lys Glu Lys Leu			
245	250	255	
Asn Leu Leu Phe Ala Glu Asn Thr Arg Gly Gly Pro Thr Pro Ala Lys			
260	265	270	
Glu Gly Val Val Tyr Glu Thr Val Asp Leu Gln Ala Pro Asn Asp Ser			
275	280	285	
Gly Asp Ala Pro Gly Lys Pro Glu Gln Val Pro Lys Pro Ser Leu Leu			
290	295	300	
Ser Ile Asn Ser Ser Ile Trp Pro Ala Asp Ile Tyr Ala Asn Ser Glu			
305	310	315	320
Ala Asp Arg Glu Ala Ser Met Val Glu Leu Lys Lys Leu Lys Asn Arg			
325	330	335	
Phe Leu Gly Lys Pro Leu Gly Pro Pro Glu Thr Thr Thr Leu Glu Ala			
340	345	350	

Phe Pro Tyr Glu Pro Glu Ala Thr Arg Thr Leu His Tyr Ser Ala Ala
 355 360 365

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

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

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

 Pro Pro Asn Leu Arg Glu Val Ser Glu Phe Asp Ser Val Val Leu Leu
 565 570 575
 Glu Thr Lys Ala Ala Ala Ala Pro Ala Val Asp Glu Ser Glu Asp Glu
 580 585 590
 Asp Ser Pro Gln Glu Gln Glu Asp Arg Ala Arg Arg Asn Phe Asn Trp

595 600 605
 Leu Arg Leu Arg Ala Ala Pro His Leu Glu Ala Gly Leu Leu Gly Asp
 610 615 620

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

 Ser Lys Asn Leu Thr Arg Phe Leu Cys Thr Pro Val Leu Asp Val Leu
 690 695 700
 Ala Leu Asp Gly Gln Leu Thr Phe Val Thr Ser Arg Ala Leu Lys Ala
 705 710 715 720
 Leu Ala Ala Asn Asp Leu Gln Val Lys Lys Pro Gly Gln Ser Ala Lys
 725 730 735
 Gly Arg Pro Phe Ala Ser Leu Ala Gly Ser Arg Ala Thr Gln Lys Met
 740 745 750

 Leu Phe Ala Arg Asn Ala Tyr Ala Pro Ala Ile Phe Gly Ala Leu Gln
 755 760 765
 Phe Phe Ser Thr Ser Thr Met Ala Asn Ala Glu Leu Leu Gly Gly Leu
 770 775 780
 Asp His Pro Gly Ile Trp Asp Ile Asn Phe Ala Ser Ser Leu Phe Thr
 785 790 795 800
 Gly Lys Gly Lys Arg Gly Trp Leu Phe Ser Arg Leu Thr Gly Ser Leu
 805 810 815

 Leu Arg Arg Leu Gly Thr Arg Leu Ala Glu Lys Ala Tyr Gln Pro Tyr
 820 825 830
 Met Met Gln Leu Leu His Gln Lys Leu Arg Pro Glu Thr Arg Lys Lys
 835 840 845

Met Phe Gln Ala Ile Gln Val Ile Val His Pro Leu Ala Leu Lys His
 850 855 860
 Leu Asn Gln Met Ala Pro Leu Tyr Ser Asp Ser Lys Gly Asn Leu Asn
 865 870 875 880

Lys Glu Gly Gly Phe Ala Glu Glu Ile Asp Asn Thr Leu Arg Glu Trp
 885 890 895
 Ser Glu Tyr Gly Met Asn Glu Lys Leu Ile Asp Arg Leu Glu Lys Gly
 900 905 910
 Gln Asn Leu Ser Ala Ser Asp Phe Ala Gly Val Asn Ile Leu Thr Met
 915 920 925
 Pro Ile Pro Ser Arg Glu Arg Met Asp Ser Leu Val Ala Glu Arg Leu
 930 935 940

Asn Gly Ala Leu Lys Arg Leu Gln Glu Asn Pro Glu Asn Val Glu Thr
 945 950 955 960
 Ser Arg Ala Ala Cys Asp Phe Leu Ser His Ala Ser Asn Ser Ile Tyr
 965 970 975
 Val Thr Asn Asp Ser Arg Tyr Leu Leu Asn Lys Phe Gly Pro Glu Asn
 980 985 990
 Leu Leu Phe Leu Gly Lys Ile Val Lys Arg Ser Glu Thr Leu Glu Lys
 995 1000 1005

Pro Gln Gly Phe Phe Ala Arg Ser Trp Ala Gly Val Glu Lys Thr
 1010 1015 1020
 Leu Lys Gly Ile Leu Arg Leu Pro Pro Tyr Met Val Arg His Phe
 1025 1030 1035
 Val Phe Ala Ala Val Lys Val Arg Glu Asp Leu Val Ser Glu Val
 1040 1045 1050
 Val Arg Glu Met Ala Ala Ile Tyr Asn Arg Phe Ser Asn Phe Phe
 1055 1060 1065

Lys Asp Glu Ile Ala Phe Arg Lys Ala Val Ser Glu Leu Ser Ile
 1070 1075 1080
 Ala Tyr Glu Asp Leu Leu Arg Gln Arg Ile Arg Glu Pro Phe Ala

1085	1090	1095
Val Pro Thr His Ser Leu Leu	Asp Asn Ile His Pro	Asp Tyr Ala
1100	1105	1110
Gln Met Asp Gly Gln Ser Arg	Asn Gln Glu Phe Gln	Ala Ser Ala
1115	1120	1125
Leu Ser His Ile Phe Ser Gln	Ala Trp Ser Leu Phe	Phe Ser Val
1130	1135	1140
Ser Met Asn Asn Tyr Ile Asn	Pro Glu Pro Leu Ala	Lys Ile Glu
1145	1150	1155
Ala Glu Tyr Ser Thr Asp Ala	Trp Lys Lys Ser Val	Asp Asp His
1160	1165	1170
Leu Ala Val Asn Ser Phe Arg	Met Ile Phe Met Gly	Ser Asp Met
1175	1180	1185
Pro Leu Lys Leu Tyr Asp Gln	Leu Ile Pro Asn Glu	Gln Lys Arg
1190	1195	1200
Met Leu Lys Arg Ala Lys Phe	Gly Val Ser Thr Met	Phe Ala Tyr
1205	1210	1215
Gln Thr Leu Leu Thr Gly Arg	Leu Tyr Glu Ala Gln	Asn Leu Pro
1220	1225	1230
Asn Leu Gly Met Phe Leu Gln	Ala Gln Gly Pro Tyr	Phe Gly Pro
1235	1240	1245
Met Ile Val Arg Trp Gln Gln	Arg Arg Arg Thr Asp	Arg Leu Ile
1250	1255	1260
Glu Ile Val Ser Trp Leu Thr	Leu Gly Ala Phe Cys	Phe Ala Ala
1265	1270	1275
Val Gly Ala Ala Met Gln Gln	Thr Thr Gln Val Val	Glu Gln Ile
1280	1285	1290
Val Gln Asn Gln Ser Ser Leu	Ala Pro Glu Leu Ser	Gly Cys Pro
1295	1300	1305
Pro Met Gly Ile Cys Met Asp	Gly Thr Ile Gly Asp	Pro Ile Ala
1310	1315	1320

Ser Pro	Pro Ala Thr	Ala Ala	Ser Ala Val	Phe Gln	Ser Ile Ala
1325		1330		1335	
Leu Val	Gly Val Gly	Met Met	Leu Gly Pro	Ala Val	Ala Ile Trp
1340		1345		1350	
Lys Ile	Ala Val Ser	His Phe	Lys Val Leu	Ala Arg	Phe Glu Met
1355		1360		1365	
Ala Ile	Gly Asn Ala	Phe Arg	Arg Met Gly	Gln Trp	Phe Arg Lys
1370		1375		1380	
Lys Trp	Arg Gly Arg	Trp Phe	Ala Asn Lys	Gln Asn	Ala Glu Ile
1385		1390		1395	
Glu Lys	Glu Met Gln	Arg His	Thr Lys Lys	Met Lys	Glu Glu Gln
1400		1405		1410	
Lys Lys	Met Ile Asp	Arg Lys	Ala Pro Asn	Leu Ile	Asp Gln Ala
1415		1420		1425	
Val Pro	Ala Thr Ala	Pro Glu	Leu Asp Leu	Val Pro	Asp Gly Pro
1430		1435		1440	
Glu Pro	Val Leu Gly	Ala Ser	Thr Ser Gly	Ser Gly	Gly Gly Phe
1445		1450		1455	
Phe Glu	Ile Ala Ser	Ala Tyr	Arg Arg Arg	Pro Arg	Phe Asp Arg
1460		1465		1470	
Leu Ala	Ser Ile Arg	Arg His	Asp Ala Leu	Leu Ala	Arg Phe Asp
1475		1480		1485	
Lys Leu					
1490					
<210>	455				
<211>	157				
<212>	PRT				
<213>	Toxoplasma gondii				
<400>	455				
Met Asp	Leu Glu Ala	Leu Ser	Ser Val	Ser Pro	Pro Arg Gly Ile Val
1	5	10	15		
Glu Asp	His Ser	Gln Ile	Ser Val	Glu Arg	Val Asn Cys Val Ala Glu

20 25 30
 Leu Val Ile Asp Ala Lys Arg Gly Gly Arg Glu Arg Glu Ala Val Glu
 35 40 45
 Gln Val Pro Pro Pro Ala Glu Arg Gln Ala Gly Gly Cys Asp Gly Gly

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

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

<210> 456

<211> 194

<212> PRT

<213> Toxoplasma gondii

<400> 456

Met Asn Phe Phe Met Ser Thr Asp Gly Ser Val Ser Leu Gly Ala Phe
 1 5 10 15

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

65						70						75						80
Leu	Pro	Leu	Phe	Lys	Thr	Ser	Glu	Asp	Gly	Pro	Gln	Pro	Val	Gln	Phe			
				85			90				95							
Leu	Val	His	Gln	Phe	Leu	Lys	Arg	Phe	Ala	Arg	Asp	Arg	Pro	Leu	Ala			
				100			105				110							
Leu	Gln	Ala	Leu	Gly	Leu	Leu	Ser	Asn	Lys	Arg	Trp	Gln	Lys	Ser	Cys			
				115			120				125							
Pro	Leu	Leu	Cys	Arg	Ser	Thr	Val	Met	Val	Glu	Arg	Gln	Gln	Glu	Glu			
130				135				140										
Thr	Val	Leu	Pro	Pro	Arg	Gly	Thr	Ser	Gln	Gly	Val	Glu	Gly	Ile	Gly			
145				150				155				160						
Gly	Lys	Gly	Cys	Asp	Gly	Leu	Val	Ser	Arg	Gly	Ala	Thr	Gly	Met	Pro			
				165			170				175							
Leu	Glu	Phe	Tyr	Asp	Val	Phe	Asp	Ala	Glu	Ala	Asn	Ala	Ser	Trp	Glu			
180				185				190										
Met Asn																		
<210>	457																	
<211>	631																	
<212>	PRT																	
<213>	Toxoplasma gondii																	
<400>	457																	
Met His Asp Pro Asp Phe Lys Val Pro Leu Asn Val Val Val Ser Ile																		
1					5					10					15			
Tyr	Arg	Arg	Gly	Ser	Ile	Lys	Cys	Val	Pro	Val	Ser	Ser	Leu	Leu	Pro			
				20			25				30							
Ile	Thr	Leu	Pro	Gly	Cys	Thr	Ser	Glu	Lys	His	Ala	Tyr	Leu	Ala	Ala			
35				40				45										
Tyr	Phe	Leu	Pro	Lys	Phe	Leu	Asn	Ile	Thr	Ser	Ala	Glu	Gln	Pro	Pro			
50				55				60										
Ala Ala Ala Arg Met Gln Leu Pro Ala Gly Ser Tyr Ile Leu Phe Gly																		

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

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

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

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

Glu Gly Ile Val Val Arg Leu Asn Gln Val Lys Ser Asp Arg Glu Arg

325 330 335

Ser Val Thr Pro Val Ala Val Lys Leu Cys Leu Ile Arg Ala Ala Val

340 345 350

Phe Ser Gly Leu Thr Trp Trp Arg Lys Arg Arg Thr Arg Thr Glu Leu

355 360 365

Met Lys Leu Phe Leu Ser Asn Glu Asn Ser Val Lys Arg Ala Leu Pro

370 375 380

Asp Leu Asp Pro Ala Glu Met Leu Glu His Gly Leu Val Val Pro His

385 390 395 400

His Ala Glu Leu Val Ser Gly Met Pro Thr Trp Phe Ala Ala Gly Asp

405 410 415

Ser Phe Phe Val Leu Pro Val Val Ser Val Ser Pro Leu Phe Thr Cys

420 425 430

Asp Leu Glu Thr Val Val Gln Asn Pro Leu Thr Phe Leu Gly Glu Asp

435 440 445

Val His Tyr Pro Pro Val Ala Lys Glu Tyr Cys Val Asp Ala Ser Lys

450 455 460

Gly Ile Ser His Asn Asp Leu Lys Leu Glu Asn Val Leu Leu Ser Ala

465 470 475 480

Asp Gly Arg Val Ala Ile Gly Asp Phe Val Phe Gln Ala Pro Phe Gly

485 490 495

Ala Ser Leu Pro Ile Arg Gly Thr His Leu Tyr Met Asp Pro Asp Ser

500 505 510

Ser Glu Ala Phe Phe Glu Gln Arg Glu Asn Glu Ile Thr Pro His Arg

515 520 525

Asp Ala Trp Ala Thr Gly Val Leu Leu Phe Tyr Leu Trp Cys Gly Val

530 535 540

Phe Pro Phe Gly Leu Gln Asn Val Ala Asn Ala Ser Pro Pro Gln Val

545 550 555 560

Met Arg Val Thr Val Met His Ala Arg Thr Thr Arg Pro Pro Pro Asn

565 570 575
Phe Arg Leu Cys Arg Arg Ile Pro Arg Glu Val Arg Asn Leu Val Thr

580 585 590
Gly Phe Leu Gln Trp Asn Glu Glu Ala Arg Arg Leu Pro Ser Asp Val

595 600 605
Ala Asp Ala Phe Leu Ala Ala Thr Asp Asp Gly Gly Arg Glu Ala Arg

610 615 620
Arg Ile Arg Thr His Gln Phe

625 630

<210> 458

<211> 131

<212> PRT

<213> *Toxoplasma gondii*

<400> 458

Met Thr Leu Lys Ile Arg Met Ile Cys Leu Ala Ala Val Gly Val Leu

1 5 10 15
Ile Gly Gly Val Ala Ile Thr Thr Val Phe Lys Pro Val Ser Pro Glu

20 25 30
Cys Thr Val His Ser Phe Ser Ile Gly Leu Ile Ser Ala Asp Ala Leu

35 40 45
Arg Ile Arg Ala Ser His Ser Ser Ser Lys Gly Glu Glu Gly Asp Gly

50 55 60
Glu Lys His Lys Asp Lys Ser Ser Glu Glu Gly Ala Gly Asp Arg Asp

65 70 75 80
Arg Glu Glu Glu Arg Asp Gly Glu Gly Glu Gly Ser Glu Lys Gly Pro

85 90 95
Gln Pro Ser Pro Ser Gly Lys Pro Leu Gln Arg Arg Asp Ala Gly Tyr

100 105 110
Trp Lys Lys Asn Ser Asp Ser Gly Lys His Glu Arg Val Lys Gly Arg

115 120 125
Lys Arg Lys

130

<210> 459

<211>

363

<212> PRT

<213> *Toxoplasma gondii*

<400> 459

Met Cys Cys Met Leu Val Gly Leu Lys His Trp Glu Tyr Cys Leu Ser

1 5 10 15

Leu Gly Ser Ala Ala Val Trp Tyr Ala Ile Val Ser Phe Cys Cys Ala

20 25 30

Val Trp Gln Leu Ala Ala Val Phe Val His Val Asp Phe Ser Gly Asp

35 40 45

Ile Thr Glu Pro Ile Val Arg Asp Asp Asp Gly Thr Arg Gln Val Val

50 55 60

Leu Gly Leu Met Ser Ile Ser His Ala Gly Ala Ala Ala Leu Asn Phe

65 70 75 80

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

85 90 95

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

100 105 110

Ser Leu Phe Leu Val Gly Val Trp Ser Ile Phe Asp Cys Ser Gln His

115 120 125

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

130 135 140

Ala Leu Leu Ala Trp Pro Ala Ala Val Ile Leu Ala Ser Leu Ala Thr

145 150 155 160

Val Gln Ser Ala Gly Asn Ser Gly Phe Glu Gly Arg Gln Arg Ile Ala

165 170 175

Ser Pro Arg Leu His Lys Pro Asp Asp Gly His Val Ser Asp Ala Trp

180 185 190

Ala Arg Val Gly Thr Trp Thr Val Gly Leu Thr Leu Gly Gln Gly Val

195 200 205

Leu Leu Leu Ser Gly Val Cys Phe Leu Met Ala Ala Lys Thr Leu Arg
 210 215 220
 Ser Phe Trp Asn Leu His Phe Val Glu Ser Tyr Glu Ala Gln Gln Ile
 225 230 235 240
 Gly Trp Ala Phe Met Leu Glu Gly Leu Ile Leu Cys Cys Leu Ala Ala
 245 250 255
 Thr Ala Phe Val Gly Thr Val Leu Thr Ser Thr Phe Ser Leu Leu Val
 260 265 270
 Ala Leu Phe Cys Cys Ile Gly Leu Gly Pro Ile Ala Thr Ile Val Ala
 275 280 285
 Val Trp Trp Asn Val Leu Leu Tyr Arg Trp Lys Val Glu Pro Gly Val
 290 295 300
 Phe Val Gly Met Gln Phe Ser Ile Ile Glu Gln Tyr Val Cys Val Phe
 305 310 315 320
 Cys Cys Trp Ala Ala Cys Arg Thr Leu Thr Gly Phe Ile Ala Ala Lys
 325 330 335
 Thr Lys Gly Arg Phe Gly Ile Asp Ile Pro Lys Asp Asp Ser Pro Glu
 340 345 350
 Ser Glu Ala Leu Val Pro Ser Ala Ser Pro Ala
 355 360
 <210> 460
 <211> 114
 <212> PRT
 <213> Toxoplasma gondii
 <400> 460
 Met Trp Val Asp Gly Ile His Leu Ser Leu Leu Ala Val Gly Met Pro
 1 5 10 15
 Thr Pro Val Arg Phe Arg Ser Met Cys Ser Ser Pro His Ser Cys Cys
 20 25 30
 Phe Val Glu Asn Ser Glu Gln Arg Glu Ile Gln Ser Leu Phe Ser Gly
 35 40 45
 His Gln Leu Leu Leu Leu Gly Ser Cys Phe Cys Asp Ala Ala Glu Ser

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

<210> 461

<211> 233

<212> PRT

<213> Toxoplasma gondii

<400> 461

Met Ala Val Gln Thr Ala Val Asp Asp Pro Glu Ala Pro Ala Glu Asp
 1 5 10 15

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

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

130 135 140

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

Lys Arg Thr Ala Glu Glu Ile Glu Glu Asp Ala Leu Ser Ala Gln Phe
210 215 220
Pro Ser Phe Ala Glu Asp Thr Pro Arg
225 230
<210> 462
<211> 479
<212> PRT
<213> Toxoplasma gondii
<400> 462

Met Ala Thr Val Pro Met Val Ser Leu Ser Ala Ala Arg Phe Thr Leu
1 5 10 15
Ser Phe Leu Phe Phe Gln Leu Cys Leu Ser Arg Leu Phe Arg Pro Glu
20 25 30

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

Val Leu Arg Arg Pro Phe Thr His Ile Arg Arg Val Ser Ser Ala Val

100	105	110	
Arg Arg Tyr Ile Ser Arg Gly Thr Ser Ser Leu Ala Ser Ser Phe Ala			
115	120	125	
Trp Lys Arg Arg Leu Arg Lys Leu Ile Arg Gly Met Ala Lys Asp Leu			
130	135	140	
Lys Gln Asn Arg Val Arg Asp Ala Gln Gln Lys Pro Gly Ser Asp Ala			
145	150	155	160
Val Ala Ser Phe Val Lys Thr Pro His Ala Leu Leu Thr Ser Leu Gly			
165	170	175	
Thr Pro Pro Ala Glu Leu Ala Asn Ala Val Gly Leu Leu Leu Pro Val			
180	185	190	
Gln His Pro Val Pro Met Lys Ser Lys Val Thr Gly Lys Ser Leu Leu			
195	200	205	
Val Ser His Ala Ala Thr Val Gly Val Ser Ser Tyr Gly Ser Val Leu			
210	215	220	
Leu Arg Cys Glu Gly Ser Gly Glu Ser Ala Ser Tyr Phe Leu Glu Ala			
225	230	235	240
Phe Pro Val Leu Arg Gly Ser Arg Glu Ala Ser Val Ser Val Arg Lys			
245	250	255	
Gln Tyr Leu Ala Ala Ile Lys Glu Leu Arg Ala Ala Ser Gly Val Ala			
260	265	270	
Gln Val Gly Val Val Val Asp Leu Leu Leu Leu Lys Arg Val Arg Asn			
275	280	285	
Thr Trp Cys Pro Arg Pro His Glu Ser His Phe Ala Phe Pro Asn Val			
290	295	300	
Phe Leu Lys Arg Ala Val Glu Gly Glu Thr Leu Arg Glu Val Leu Leu			
305	310	315	320
His Ile Ala Ser Thr Ala Ala Thr Asp Thr Pro Gly Thr Gly Pro Ala			
325	330	335	
His Asp Ala Arg Val Ser Leu Thr Glu Gln Val His Lys Leu Ala Arg			
340	345	350	

Ser Ala Ala Glu Leu Gly Ser Arg Gly Gly Lys Ile Asn Ile Asp Thr
355 360 365

Phe Phe Val Thr Leu Asp Gly Ile Val His Leu Gln Pro Val Ser Leu
370 375 380

Val Glu Ser Pro Pro Val His Arg Gly Ser Ala Gly Leu Glu Ser Pro
385 390 395 400

Ile Ala Ala Glu Leu Glu Glu Gly Glu Glu Lys Pro Ser Pro Glu Lys
405 410 415

Arg Met Thr Asp Asp Leu Ala Leu Ala Ile Val Leu Ala Gln Ile Trp
420 425 430

Cys Pro Gln Arg Arg Phe Asp Asp Val Ala Tyr Glu Leu Leu Leu Leu
435 440 445

His Arg Phe Glu Arg Glu Val Thr Glu Glu Phe Phe Glu Arg Cys Ala
450 455 460

Asp Pro Pro Glu Ala Val Gln Val Leu Val Thr Met Leu Ala Phe
465 470 475

<210> 463
<211> 226
<212> PRT
<213> Toxoplasma gondii
<400> 463

Met Asp Leu Trp Gly Arg Asp Ile Ser Arg Val Glu Ala Leu Lys Asp
1 5 10 15

Glu Ile Phe Ser Leu Leu Gln Gln Arg Glu Lys Gln Arg Gly Pro Gly
20 25 30

Gly Ser Ala Ser Ser Ser Gly Arg Ser Ser Ala Leu Leu Arg Gly Lys
35 40 45

Phe Tyr Gln Phe Cys Gln Asp Val Glu His Leu Glu Arg Val Met Lys
50 55 60

Ala Ser Glu Ala Glu Arg Ser Ser Asp Met Ser Ser Ala Asp Trp Arg
65 70 75 80

Arg Arg Arg Glu Gln Met Ser Arg Leu Leu Ala Glu Lys Ser Glu Leu

85 90 95
Gln Leu Ser Phe Ser Arg Ala Phe Ser Ser Thr Glu Asp Asp Leu Cys
100 105 110
Gly Leu Pro Glu Ser Gly Ala Val Trp Val Asp Val Ser Gly Gly Ala

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

180 185 190
Glu Leu Leu Lys Lys Ile Val Asp Arg Gln Ser Thr Ala Cys Leu Leu
195 200 205
Phe Thr Ala Leu Ala Leu Leu Val Val Leu Ile Phe Leu Val Val Ala
210 215 220

Thr Ala

225

<210> 464

<211> 823

<212> PRT

<213> *Toxoplasma gondii*

<400> 464

Met Ser Ala His Thr Glu Thr Met Thr Leu Gly Ile Pro Leu Ser Pro
1 5 10 15

Thr Gly Glu Leu Val Asp Ala Val Pro His Ala Thr Ala Ala Thr Glu
20 25 30
His Leu His Glu His Ala Ile Val Met Ile Ile Ala Ser Ile Ser Phe
35 40 45
Ile Tyr Leu Leu Ser Ala Val Leu Ala Gly Leu Val Gly Leu Leu Pro
50 55 60

Lys Phe Arg Pro Pro Ile Thr Val Val Leu Phe Leu Ala Gly Met Ser
65 70 75 80

Leu Gln Pro Leu Leu Glu Trp Met Gln Asn Arg Val Leu Leu Gln Gly
85 90 95

Ile Arg Leu Ile Gly Asn Val Asp Pro Tyr Leu Ile Phe Phe Ala Leu
100 105 110

Leu Pro Met Cys Leu Tyr Glu Ser Ser Ala Phe Val Asn Tyr His Met
115 120 125

Phe Lys Gln Val Leu Pro Ser Ser Leu Leu Leu Ala Ile Pro Gly Val
130 135 140

Ala Val Asn Ile Gly Leu Val Gly Val Phe Leu Arg Tyr Gly Val Ser
145 150 155 160

Arg Val Tyr Asp Trp Pro Ala Ala Leu Met Thr Ala Ser Ile Val Ser
165 170 175

Ala Thr Asp Pro Val Ala Val Ile Ala Cys Leu Arg Ala Leu Gly Ala
180 185 190

Pro Glu Lys Leu Ser Ser Leu Ile Asp Gly Glu Ser Leu Leu Asn Asp
195 200 205

Gly Ser Ala Val Val Phe Phe Glu Val Phe Arg Ser Ile Val Ile Gly
210 215 220

Thr Tyr Thr Gly Val Gly Ser Ser Val Val Leu Phe Ser Gln Leu Ser
225 230 235 240

Phe Gly Ala Leu Gly Tyr Gly Leu Ala Val Ala Ile Val Leu Tyr Leu
245 250 255

Trp Leu Leu Thr Val Arg Glu Phe Glu Ile Val Gln Val Thr Gly Thr
260 265 270

Ile Ala Ala Val Phe Thr Val Phe Phe Thr Ala Asp His Phe Leu His
275 280 285

Val Ser Gly Val Leu Ala Val Val Thr Leu Gly Ile Phe Met Ala Ala
290 295 300

Lys Gly Ser Thr Ala Leu Gln Arg Ser Ile Gln Lys Leu His His Glu

305 310 315 320
 Ser Val Glu Leu Leu Ser Thr Leu Ser Val Gln Ala Ile Phe Val Cys
 325 330 335

 Gly Gly Val Ile Ala Ser Arg Leu Leu Ile Gln Tyr Ala Asp Thr Trp
 340 345 350
 Gln Glu Trp Val Glu Leu Leu Leu Leu Phe Ala Val Leu Gln Thr Ala
 355 360 365
 Arg Phe Ala Val Val Phe Gly Ser Trp Pro Phe Ile Thr Trp Met Gly
 370 375 380
 Leu Pro Leu Ser Trp Lys Glu Cys Phe Ile Ile Ser Tyr Gly Gly Leu
 385 390 395 400

 Arg Gly Val Ile Cys Leu Ala Leu Gly Leu Val Val Glu Ala Asp Pro
 405 410 415
 Leu Ile Ser Pro Thr Leu Arg Glu His Val Gly Ile Cys Val Ala Gly
 420 425 430
 Thr Val Ile Phe Thr Leu Leu Ile Asn Gly Thr Thr Ala Glu Leu Ala
 435 440 445
 Tyr Thr Arg Leu Arg Leu Tyr Pro Ile Ser Lys Tyr Arg Arg Glu Tyr
 450 455 460

 Leu Asp Ser Val Leu Ala Ser Ile Asp Val Ser Phe Asn Arg Lys Lys
 465 470 475 480
 Asn Glu Leu Lys Asp Tyr Trp Leu Phe Arg Gly Thr Asp Val Val Gln
 485 490 495
 Ala Ala Asn Glu Ala Leu Pro Gln Phe Ser Lys Gly His Leu Asp Val
 500 505 510
 Asn Gly Asn Leu His Ile Pro Thr Lys Ser Phe Arg Glu Val Leu Arg
 515 520 525

 Asn Pro Pro Ser Cys Glu Asn Trp Asn Val Gln Ala Gln Val Thr Gly
 530 535 540
 Leu Ala Lys Leu Glu Ser Arg Asp Phe Gly Val Pro Ser Gln Leu Gly
 545 550 555 560

Asp Trp Thr His Gly Leu Val Ser Thr Ile Lys Asn Val Lys Gln Leu
 565 570 575
 Thr Ser Arg Gln Gln Arg Ser Pro Glu Ser Arg Asp Asp Gln His Asn
 580 585 590

 Pro Glu Glu Val Thr Leu Val Asp Lys Glu Ala Gly Gln Leu Glu Lys
 595 600 605
 Glu Val His Val Leu His Ile Met Phe Ser Ala Met Arg Glu Phe Tyr
 610 615 620
 Ser Gly Met Tyr Lys Arg Ser Asn Ile Gly Gly Thr Ala Cys Leu Leu
 625 630 635 640
 Leu Thr Ser Thr Val Asp Lys Cys His Ser His Leu Asp Ala Gln Leu
 645 650 655

 His Asp Met Thr Thr Asn Lys Lys Ser Arg Lys Asn Ala Asn Asn Thr
 660 665 670
 Asn Val Phe Ser Phe Glu Trp Glu Val Leu Leu Ala Ser Leu Arg Thr
 675 680 685
 Arg Tyr Gly Leu Trp Lys Cys Leu Asn Ala Met Pro Cys Asp Ala Phe
 690 695 700
 Asp Leu Leu Lys Ser Tyr Leu Ile Ser Ile Ile Glu Thr Leu Tyr Ala
 705 710 715 720

 Val Val Glu Ala His Glu Phe Val Asn Gln Ser Asn Arg Lys Glu Met
 725 730 735
 Glu Glu Leu Ile Ser Gln Ala Thr Leu Met Pro Ser Asp Asp Val Val
 740 745 750
 Thr Ser Ala Lys Glu Leu Leu Glu Lys Leu Arg Asn Thr Phe Pro Val
 755 760 765
 Ala Phe Ser Gln Cys Leu Val Ile Ile Ala Ala His Met Leu Leu Asn
 770 775 780

 Ala Lys Gln Lys Val Leu Asp Glu Glu Ile Glu Arg Gly Leu Val Phe
 785 790 795 800
 Pro Glu Asp Ala Asp Lys Leu Asn Glu Ala Leu Ile Glu Gln Arg Met

805 810 815
 Met Leu Glu Arg Ile Ile Arg
 820
 <210> 465
 <211> 1300
 <212> PRT
 <213> Toxoplasma gondii
 <400> 465
 Met Ala Arg Arg Arg Pro Ser Ala Ile Ala Thr Cys Phe Arg Met Ile
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 Leu Ala Phe Phe Leu Ser Phe Thr Phe Ser Ser Gly Ala Asp Ser Leu
 20 25 30
 Leu Ala Pro Ser Thr Thr Gln Ala Arg Arg Leu Gln Ala Arg Ser Gly
 35 40 45
 Asp Asn Ala Leu Ser Asn Gly Gly Arg Leu Pro Asn Gly Glu His Asn
 50 55 60
 Gln Phe Arg Ala Leu Arg Arg Gly Asp Gln Lys Val Glu Lys Asp Ala
 65 70 75 80

 Phe Gly Ala Val Asn Ala Glu Gln Arg Thr Ala Val Ser Gly Ser Lys
 85 90 95
 Phe Glu Arg Glu Lys Trp Thr Pro Ile Ser Phe Thr Glu Lys Gly Leu
 100 105 110
 Phe Asp Val Ile Asn Pro Thr Ile Ala Gly Asp Glu Lys Asp Glu Leu
 115 120 125
 Asn Trp Ser Thr His Gln Arg Ile Glu Gly Arg Gly Thr Glu Pro Thr
 130 135 140

 Arg Ser Asp Ser Gln Gln Arg Asp Gln Ala Lys Pro Arg Ala Leu Glu
 145 150 155 160
 Arg Arg Glu Glu Ala Gly Gln Pro Pro Arg Asp Glu His Gln Asp Thr
 165 170 175
 Asp Val Glu Gln Ala Pro Leu Ile Lys Glu Asp Glu Ser Asp Ser Pro
 180 185 190

Ser Val Glu Glu Pro Arg Ala Gln Pro Pro Glu Asn Lys Glu Asp Ala
195 200 205

Ile Thr Lys Pro Trp Asp Ala Asp Trp Asn Pro Trp Lys Phe Leu Asp
210 215 220

Glu Asn Pro Leu Pro Ile Tyr Arg Asp Asp Trp Asp Glu Glu Glu Asp
225 230 235 240

Asn Arg Asp Asp Ala Asp His Asp Pro Gly Phe Ala Glu Pro Pro Asn
245 250 255

Ser Pro Pro Ala Gly Gly Val Pro Lys Arg Glu Asp Asp Asn Ala Pro
260 265 270

Asp Tyr Pro Gly Asp Asp Thr Ala Ser Ser Pro Pro Tyr Asp Met Arg
275 280 285

Pro Asn Pro Glu Asp His Ser Arg Thr Gln Pro Gly Glu Tyr Gly Gly
290 295 300

Gly Val Asp Asp Glu Gly Glu Leu Pro Asp Glu Asp Thr Ala Lys Gly
305 310 315 320

Met Pro Arg Ser Ser Thr Pro Pro Pro Asn Glu Glu Ser Ile Pro Ala
325 330 335

Val Pro Thr Glu Ser Glu Trp Ser Gly Ser Gly Val Tyr Glu Gly Ile
340 345 350

Ala Ile Thr Val Asn Ala Arg Trp Ile Asp Thr Arg Thr Ile Gly Glu
355 360 365

Gly Gly Ile Gln Leu Gln His Gln Pro Thr Val Phe Pro Ala Pro Pro
370 375 380

Val Leu Arg Lys Val Gly Leu Lys Ser Lys Trp Lys His Thr Ile Lys
385 390 395 400

Ile Phe Val Arg Thr Thr Gly Ala Lys Phe Val Pro Ala Arg Arg Gln
405 410 415

Val Phe Val Pro Leu Asp Glu Thr Pro Thr Ser Ser Ser Thr Leu Leu
420 425 430

Pro Trp Trp Ala Asn Trp Ser Ile Ser Ala Val Lys Ala Ala Ser Ala

435 440 445
 Thr Thr Ser Ser Val Ala Ala Phe Leu Phe Gly Thr Gly Arg Ala Val
 450 455 460

 Asp Gly Gly Glu Gly Ile Ser Glu Gly Lys Gly Pro Thr Ile Thr Ser
 465 470 475 480
 Ile Lys Asn Met Leu Lys Gln Tyr Lys Arg Phe Lys Arg Lys His Pro
 485 490 495
 Gly Lys Pro Gly Glu Leu Val Ile Asp Leu Cys Lys Asp Glu Glu Asp
 500 505 510
 Ala Ser Ser Ala Ala Arg Thr Pro Ser Pro Ser Ser Ala Ser Glu Ser
 515 520 525

 Ser Ser Asp Gly Gly Val Trp Glu Ser Leu Glu Ser Pro Ala Pro Ala
 530 535 540
 Pro Met Pro Ser Leu Thr Ser Ser Ser Pro Ser Gly Ser Ser Pro Phe
 545 550 555 560
 Val Val Lys Gln Ser Pro Glu Gly Asp Leu Lys Thr Glu Ser Glu Gly
 565 570 575
 Pro Ala Arg Leu Thr Thr Pro Ser Glu Lys Arg Pro Ala Lys Ala Lys
 580 585 590

 Pro Gln Asn Thr Lys Lys Lys Thr Lys Arg Arg Lys Arg Thr Val Ala
 595 600 605
 Asn Ala Tyr Asn Ile Leu Gln Thr Gln Glu Gly Leu Ala Leu Val Asn
 610 615 620
 Lys Ile Arg Asp Thr Met Ala Glu Ile Phe Ser Ser Pro Ser Thr Ser
 625 630 635 640
 Val Gln Val Leu Thr Ser Thr Gly His Leu Val Ile Thr Leu Pro Ser
 645 650 655

 Glu Gly Val Asp Arg Tyr Lys Leu Lys Gly Phe Leu Gln Thr Val Gln
 660 665 670
 Glu Thr Phe Gly Asp Asn Ile Gln Gln Trp Ser Phe Ser Glu Ile Val
 675 680 685

Gln Leu Arg Ser Glu Val Pro Glu Pro His Ile Pro Pro Arg Ala Gln
690 695 700

Met Ala Ala Lys Met Glu Ser Leu Ser Gly Lys Ser Thr Lys Thr Ser
705 710 715 720

Lys Lys Leu Asn Gly Arg Ser Leu Pro Ala Ser Met Ser Glu Thr Thr
725 730 735

Ser Lys Lys Thr Pro Phe Glu Ala Ser Met Pro Thr Asp Ser Ala Leu
740 745 750

Glu Ser Lys Leu Tyr Gly Met His Met Ile Thr Ala Thr His Ala Trp
755 760 765

Ile His Gly Glu Ala Gly Asp Gly Thr Val Val Ala Val Val Asp Ser
770 775 780

Gly Ile Ser Arg His His Asp Leu Asp Cys Asn Leu Trp Gln Asn Pro
785 790 795 800

His Glu Gln Gln Asp Gly Arg Asp Asp Asp Gly Asn Gly Leu Ile Asp
805 810 815

Asp Asn His Gly Tyr Asp Phe Gln Glu Asn Lys Ser Glu Pro Glu Asp
820 825 830

Glu Asn Gly His Gly Thr His Val Ala Gly Ile Ile Gly Ala Cys Val
835 840 845

Asn Gly Gly Gly Val Val Gly Gly Ala Pro Lys Thr Gln Leu Met Ala
850 855 860

Leu Arg Phe Ile Asp Lys Gly Gly Gln Gly Ser Met Ala Asn Ser Ile
865 870 875 880

Arg Ala Leu Asn Tyr Ala Ile Asp His Glu Val Gln Val Ile Asn Asn
885 890 895

Ser Trp Gly Gly Pro Gln Ser Thr Thr Val Leu Arg Arg Leu Val His
900 905 910

Met Ser Ala Val Ala Arg Asn Gly Lys Gly Ile Leu Leu Ile Asn Ala
915 920 925

Ala Gly Asn Glu Ser Ser Asn Asn Asp Val Asn Pro Ser Tyr Pro Ala

930	935	940	
Asn Trp Asp Gln Asp Asn Thr Ile Ser Val Ala Ala Ile Asp Ile Asn			
945	950	955	960
Gly Asp Leu Ala Asp Phe Ser Asn Tyr Gly Lys Ser Ser Val Asp Met			
	965	970	975
Ala Ala Pro Gly Val Lys Ile Tyr Ser Thr Lys Pro Gly Gly Asp Tyr			
	980	985	990
Gln His Met Ser Gly Thr Ser Met Ala Thr Pro His Val Ser Ala Val			
	995	1000	1005
Ala Ala Leu Val Phe Gly Ala Phe Leu Arg Asn Gly Tyr Asp Ala			
	1010	1015	1020
Pro Ala Ala Glu Val Lys Asp Ile Ile Arg Ile Thr Ala Ser Pro			
	1025	1030	1035
Val Glu Gln Leu Gln Gly Val Thr Arg Trp Gly Ser Ile Pro His			
	1040	1045	1050
Ala Arg Asp Ala Val Leu Met Ala Arg Met Gly Gly Met Phe Leu			
	1055	1060	1065
Gln Ala Lys Cys Glu Asp Met Val Phe Glu Leu Asp Ala Gly Ser			
	1070	1075	1080
Ala His Val Val Asp Leu His Leu Met Pro Tyr Arg Gln Gly Asn			
	1085	1090	1095
Tyr Thr Ala Asp Leu Thr Phe Asp Val Phe Thr Glu Asp Gly Tyr			
	1100	1105	1110
Arg Leu Asp Gln Ile Lys Val Pro Val Lys Leu Ala Ile Ser Ala			
	1115	1120	1125
Glu Pro Arg Gln Gly Asn Ser Asp Ser Leu Ala Ala Ala Ala Phe			
	1130	1135	1140
Ser Ser Val Val Ser Thr Phe Ala Ala His Pro Thr Glu Gly Phe			
	1145	1150	1155
Glu Glu Leu Cys Arg Leu Gln Ala Lys Ile His Val Val Gln Glu			
	1160	1165	1170

Met Ser Thr Ala Met Ile Val Ile Ile Cys Leu Gly Val Ile Ala
1175 1180 1185

Ala Ile Ser Val Leu Val Leu Val Tyr Cys Cys Ser Arg Asn Gly
1190 1195 1200

Gln Arg Arg Ser Asp Ala Ala Lys Arg Arg Arg Glu Ser Val Arg
1205 1210 1215

Asp Ser Ala Gly Glu Glu Arg Arg Asn Gln Leu Thr Glu Thr His
1220 1225 1230

Arg Ala Arg Lys His Ala Asp Thr Ser Ala Glu Ala Asn Lys Glu
1235 1240 1245

Phe Leu Asn Cys Ser Ser Arg Ala Glu Asp Asp Ala Asn Asp Arg
1250 1255 1260

Ser Glu Thr His Thr Asn Pro Thr Asp Pro Leu Cys Arg Lys Glu
1265 1270 1275

His Val Phe Leu Pro Ala Thr Thr Leu Glu Gln Phe Ala Leu Ser
1280 1285 1290

Thr Pro Asn Glu Asn Glu Ser
1295 1300

<210> 466

<211> 243

<212> PRT

<213> Toxoplasma gondii

<400> 466

Met Ala Gln Tyr Lys Ser Arg Pro Leu Ala Ala Val Leu Leu Leu Ile
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Thr Val Gly Ser Leu Leu Thr Ala Ser Glu Ser Val Gln Leu Ser Glu
20 25 30

Gly Met Lys Arg Leu Ser Met Arg Gly Arg Ser Pro Ser Pro Lys Thr
35 40 45

Gly Arg Phe Glu Ser Gly Asp Glu Gly Thr Ser Thr Met Ser Pro Ser
50 55 60

Val Ala Ala Arg Gln Gln Glu Leu Gly Leu Leu Arg Pro Glu Glu Arg

65 70 75 80
 Leu Ile Ala Gly Gln Ala Lys Ala Ala Ala Leu Gln Thr Val His Gln
 85 90 95

Leu Gly Ala Val Val Leu Thr Pro Glu Gln Ala Lys Ala Ala Leu Leu
 100 105 110
 Asp Glu Ile Leu Arg Ala Thr Gln Asn Leu Asp Leu Lys Lys Tyr Glu
 115 120 125
 Asn Leu Asn Thr Glu Gln Gln Lys Ala Tyr Glu Gln Val Gln Lys Asp
 130 135 140
 Leu Ser Leu Leu Ser Pro Glu Thr Lys Ala Leu Leu Ile Glu Asn His
 145 150 155 160

Arg Lys Glu Lys Ser Leu Leu Glu Gln Ala Lys Arg Leu Phe Arg Lys
 165 170 175
 Arg His Tyr His Val Thr Arg Gln Ala Ala Leu Ala Gly Gln Ile Leu
 180 185 190
 Asn Glu Gln Arg Asp Ala Ser Gly Ala Leu Gln Ser Gly Ala Val Lys
 195 200 205
 Ala Ala Ile Arg Lys Ala Asn Glu Gln Tyr Asn Val Ala Glu Glu Asp
 210 215 220

Lys Asn Phe Asn Glu Glu Gln His Ala Ala Gln Leu Lys Lys Val Gly
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<210> 467

<211> 3262

<212> DNA

<213> Toxoplasma gondii

<400> 467

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<211> 1849
<212> DNA
<213> Toxoplasma gondii
<400> 468
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cttgacccaa gcagatgata tctttcctgc tggttgagca aagctaagcg ctgcaggaac 180

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gccgcaggct taggcaaagg agacgaggag tgagacagcc agctgttcct ggtaggtca 300

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ggcgtacagt gcgtatagt gacggaatg gatttggaag gaaaggagtc 720

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cgggtcagaa caactggata acagacaatt ttgcggaac ctacgaacga gacaaagagc 960

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tctgctgcat aaacgtgcc taaaattctg gcgttgctgt caagtcгааg gctctctagg 1560

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cccctgagcg ttaagtctga gtgtgactac agaagctaga ctgagtcgaa ctgagggaga 1800

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<210> 469

<211> 4139

<212> DNA

<213> *Toxoplasma gondii*

<400> 469

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cggactctga acttccgcgt cgacgccgca ggtcgtctgc cgcggctcga cgcgtgagcc	300
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<213> Toxoplasma gondii

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<212> DNA

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<211> 3721

<212> DNA

<213> Toxoplasma gondii

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<213> *Toxoplasma gondii*

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<211> 4124

<212> DNA

<213> *Toxoplasma gondii*

<400> 492

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<210> 493

<211> 1221

<212> DNA

<213> *Toxoplasma gondii*

<400> 493

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<210> 494

<211> 1922

<212> DNA

<213> Toxoplasma gondii

<400> 494

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<210> 495
<211> 2979
<212> DNA
<213> *Toxoplasma gondii*

<400> 495

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<211> 1717

<212> DNA

<213> *Toxoplasma gondii*

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<400> 506

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<211> 2059

<212> DNA

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<211> 2415

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<213> Toxoplasma gondii

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<213> Toxoplasma gondii

<400> 522

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<212> DNA

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<211> 3215

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<211> 1781

<212> DNA

<213> Toxoplasma gondii

<400> 525

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 <213> Toxoplasma gondii
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<400> 527

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<212> DNA

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<400> 528

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<212> DNA

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<211> 2005

<212> DNA

<213> Toxoplasma gondii

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<400> 569

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<210> 573
<211> 1947
<212> DNA
<213> Toxoplasma gondii
<400> 573

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<210> 574

<211> 4739

<212> DNA

<213> Toxoplasma gondii

<400> 574

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<211> 1918

<212> DNA

<213> *Toxoplasma gondii*

<400> 575

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 <211> 3078
 <212> DNA
 <213> Toxoplasma gondii

<400> 576

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<210> 579

<211> 1278

<212> DNA

<213> Toxoplasma gondii

<400> 579

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<211> 1833

<212> DNA

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<213> Toxoplasma gondii

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<400> 591

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<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

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<400> 624

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<211> 1776

<212> DNA

<213> *Toxoplasma gondii*

<400> 629

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<211> 3463

<212> DNA

<213> Toxoplasma gondii

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<211> 4316

<212> DNA

<213> Toxoplasma gondii

<400> 631

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<210> 639

<211> 3131

<212> DNA

<213> *Toxoplasma gondii*

<400> 639

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 <211> 3022
 <212> DNA
 <213> *Toxoplasma gondii*
 <400> 640

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<210> 641

<211> 2668

<212> DNA

<213> *Toxoplasma gondii*

<400> 641

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<211> 1508
<212> DNA

<213> Toxoplasma gondii

<400> 642

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<210> 643

<211> 1742

<212> DNA

<213> Toxoplasma gondii

<400> 643

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<211> 2104

<212> DNA

<213> *Toxoplasma gondii*

<400> 661

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<211> 2218
<212> DNA
<213> Toxoplasma gondii
<400> 662

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<210> 663

<211> 1096

<212> DNA

<213> *Toxoplasma gondii*

<400> 663

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<210> 664

<211> 1426

<212> DNA

<213> *Toxoplasma gondii*

<400> 664

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<211> 2140
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<213> Toxoplasma gondii
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<211> 2566

<212> DNA

<213> Toxoplasma gondii

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<210> 685

<211> 4058

<212> DNA

<213> *Toxoplasma gondii*

<400> 685

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<210> 686

<211> 1848

<212> DNA

<213> *Toxoplasma gondii*

<400> 686

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<210> 687

<211> 1504

<212> DNA

<213> Toxoplasma gondii

<400> 687

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<211> 1884
<212> DNA

<213> Toxoplasma gondii

<400> 689

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<212> DNA

<213> *Toxoplasma gondii*

<400> 704

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<211> 1690

<212> DNA

<213> Toxoplasma gondii

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 <212> DNA

<213> Toxoplasma gondii

<400> 742

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<211> 3479

<212> DNA

<213> Toxoplasma gondii

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<211> 1728

<212> DNA

<213> *Toxoplasma gondii*

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<213> Toxoplasma gondii

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<210> 767

<211> 1881

<212> DNA

<213> Toxoplasma gondii

<400> 767

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<210> 768
<211> 2019
<212> DNA
<213> *Toxoplasma gondii*

<400> 768

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<210> 769

<211> 2612

<212> DNA

<213> Toxoplasma gondii

<400> 769

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<211> 2067

<212> DNA

<213> *Toxoplasma gondii*

<400> 770

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 <400> 771

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<213> *Toxoplasma gondii*

<400> 793

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<212> DNA

<213> *Toxoplasma gondii*

<400> 831

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<211> 2235

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<400> 832

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<210> 842

<211> 4217

<212> DNA

<213> Toxoplasma gondii

<400> 842

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<210> 843

<211> 2594

<212> DNA

<213> Toxoplasma gondii

<400> 843

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<210> 844

<211> 1665

<212> DNA

<213> *Toxoplasma gondii*

<400> 844

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<210> 845

<211> 3990

<212> DNA

<213> *Toxoplasma gondii*

<400> 845

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<210> 862

<211> 2370

<212> DNA

<213> Toxoplasma gondii

<400> 862

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<210> 863
<211> 2219
<212> DNA
<213> Toxoplasma gondii
<400> 863

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<210> 864

<211> 1591

<212> DNA

<213> Toxoplasma gondii

<400> 864

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<210> 865
<211> 1429
<212> DNA
<213> *Toxoplasma gondii*

<400> 865

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<210> 867

<211> 4444

<212> DNA

<213> *Toxoplasma gondii*

<400> 867

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<400> 887

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<212> DNA
<213> *Toxoplasma gondii*

<400> 914

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<211> 1983

<212> DNA

<213> Toxoplasma gondii

<400> 915

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<210> 916

<211> 1905

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> Toxoplasma gondii

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<211> 2525

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<213> *Toxoplasma gondii*

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<400> 941

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<212> DNA
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<211> 1678

<212> DNA

<213> Toxoplasma gondii

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<210> 945

<211> 2771

<212> DNA

<213> *Toxoplasma gondii*

<400> 945

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<211> 1932

<212> DNA

<213> Toxoplasma gondii

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<211> 2484

<212> DNA

<213> Toxoplasma gondii

<400> 961

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<210> 962

<211> 1970

<212> DNA

<213> *Toxoplasma gondii*

<400> 962

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<211> 1982

<212> DNA

<213> *Toxoplasma gondii*

<400> 963

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<212> DNA

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<400> 965

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<211> 2250

<212> DNA

<213> Toxoplasma gondii

<400> 966

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<210> 967

<211> 2271

<212> DNA

<213> Toxoplasma gondii

<400> 967

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<210> 968

<211> 1607

<212> DNA

<213> Toxoplasma gondii

<400> 968

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<212> DNA
<213> Toxoplasma gondii
<400> 969

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<212> DNA
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<400> 970

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<210> 971

<211> 4117

<212> DNA

<213> *Toxoplasma gondii*

<400> 971

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<211> 4830

<212> DNA

<213> Toxoplasma gondii

<400> 972

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<211> 2173

<212> DNA

<213> Toxoplasma gondii

<400> 973

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

<400> 975

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<212> DNA

<213> *Toxoplasma gondii*

<400> 976

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<212> DNA
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<400> 977

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<211> 3612

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<211> 3024

<212> DNA

<213> *Toxoplasma gondii*

<400> 990

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<211> 1734

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

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<211> 2202

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<213> *Toxoplasma gondii*

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<211> 2881

<212> DNA

<213> *Toxoplasma gondii*

<400> 1019

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<210> 1027

<211> 4364

<212> DNA

<213> Toxoplasma gondii

<400> 1027

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 <212> DNA

<213> *Toxoplasma gondii*

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<211> 3024

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

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<211> 1273

<212> DNA

<213> Toxoplasma gondii

<400> 1060

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<211> 1857

<212> DNA

<213> Toxoplasma gondii

<400> 1061

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<211> 1774
<212> DNA

<213> Toxoplasma gondii

<400> 1062

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<210> 1063

<211> 1695

<212> DNA

<213> Toxoplasma gondii

<400> 1063

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<213> Toxoplasma gondii
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<211> 1974
<212> DNA

<213> Toxoplasma gondii

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<211> 2284

<212> DNA

<213> Toxoplasma gondii

<400> 1066

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<211> 1956
<212> DNA
<213> Toxoplasma gondii
<400> 1067

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<210> 1068

<211> 4026

<212> DNA

<213> Toxoplasma gondii

<400> 1068

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<211> 2776

<212> DNA

<213> *Toxoplasma gondii*

<400> 1069

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<211> 4905

<212> DNA

<213> *Toxoplasma gondii*

<400> 1070

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<213> Toxoplasma gondii
<400> 1072

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<211> 2320

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<213> *Toxoplasma gondii*

<400> 1073

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<211> 2687

<212> DNA

<213> Toxoplasma gondii

<400> 1074

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<400> 1082

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 <211> 2956
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<213> Toxoplasma gondii

<400> 1083

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<211> 3680

<212> DNA

<213> Toxoplasma gondii

<400> 1084

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<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

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<211> 1487

<212> DNA

<213> *Toxoplasma gondii*

<400> 1087

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<211> 1835

<212> DNA

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<213> Toxoplasma gondii

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<212> DNA

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<211> 3334

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1477

<212> DNA

<213> Toxoplasma gondii

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<211> 3544

<212> DNA

<213> Toxoplasma gondii

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<211> 2431

<212> DNA

<213> Toxoplasma gondii

<400> 1113

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<211> 1929

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<213> Toxoplasma gondii

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<400> 1115

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<212> DNA
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<400> 1116

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<211> 1281

<212> DNA

<213> *Toxoplasma gondii*

<400> 1117

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<211> 1223

<212> DNA

<213> Toxoplasma gondii

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<211> 2094

<212> DNA

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<211> 2894

<212> DNA

<213> *Toxoplasma gondii*

<400> 1132

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<211> 2001

<212> DNA

<213> *Toxoplasma gondii*

<400> 1133

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<211> 2384
<212> DNA
<213> Toxoplasma gondii
<400> 1134

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<211> 1918

<212> DNA

<213> Toxoplasma gondii

<400> 1135

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<213> *Toxoplasma gondii*

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<211> 3549

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<213> Toxoplasma gondii

<400> 1152

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<213> *Toxoplasma gondii*

<400> 1153

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<211> 4355

<212> DNA

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<400> 1154

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<210> 1166

<211> 1625

<212> DNA

<213> Toxoplasma gondii

<400> 1166

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<210> 1167

<211> 629

<212> DNA

<213> Toxoplasma gondii

<400> 1167

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<210> 1168

<211> 1977

<212> DNA

<213> Toxoplasma gondii

<400> 1168

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<210> 1169

<211> 1742

<212> DNA

<213> Toxoplasma gondii

<400> 1169

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<210> 1170

<211> 4194

<212> DNA

<213> *Toxoplasma gondii*

<400> 1170

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<210> 1171
<211> 2142
<212> DNA
<213> *Toxoplasma gondii*
<400> 1171

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<211> 2660

<212> DNA

<213> Toxoplasma gondii

<400> 1172

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<210> 1173

<211> 3582

<212> DNA

<213> *Toxoplasma gondii*

<400> 1173

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<211> 1134

<212> DNA

<213> Toxoplasma gondii

<400> 1174

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<211> 1427
<212> DNA
<213> Toxoplasma gondii
<400> 1175

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2162

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<211> 2352

<212> DNA

<213> *Toxoplasma gondii*

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<211> 2878

<212> DNA

<213> Toxoplasma gondii

<400> 1187

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<212> DNA

<213> Toxoplasma gondii

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<211> 2444
<212> DNA
<213> Toxoplasma gondii
<400> 1194

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<211> 1934

<212> DNA

<213> *Toxoplasma gondii*

<400> 1195

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<212> DNA
<213> Toxoplasma gondii

<400> 1196

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 <211> 1572

<212> DNA

<213> *Toxoplasma gondii*

<400> 1197

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<211> 2118

<212> DNA

<213> Toxoplasma gondii

<400> 1217

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<211> 2851

<212> DNA

<213> Toxoplasma gondii

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<211> 2008

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

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<210> 1230

<211> 4233

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> Toxoplasma gondii

<400> 1231

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<211> 2345

<212> DNA

<213> *Toxoplasma gondii*

<400> 1233

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<211> 2387

<212> DNA

<213> Toxoplasma gondii

<400> 1234

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 <400> 1236

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 <213> Toxoplasma gondii

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<211> 1716

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<213> Toxoplasma gondii

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<212> DNA
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<211> 811

<212> DNA

<213> Toxoplasma gondii

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<211> 4564

<212> DNA

<213> *Toxoplasma gondii*

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<213> Toxoplasma gondii

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<211> 4615

<212> DNA

<213> Toxoplasma gondii

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<211> 2362

<212> DNA

<213> *Toxoplasma gondii*

<400> 1252

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<211> 4611

<212> DNA

<213> Toxoplasma gondii

<400> 1253

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<211> 1793

<212> DNA

<213> Toxoplasma gondii

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<211> 2219

<212> DNA

<213> Toxoplasma gondii

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<210> 1271

<211> 3409

<212> DNA

<213> *Toxoplasma gondii*

<400> 1271

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<211> 1762

<212> DNA

<213> Toxoplasma gondii

<400> 1272

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<210> 1273
 <211> 1764
 <212> DNA
 <213> Toxoplasma gondii
 <400> 1273

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<210> 1274

<211> 2072

<212> DNA

<213> *Toxoplasma gondii*

<400> 1274

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<210> 1275

<211> 2370

<212> DNA

<213> *Toxoplasma gondii*

<400> 1275

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<211> 3550

<212> DNA

<213> *Toxoplasma gondii*

<400> 1276

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<213> Toxoplasma gondii

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<400> 1288

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<211> 1894
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<210> 1291

<211> 2339

<212> DNA

<213> Toxoplasma gondii

<400> 1291

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<211> 4574

<212> DNA

<213> Toxoplasma gondii

<400> 1307

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<213> Toxoplasma gondii

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<212> DNA

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<213> Toxoplasma gondii

<400> 1333

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<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

<400> 1341

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<211> 3322

<212> DNA

<213> Toxoplasma gondii

<400> 1342

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<211> 1653

<212> DNA

<213> Toxoplasma gondii

<400> 1343

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<213> Toxoplasma gondii
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<400> 1374

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<211> 1689

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<211> 3843

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

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<211> 2264

<212> DNA

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<400> 1396

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<211> 2624

<212> DNA

<213> Toxoplasma gondii

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<211> 4276

<212> DNA

<213> Toxoplasma gondii

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<211> 1581

<212> DNA

<213> Toxoplasma gondii

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<211> 1521

<212> DNA

<213> *Toxoplasma gondii*

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<211> 2457

<212> DNA

<213> *Toxoplasma gondii*

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<211> 2166

<212> DNA

<213> Toxoplasma gondii

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<211> 2221

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<213> Toxoplasma gondii

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<211> 2565

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

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<211> 3888

<212> DNA

<213> Toxoplasma gondii

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<211> 1951

<212> DNA

<213> Toxoplasma gondii

<400> 1474

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 <212> DNA
 <213> Toxoplasma gondii
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<211> 2022

<212> DNA

<213> *Toxoplasma gondii*

<400> 1476

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<211> 1966

<212> DNA

<213> Toxoplasma gondii

<400> 1477

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<213> Toxoplasma gondii

<400> 1484

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

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<400> 1493

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<212> DNA

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<210> 1497

<211> 1800

<212> DNA

<213> *Toxoplasma gondii*

<400> 1497

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<211> 1494

<212> DNA

<213> *Toxoplasma gondii*

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<211> 3271

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<213> Toxoplasma gondii

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<400> 1526

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<211> 2098

<212> DNA

<213> Toxoplasma gondii

<400> 1527

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<211> 3997

<212> DNA

<213> Toxoplasma gondii

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 <213> Toxoplasma gondii
 <400> 1529

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<211> 1598

<212> DNA

<213> Toxoplasma gondii

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<211> 2057
<212> DNA
<213> Toxoplasma gondii
<400> 1531

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<211> 2487

<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii
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<211> 1980

<212> DNA

<213> Toxoplasma gondii

<400> 1535

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<211> 1903

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<213> *Toxoplasma gondii*

<400> 1551

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<211> 4205

<212> DNA

<213> Toxoplasma gondii

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<211> 3380

<212> DNA

<213> Toxoplasma gondii

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<211> 2347

<212> DNA

<213> Toxoplasma gondii

<400> 1568

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<211> 4372

<212> DNA

<213> Toxoplasma gondii

<400> 1570

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<211> 1936

<212> DNA

<213> Toxoplasma gondii

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<211> 2097

<212> DNA

<213> Toxoplasma gondii

<400> 1572

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<400> 1576

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<210> 1577

<211> 1649

<212> DNA

<213> Toxoplasma gondii

<400> 1577

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<211> 1674

<212> DNA

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<400> 1579

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<400> 1581

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<212> DNA

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<212> DNA

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<210> 1589

<211> 1812

<212> DNA

<213> *Toxoplasma gondii*

<400> 1589

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<212> DNA

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<211> 2816

<212> DNA

<213> *Toxoplasma gondii*

<400> 1599

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<211> 2058

<212> DNA

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<210> 1609

<211> 2945

<212> DNA

<213> Toxoplasma gondii

<400> 1609

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<210> 1610

<211> 2096

<212> DNA

<213> *Toxoplasma gondii*

<400> 1610

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<210> 1611
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<212> DNA
<213> *Toxoplasma gondii*

<400> 1611

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<211> 1583

<212> DNA

<213> Toxoplasma gondii

<400> 1612

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<210> 1613
<211> 2394
<212> DNA
<213> Toxoplasma gondii
<400> 1613

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<211> 3280

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> Toxoplasma gondii

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<400> 1625

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<211> 1688

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<212> DNA

<213> Toxoplasma gondii

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<211> 4212

<212> DNA

<213> *Toxoplasma gondii*

<400> 1647

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<211> 2304

<212> DNA

<213> Toxoplasma gondii

<400> 1648

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<211> 1861

<212> DNA

<213> *Toxoplasma gondii*

<400> 1649

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<210> 1650

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<212> DNA

<213> *Toxoplasma gondii*

<400> 1650

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<210> 1651

<211> 2715

<212> DNA

<213> Toxoplasma gondii

<400> 1651

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<210> 1652

<211> 1479

<212> DNA

<213> Toxoplasma gondii

<400> 1652

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<210> 1653

<211> 2133

<212> DNA

<213> *Toxoplasma gondii*

<400> 1653

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<210> 1654

<211> 3304

<212> DNA

<213> Toxoplasma gondii

<400> 1654

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<211> 4881

<212> DNA

<213> *Toxoplasma gondii*

<400> 1655

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<400> 1675

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 <212> DNA
 <213> Toxoplasma gondii
 <400> 1676

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<212> DNA

<213> Toxoplasma gondii

<400> 1677

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<210> 1678

<211> 1608

<212> DNA

<213> *Toxoplasma gondii*

<400> 1678

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 <213> *Toxoplasma gondii*

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<212> DNA

<213> *Toxoplasma gondii*

<400> 1702

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<212> DNA

<213> *Toxoplasma gondii*

<400> 1703

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<213> Toxoplasma gondii

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<211> 4858

<212> DNA

<213> *Toxoplasma gondii*

<400> 1706

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<211> 3448

<212> DNA

<213> Toxoplasma gondii

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<211> 2386

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<213> Toxoplasma gondii

<400> 1709

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<211> 1875

<212> DNA

<213> *Toxoplasma gondii*

<400> 1714

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<210> 1715

<211> 2030

<212> DNA

<213> Toxoplasma gondii

<400> 1715

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<211> 2360
<212> DNA
<213> *Toxoplasma gondii*

<400> 1716

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<211> 3342

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 <400> 1718

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<211> 2016

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<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

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<211> 1563

<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

<400> 1756

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<210> 1758

<211> 2406

<212> DNA

<213> Toxoplasma gondii

<400> 1758

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<213> Toxoplasma gondii

<400> 1759

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<211> 4434

<212> DNA

<213> Toxoplasma gondii

<400> 1760

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<212> DNA

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<211> 2183

<212> DNA

<213> Toxoplasma gondii

<400> 1775

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<211> 1574

<212> DNA

<213> *Toxoplasma gondii*

<400> 1777

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<211> 3063

<212> DNA

<213> Toxoplasma gondii

<400> 1778

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 <213> *Toxoplasma gondii*

<400> 1780

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<212> DNA

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<211> 3242

<212> DNA

<213> Toxoplasma gondii

<400> 1820

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<211> 1574

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<211> 1837

<212> DNA

<213> *Toxoplasma gondii*

<400> 1822

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<210> 1823

<211> 2386

<212> DNA

<213> Toxoplasma gondii

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<211> 4789

<212> DNA

<213> Toxoplasma gondii

<400> 1825

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<210> 1826

<211> 4984

<212> DNA

<213> Toxoplasma gondii

<400> 1826

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<211> 1623

<212> DNA

<213> Toxoplasma gondii

<400> 1827

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<213> *Toxoplasma gondii*

<400> 1829

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<211> 5008

<212> DNA

<213> Toxoplasma gondii

<400> 1830

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<211> 4250

<212> DNA

<213> Toxoplasma gondii

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<211> 1926
<212> DNA
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<400> 1840

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<211> 1495

<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii
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<212> DNA

<213> Toxoplasma gondii

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<210> 1861

<211> 2938

<212> DNA

<213> *Toxoplasma gondii*

<400> 1861

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<210> 1862

<211> 1447

<212> DNA

<213> *Toxoplasma gondii*

<400> 1862

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<210> 1863

<211> 2182

<212> DNA

<213> *Toxoplasma gondii*

<400> 1863

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<210> 1864

<211> 2396

<212> DNA

<213> Toxoplasma gondii

<400> 1864

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<211> 946
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<213> Toxoplasma gondii
<400> 1875

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<210> 1876

<211> 2689

<212> DNA

<213> Toxoplasma gondii

<400> 1876

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<210> 1877

<211> 1925

<212> DNA

<213> Toxoplasma gondii

<400> 1877

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<210> 1878

<211> 4701

<212> DNA

<213> *Toxoplasma gondii*

<400> 1878

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<211> 4190

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1647

<212> DNA

<213> Toxoplasma gondii

<400> 1881

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<211> 3847

<212> DNA

<213> Toxoplasma gondii

<400> 1882

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<213> *Toxoplasma gondii*

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<211> 4967

<212> DNA

<213> Toxoplasma gondii

<400> 1887

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<211> 4865

<212> DNA

<213> *Toxoplasma gondii*

<400> 1888

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<210> 1895

<211> 1941

<212> DNA

<213> *Toxoplasma gondii*

<400> 1895

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<210> 1896

<211> 2142

<212> DNA

<213> Toxoplasma gondii

<400> 1896

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 <212> DNA
 <213> Toxoplasma gondii
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<210> 1898
<211> 1740
<212> DNA
<213> *Toxoplasma gondii*
<400> 1898

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<210> 1899

<211> 3827

<212> DNA

<213> Toxoplasma gondii

<400> 1899

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<211> 3101

<212> DNA

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<211> 2800

<212> DNA

<213> *Toxoplasma gondii*

<400> 1904

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<212> DNA

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<212> DNA

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<211> 4719

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<400> 1917

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<211> 4683

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<213> Toxoplasma gondii

<400> 1918

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<400> 1919

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<210> 1925

<211> 1584

<212> DNA

<213> *Toxoplasma gondii*

<400> 1925

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<213> Toxoplasma gondii	
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<210> 1927
<211> 2681
<212> DNA
<213> *Toxoplasma gondii*

<400> 1927

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<210> 1928

<211> 1482

<212> DNA

<213> *Toxoplasma gondii*

<400> 1928

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<210> 1929

<211> 1536

<212> DNA

<213> *Toxoplasma gondii*

<400> 1929

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<210> 1930

<211> 1873

<212> DNA

<213> *Toxoplasma gondii*

<400> 1930

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 <211> 775
 <212> DNA
 <213> Toxoplasma gondii
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<211> 2315

<212> DNA

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<400> 1933

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<211> 1847

<212> DNA

<213> Toxoplasma gondii

<400> 1934

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<211> 2818

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<213> Toxoplasma gondii

<400> 1935

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<211> 2390
<212> DNA
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<400> 1937

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<400> 1938

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<211> 2773

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<400> 1941

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<210> 1942

<211> 2392

<212> DNA

<213> Toxoplasma gondii

<400> 1942

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<210> 1943

<211> 4204

<212> DNA

<213> *Toxoplasma gondii*

<400> 1943

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<211> 2270

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<213> Toxoplasma gondii

<400> 1944

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<211> 2396

<212> DNA

<213> Toxoplasma gondii

<400> 1945

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<400> 1951

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<210> 1952

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<400> 1952

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<211> 3319

<212> DNA

<213> *Toxoplasma gondii*

<400> 1953

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<210> 1963

<211> 2143

<212> DNA

<213> Toxoplasma gondii

<400> 1963

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<210> 1964

<211> 1369

<212> DNA

<213> Toxoplasma gondii

<400> 1964

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<210> 1965
<211> 1783
<212> DNA
<213> Toxoplasma gondii
<400> 1965

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<210> 1966
<211> 2069
<212> DNA
<213> Toxoplasma gondii
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 <210> 1967
 <211> 2164
 <212> DNA
 <213> *Toxoplasma gondii*

<400> 1967

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<210> 1969
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<211> 4153

<212> DNA

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<212> DNA

<213> Toxoplasma gondii

<400> 1971

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<212> DNA

<213> *Toxoplasma gondii*

<400> 1972

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<210> 1973

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<210> 1974

<211> 3776

<212> DNA

<213> *Toxoplasma gondii*

<400> 1974

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<211> 1642

<212> DNA

<213> Toxoplasma gondii

<400> 1977

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<211> 1922
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<211> 3187

<212> DNA

<213> *Toxoplasma gondii*

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<211> 2204
<212> DNA
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<213> *Toxoplasma gondii*

<400> 1986

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<211> 4520

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<213> *Toxoplasma gondii*

<400> 1989

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<211> 2495
<212> DNA
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<400> 1991

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<211> 1469

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<213> Toxoplasma gondii

<400> 1992

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<210> 1993

<211> 1838

<212> DNA

<213> *Toxoplasma gondii*

<400> 1993

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 <211> 1896
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<210> 1995

<211> 978

<212> DNA

<213> *Toxoplasma gondii*

<400> 1995

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<213> *Toxoplasma gondii*

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<211> 2533

<212> DNA

<213> Toxoplasma gondii

<400> 2003

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<211> 1622

<212> DNA

<213> Toxoplasma gondii

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 <213> Toxoplasma gondii
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<210> 2012

<211> 1092

<212> DNA

<213> *Toxoplasma gondii*

<400> 2012

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<210> 2014

<211> 2901

<212> DNA

<213> *Toxoplasma gondii*

<400> 2014

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<211> 1917

<212> DNA

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<211> 2083

<212> DNA

<213> *Toxoplasma gondii*

<400> 2020

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<210> 2021

<211> 3051

<212> DNA

<213> *Toxoplasma gondii*

<400> 2021

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<211> 2441

<212> DNA

<213> Toxoplasma gondii

<400> 2022

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<211> 2292

<212> DNA

<213> Toxoplasma gondii

<400> 2023

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<212> DNA

<213> Toxoplasma gondii

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<211> 1297

<212> DNA

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<212> DNA

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<211> 2241

<212> DNA

<213> Toxoplasma gondii

<400> 2062

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 <212> DNA
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<210> 2065

<211> 2604

<212> DNA

<213> *Toxoplasma gondii*

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<213> Toxoplasma gondii

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<211> 4844

<212> DNA

<213> Toxoplasma gondii

<400> 2093

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<211> 2771

<212> DNA

<213> Toxoplasma gondii

<400> 2094

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 <213> Toxoplasma gondii
 <400> 2095

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<211> 2481

<212> DNA

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<400> 2096

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<211> 3534

<212> DNA

<213> Toxoplasma gondii

<400> 2097

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<211> 2731

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

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<210> 2122

<211> 923

<212> DNA

<213> *Toxoplasma gondii*

<400> 2122

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<211> 2389

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1834

<212> DNA

<213> Toxoplasma gondii

<400> 2124

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<212> DNA
<213> *Toxoplasma gondii*

<400> 2130

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<211> 2141

<212> DNA

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<400> 2131

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<213> Toxoplasma gondii

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<210> 2133

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<213> Toxoplasma gondii

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<211> 1928

<212> DNA

<213> *Toxoplasma gondii*

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<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<211> 3327

<212> DNA

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<212> DNA

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<211> 1803
<212> DNA
<213> *Toxoplasma gondii*

<400> 2287

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<211> 4425

<212> DNA

<213> Toxoplasma gondii

<400> 2288

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<212> DNA

<213> Toxoplasma gondii

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<211> 2224

<212> DNA

<213> *Toxoplasma gondii*

<400> 2308

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agaaagagac tgagagcttg agttctgacc ctttcacgc tcagttttgc cgtgttgccg 480

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<210> 2309

<211> 2197

<212> DNA

<213> Toxoplasma gondii

<400> 2309

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<210> 2310
<211> 1674
<212> DNA
<213> *Toxoplasma gondii*

<400> 2310

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tgtttatctg aatgtaggtg	360
tacccaatt gtgccaatgg	420
accgatctgt acacctaacg	480
gaccgtagca tcgaagccgt	540
gctctgtacc acgcgtatgt	600
aaaaaatata catcctaaga	660
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gaggaagaca atcaagaagg	780
ctgaagtcca catgaaacca	840
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gtggcagtga gagagtcgtt	1020
aagcttggtc ttggacgacg	1080
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gcccagttg ccggcgctcg	1200
atgtatctga aagtgtttct	1260
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gtggacttca tgggtgtccg	1380
ggccgtgagt gtttttggtt	1440
tggggcattt catcacctc	1500
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<210> 2311

<211> 1743

<212> DNA

<213> *Toxoplasma gondii*

<400> 2311

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<210> 2312

<211> 2326

<212> DNA

<213> Toxoplasma gondii

<400> 2312

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<210> 2313
<211> 2024
<212> DNA
<213> *Toxoplasma gondii*

<400> 2313

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<210> 2314
<211> 1860
<212> DNA
<213> Toxoplasma gondii

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<400> 2335

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<211> 2048

<212> DNA

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<213> *Toxoplasma gondii*

<400> 2358

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<211> 2226

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<213> *Toxoplasma gondii*

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<213> Toxoplasma gondii

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<211> 1876

<212> DNA

<213> *Toxoplasma gondii*

<400> 2375

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<210> 2376

<211> 3584

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1278

<212> DNA

<213> Toxoplasma gondii

<400> 2377

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<400> 2378

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<211> 4184

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<400> 2382

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<213> *Toxoplasma gondii*

<400> 2384

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<212> DNA

<213> Toxoplasma gondii

<400> 2386

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<211> 2944

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1372

<212> DNA

<213> Toxoplasma gondii

<400> 2441

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<212> DNA

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<211> 3094

<212> DNA

<213> Toxoplasma gondii

<400> 2444

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<211> 1931

<212> DNA

<213> Toxoplasma gondii

<400> 2465

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<212> DNA

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<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

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<211> 3695

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<400> 2490

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<211> 1643

<212> DNA

<213> *Toxoplasma gondii*

<400> 2491

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<211> 2011

<212> DNA

<213> Toxoplasma gondii

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<211> 2009
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<211> 3686

<212> DNA

<213> Toxoplasma gondii

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<211> 1484

<212> DNA

<213> Toxoplasma gondii

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<210> 2506

<211> 1607

<212> DNA

<213> *Toxoplasma gondii*

<400> 2506

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<211> 1431

<212> DNA

<213> *Toxoplasma gondii*

<400> 2507

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<211> 4884

<212> DNA

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<211> 2316

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<400> 2521

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<211> 4470

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

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<211> 1574

<212> DNA

<213> Toxoplasma gondii

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<211> 1363

<212> DNA

<213> Toxoplasma gondii

<400> 2529

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<212> DNA

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<211> 1944

<212> DNA

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<211> 2211

<212> DNA

<213> Toxoplasma gondii

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<211> 1931

<212> DNA

<213> *Toxoplasma gondii*

<400> 2565

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<212> DNA

<213> Toxoplasma gondii

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<211> 2717

<212> DNA

<213> Toxoplasma gondii

<400> 2567

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<211> 3744

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<213> Toxoplasma gondii

<400> 2568

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<211> 3616

<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<212> DNA

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<212> DNA

<213> Toxoplasma gondii

<400> 2593

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<211> 2221

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<212> DNA

<213> *Toxoplasma gondii*

<400> 2595

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<211> 2627

<212> DNA

<213> *Toxoplasma gondii*

<400> 2621

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<211> 2181

<212> DNA

<213> Toxoplasma gondii

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<211> 2310

<212> DNA

<213> *Toxoplasma gondii*

<400> 2624

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<211> 4593

<212> DNA

<213> Toxoplasma gondii

<400> 2625

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<211> 1875

<212> DNA

<213> Toxoplasma gondii

<400> 2626

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<210> 2627

<211> 2114

<212> DNA

<213> Toxoplasma gondii

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<211> 2703

<212> DNA

<213> Toxoplasma gondii

<400> 2641

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<211> 1810
<212> DNA
<213> *Toxoplasma gondii*

<400> 2642

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<211> 2126

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<400> 2643

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<210> 2644

<211> 2481

<212> DNA

<213> Toxoplasma gondii

<400> 2644

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<211> 4689
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<211> 2669

<212> DNA

<213> *Toxoplasma gondii*

<400> 2661

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<210> 2662

<211> 2343

<212> DNA

<213> Toxoplasma gondii

<400> 2662

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<211> 1680

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

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<400> 2681

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<211> 4851

<212> DNA

<213> Toxoplasma gondii

<400> 2699

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<211> 1650

<212> DNA

<213> Toxoplasma gondii

<400> 2700

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<212> DNA

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<400> 2701

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<211> 3287

<212> DNA

<213> *Toxoplasma gondii*

<400> 2702

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<211> 2084

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<211> 2223

<212> DNA

<213> Toxoplasma gondii

<400> 2736

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<211> 4438

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

<400> 2738

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<211> 1883

<212> DNA

<213> Toxoplasma gondii

<400> 2751

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<211> 2204

<212> DNA

<213> Toxoplasma gondii

<400> 2752

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<211> 2287

<212> DNA

<213> Toxoplasma gondii

<400> 2754

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<400> 2755

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<212> DNA

<213> Toxoplasma gondii

<400> 2757

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

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<400> 2786

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<400> 2788

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<211> 2025

<212> DNA

<213> Toxoplasma gondii

<400> 2789

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<211> 2141

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<213> Toxoplasma gondii

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<211> 4259

<212> DNA

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<212> DNA

<213> Toxoplasma gondii

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<211> 1384

<212> DNA

<213> *Toxoplasma gondii*

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<210> 2804

<211> 1606

<212> DNA

<213> Toxoplasma gondii

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<211> 2418

<212> DNA

<213> Toxoplasma gondii

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<211> 2364
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<213> *Toxoplasma gondii*

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<211> 2872

<212> DNA

<213> Toxoplasma gondii

<400> 2813

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<211> 1145

<212> DNA

<213> Toxoplasma gondii

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<211> 673

<212> DNA

<213> Toxoplasma gondii

<400> 2815

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<210> 2816

<211> 1908

<212> DNA

<213> Toxoplasma gondii

<400> 2816

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<213> *Toxoplasma gondii*

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<211> 1199

<212> DNA

<213> *Toxoplasma gondii*

<400> 2859

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<211> 3618

<212> DNA

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<211> 1889

<212> DNA

<213> Toxoplasma gondii

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 <211> 2037
 <212> DNA
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<211> 1952

<212> DNA

<213> Toxoplasma gondii

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<400> 2878

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

<400> 2897

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<210> 2898

<211> 1537

<212> DNA

<213> *Toxoplasma gondii*

<400> 2898

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<211> 1428

<212> DNA

<213> *Toxoplasma gondii*

<400> 2899

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<211> 1610

<212> DNA

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<211> 2926

<212> DNA

<213> Toxoplasma gondii

<400> 2901

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<211> 1722

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<212> DNA

<213> Toxoplasma gondii

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<211> 1755

<212> DNA

<213> Toxoplasma gondii

<400> 2936

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<210> 2937

<211> 2351

<212> DNA

<213> Toxoplasma gondii

<400> 2937

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<211> 3084

<212> DNA

<213> Toxoplasma gondii

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<211> 1847

<212> DNA

<213> Toxoplasma gondii

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<211> 4003

<212> DNA

<213> Toxoplasma gondii

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<211> 2401

<212> DNA

<213> Toxoplasma gondii

<400> 3005

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<211> 1717

<212> DNA

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<210> 3007

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

<400> 3008

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<211> 2436

<212> DNA

<213> Toxoplasma gondii

<400> 3009

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<211> 2187

<212> DNA

<213> *Toxoplasma gondii*

<400> 3011

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<211> 1553

<212> DNA

<213> Toxoplasma gondii

<400> 3012

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<210> 3013

<211> 2033

<212> DNA

<213> *Toxoplasma gondii*

<400> 3013

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<210> 3014

<211> 2668

<212> DNA

<213> Toxoplasma gondii

<400> 3014

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<211> 2726

<212> DNA

<213> *Toxoplasma gondii*

<400> 3015

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<213> Toxoplasma gondii

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 <211> 3214
 <212> DNA

<213> *Toxoplasma gondii*

<400> 3064

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<212> DNA
<213> Toxoplasma gondii
<400> 3065

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<212> DNA

<213> Toxoplasma gondii

<400> 3066

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<211> 2183

<212> DNA

<213> Toxoplasma gondii

<400> 3067

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<211> 2819

<212> DNA

<213> Toxoplasma gondii

<400> 3069

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<400> 3081

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<211> 2261

<212> DNA

<213> Toxoplasma gondii

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<211> 1402

<212> DNA

<213> Toxoplasma gondii

<400> 3087

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<210> 3088

<211> 2598

<212> DNA

<213> Toxoplasma gondii

<400> 3088

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<212> DNA

<213> *Toxoplasma gondii*

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<211> 1794

<212> DNA

<213> *Toxoplasma gondii*

<400> 3095

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<210> 3096

<211> 1902

<212> DNA

<213> *Toxoplasma gondii*

<400> 3096

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 <212> DNA
 <213> Toxoplasma gondii
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<211> 2758

<212> DNA

<213> Toxoplasma gondii

<400> 3098

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<211> 2452

<212> DNA

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<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<210> 3134

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<211> 2282

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<213> Toxoplasma gondii

<400> 3145

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<211> 1624

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<213> *Toxoplasma gondii*

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<211> 2970

<212> DNA

<213> Toxoplasma gondii

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<213> *Toxoplasma gondii*

<400> 3152

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<213> Toxoplasma gondii
<400> 3153

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<210> 3154

<211> 1243

<212> DNA

<213> Toxoplasma gondii

<400> 3154

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<211> 2862
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<212> DNA

<213> *Toxoplasma gondii*

<400> 3156

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<211> 3283

<212> DNA

<213> *Toxoplasma gondii*

<400> 3157

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<212> DNA

<213> *Toxoplasma gondii*

<400> 3163

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<211> 2796

<212> DNA

<213> *Toxoplasma gondii*

<400> 3164

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<211> 1859

<212> DNA

<213> Toxoplasma gondii

<400> 3165

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<210> 3167

<211> 4221

<212> DNA

<213> *Toxoplasma gondii*

<400> 3167

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<212> DNA

<213> Toxoplasma gondii

<400> 3174

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<400> 3177

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<211> 2000

<212> DNA

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<211> 1800

<212> DNA

<213> Toxoplasma gondii

<400> 3179

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<211> 4727

<212> DNA

<213> *Toxoplasma gondii*

<400> 3180

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<212> DNA

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<211> 1567

<212> DNA

<213> *Toxoplasma gondii*

<400> 3182

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<400> 3183

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<211> 2262
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<213> Toxoplasma gondii
<400> 3201

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<212> DNA

<213> Toxoplasma gondii

<400> 3202

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<210> 3203

<211> 2272

<212> DNA

<213> Toxoplasma gondii

<400> 3203

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<211> 2538

<212> DNA

<213> Toxoplasma gondii

<400> 3204

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<213> Toxoplasma gondii

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<212> DNA

<213> Toxoplasma gondii

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<211> 1592

<212> DNA

<213> Toxoplasma gondii

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<212> DNA
<213> Toxoplasma gondii
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<212> DNA

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<213> Toxoplasma gondii

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<213> *Toxoplasma gondii*

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<211> 3650

<212> DNA

<213> Toxoplasma gondii

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<211> 2516

<212> DNA

<213> Toxoplasma gondii

<400> 3314

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<211> 3240

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<213> Toxoplasma gondii

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<211> 3018

<212> DNA

<213> *Toxoplasma gondii*

<400> 3371

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<211> 1983
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<400> 3372

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<210> 3373

<211> 2097

<212> DNA

<213> Toxoplasma gondii

<400> 3373

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<211> 1991

<212> DNA

<213> *Toxoplasma gondii*

<400> 3378

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<211> 4475

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<211> 1881

<212> DNA

<213> Toxoplasma gondii

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<211> 1906

<212> DNA

<213> Toxoplasma gondii

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<212> DNA

<213> *Toxoplasma gondii*

<400> 3427

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<211> 1865

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1808

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<213> Toxoplasma gondii

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 <213> Toxoplasma gondii

<400> 3451

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<211> 4932

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<212> DNA

<213> Toxoplasma gondii

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<212> DNA

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<211> 2023

<212> DNA

<213> Toxoplasma gondii

<400> 3565

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<210> 3566

<211> 3151

<212> DNA

<213> Toxoplasma gondii

<400> 3566

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<210> 3567

<211> 1965

<212> DNA

<213> Toxoplasma gondii

<400> 3567

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<210> 3568

<211> 2092

<212> DNA

<213> *Toxoplasma gondii*

<400> 3568

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<210> 3569

<211> 1820

<212> DNA

<213> *Toxoplasma gondii*

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<210> 3576

<211> 1880

<212> DNA

<213> Toxoplasma gondii

<400> 3576

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<210> 3577
<211> 2900
<212> DNA
<213> *Toxoplasma gondii*

<400> 3577

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<210> 3578

<211> 2003

<212> DNA

<213> *Toxoplasma gondii*

<400> 3578

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<210> 3579

<211> 1936

<212> DNA

<213> Toxoplasma gondii

<400> 3579

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<210> 3580

<211> 2411

<212> DNA

<213> Toxoplasma gondii

<400> 3580

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<211> 3125
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<400> 3581

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<213> Toxoplasma gondii

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<211> 1328

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<213> Toxoplasma gondii

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<213> *Toxoplasma gondii*

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<210> 3602

<211> 2238

<212> DNA

<213> Toxoplasma gondii

<400> 3602

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<210> 3603

<211> 1760

<212> DNA

<213> Toxoplasma gondii

<400> 3603

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<211> 2013
<212> DNA
<213> Toxoplasma gondii
<400> 3604

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<210> 3605

<211> 4505

<212> DNA

<213> *Toxoplasma gondii*

<400> 3605

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<210> 3606

<211> 2049

<212> DNA

<213> Toxoplasma gondii

<400> 3606

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<210> 3607

<211> 3067

<212> DNA

<213> *Toxoplasma gondii*

<400> 3607

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<211> 1947

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<213> Toxoplasma gondii

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<211> 1772

<212> DNA

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<211> 4635

<212> DNA

<213> Toxoplasma gondii

<400> 3619

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<211> 2309

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<213> Toxoplasma gondii

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<211> 1867

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> *Toxoplasma gondii*

<400> 3632

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<211> 1499

<212> DNA

<213> Toxoplasma gondii

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<211> 3798

<212> DNA

<213> Toxoplasma gondii

<400> 3635

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<211> 3745

<212> DNA

<213> Toxoplasma gondii

<400> 3636

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<212> DNA
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<400> 3643

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<212> DNA

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<211> 1121

<212> DNA

<213> Toxoplasma gondii

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<211> 2524

<212> DNA

<213> Toxoplasma gondii

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<211> 2709

<212> DNA

<213> *Toxoplasma gondii*

<400> 3672

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<210> 3673

<211> 3810

<212> DNA

<213> Toxoplasma gondii

<400> 3673

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<210> 3674

<211> 1587

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> Toxoplasma gondii

<400> 3675

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 <212> DNA
 <213> Toxoplasma gondii

<400> 3676

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<213> Toxoplasma gondii

<400> 3696

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<212> DNA

<213> Toxoplasma gondii

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<213> *Toxoplasma gondii*

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 <211> 1248
 <212> DNA
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 <400> 3740

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<210> 3741

<211> 1983

<212> DNA

<213> *Toxoplasma gondii*

<400> 3741

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<210> 3742

<211> 3127

<212> DNA

<213> Toxoplasma gondii

<400> 3742

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<210> 3743

<211> 3684

<212> DNA

<213> Toxoplasma gondii

<400> 3743

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<210> 3744

<211> 3752

<212> DNA

<213> Toxoplasma gondii

<400> 3744

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<212> DNA

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<400> 3766

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<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<400> 3776

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<212> DNA

<213> *Toxoplasma gondii*

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<211> 4533

<212> DNA

<213> *Toxoplasma gondii*

<400> 3803

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<211> 4831

<212> DNA

<213> Toxoplasma gondii

<400> 3804

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<210> 3810

<211> 4760

<212> DNA

<213> *Toxoplasma gondii*

<400> 3810

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<211> 2042

<212> DNA

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<400> 3811

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<210> 3812
 <211> 4655
 <212> DNA
 <213> Toxoplasma gondii
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<211> 1917

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<213> Toxoplasma gondii

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<211> 2629

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<211> 1265

<212> DNA

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<400> 3863

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<213> Toxoplasma gondii

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<211> 1704

<212> DNA

<213> Toxoplasma gondii

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<211> 1484

<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<211> 2768

<212> DNA

<213> Toxoplasma gondii

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<211> 1957
<212> DNA
<213> Toxoplasma gondii

<400> 3903

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<210> 3904

<211> 4176

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1884

<212> DNA

<213> Toxoplasma gondii

<400> 3905

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<213> Toxoplasma gondii
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<213> Toxoplasma gondii

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<213> *Toxoplasma gondii*

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<211> 4818

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<211> 2551

<212> DNA

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 <213> Toxoplasma gondii
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<211> 2288

<212> DNA

<213> Toxoplasma gondii

<400> 3938

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<211> 2051
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<400> 3939

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<211> 2126

<212> DNA

<213> Toxoplasma gondii

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<211> 3387

<212> DNA

<213> *Toxoplasma gondii*

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<212> DNA

<213> Toxoplasma gondii

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<211> 2387

<212> DNA

<213> Toxoplasma gondii

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<211> 2471

<212> DNA

<213> Toxoplasma gondii

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<211> 1158

<212> DNA

<213> *Toxoplasma gondii*

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<211> 1723

<212> DNA

<213> *Toxoplasma gondii*

<400> 3946

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<211> 701

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<213> Toxoplasma gondii

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<400> 3965

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<211> 4702

<212> DNA

<213> *Toxoplasma gondii*

<400> 3978

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 <211> 2023
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 <213> Toxoplasma gondii

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<210> 3980

<211> 3982

<212> DNA

<213> *Toxoplasma gondii*

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<211> 3482

<212> DNA

<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<213> Toxoplasma gondii

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<212> DNA

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<400> 4030

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<211> 492

<212> DNA

<213> Artificial Sequence

<220><223> 5RT70constitutive promotor

<400> 4031

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<400> 4032

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<210> 4033

<211> 1205

<212> DNA

<213> Artificial Sequence

<220><223> MIC2constitutive promotor

<400> 4033

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<213> Artificial Sequence	
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<210> 4035

<211> 806

<212> DNA

<213> Artificial Sequence

<220><223> SAG1constitutive promotor

<400> 4035

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<210> 4036

<211> 639

<212> DNA

<213> Artificial Sequence

<220><223> Tet07SAG1 inducible promotor

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<210> 4037

<211> 716

<212> DNA

<213> Artificial Sequence

<220><223> Tet07SAG4 inducible promotor

<400> 4037

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<211> 498

<212> DNA

<213> Artificial Sequence

<220><223> TUB1 constitutive promotor

<220><221> misc_feature

<222> (290)..(290)

<223> n is a, c, g, or t

<400> 4038

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<210> 4039

<211> 485

<212> DNA

<213> Artificial Sequence

<220><223> TUB8 constitutive promotor

<400> 4039

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 Leu Lys Met Asp Gln Ala Leu Leu Leu Ile His Asn Glu Leu Leu Trp
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 Thr Asn Leu Thr Val Tyr Trp Lys Ser Glu Cys Cys Tyr His Cys Leu
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 Phe Gln Val Leu Val Asn Val Pro Gln Ser Pro Lys Ala Gly Lys Pro
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 Ser Ala Ala Ala Ala Ser Val Ser Thr Gln His Gly Ser Ile Leu Gln
 100 105 110

Leu Asn Asp Thr Leu Glu Glu Lys Glu Val Cys Arg Leu Glu Tyr Arg
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 Phe Gly Glu Phe Gly Asn Tyr Ser Leu Leu Val Lys Asn Ile His Asn
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 Gly Val Ser Glu Ile Ala Cys Asp Leu Ala Val Asn Glu Asp Pro Val
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 Ile Ile Val Ile Ser Phe Leu Arg Leu Leu Leu Ser Leu Asp Asp Phe
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 Arg Ser Val Asp Thr Phe Arg Gly Ile Ala Leu Ile Leu Met Val Phe
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 Pro Leu Ser Trp Asp Lys Val Arg Ile Pro Gly Val Leu Gln Arg Leu
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Gly Leu Trp Leu Gly Leu Thr Phe Leu Leu Pro Val Pro Gly Cys Pro			
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Thr Gly Tyr Leu Gly Pro Gly Gly Ile Gly Asp Phe Gly Lys Tyr Pro			
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Asn Cys Thr Gly Gly Ala Ala Gly Tyr Ile Asp Arg Leu Leu Leu Gly			
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Asp Asp His Leu Tyr Gln His Pro Ser Ser Ala Val Leu Tyr His Thr			
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Glu Val Ala Tyr Asp Pro Glu Gly Ile Leu Gly Thr Ile Asn Ser Ile			
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Val Met Ala Phe Leu Gly Val Gln Ala Gly Lys Ile Leu Leu Tyr Tyr			
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Lys Ala Arg Thr Lys Asp Ile Leu Ile Arg Phe Thr Ala Trp Cys Cys			
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Gly Phe Ile Pro Val Asn Lys Asn Leu Trp Ser Leu Ser Tyr Val Thr			
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Thr Leu Ser Ser Phe Ala Phe Phe Ile Leu Leu Val Leu Tyr Pro Val			
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Val Asp Val Lys Gly Leu Trp Thr Gly Thr Pro Phe Phe Tyr Pro Gly			
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Phe Pro Phe Gln Trp Lys Leu Lys Asp Asn Gln Ser His Lys Glu His			
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Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe

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45

Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys

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Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr

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Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu Asn Lys Gly Cys

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90

95

Glu Ser Pro Asp Pro Asp Ser Ser Tyr Ala Leu Thr Pro Arg Thr Glu

100

105

110

Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Ile Lys Ser

115

120

125

His Lys Ile Pro Ala Val Pro Pro Pro Asn Phe Glu Met Pro Val Ser

130

135

140

Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro Val Ser

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160

Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser Leu Gln

165

170

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Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser Ala Gly

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Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly Leu Leu		
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Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg Val Leu		
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Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln Arg Ile		
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Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val Ser Val		
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Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro Ser Ala		
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Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala Asp Leu		
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Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser Glu Pro		
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Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr Pro Gln		
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His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu Ser Ser		
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Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg Asn Glu		
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Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr

65 70 75 80

Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys

85 90 95

Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu

100 105 110

Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile

115 120 125

Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro

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Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro

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165 170 175

Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser

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Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala

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Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser

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Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg

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Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Ser Glu

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Gln Ser Leu Ala Thr Pro Val Val Ser Val Ala Thr Pro Thr Leu Pro

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Gly Gln Gly Met Gly Gly Tyr Pro Ser Ala Ile Ser Thr Thr Tyr Gly

305 310 315 320

Thr Glu Tyr Ser Leu Ser Ser Ala Asp Leu Ser Ser Leu Ser Gly Phe

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<213> homo sapiens

<400> 4305

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly

1

5

10

15

Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly

20

25

30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly

35

40

45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu

50

55

60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu

65

70

75

80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro

85

90

95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly

100

105

110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys

115

120

125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro

130

135

140

Lys Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys

145

150

155

160

His Leu Cys Gly Asp Ala Val Pro Arg Arg

165 170

<210> 4306

<211> 533

<212> PRT

<213> homo sapiens

<400> 4306

Met Ser Ile Gln Val Glu His Pro Ala Gly Gly Tyr Lys Lys Leu Phe

1 5 10 15

Glu Thr Val Glu Glu Leu Ser Ser Pro Leu Thr Ala His Val Thr Gly

20 25 30

Arg Ile Pro Leu Trp Leu Thr Gly Ser Leu Leu Arg Cys Gly Pro Gly

35 40 45

Leu Phe Glu Val Gly Ser Glu Pro Phe Tyr His Leu Phe Asp Gly Gln

50 55 60

Ala Leu Leu His Lys Phe Asp Phe Lys Glu Gly His Val Thr Tyr His

65 70 75 80

Arg Arg Phe Ile Arg Thr Asp Ala Tyr Val Arg Ala Met Thr Glu Lys

85 90 95

Arg Ile Val Ile Thr Glu Phe Gly Thr Cys Ala Phe Pro Asp Pro Cys

100 105 110

Lys Asn Ile Phe Ser Arg Phe Phe Ser Tyr Phe Arg Gly Val Glu Val

115 120 125

Thr Asp Asn Ala Leu Val Asn Val Tyr Pro Val Gly Glu Asp Tyr Tyr

130 135 140

Ala Cys Thr Glu Thr Asn Phe Ile Thr Lys Ile Asn Pro Glu Thr Leu

145 150 155 160

Glu Thr Ile Lys Gln Val Asp Leu Cys Asn Tyr Val Ser Val Asn Gly

165 170 175

Ala Thr Ala His Pro His Ile Glu Asn Asp Gly Thr Val Tyr Asn Ile

180 185 190

Gly Asn Cys Phe Gly Lys Asn Phe Ser Ile Ala Tyr Asn Ile Val Lys

195 200 205
 Ile Pro Pro Leu Gln Ala Asp Lys Glu Asp Pro Ile Ser Lys Ser Glu
 210 215 220
 Ile Val Val Gln Phe Pro Cys Ser Asp Arg Phe Lys Pro Ser Tyr Val

 225 230 235 240
 His Ser Phe Gly Leu Thr Pro Asn Tyr Ile Val Phe Val Glu Thr Pro
 245 250 255
 Val Lys Ile Asn Leu Phe Lys Phe Leu Ser Ser Trp Ser Leu Trp Gly
 260 265 270
 Ala Asn Tyr Met Asp Cys Phe Glu Ser Asn Glu Thr Met Gly Val Trp
 275 280 285
 Leu His Ile Ala Asp Lys Lys Arg Lys Lys Tyr Leu Asn Asn Lys Tyr

 290 295 300
 Arg Thr Ser Pro Phe Asn Leu Phe His His Ile Asn Thr Tyr Glu Asp
 305 310 315 320
 Asn Gly Phe Leu Ile Val Asp Leu Cys Cys Trp Lys Gly Phe Glu Phe
 325 330 335
 Val Tyr Asn Tyr Leu Tyr Leu Ala Asn Leu Arg Glu Asn Trp Glu Glu
 340 345 350
 Val Lys Lys Asn Ala Arg Lys Ala Pro Gln Pro Glu Val Arg Arg Tyr

 355 360 365
 Val Leu Pro Leu Asn Ile Asp Lys Ala Asp Thr Gly Lys Asn Leu Val
 370 375 380
 Thr Leu Pro Asn Thr Thr Ala Thr Ala Ile Leu Cys Ser Asp Glu Thr
 385 390 395 400
 Ile Trp Leu Glu Pro Glu Val Leu Phe Ser Gly Pro Arg Gln Ala Phe
 405 410 415
 Glu Phe Pro Gln Ile Asn Tyr Gln Lys Tyr Cys Gly Lys Pro Tyr Thr

 420 425 430
 Tyr Ala Tyr Gly Leu Gly Leu Asn His Phe Val Pro Asp Arg Leu Cys
 435 440 445

Lys Leu Asn Val Lys Thr Lys Glu Thr Trp Val Trp Gln Glu Pro Asp
450 455 460

Ser Tyr Pro Ser Glu Pro Ile Phe Val Ser His Pro Asp Ala Leu Glu
465 470 475 480

Glu Asp Asp Gly Val Val Leu Ser Val Val Val Ser Pro Gly Ala Gly
485 490 495

Gln Lys Pro Ala Tyr Leu Leu Ile Leu Asn Ala Lys Asp Leu Ser Glu
500 505 510

Val Ala Arg Ala Glu Val Glu Ile Asn Ile Pro Val Thr Phe His Gly
515 520 525

Leu Phe Lys Lys Ser
530

<210> 4307
<211> 211
<212> PRT
<213> homo sapiens
<400> 4307

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr

115 120 125
Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr

130 135 140
Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu

145 150 155 160
Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln

165 170 175
Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp

180 185 190
Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys

195 200 205
Gly Cys Ile

210

<210> 4308

<211> 185

<212> PRT

<213> homo sapiens

<400> 4308

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr

1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Ala Asn Met Pro Glu Asp Tyr Pro

20 25 30

Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg

35 40 45

Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu

50 55 60

Arg Asn Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys

65 70 75 80

Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala

85 90 95

Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu

100 105 110
 Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr
 115 120 125
 Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val
 130 135 140
 Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp
 145 150 155 160
 Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys
 165 170 175

 His Ser Ala Lys Arg Cys Gly Cys Ile
 180 185
 <210> 4309
 <211> 809
 <212> PRT
 <213> homo sapiens
 <400> 4309
 Met Phe Lys Ser Leu Thr Lys Val Asn Lys Val Lys Pro Ile Gly Glu
 1 5 10 15
 Asn Asn Glu Asn Glu Gln Ser Ser Arg Arg Asn Glu Glu Gly Ser His
 20 25 30
 Pro Ser Asn Gln Ser Gln Gln Thr Thr Ala Gln Glu Glu Asn Lys Gly
 35 40 45

 Glu Glu Lys Ser Leu Lys Thr Lys Ser Thr Pro Val Thr Ser Glu Glu
 50 55 60
 Pro His Thr Asn Ile Gln Asp Lys Leu Ser Lys Lys Asn Ser Ser Gly
 65 70 75 80
 Asp Leu Thr Thr Asn Pro Asp Pro Gln Asn Ala Ala Glu Pro Thr Gly
 85 90 95
 Thr Val Pro Glu Gln Lys Glu Met Asp Pro Gly Lys Glu Gly Pro Asn
 100 105 110

 Ser Pro Gln Asn Lys Pro Pro Ala Ala Pro Val Ile Asn Glu Tyr Ala

115	120	125	
Asp Ala Gln Leu His Asn Leu Val Lys Arg Met Arg Gln Arg Thr Ala			
130	135	140	
Leu Tyr Lys Lys Lys Leu Val Glu Gly Asp Leu Ser Ser Pro Glu Ala			
145	150	155	160
Ser Pro Gln Thr Ala Lys Pro Thr Ala Val Pro Pro Val Lys Glu Ser			
165	170	175	
Asp Asp Lys Pro Thr Glu His Tyr Tyr Arg Leu Leu Trp Phe Lys Val			
180	185	190	
Lys Lys Met Pro Leu Thr Glu Tyr Leu Lys Arg Ile Lys Leu Pro Asn			
195	200	205	
Ser Ile Asp Ser Tyr Thr Asp Arg Leu Tyr Leu Leu Trp Leu Leu Leu			
210	215	220	
Val Thr Leu Ala Tyr Asn Trp Asn Cys Cys Phe Ile Pro Leu Arg Leu			
225	230	235	240
Val Phe Pro Tyr Gln Thr Ala Asp Asn Ile His Tyr Trp Leu Ile Ala			
245	250	255	
Asp Ile Ile Cys Asp Ile Ile Tyr Leu Tyr Asp Met Leu Phe Ile Gln			
260	265	270	
Pro Arg Leu Gln Phe Val Arg Gly Gly Asp Ile Ile Val Asp Ser Asn			
275	280	285	
Glu Leu Arg Lys His Tyr Arg Thr Ser Thr Lys Phe Gln Leu Asp Val			
290	295	300	
Ala Ser Ile Ile Pro Phe Asp Ile Cys Tyr Leu Phe Phe Gly Phe Asn			
305	310	315	320
Pro Met Phe Arg Ala Asn Arg Met Leu Lys Tyr Thr Ser Phe Phe Glu			
325	330	335	
Phe Asn His His Leu Glu Ser Ile Met Asp Lys Ala Tyr Ile Tyr Arg			
340	345	350	
Val Ile Arg Thr Thr Gly Tyr Leu Leu Phe Ile Leu His Ile Asn Ala			
355	360	365	

Cys Val Tyr Tyr Trp Ala Ser Asn Tyr Glu Gly Ile Gly Thr Thr Arg
 370 375 380
 Trp Val Tyr Asp Gly Glu Gly Asn Glu Tyr Leu Arg Cys Tyr Tyr Trp
 385 390 395 400
 Ala Val Arg Thr Leu Ile Thr Ile Gly Gly Leu Pro Glu Pro Gln Thr
 405 410 415
 Leu Phe Glu Ile Val Phe Gln Leu Leu Asn Phe Phe Ser Gly Val Phe
 420 425 430

 Val Phe Ser Ser Leu Ile Gly Gln Met Arg Asp Val Ile Gly Ala Ala
 435 440 445
 Thr Ala Asn Gln Asn Tyr Phe Arg Ala Cys Met Asp Asp Thr Ile Ala
 450 455 460
 Tyr Met Asn Asn Tyr Ser Ile Pro Lys Leu Val Gln Lys Arg Val Arg
 465 470 475 480
 Thr Trp Tyr Glu Tyr Thr Trp Asp Ser Gln Arg Met Leu Asp Glu Ser
 485 490 495

 Asp Leu Leu Lys Thr Leu Pro Thr Thr Val Gln Leu Ala Leu Ala Ile
 500 505 510
 Asp Val Asn Phe Ser Ile Ile Ser Lys Val Asp Leu Phe Lys Gly Cys
 515 520 525
 Asp Thr Gln Met Ile Tyr Asp Met Leu Leu Arg Leu Lys Ser Val Leu
 530 535 540
 Tyr Leu Pro Gly Asp Phe Val Cys Lys Lys Gly Glu Ile Gly Lys Glu
 545 550 555 560

 Met Tyr Ile Ile Lys His Gly Glu Val Gln Val Leu Gly Gly Pro Asp
 565 570 575
 Gly Thr Lys Val Leu Val Thr Leu Lys Ala Gly Ser Val Phe Gly Glu
 580 585 590
 Ile Ser Leu Leu Ala Ala Gly Gly Gly Asn Arg Arg Thr Ala Asn Val
 595 600 605
 Val Ala His Gly Phe Ala Asn Leu Leu Thr Leu Asp Lys Lys Thr Leu

610 615 620

 Gln Glu Ile Leu Val His Tyr Pro Asp Ser Glu Arg Ile Leu Met Lys
 625 630 635 640
 Lys Ala Arg Val Leu Leu Lys Gln Lys Ala Lys Thr Ala Glu Ala Thr
 645 650 655
 Pro Pro Arg Lys Asp Leu Ala Leu Leu Phe Pro Pro Lys Glu Glu Thr
 660 665 670
 Pro Lys Leu Phe Lys Thr Leu Leu Gly Gly Thr Gly Lys Ala Ser Leu
 675 680 685

 Ala Arg Leu Leu Lys Leu Lys Arg Glu Gln Ala Ala Gln Lys Lys Glu
 690 695 700
 Asn Ser Glu Gly Gly Glu Glu Glu Gly Lys Glu Asn Glu Asp Lys Gln
 705 710 715 720
 Lys Glu Asn Glu Asp Lys Gln Lys Glu Asn Glu Asp Lys Gly Lys Glu
 725 730 735
 Asn Glu Asp Lys Asp Lys Gly Arg Glu Pro Glu Glu Lys Pro Leu Asp
 740 745 750

 Arg Pro Glu Cys Thr Ala Ser Pro Ile Ala Val Glu Glu Glu Pro His
 755 760 765
 Ser Val Arg Arg Thr Val Leu Pro Arg Gly Thr Ser Arg Gln Ser Leu
 770 775 780
 Ile Ile Ser Met Ala Pro Ser Ala Glu Gly Gly Glu Glu Val Leu Thr
 785 790 795 800
 Ile Glu Val Lys Glu Lys Ala Lys Gln
 805
 <210> 4310
 <211> 247
 <212> PRT

 <213> homo sapiens
 <400> 4310
 Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met

1 5 10 15
 Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
 20 25 30
 Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
 35 40 45
 Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
 50 55 60

 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
 100 105 110
 Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
 115 120 125

 His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
 130 135 140
 Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
 145 150 155 160
 Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
 165 170 175
 Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
 180 185 190

 Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
 195 200 205
 Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
 210 215 220
 Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
 225 230 235 240
 Leu Thr Ile Lys Arg Gly Arg
 245
 <210> 4311

<211> 247

<212> PRT

<213> homo sapiens

<400> 4311

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met

1 5 10 15

Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu

20 25 30

Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly

35 40 45

Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu

50 55 60

His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn

65 70 75 80

Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu

85 90 95

Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu

100 105 110

Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg

115 120 125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile

130 135 140

Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser

145 150 155 160

Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln

165 170 175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr

180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys

195 200 205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys

210 215 220
 Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
 225 230 235 240
 Leu Thr Ile Lys Arg Gly Arg
 245
 <210> 4312
 <211> 247
 <212> PRT
 <213> homo sapiens

 <400> 4312
 Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
 1 5 10 15
 Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
 20 25 30
 Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
 35 40 45
 Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
 50 55 60

 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
 100 105 110
 Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
 115 120 125

 His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
 130 135 140
 Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
 145 150 155 160
 Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
 165 170 175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
195 200 205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
210 215 220

Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
225 230 235 240

Leu Thr Ile Lys Arg Gly Arg
245

<210> 4313

<211> 247

<212> PRT

<213> homo sapiens

<400> 4313

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
1 5 10 15

Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
20 25 30

Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
35 40 45

Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
50 55 60

His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
65 70 75 80

Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
85 90 95

Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
100 105 110

Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
115 120 125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
130 135 140

Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
145 150 155 160

Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
165 170 175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
195 200 205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
210 215 220

Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
225 230 235 240

Leu Thr Ile Lys Arg Gly Arg
245

<210> 4314

<211> 247

<212> PRT

<213> homo sapiens

<400> 4314

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
1 5 10 15

Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
20 25 30

Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
35 40 45

Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
50 55 60

His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
65 70 75 80

Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu

85 90 95
Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
100 105 110
Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
115 120 125

His	Ser	Asp	Pro	Ala	Arg	Arg	Gly	Glu	Leu	Ser	Val	Cys	Asp	Ser	Ile		
130					135					140							
Ser	Glu	Trp	Val	Thr	Ala	Ala	Asp	Lys	Lys	Thr	Ala	Val	Asp	Met	Ser		
145					150					155						160	
Gly	Gly	Thr	Val	Thr	Val	Leu	Glu	Lys	Val	Pro	Val	Ser	Lys	Gly	Gln		
165						170						175					
Leu	Lys	Gln	Tyr	Phe	Tyr	Glu	Thr	Lys	Cys	Asn	Pro	Met	Gly	Tyr	Thr		
180					185					190							

Lys	Glu	Gly	Cys	Arg	Gly	Ile	Asp	Lys	Arg	His	Trp	Asn	Ser	Gln	Cys
195				200				205							
Arg	Thr	Thr	Gln	Ser	Tyr	Val	Arg	Ala	Leu	Thr	Met	Asp	Ser	Lys	Lys
210				215				220							
Arg	Ile	Gly	Trp	Arg	Phe	Ile	Arg	Ile	Asp	Thr	Ser	Cys	Val	Cys	Thr
225				230				235				240			
Leu	Thr	Ile	Lys	Arg	Gly	Arg									
245															

<210> 4315

<211> 262

<212> PRT

<213> homo sapiens

<400> 4315

Met	Gln	Ser	Arg	Glu	Glu	Glu	Trp	Phe	His	Gln	Val	Arg	Arg	Val	Met
1				5				10						15	
Thr	Ile	Leu	Phe	Leu	Thr	Met	Val	Ile	Ser	Tyr	Phe	Gly	Cys	Met	Lys
			20					25					30		
Ala	Ala	Pro	Met	Lys	Glu	Ala	Asn	Ile	Arg	Gly	Gln	Gly	Gly	Leu	Ala
		35					40					45			

Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly Pro
50 55 60

Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu His
65 70 75 80

Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn Glu
85 90 95

Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu Ser
100 105 110

Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu Tyr
115 120 125

Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg His
130 135 140

Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile Ser
145 150 155 160

Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser Gly
165 170 175

Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln Leu
180 185 190

Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr Lys
195 200 205

Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys Arg
210 215 220

Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys Arg
225 230 235 240

Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr Leu
245 250 255

Thr Ile Lys Arg Gly Arg
260

<210> 4316

<211> 247

<212> PRT

<213> homo sapiens

<400> 4316

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met

1 5 10 15

Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu

20 25 30

Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly

35 40 45

Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu

50 55 60

His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn

65 70 75 80

Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu

85 90 95

Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu

100 105 110

Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg

115 120 125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile

130 135 140

Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser

145 150 155 160

Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln

165 170 175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr

180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys

195 200 205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys

210 215 220

Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr

225					230					235					240
Leu	Thr	Ile	Lys	Arg	Gly	Arg									
				245											
<210>	4317														
<211>	255														
<212>	PRT														
<213>	homo sapiens														
<400>	4317														
Met	Phe	His	Gln	Val	Arg	Arg	Val	Met	Thr	Ile	Leu	Phe	Leu	Thr	Met
1				5				10				15			
Val	Ile	Ser	Tyr	Phe	Gly	Cys	Met	Lys	Ala	Ala	Pro	Met	Lys	Glu	Ala
			20				25				30				
Asn	Ile	Arg	Gly	Gln	Gly	Gly	Leu	Ala	Tyr	Pro	Gly	Val	Arg	Thr	His
			35				40				45				
Gly	Thr	Leu	Glu	Ser	Val	Asn	Gly	Pro	Lys	Ala	Gly	Ser	Arg	Gly	Leu
		50				55				60					
Thr	Ser	Leu	Ala	Asp	Thr	Phe	Glu	His	Val	Ile	Glu	Glu	Leu	Leu	Asp
65					70					75					80
Glu	Asp	Gln	Lys	Val	Arg	Pro	Asn	Glu	Glu	Asn	Asn	Lys	Asp	Ala	Asp
			85				90				95				
Leu	Tyr	Thr	Ser	Arg	Val	Met	Leu	Ser	Ser	Gln	Val	Pro	Leu	Glu	Pro
			100				105				110				
Pro	Leu	Leu	Phe	Leu	Leu	Glu	Glu	Tyr	Lys	Asn	Tyr	Leu	Asp	Ala	Ala
			115				120				125				
Asn	Met	Ser	Met	Arg	Val	Arg	Arg	His	Ser	Asp	Pro	Ala	Arg	Arg	Gly
			130				135				140				
Glu	Leu	Ser	Val	Cys	Asp	Ser	Ile	Ser	Glu	Trp	Val	Thr	Ala	Ala	Asp
145					150					155					160
Lys	Lys	Thr	Ala	Val	Asp	Met	Ser	Gly	Gly	Thr	Val	Thr	Val	Leu	Glu
			165				170				175				
Lys	Val	Pro	Val	Ser	Lys	Gly	Gln	Leu	Lys	Gln	Tyr	Phe	Tyr	Glu	Thr

180 185 190
 Lys Cys Asn Pro Met Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp
 195 200 205
 Lys Arg His Trp Asn Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg
 210 215 220
 Ala Leu Thr Met Asp Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg
 225 230 235 240

Ile Asp Thr Ser Cys Val Cys Thr Leu Thr Ile Lys Arg Gly Arg
 245 250 255

<210> 4318

<211> 247

<212> PRT

<213> homo sapiens

<400> 4318

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
 1 5 10 15
 Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
 20 25 30
 Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly

35 40 45
 Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
 50 55 60
 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu

100 105 110
 Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
 115 120 125
 His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
 130 135 140

Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
145 150 155 160
Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
165 170 175
Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
180 185 190
Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
195 200 205
Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
210 215 220
Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
225 230 235 240
Leu Thr Ile Lys Arg Gly Arg
245
<210> 4319
<211> 247
<212> PRT
<213> homo sapiens
<400> 4319
Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
1 5 10 15
Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
20 25 30
Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
35 40 45
Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
50 55 60
His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
65 70 75 80
Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
85 90 95

Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu

100 105 110
Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
115 120 125
His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
130 135 140
Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
145 150 155 160
Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln

165 170 175
Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
180 185 190
Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
195 200 205
Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
210 215 220
Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr

225 230 235 240
Leu Thr Ile Lys Arg Gly Arg
245

<210> 4320

<211> 276

<212> PRT

<213> homo sapiens

<400> 4320

Met Leu Cys Ala Ile Ser Leu Cys Ala Arg Val Arg Lys Leu Arg Ser
1 5 10 15
Ala Gly Arg Cys Gly Lys Phe His Gln Val Arg Arg Val Met Thr Ile
20 25 30
Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met Lys Ala Ala

35

40

45

Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu Ala Tyr Pro
50 55 60
Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly Pro Lys Ala
65 70 75 80
Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu His Val Ile
85 90 95
Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn Glu Glu Asn
100 105 110
Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu Ser Ser Gln
115 120 125
Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu Tyr Lys Asn
130 135 140
Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg His Ser Asp
145 150 155 160
Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile Ser Glu Trp
165 170 175
Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser Gly Gly Thr
180 185 190
Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln Leu Lys Gln
195 200 205
Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr Lys Glu Gly
210 215 220
Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys Arg Thr Thr
225 230 235 240
Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys Arg Ile Gly
245 250 255
Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr Leu Thr Ile
260 265 270
Lys Arg Gly Arg
275
<210> 4321
<211> 329

<212> PRT

<213> homo sapiens

<400> 4321

Met Cys Gly Ala Thr Ser Phe Leu His Glu Cys Thr Arg Leu Ile Leu

1 5 10 15

Val Thr Thr Gln Asn Ala Glu Phe Leu Gln Lys Gly Leu Gln Val His

20 25 30

Thr Cys Phe Gly Val Tyr Pro His Ala Ser Val Trp His Asp Cys Ala

35 40 45

Ser Gln Lys Lys Gly Cys Ala Val Tyr Leu His Val Ser Val Glu Phe

50 55 60

Asn Lys Leu Ile Pro Glu Asn Gly Phe Ile Lys Phe His Gln Val Arg

65 70 75 80

Arg Val Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly

85 90 95

Cys Met Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly

100 105 110

Gly Leu Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val

115 120 125

Asn Gly Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr

130 135 140

Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg

145 150 155 160

Pro Asn Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val

165 170 175

Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu

180 185 190

Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val

195 200 205

Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp

210 215 220

Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp
 225 230 235 240
 Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys
 245 250 255
 Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly
 260 265 270
 Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser
 275 280 285
 Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser
 290 295 300
 Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val
 305 310 315 320
 Cys Thr Leu Thr Ile Lys Arg Gly Arg
 325

<210> 4322

<211> 247

<212> PRT

<213> homo sapiens

<400> 4322

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
 1 5 10 15
 Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
 20 25 30
 Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
 35 40 45
 Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
 50 55 60
 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu

100 105 110
Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
115 120 125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
130 135 140
Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
145 150 155 160
Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
165 170 175
Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
195 200 205
Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
210 215 220
Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
225 230 235 240
Leu Thr Ile Lys Arg Gly Arg
245

<210> 4323

<211> 247

<212> PRT

<213> homo sapiens

<400> 4323

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
1 5 10 15
Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
20 25 30
Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
35 40 45
Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu

50 55 60
 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
 100 105 110
 Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
 115 120 125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
 130 135 140
 Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
 145 150 155 160
 Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
 165 170 175
 Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
 180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
 195 200 205
 Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
 210 215 220
 Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
 225 230 235 240
 Leu Thr Ile Lys Arg Gly Arg
 245

<210> 4324

<211> 247

<212> PRT

<213> homo sapiens

<400> 4324

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met

1 5 10 15
 Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
 20 25 30
 Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
 35 40 45
 Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
 50 55 60

 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
 100 105 110
 Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
 115 120 125

 His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
 130 135 140
 Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
 145 150 155 160
 Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
 165 170 175
 Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
 180 185 190

 Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
 195 200 205
 Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
 210 215 220
 Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
 225 230 235 240
 Leu Thr Ile Lys Arg Gly Arg
 245
 <210> 4325

<211> 247

<212> PRT

<213> homo sapiens

<400> 4325

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met

1 5 10 15

Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu

20 25 30

Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly

35 40 45

Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu

50 55 60

His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn

65 70 75 80

Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu

85 90 95

Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu

100 105 110

Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg

115 120 125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile

130 135 140

Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser

145 150 155 160

Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln

165 170 175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr

180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys

195 200 205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys

210 215 220
 Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
 225 230 235 240
 Leu Thr Ile Lys Arg Gly Arg
 245
 <210> 4326
 <211> 247
 <212> PRT
 <213> homo sapiens

 <400> 4326
 Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met
 1 5 10 15
 Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu
 20 25 30
 Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly
 35 40 45
 Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu
 50 55 60

 His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val Arg Pro Asn
 65 70 75 80
 Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu
 85 90 95
 Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu
 100 105 110
 Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg Val Arg Arg
 115 120 125

 His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile
 130 135 140
 Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser
 145 150 155 160
 Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln
 165 170 175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr
180 185 190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys
195 200 205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys
210 215 220

Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr
225 230 235 240

Leu Thr Ile Lys Arg Gly Arg
245

<210> 4327

<211> 639

<212> PRT

<213> homo sapiens

<400> 4327

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Tyr Pro Glu Leu Gln Ile Thr Asn Val Val Glu Ala
20 25 30

Asn Gln Pro Val Thr Ile Gln Asn Trp Cys Lys Arg Gly Arg Lys Gln
35 40 45

Cys Lys Thr His Pro His Phe Val Ile Pro Tyr Arg Cys Leu Val Gly
50 55 60

Glu Phe Val Ser Asp Ala Leu Leu Val Pro Asp Lys Cys Lys Phe Leu
65 70 75 80

His Gln Glu Arg Met Asp Val Cys Glu Thr His Leu His Trp His Thr
85 90 95

Val Ala Lys Glu Thr Cys Ser Glu Lys Ser Thr Asn Leu His Asp Tyr
100 105 110

Gly Met Leu Leu Pro Cys Gly Ile Asp Lys Phe Arg Gly Val Glu Phe
115 120 125

Val Cys Cys Pro Leu Ala Glu Glu Ser Asp Asn Val Asp Ser Ala Asp
130 135 140

Ala Glu Glu Asp Asp Ser Asp Val Trp Trp Gly Gly Ala Asp Thr Asp
145 150 155 160

Tyr Ala Asp Gly Ser Glu Asp Lys Val Val Glu Val Ala Glu Glu Glu
165 170 175

Glu Val Ala Glu Val Glu Glu Glu Glu Ala Asp Asp Asp Glu Asp Asp
180 185 190

Glu Asp Gly Asp Glu Val Glu Glu Glu Ala Glu Glu Pro Tyr Glu Glu
195 200 205

Ala Thr Glu Arg Thr Thr Ser Ile Ala Thr Thr Thr Thr Thr Thr Thr
210 215 220

Glu Ser Val Glu Glu Val Val Arg Val Pro Thr Thr Ala Ala Ser Thr
225 230 235 240

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
245 250 255

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg
260 265 270

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
275 280 285

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
290 295 300

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
305 310 315 320

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp
325 330 335

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
340 345 350

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
355 360 365

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val

370	375	380	
Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met			
385	390	395	400
Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu			
	405	410	415
Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp			
	420	425	430
Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn			
	435	440	445
Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro			
	450	455	460
Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly			
465	470	475	480
Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp			
	485	490	495
Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg			
	500	505	510
Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr			
	515	520	525
Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe			
	530	535	540
Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe			
545	550	555	560
Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val			
	565	570	575
Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu			
	580	585	590
Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp			
	595	600	605
Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn			
610	615	620	

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn

625 630 635

<210> 4328

<211> 695

<212> PRT

<213> homo sapiens

<400> 4328

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg

1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro

20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln

35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp

50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu

65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn

85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val

100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu

115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys

130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu

145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile

165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu

180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
 290 295 300
 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
 305 310 315 320
 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
 325 330 335
 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
 340 345 350
 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
 355 360 365
 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
 370 375 380
 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
 385 390 395 400
 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe
 405 410 415
 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
 420 425 430
 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala

435 440 445
 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
 450 455 460
 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
 465 470 475 480
 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
 485 490 495
 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser

 500 505 510
 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
 515 520 525
 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
 530 535 540
 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
 545 550 555 560
 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr

 565 570 575
 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
 580 585 590
 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
 595 600 605
 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
 610 615 620
 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val

 625 630 635 640
 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
 645 650 655
 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
 660 665 670
 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
 675 680 685
 Phe Phe Glu Gln Met Gln Asn

690

695

<210> 4329

<211> 751

<212> PRT

<213> homo sapiens

<400> 4329

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg

1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro

20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln

35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp

50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu

65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn

85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val

100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu

115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys

130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu

145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile

165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu

180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val

195 200 205
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
 210 215 220
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu

 245 250 255
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
 260 265 270
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
 275 280 285
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
 290 295 300
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe

 305 310 315 320
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
 325 330 335
 Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr
 340 345 350
 Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu
 355 360 365
 His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg

 370 375 380
 Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln
 385 390 395 400
 Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe
 405 410 415
 Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln
 420 425 430
 Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp

 435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val
 450 455 460
 Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg
 465 470 475 480
 Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val
 485 490 495
 Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met
 500 505 510
 Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu
 515 520 525
 Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp
 530 535 540
 Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn
 545 550 555 560
 Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro
 565 570 575
 Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly
 580 585 590
 Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp
 595 600 605
 Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg
 610 615 620
 Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr
 625 630 635 640
 Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe
 645 650 655
 Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe
 660 665 670
 Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val
 675 680 685
 Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu

690 695 700
 Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp
 705 710 715 720
 Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn
 725 730 735
 Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
 740 745 750
 <210> 4330
 <211> 714
 <212> PRT
 <213> homo sapiens

 <400> 4330
 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
 1 5 10 15
 Ala Leu Glu Val Tyr Pro Glu Leu Gln Ile Thr Asn Val Val Glu Ala
 20 25 30
 Asn Gln Pro Val Thr Ile Gln Asn Trp Cys Lys Arg Gly Arg Lys Gln
 35 40 45
 Cys Lys Thr His Pro His Phe Val Ile Pro Tyr Arg Cys Leu Val Gly
 50 55 60

 Glu Phe Val Ser Asp Ala Leu Leu Val Pro Asp Lys Cys Lys Phe Leu
 65 70 75 80
 His Gln Glu Arg Met Asp Val Cys Glu Thr His Leu His Trp His Thr
 85 90 95
 Val Ala Lys Glu Thr Cys Ser Glu Lys Ser Thr Asn Leu His Asp Tyr
 100 105 110
 Gly Met Leu Leu Pro Cys Gly Ile Asp Lys Phe Arg Gly Val Glu Phe
 115 120 125

 Val Cys Cys Pro Leu Ala Glu Glu Ser Asp Asn Val Asp Ser Ala Asp
 130 135 140
 Ala Glu Glu Asp Asp Ser Asp Val Trp Trp Gly Gly Ala Asp Thr Asp
 145 150 155 160

Tyr Ala Asp Gly Ser Glu Asp Lys Val Val Glu Val Ala Glu Glu Glu
 165 170 175
 Glu Val Ala Glu Val Glu Glu Glu Glu Ala Asp Asp Asp Glu Asp Asp
 180 185 190

 Glu Asp Gly Asp Glu Val Glu Glu Glu Ala Glu Glu Pro Tyr Glu Glu
 195 200 205
 Ala Thr Glu Arg Thr Thr Ser Ile Ala Thr Thr Thr Thr Thr Thr Thr
 210 215 220
 Glu Ser Val Glu Glu Val Val Arg Glu Val Cys Ser Glu Gln Ala Glu
 225 230 235 240
 Thr Gly Pro Cys Arg Ala Met Ile Ser Arg Trp Tyr Phe Asp Val Thr
 245 250 255

 Glu Gly Lys Cys Ala Pro Phe Phe Tyr Gly Gly Cys Gly Gly Asn Arg
 260 265 270
 Asn Asn Phe Asp Thr Glu Glu Tyr Cys Met Ala Val Cys Gly Ser Ala
 275 280 285
 Met Ser Gln Ser Leu Leu Lys Thr Thr Gln Glu Pro Leu Ala Arg Asp
 290 295 300
 Pro Val Lys Leu Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp
 305 310 315 320

 Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln
 325 330 335
 Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln
 340 345 350
 Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro
 355 360 365
 Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu
 370 375 380

 Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr
 385 390 395 400
 His Met Ala Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala

405 410 415
 Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg
 420 425 430
 His Val Phe Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp
 435 440 445

 Arg Gln His Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro
 450 455 460
 Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val
 465 470 475 480
 Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro
 485 490 495
 Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys
 500 505 510

 Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro
 515 520 525
 Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr
 530 535 540
 Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp
 545 550 555 560
 Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn
 565 570 575

 Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg
 580 585 590
 Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu
 595 600 605
 Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly
 610 615 620
 Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly
 625 630 635 640

 Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile
 645 650 655

Ala Thr Val Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr
660 665 670
Thr Ser Ile His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro
675 680 685
Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro
690 695 700

Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
705 710

<210> 4331

<211> 746

<212> PRT

<213> homo sapiens

<400> 4331

Met Asp Gln Leu Glu Asp Leu Leu Val Leu Phe Ile Asn Tyr Val Pro
1 5 10 15
Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro Gln Ile Ala Met Phe
20 25 30
Cys Gly Arg Leu Asn Met His Met Asn Val Gln Asn Gly Lys Trp Asp
35 40 45

Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp Thr Lys Glu Gly Ile
50 55 60
Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu Gln Ile Thr Asn Val
65 70 75 80
Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn Trp Cys Lys Arg Gly
85 90 95
Arg Lys Gln Cys Lys Thr His Pro His Phe Val Ile Pro Tyr Arg Cys
100 105 110

Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu Val Pro Asp Lys Cys
115 120 125
Lys Phe Leu His Gln Glu Arg Met Asp Val Cys Glu Thr His Leu His
130 135 140
Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu Lys Ser Thr Asn Leu

145 150 155 160
 His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile Asp Lys Phe Arg Gly
 165 170 175

 Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu Ser Asp Asn Val Asp
 180 185 190
 Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val Trp Trp Gly Gly Ala
 195 200 205
 Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys Val Val Glu Val Ala
 210 215 220
 Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu Glu Ala Asp Asp Asp
 225 230 235 240

 Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu Glu Ala Glu Glu Pro
 245 250 255
 Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile Ala Thr Thr Thr Thr
 260 265 270
 Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg Glu Val Cys Ser Glu
 275 280 285
 Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile Ser Arg Trp Tyr Phe
 290 295 300

 Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe Tyr Gly Gly Cys Gly
 305 310 315 320
 Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr Cys Met Ala Val Cys
 325 330 335
 Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp
 340 345 350
 Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln
 355 360 365

 Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln
 370 375 380
 Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro
 385 390 395 400

Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu
 405 410 415
 Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr
 420 425 430

 His Met Ala Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala
 435 440 445
 Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg
 450 455 460
 His Val Phe Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp
 465 470 475 480
 Arg Gln His Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro
 485 490 495

 Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val
 500 505 510
 Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro
 515 520 525
 Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys
 530 535 540
 Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro
 545 550 555 560

 Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr
 565 570 575
 Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp
 580 585 590
 Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn
 595 600 605
 Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg
 610 615 620

 Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu
 625 630 635 640
 Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly

645 650 655
Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly
660 665 670
Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile
675 680 685

Ala Thr Val Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr
690 695 700
Thr Ser Ile His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro
705 710 715 720
Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro
725 730 735

Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn
740 745

<210> 4332

<211> 770

<212>

> PRT

<213> homo sapiens

<400> 4332

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15
Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30
Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala

355	360	365	
Ala Ser Thr Pro Asp	Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp		
370	375	380	
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala			
385	390	395	400
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala			
405	410	415	
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile			
420	425	430	
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn			
435	440	445	
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met			
450	455	460	
Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu			
465	470	475	480
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys			
485	490	495	
Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe			
500	505	510	
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser			
515	520	525	
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser			
530	535	540	
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp			
545	550	555	560
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val			
565	570	575	
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala			
580	585	590	
Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro			
595	600	605	

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 4333

<211> 660

<212> PRT

<213> homo sapiens

<400> 4333

Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln Asn Gly Lys
1 5 10 15

Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp Thr Lys Glu
20 25 30

Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu Gln Ile Thr

35 40 45
 Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn Trp Cys Lys

 50 55 60
 Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val Ile Pro Tyr
 65 70 75 80
 Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu Val Pro Asp
 85 90 95
 Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys Glu Thr His
 100 105 110
 Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu Lys Ser Thr

 115 120 125
 Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile Asp Lys Phe
 130 135 140
 Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu Ser Asp Asn
 145 150 155 160
 Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val Trp Trp Gly
 165 170 175
 Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys Val Val Glu

 180 185 190
 Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu Glu Ala Asp
 195 200 205
 Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu Glu Ala Glu
 210 215 220
 Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile Ala Thr Thr
 225 230 235 240
 Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg Val Pro Thr

 245 250 255
 Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro
 260 265 270
 Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu
 275 280 285

Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu
 290 295 300
 Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala

 305 310 315 320
 Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala
 325 330 335
 Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu
 340 345 350
 Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr
 355 360 365
 Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu

 370 375 380
 Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys
 385 390 395 400
 His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile
 405 410 415
 Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn
 420 425 430
 Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile

 435 440 445
 Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp
 450 455 460
 Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn
 465 470 475 480
 Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu
 485 490 495
 Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His

 500 505 510
 Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu
 515 520 525
 Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro

530 535 540
 Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys
 545 550 555 560
 Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln

 565 570 575
 Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile
 580 585 590
 Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile
 595 600 605
 Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly
 610 615 620
 Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser

 625 630 635 640
 Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu
 645 650 655
 Gln Met Gln Asn
 660
 <210> 4334
 <211> 313
 <212> PRT
 <213> homo sapiens
 <400> 4334
 Met Thr Ser Cys His Ile Ala Glu Glu His Ile Gln Lys Val Ala Ile
 1 5 10 15
 Phe Gly Gly Thr His Gly Asn Glu Leu Thr Gly Val Phe Leu Val Lys
 20 25 30

 His Trp Leu Glu Asn Gly Ala Glu Ile Gln Arg Thr Gly Leu Glu Val
 35 40 45
 Lys Pro Phe Ile Thr Asn Pro Arg Ala Val Lys Lys Cys Thr Arg Tyr
 50 55 60
 Ile Asp Cys Asp Leu Asn Arg Ile Phe Asp Leu Glu Asn Leu Gly Lys
 65 70 75 80

Lys Met Ser Glu Asp Leu Pro Tyr Glu Val Arg Arg Ala Gln Glu Ile
85 90 95

Asn His Leu Phe Gly Pro Lys Asp Ser Glu Asp Ser Tyr Asp Ile Ile
100 105 110

Phe Asp Leu His Asn Thr Thr Ser Asn Met Gly Cys Thr Leu Ile Leu
115 120 125

Glu Asp Ser Arg Asn Asn Phe Leu Ile Gln Met Phe His Tyr Ile Lys
130 135 140

Thr Ser Leu Ala Pro Leu Pro Cys Tyr Val Tyr Leu Ile Glu His Pro
145 150 155 160

Ser Leu Lys Tyr Ala Thr Thr Arg Ser Ile Ala Lys Tyr Pro Val Gly
165 170 175

Ile Glu Val Gly Pro Gln Pro Gln Gly Val Leu Arg Ala Asp Ile Leu
180 185 190

Asp Gln Met Arg Lys Met Ile Lys His Ala Leu Asp Phe Ile His His
195 200 205

Phe Asn Glu Gly Lys Glu Phe Pro Pro Cys Ala Ile Glu Val Tyr Lys
210 215 220

Ile Ile Glu Lys Val Asp Tyr Pro Arg Asp Glu Asn Gly Glu Ile Ala
225 230 235 240

Ala Ile Ile His Pro Asn Leu Gln Asp Gln Asp Trp Lys Pro Leu His
245 250 255

Pro Gly Asp Pro Met Phe Leu Thr Leu Asp Gly Lys Thr Ile Pro Leu
260 265 270

Gly Gly Asp Cys Thr Val Tyr Pro Val Phe Val Asn Glu Ala Ala Tyr
275 280 285

Tyr Glu Lys Lys Glu Ala Phe Ala Lys Thr Thr Lys Leu Thr Leu Asn
290 295 300

Ala Lys Ser Ile Arg Cys Cys Leu His
305 310

<210> 4335

<211> 313

<212> PRT

<213> homo sapiens

<400> 4335

Met Thr Ser Cys His Ile Ala Glu Glu His Ile Gln Lys Val Ala Ile

1 5 10 15

Phe Gly Gly Thr His Gly Asn Glu Leu Thr Gly Val Phe Leu Val Lys

20 25 30

His Trp Leu Glu Asn Gly Ala Glu Ile Gln Arg Thr Gly Leu Glu Val

35 40 45

Lys Pro Phe Ile Thr Asn Pro Arg Ala Val Lys Lys Cys Thr Arg Tyr

50 55 60

Ile Asp Cys Asp Leu Asn Arg Ile Phe Asp Leu Glu Asn Leu Gly Lys

65 70 75 80

Lys Met Ser Glu Asp Leu Pro Tyr Glu Val Arg Arg Ala Gln Glu Ile

85 90 95

Asn His Leu Phe Gly Pro Lys Asp Ser Glu Asp Ser Tyr Asp Ile Ile

100 105 110

Phe Asp Leu His Asn Thr Thr Ser Asn Met Gly Cys Thr Leu Ile Leu

115 120 125

Glu Asp Ser Arg Asn Asn Phe Leu Ile Gln Met Phe His Tyr Ile Lys

130 135 140

Thr Ser Leu Ala Pro Leu Pro Cys Tyr Val Tyr Leu Ile Glu His Pro

145 150 155 160

Ser Leu Lys Tyr Ala Thr Thr Arg Ser Ile Ala Lys Tyr Pro Val Gly

165 170 175

Ile Glu Val Gly Pro Gln Pro Gln Gly Val Leu Arg Ala Asp Ile Leu

180 185 190

Asp Gln Met Arg Lys Met Ile Lys His Ala Leu Asp Phe Ile His His

195 200 205

Phe Asn Glu Gly Lys Glu Phe Pro Pro Cys Ala Ile Glu Val Tyr Lys

210						215						220					
Ile	Ile	Glu	Lys	Val	Asp	Tyr	Pro	Arg	Asp	Glu	Asn	Gly	Glu	Ile	Ala		
225						230						235					
Ala	Ile	Ile	His	Pro	Asn	Leu	Gln	Asp	Gln	Asp	Trp	Lys	Pro	Leu	His		
					245						250						
Pro	Gly	Asp	Pro	Met	Phe	Leu	Thr	Leu	Asp	Gly	Lys	Thr	Ile	Pro	Leu		
					260						265						
Gly	Gly	Asp	Cys	Thr	Val	Tyr	Pro	Val	Phe	Val	Asn	Glu	Ala	Ala	Tyr		
					275						280						
Tyr	Glu	Lys	Lys	Glu	Ala	Phe	Ala	Lys	Thr	Thr	Lys	Leu	Thr	Leu	Asn		
					290						300						
Ala	Lys	Ser	Ile	Arg	Cys	Cys	Leu	His									
305						310											
<210>	4336																
<211>	382																
<212>	PRT																
<213>	homo sapiens																
<400>	4336																
Met	Gly	Pro	Thr	Ser	Val	Pro	Leu	Val	Lys	Ala	His	Arg	Ser	Ser	Val		
1				5				10				15					
Ser	Asp	Tyr	Val	Asn	Tyr	Asp	Ile	Ile	Val	Arg	His	Tyr	Asn	Tyr	Thr		
				20					25					30			
Gly	Lys	Leu	Asn	Ile	Ser	Ala	Asp	Lys	Glu	Asn	Ser	Ile	Lys	Leu	Thr		
				35					40					45			
Ser	Val	Val	Phe	Ile	Leu	Ile	Cys	Cys	Phe	Ile	Ile	Leu	Glu	Asn	Ile		
			50				55				60						
Phe	Val	Leu	Leu	Thr	Ile	Trp	Lys	Thr	Lys	Lys	Phe	His	Arg	Pro	Met		
65						70						75					
Tyr	Tyr	Phe	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Ala	Gly	Val		
					85						90						
Ala	Tyr	Thr	Ala	Asn	Leu	Leu	Leu	Ser	Gly	Ala	Thr	Thr	Tyr	Lys	Leu		

100	105	110	
Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu			
115	120	125	
Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile			
130	135	140	
Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu			
145	150	155	160
Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly			
165	170	175	
Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser			
180	185	190	
Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr			
195	200	205	
Val Phe Thr Leu Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile			
210	215	220	
Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys Asn			
225	230	235	240
Ile Ser Lys Ala Ser Arg Ser Ser Glu Lys Ser Leu Ala Leu Leu Lys			
245	250	255	
Thr Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu			
260	265	270	
Phe Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp			
275	280	285	
Ile Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser			
290	295	300	
Gly Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg			
305	310	315	320
Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp Ser			
325	330	335	
Ala Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg			
340	345	350	

Ser Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn
355 360 365
Pro Glu Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser Ser
370 375 380
<210> 4337
<211> 460
<212> PRT
<213> homo sapiens
<400> 4337
Met Pro Leu Arg Arg Arg Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn
1 5 10 15
Ser Tyr Trp Arg Val His Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr
20 25 30
Phe Lys Glu Asn Gly Tyr Val Thr Met Ser Val Gly Lys Val Phe His
35 40 45
Pro Gly Ile Ser Ser Asn His Thr Asp Asp Ser Pro Tyr Ser Trp Ser
50 55 60
Phe Pro Pro Tyr His Pro Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr
65 70 75 80
Cys Arg Gly Pro Asp Gly Glu Leu His Ala Asn Leu Leu Cys Pro Val
85 90 95
Asp Val Leu Asp Val Pro Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr
100 105 110
Glu Gln Ala Ile Gln Leu Leu Glu Lys Met Lys Thr Ser Ala Ser Pro
115 120 125
Phe Phe Leu Ala Val Gly Tyr His Lys Pro His Ile Pro Phe Arg Tyr
130 135 140
Pro Lys Glu Phe Gln Lys Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala
145 150 155 160
Pro Asp Pro Glu Val Pro Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro
165 170 175
Trp Met Asp Ile Arg Gln Arg Glu Asp Val Gln Ala Leu Asn Ile Ser

180 185 190
Val Pro Tyr Gly Pro Ile Pro Val Asp Phe Gln Arg Lys Ile Arg Gln
195 200 205
Ser Tyr Phe Ala Ser Val Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu

210 215 220
Leu Ser Ala Leu Asp Asp Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala
225 230 235 240
Phe Thr Ser Asp His Gly Trp Ala Leu Gly Glu His Gly Glu Trp Ala
245 250 255
Lys Tyr Ser Asn Phe Asp Val Ala Thr His Val Pro Leu Ile Phe Tyr
260 265 270
Val Pro Gly Arg Thr Ala Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe

275 280 285
Pro Tyr Leu Asp Pro Phe Asp Ser Ala Ser Gln Leu Met Glu Pro Gly
290 295 300
Arg Gln Ser Met Asp Leu Val Glu Leu Val Ser Leu Phe Pro Thr Leu
305 310 315 320
Ala Gly Leu Ala Gly Leu Gln Val Pro Pro Arg Cys Pro Val Pro Ser
325 330 335
Phe His Val Glu Leu Cys Arg Glu Gly Lys Asn Leu Leu Lys His Phe

340 345 350
Arg Phe Arg Asp Leu Glu Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg
355 360 365
Glu Leu Ile Ala Tyr Ser Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln
370 375 380
Trp Asn Ser Asp Lys Pro Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr
385 390 395 400
Ser Ile Arg Thr Ile Asp Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn

405 410 415
Pro Asp Glu Phe Leu Ala Asn Phe Ser Asp Ile His Ala Gly Glu Leu
420 425 430

Tyr Phe Val Asp Ser Asp Pro Leu Gln Asp His Asn Met Tyr Asn Asp
 435 440 445
 Ser Gln Gly Gly Asp Leu Phe Gln Leu Leu Met Pro
 450 455 460
 <210> 4338
 <211> 343
 <212> PRT
 <213> homo sapiens
 <400> 4338
 Met Pro Pro Pro Arg Thr Gly Arg Gly Leu Leu Trp Leu Gly Leu Val

 1 5 10 15
 Leu Ser Ser Val Cys Val Ala Leu Gly Ser Glu Thr Gln Ala Asn Ser
 20 25 30
 Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg
 35 40 45
 Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn Ile
 50 55 60
 Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala Gln

 65 70 75 80
 Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg Arg
 85 90 95
 Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val His
 100 105 110
 Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr
 115 120 125
 Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn

 130 135 140
 His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro
 145 150 155 160
 Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly
 165 170 175
 Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro

180 185 190
Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu

195 200 205
Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val Gly

210 215 220
Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln Lys

225 230 235 240
Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro

245 250 255
Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln

260 265 270
Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile

275 280 285
Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val

290 295 300
Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp

305 310 315 320
Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly

325 330 335
Phe Leu Met Arg Thr Asn Thr

340

<210> 4339

<211> 550

<212> PRT

<213> homo sapiens

<400> 4339

Met Pro Pro Pro Arg Thr Gly Arg Gly Leu Leu Trp Leu Gly Leu Val

1 5 10 15

Leu Ser Ser Val Cys Val Ala Leu Gly Ser Glu Thr Gln Ala Asn Ser

20 25 30

Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg

35	40	45	
Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn Ile			
50	55	60	
Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala Gln			
65	70	75	80
Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg Arg			
85	90	95	
Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val His			
100	105	110	
Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr			
115	120	125	
Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn			
130	135	140	
His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro			
145	150	155	160
Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly			
165	170	175	
Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro			
180	185	190	
Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu			
195	200	205	
Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val Gly			
210	215	220	
Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln Lys			
225	230	235	240
Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro			
245	250	255	
Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln			
260	265	270	
Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile			
275	280	285	

Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val

290 295 300

Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp

305 310 315 320

Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly

325 330 335

Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe Asp

340 345 350

Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr Ala

355 360 365

Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro Phe

370 375 380

Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp Leu

385 390 395 400

Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly Leu

405 410 415

Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu Cys

420 425 430

Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu Glu

435 440 445

Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr Ser

450 455 460

Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys Pro

465 470 475 480

Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile Asp

485 490 495

Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu Ala

500 505 510

Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser Asp

515 520 525

Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp Leu

530 535 540
Phe Gln Leu Leu Met Pro
545 550

<210> 4340
<211> 361
<212> PRT
<213> homo sapiens
<400> 4340

Met Ala Ala Pro Arg Ala Gly Arg Gly Ala Gly Trp Ser Leu Arg Ala
1 5 10 15
Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
20 25 30
Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
35 40 45
Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly

50 55 60
Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
65 70 75 80
Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
85 90 95
Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
100 105 110
Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro

115 120 125
Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg
130 135 140
Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
145 150 155 160
Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
165 170 175
Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu

180 185 190
 Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val
 195 200 205
 Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
 210 215 220
 Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Phe Gly Asn
 225 230 235 240
 Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val Asn

245 250 255
 Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp Arg
 260 265 270
 Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser Gly
 275 280 285
 Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr Leu
 290 295 300
 Ser Pro Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile Gly

305 310 315 320
 Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg Thr
 325 330 335
 Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu Thr
 340 345 350
 Leu Tyr Val Thr Pro Glu Val Thr Glu
 355 360

<210> 4341

<211> 458

<212> PRT

<213> homo sapiens

<400> 4341

Met Ala Ala Pro Arg Ala Gly Arg Gly Ala Gly Trp Ser Leu Arg Ala

1 5 10 15
 Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
 20 25 30

Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
35 40 45
Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly
50 55 60
Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
65 70 75 80
Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
85 90 95
Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
100 105 110
Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro
115 120 125
Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Pro Ala Ser Pro Arg
130 135 140
Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
145 150 155 160
Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
165 170 175
Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu
180 185 190
Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val
195 200 205
Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
210 215 220
Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu
225 230 235 240
Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe
245 250 255
Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser
260 265 270
Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro

275 280 285
 Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly
 290 295 300
 Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val
 305 310 315 320
 Asn Thr Met Lys Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp

325 330 335
 Arg Leu Arg Glu Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser
 340 345 350
 Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr
 355 360 365
 Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe
 370 375 380
 Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser

385 390 395 400
 Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile
 405 410 415
 Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg
 420 425 430
 Thr Gln Ser Gln Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu
 435 440 445
 Thr Leu Tyr Val Thr Pro Glu Val Thr Glu
 450 455

<210> 4342

<211> 187

<212> PRT

<213> homo sapiens

<400> 4342

Met Trp Cys Ala Ser Pro Val Ala Val Val Ala Phe Cys Ala Gly Leu
 1 5 10 15
 Leu Val Ser His Pro Val Leu Thr Gln Gly Gln Glu Ala Gly Gly Arg
 20 25 30

Pro Gly Ala Asp Cys Glu Val Cys Lys Glu Phe Leu Asn Arg Phe Tyr
35 40 45
Lys Ser Leu Ile Asp Arg Gly Val Asn Phe Ser Leu Asp Thr Ile Glu
50 55 60
Lys Glu Leu Ile Ser Phe Cys Leu Asp Thr Lys Gly Lys Glu Asn Arg
65 70 75 80
Leu Cys Tyr Tyr Leu Gly Ala Thr Lys Asp Ala Ala Thr Lys Ile Leu
85 90 95
Ser Glu Val Thr Arg Pro Met Ser Val His Met Pro Ala Met Lys Ile
100 105 110
Cys Glu Lys Leu Lys Lys Leu Asp Ser Gln Ile Cys Glu Leu Lys Tyr
115 120 125
Glu Lys Thr Leu Asp Leu Ala Ser Val Asp Leu Arg Lys Met Arg Val
130 135 140
Ala Glu Leu Lys Gln Ile Leu His Ser Trp Gly Glu Glu Cys Arg Ala
145 150 155 160
Cys Ala Glu Lys Thr Asp Tyr Val Asn Leu Ile Gln Glu Leu Ala Pro
165 170 175
Lys Tyr Ala Ala Thr His Pro Lys Thr Glu Leu
180 185
<210> 4343
<211> 198
<212> PRT
<213> homo sapiens
<400> 4343
Met Ala Asp Gln Arg Gln Arg Ser Leu Ser Thr Ser Gly Glu Ser Leu
1 5 10 15
Tyr His Val Leu Gly Leu Asp Lys Asn Ala Thr Ser Asp Asp Ile Lys
20 25 30
Lys Ser Tyr Arg Lys Leu Ala Leu Lys Tyr His Pro Asp Lys Asn Pro
35 40 45

Asp Asn Pro Glu Ala Ala Asp Lys Phe Lys Glu Ile Asn Asn Ala His

50

55

60

Ala Ile Leu Thr Asp Ala Thr Lys Arg Asn Ile Tyr Asp Lys Tyr Gly

65

70

75

80

Ser Leu Gly Leu Tyr Val Ala Glu Gln Phe Gly Glu Glu Asn Val Asn

85

90

95

Thr Tyr Phe Val Leu Ser Ser Trp Trp Ala Lys Ala Leu Phe Val Phe

100

105

110

Cys Gly Leu Leu Thr Cys Cys Tyr Cys Cys Cys Cys Leu Cys Cys Cys

115

120

125

Phe Asn Cys Cys Cys Gly Lys Cys Lys Pro Lys Ala Pro Glu Gly Glu

130

135

140

Glu Thr Glu Phe Tyr Val Ser Pro Glu Asp Leu Glu Ala Gln Leu Gln

145

150

155

160

Ser Asp Glu Arg Glu Ala Thr Asp Thr Pro Ile Val Ile Gln Pro Ala

165

170

175

Ser Ala Thr Glu Thr Thr Gln Leu Thr Ala Asp Ser His Pro Ser Tyr

180

185

190

His Thr Asp Gly Phe Asn

195

<210> 4344

<211> 653

<212> PRT

<213> homo sapiens

<400> 4344

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser

1

5

10

15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val

20

25

30

His Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg

35

40

45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
 50 55 60
 Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
 65 70 75 80
 Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
 85 90 95
 Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr
 100 105 110
 His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
 115 120 125
 Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
 130 135 140
 Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
 145 150 155 160
 Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
 165 170 175
 Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
 180 185 190
 Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
 195 200 205
 Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
 210 215 220
 Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
 225 230 235 240
 Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
 245 250 255
 Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
 260 265 270
 Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
 275 280 285
 Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val

290 295 300
 Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
 305 310 315 320
 Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
 325 330 335
 Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
 340 345 350
 Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg

 355 360 365
 Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
 370 375 380
 Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
 385 390 395 400
 Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
 405 410 415
 Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp

 420 425 430
 Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
 435 440 445
 His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
 450 455 460
 Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
 465 470 475 480
 Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro

 485 490 495
 Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
 500 505 510
 Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
 515 520 525
 Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
 530 535 540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr

545 550 555 560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys

565 570 575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr

580 585 590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser

595 600 605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp

610 615 620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu

625 630 635 640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

645 650

<210> 4345

<211> 807

<212> PRT

<213> homo sapiens

<400> 4345

Met Arg Leu Ser Pro Ala Pro Leu Lys Leu Ser Arg Thr Pro Ala Leu

1 5 10 15

Leu Ala Leu Ala Leu Pro Leu Ala Ala Ala Leu Ala Phe Ser Asp Glu

20 25 30

Thr Leu Asp Lys Val Pro Lys Ser Glu Gly Tyr Cys Ser Arg Ile Leu

35 40 45

Arg Ala Gln Gly Thr Arg Arg Glu Gly Tyr Thr Glu Phe Ser Leu Arg

50 55 60

Val Glu Gly Asp Pro Asp Phe Tyr Lys Pro Gly Thr Ser Tyr Arg Val

65 70 75 80

Thr Leu Ser Ala Ala Pro Pro Ser Tyr Phe Arg Gly Phe Thr Leu Ile

85 90 95

Ala Leu Arg Glu Asn Arg Glu Gly Asp Lys Glu Glu Asp His Ala Gly
100 105 110

Thr Phe Gln Ile Ile Asp Glu Glu Glu Thr Gln Phe Met Ser Asn Cys
115 120 125

Pro Val Ala Val Thr Glu Ser Thr Pro Arg Arg Arg Thr Arg Ile Gln
130 135 140

Val Phe Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Ile Leu Lys
145 150 155 160

Ala Ser Ile Val Gln Lys Arg Ile Ile Tyr Phe Gln Asp Glu Gly Ser
165 170 175

Leu Thr Lys Lys Leu Cys Glu Gln Asp Ser Thr Phe Asp Gly Val Thr
180 185 190

Asp Lys Pro Ile Leu Asp Cys Cys Ala Cys Gly Thr Ala Lys Tyr Arg
195 200 205

Leu Thr Phe Tyr Gly Asn Trp Ser Glu Lys Thr His Pro Lys Asp Tyr
210 215 220

Pro Arg Arg Ala Asn His Trp Ser Ala Ile Ile Gly Gly Ser His Ser
225 230 235 240

Lys Asn Tyr Val Leu Trp Glu Tyr Gly Gly Tyr Ala Ser Glu Gly Val
245 250 255

Lys Gln Val Ala Glu Leu Gly Ser Pro Val Lys Met Glu Glu Glu Ile
260 265 270

Arg Gln Gln Ser Asp Glu Val Leu Thr Val Ile Lys Ala Lys Ala Gln
275 280 285

Trp Pro Ala Trp Gln Pro Leu Asn Val Arg Ala Ala Pro Ser Ala Glu
290 295 300

Phe Ser Val Asp Arg Thr Arg His Leu Met Ser Phe Leu Thr Met Met
305 310 315 320

Gly Pro Ser Pro Asp Trp Asn Val Gly Leu Ser Ala Glu Asp Leu Cys
325 330 335

Thr Lys Glu Cys Gly Trp Val Gln Lys Val Val Gln Asp Leu Ile Pro

340 345 350
 Trp Asp Ala Gly Thr Asp Ser Gly Val Thr Tyr Glu Ser Pro Asn Lys
 355 360 365
 Pro Thr Ile Pro Gln Glu Lys Ile Arg Pro Leu Thr Ser Leu Asp His
 370 375 380
 Pro Gln Ser Pro Phe Tyr Asp Pro Glu Gly Gly Ser Ile Thr Gln Val
 385 390 395 400

 Ala Arg Val Val Ile Glu Arg Ile Ala Arg Lys Gly Glu Gln Cys Asn
 405 410 415
 Ile Val Pro Asp Asn Val Asp Asp Ile Val Ala Asp Leu Ala Pro Glu
 420 425 430
 Glu Lys Asp Glu Asp Asp Thr Pro Glu Thr Cys Ile Tyr Ser Asn Trp
 435 440 445
 Ser Pro Trp Ser Ala Cys Ser Ser Ser Thr Cys Asp Lys Gly Lys Arg
 450 455 460

 Met Arg Gln Arg Met Leu Lys Ala Gln Leu Asp Leu Ser Val Pro Cys
 465 470 475 480
 Pro Asp Thr Gln Asp Phe Gln Pro Cys Met Gly Pro Gly Cys Ser Asp
 485 490 495
 Glu Asp Gly Ser Thr Cys Thr Met Ser Glu Trp Ile Thr Trp Ser Pro
 500 505 510
 Cys Ser Ile Ser Cys Gly Met Gly Met Arg Ser Arg Glu Arg Tyr Val
 515 520 525

 Lys Gln Phe Pro Glu Asp Gly Ser Val Cys Thr Leu Pro Thr Glu Glu
 530 535 540
 Thr Glu Lys Cys Thr Val Asn Glu Glu Cys Ser Pro Ser Ser Cys Leu
 545 550 555 560
 Met Thr Glu Trp Gly Glu Trp Asp Glu Cys Ser Ala Thr Cys Gly Met
 565 570 575
 Gly Met Lys Lys Arg His Arg Met Ile Lys Met Asn Pro Ala Asp Gly
 580 585 590

Ser Met Cys Lys Ala Glu Thr Ser Gln Ala Glu Lys Cys Met Met Pro
595 600 605

Glu Cys His Thr Ile Pro Cys Leu Leu Ser Pro Trp Ser Glu Trp Ser
610 615 620

Asp Cys Ser Val Thr Cys Gly Lys Gly Met Arg Thr Arg Gln Arg Met
625 630 635 640

Leu Lys Ser Leu Ala Glu Leu Gly Asp Cys Asn Glu Asp Leu Glu Gln
645 650 655

Val Glu Lys Cys Met Leu Pro Glu Cys Pro Ile Asp Cys Glu Leu Thr
660 665 670

Glu Trp Ser Gln Trp Ser Glu Cys Asn Lys Ser Cys Gly Lys Gly His
675 680 685

Val Ile Arg Thr Arg Met Ile Gln Met Glu Pro Gln Phe Gly Gly Ala
690 695 700

Pro Cys Pro Glu Thr Val Gln Arg Lys Lys Cys Arg Ile Arg Lys Cys
705 710 715 720

Leu Arg Asn Pro Ser Ile Gln Lys Leu Arg Trp Arg Glu Ala Arg Glu
725 730 735

Ser Arg Arg Ser Glu Gln Leu Lys Glu Glu Ser Glu Gly Glu Gln Phe
740 745 750

Pro Gly Cys Arg Met Arg Pro Trp Thr Ala Trp Ser Glu Cys Thr Lys
755 760 765

Leu Cys Gly Gly Gly Ile Gln Glu Arg Tyr Met Thr Val Lys Lys Arg
770 775 780

Phe Lys Ser Ser Gln Phe Thr Ser Cys Lys Asp Lys Lys Glu Ile Arg
785 790 795 800

Ala Cys Asn Val His Pro Cys
805

<210> 4346

<211> 302

<212> PRT

<213> homo sapiens

<400> 4346

Met Glu Ile Gln Glu Leu Glu Glu Ile Gln Ala Cys Gln Gly Leu Trp

1 5 10 15

Glu Val Phe Val Thr Leu Ser Glu Arg Ala Arg Asp Tyr Leu His Lys

20 25 30

Thr Gly Arg Phe Ile Val Ile Gly Gly Ile Val Ser Pro Val His Asp

35 40 45

Ser Tyr Gly Lys Gln Gly Leu Val Ser Ser Arg His Arg Leu Ile Met

50 55 60

Cys Gln Leu Ala Val Gln Asn Ser Asp Trp Ile Arg Val Asp Pro Trp

65 70 75 80

Glu Cys Tyr Gln Asp Thr Trp Gln Thr Thr Cys Ser Val Leu Glu His

85 90 95

His Arg Asp Leu Met Lys Arg Val Thr Gly Cys Ile Leu Ser Asn Val

100 105 110

Asn Thr Pro Ser Met Thr Pro Val Ile Gly Gln Pro Gln Asn Glu Thr

115 120 125

Pro Gln Pro Ile Tyr Gln Asn Ser Asn Val Ala Thr Lys Pro Thr Ala

130 135 140

Ala Lys Ile Leu Gly Lys Val Gly Glu Ser Leu Ser Arg Ile Cys Cys

145 150 155 160

Val Arg Pro Pro Val Glu Arg Phe Thr Phe Val Asp Glu Asn Ala Asn

165 170 175

Leu Gly Thr Val Met Arg Tyr Glu Glu Ile Glu Leu Arg Ile Leu Leu

180 185 190

Leu Cys Gly Ser Asp Leu Leu Glu Ser Phe Cys Ile Pro Gly Leu Trp

195 200 205

Asn Glu Ala Asp Met Glu Val Ile Val Gly Asp Phe Gly Ile Val Val

210 215 220

Val Pro Arg Asp Ala Ala Asp Thr Asp Arg Ile Met Asn His Ser Ser

225 230 235 240

Ile Leu Arg Lys Tyr Lys Asn Asn Ile Met Val Val Lys Asp Asp Ile
245 250 255

Asn His Pro Met Ser Val Val Ser Ser Thr Lys Ser Arg Leu Ala Leu
260 265 270

Gln His Gly Asp Gly His Val Val Asp Tyr Leu Ser Gln Pro Val Ile
275 280 285

Asp Tyr Ile Leu Lys Ser Gln Leu Tyr Ile Asn Ala Ser Gly
290 295 300

<210> 4347

<211> 307

<212> PRT

<213> homo sapiens

<400> 4347

Met Thr Glu Thr Thr Lys Thr His Val Ile Leu Leu Ala Cys Gly Ser
1 5 10 15

Phe Asn Pro Ile Thr Lys Gly His Ile Gln Met Phe Glu Arg Ala Arg
20 25 30

Asp Tyr Leu His Lys Thr Gly Arg Phe Ile Val Ile Gly Gly Ile Val
35 40 45

Ser Pro Val His Asp Ser Tyr Gly Lys Gln Gly Leu Val Ser Ser Arg
50 55 60

His Arg Leu Ile Met Cys Gln Leu Ala Val Gln Asn Ser Asp Trp Ile
65 70 75 80

Arg Val Asp Pro Trp Glu Cys Tyr Gln Asp Thr Trp Gln Thr Thr Cys
85 90 95

Ser Val Leu Glu His His Arg Asp Leu Met Lys Arg Val Thr Gly Cys
100 105 110

Ile Leu Ser Asn Val Asn Thr Pro Ser Met Thr Pro Val Ile Gly Gln
115 120 125

Pro Gln Asn Glu Thr Pro Gln Pro Ile Tyr Gln Asn Ser Asn Val Ala
130 135 140

Thr Lys Pro Thr Ala Ala Lys Ile Leu Gly Lys Val Gly Glu Ser Leu

145 150 155 160
Ser Arg Ile Cys Cys Val Arg Pro Pro Val Glu Arg Phe Thr Phe Val

 165 170 175
Asp Glu Asn Ala Asn Leu Gly Thr Val Met Arg Tyr Glu Glu Ile Glu

 180 185 190
Leu Arg Ile Leu Leu Leu Cys Gly Ser Asp Leu Leu Glu Ser Phe Cys

 195 200 205
Ile Pro Gly Leu Trp Asn Glu Ala Asp Met Glu Val Ile Val Gly Asp

 210 215 220
Phe Gly Ile Val Val Val Pro Arg Asp Ala Ala Asp Thr Asp Arg Ile

225 230 235 240
Met Asn His Ser Ser Ile Leu Arg Lys Tyr Lys Asn Asn Ile Met Val

 245 250 255
Val Lys Asp Asp Ile Asn His Pro Met Ser Val Val Ser Ser Thr Lys

 260 265 270
Ser Arg Leu Ala Leu Gln His Gly Asp Gly His Val Val Asp Tyr Leu

 275 280 285
Ser Gln Pro Val Ile Asp Tyr Ile Leu Lys Ser Gln Leu Tyr Ile Asn

 290 295 300
Ala Ser Gly

305

<210> 4348

<211> 632

<212> PRT

<213> homo sapiens

<400> 4348

Met Glu Glu Leu Val Val Glu Val Arg Gly Ser Asn Gly Ala Phe Tyr

1 5 10 15

Lys Ala Phe Val Lys Asp Val His Glu Asp Ser Ile Thr Val Ala Phe

20 25 30

Glu Asn Asn Trp Gln Pro Asp Arg Gln Ile Pro Phe His Asp Val Arg

35	40	45
Phe Pro Pro Pro Val Gly Tyr Asn Lys Asp Ile Asn Glu Ser Asp Glu		
50	55	60
Val Glu Val Tyr Ser Arg Ala Asn Glu Lys Glu Pro Cys Cys Trp Trp		
65	70	75
Leu Ala Lys Val Arg Met Ile Lys Gly Glu Phe Tyr Val Ile Glu Tyr		
85	90	95
Ala Ala Cys Asp Ala Thr Tyr Asn Glu Ile Val Thr Ile Glu Arg Leu		
100	105	110
Arg Ser Val Asn Pro Asn Lys Pro Ala Thr Lys Asp Thr Phe His Lys		
115	120	125
Ile Lys Leu Asp Val Pro Glu Asp Leu Arg Gln Met Cys Ala Lys Glu		
130	135	140
Ala Ala His Lys Asp Phe Lys Lys Ala Val Gly Ala Phe Ser Val Thr		
145	150	155
Tyr Asp Pro Glu Asn Tyr Gln Leu Val Ile Leu Ser Ile Asn Glu Val		
165	170	175
Thr Ser Lys Arg Ala His Met Leu Ile Asp Met His Phe Arg Ser Leu		
180	185	190
Arg Thr Lys Leu Ser Leu Ile Met Arg Asn Glu Glu Ala Ser Lys Gln		
195	200	205
Leu Glu Ser Ser Arg Gln Leu Ala Ser Arg Phe His Glu Gln Phe Ile		
210	215	220
Val Arg Glu Asp Leu Met Gly Leu Ala Ile Gly Thr His Gly Ala Asn		
225	230	235
Ile Gln Gln Ala Arg Lys Val Pro Gly Val Thr Ala Ile Asp Leu Asp		
245	250	255
Glu Asp Thr Cys Thr Phe His Ile Tyr Gly Glu Asp Gln Asp Ala Val		
260	265	270
Lys Lys Ala Arg Ser Phe Leu Glu Phe Ala Glu Asp Val Ile Gln Val		
275	280	285

Pro Arg Asn Leu Val Gly Lys Val Ile Gly Lys Asn Gly Lys Leu Ile
290 295 300

Gln Glu Ile Val Asp Lys Ser Gly Val Val Arg Val Arg Ile Glu Ala
305 310 315 320

Glu Asn Glu Lys Asn Val Pro Gln Glu Glu Glu Ile Met Pro Pro Asn
325 330 335

Ser Leu Pro Ser Asn Asn Ser Arg Val Gly Pro Asn Ala Pro Glu Glu
340 345 350

Lys Lys His Leu Asp Ile Lys Glu Asn Ser Thr His Phe Ser Gln Pro
355 360 365

Asn Ser Thr Lys Val Gln Arg Val Leu Val Ala Ser Ser Val Val Ala
370 375 380

Gly Glu Ser Gln Lys Pro Glu Leu Lys Ala Trp Gln Gly Met Val Pro
385 390 395 400

Phe Val Phe Val Gly Thr Lys Asp Ser Ile Ala Asn Ala Thr Val Leu
405 410 415

Leu Asp Tyr His Leu Asn Tyr Leu Lys Glu Val Asp Gln Leu Arg Leu
420 425 430

Glu Arg Leu Gln Ile Asp Glu Gln Leu Arg Gln Ile Gly Ala Ser Ser
435 440 445

Arg Pro Pro Pro Asn Arg Thr Asp Lys Glu Lys Ser Tyr Val Thr Asp
450 455 460

Asp Gly Gln Gly Met Gly Arg Gly Ser Arg Pro Tyr Arg Asn Arg Gly
465 470 475 480

His Gly Arg Arg Gly Pro Gly Tyr Thr Ser Gly Thr Asn Ser Glu Ala
485 490 495

Ser Asn Ala Ser Glu Thr Glu Ser Asp His Arg Asp Glu Leu Ser Asp
500 505 510

Trp Ser Leu Ala Pro Thr Glu Glu Glu Arg Glu Ser Phe Leu Arg Arg
515 520 525

Gly Asp Gly Arg Arg Arg Gly Gly Gly Arg Gly Gln Gly Gly Arg

530 535 540
 Gly Arg Gly Gly Gly Phe Lys Gly Asn Asp Asp His Ser Arg Thr Asp
 545 550 555 560

Asn Arg Pro Arg Asn Pro Arg Glu Ala Lys Gly Arg Thr Thr Asp Gly
 565 570 575
 Ser Leu Gln Ile Arg Val Asp Cys Asn Asn Glu Arg Ser Val His Thr
 580 585 590
 Lys Thr Leu Gln Asn Thr Ser Ser Glu Gly Ser Arg Leu Arg Thr Gly
 595 600 605
 Lys Asp Arg Asn Gln Lys Lys Glu Lys Pro Asp Ser Val Asp Gly Gln
 610 615 620

Gln Pro Leu Val Asn Gly Val Pro

625 630

<210> 4349

<211> 486

<212> PRT

<213> homo sapiens

<400> 4349

Met Val Ala Gly Met Leu Gly Leu Arg Glu Glu Lys Ser Glu Asp Gln
 1 5 10 15
 Asp Leu Gln Gly Leu Lys Asp Lys Pro Leu Lys Phe Lys Lys Val Lys
 20 25 30
 Lys Asp Lys Lys Glu Glu Lys Glu Gly Lys His Glu Pro Val Gln Pro
 35 40 45

Ser Ala His His Ser Ala Glu Pro Ala Glu Ala Gly Lys Ala Glu Thr
 50 55 60
 Ser Glu Gly Ser Gly Ser Ala Pro Ala Val Pro Glu Ala Ser Ala Ser
 65 70 75 80
 Pro Lys Gln Arg Arg Ser Ile Ile Arg Asp Arg Gly Pro Met Tyr Asp
 85 90 95
 Asp Pro Thr Leu Pro Glu Gly Trp Thr Arg Lys Leu Lys Gln Arg Lys

100	105	110	
Ser Gly Arg Ser Ala Gly Lys Tyr Asp Val Tyr Leu Ile Asn Pro Gln			
115	120	125	
Gly Lys Ala Phe Arg Ser Lys Val Glu Leu Ile Ala Tyr Phe Glu Lys			
130	135	140	
Val Gly Asp Thr Ser Leu Asp Pro Asn Asp Phe Asp Phe Thr Val Thr			
145	150	155	160
Gly Arg Gly Ser Pro Ser Arg Arg Glu Gln Lys Pro Pro Lys Lys Pro			
165	170	175	
Lys Ser Pro Lys Ala Pro Gly Thr Gly Arg Gly Arg Gly Arg Pro Lys			
180	185	190	
Gly Ser Gly Thr Thr Arg Pro Lys Ala Ala Thr Ser Glu Gly Val Gln			
195	200	205	
Val Lys Arg Val Leu Glu Lys Ser Pro Gly Lys Leu Leu Val Lys Met			
210	215	220	
Pro Phe Gln Thr Ser Pro Gly Gly Lys Ala Glu Gly Gly Gly Ala Thr			
225	230	235	240
Thr Ser Thr Gln Val Met Val Ile Lys Arg Pro Gly Arg Lys Arg Lys			
245	250	255	
Ala Glu Ala Asp Pro Gln Ala Ile Pro Lys Lys Arg Gly Arg Lys Pro			
260	265	270	
Gly Ser Val Val Ala Ala Ala Ala Ala Glu Ala Lys Lys Lys Ala Val			
275	280	285	
Lys Glu Ser Ser Ile Arg Ser Val Gln Glu Thr Val Leu Pro Ile Lys			
290	295	300	
Lys Arg Lys Thr Arg Glu Thr Val Ser Ile Glu Val Lys Glu Val Val			
305	310	315	320
Lys Pro Leu Leu Val Ser Thr Leu Gly Glu Lys Ser Gly Lys Gly Leu			
325	330	335	
Lys Thr Cys Lys Ser Pro Gly Arg Lys Ser Lys Glu Ser Ser Pro Lys			
340	345	350	

Gly Arg Ser Ser Ser Ala Ser Ser Pro Pro Lys Lys Glu His His His
355 360 365

His His His His Ser Glu Ser Pro Lys Ala Pro Val Pro Leu Leu Pro
370 375 380

Pro Leu Pro Pro Pro Pro Pro Glu Pro Glu Ser Ser Glu Asp Pro Thr
385 390 395 400

Ser Pro Pro Glu Pro Gln Asp Leu Ser Ser Ser Val Cys Lys Glu Glu
405 410 415

Lys Met Pro Arg Gly Gly Ser Leu Glu Ser Asp Gly Cys Pro Lys Glu
420 425 430

Pro Ala Lys Thr Gln Pro Ala Val Ala Thr Ala Ala Thr Ala Ala Glu
435 440 445

Lys Tyr Lys His Arg Gly Glu Gly Glu Arg Lys Asp Ile Val Ser Ser
450 455 460

Ser Met Pro Arg Pro Asn Arg Glu Glu Pro Val Asp Ser Arg Thr Pro
465 470 475 480

Val Thr Glu Arg Val Ser
485

<210> 4350

<211> 498

<212> PRT

<213> homo sapiens

<400> 4350

Met Ala Ala Ala Ala Ala Ala Ala Pro Ser Gly Gly Gly Gly Gly Gly
1 5 10 15

Glu Glu Glu Arg Leu Glu Glu Lys Ser Glu Asp Gln Asp Leu Gln Gly
20 25 30

Leu Lys Asp Lys Pro Leu Lys Phe Lys Lys Val Lys Lys Asp Lys Lys
35 40 45

Glu Glu Lys Glu Gly Lys His Glu Pro Val Gln Pro Ser Ala His His
50 55 60

Ser	Ala	Glu	Pro	Ala	Glu	Ala	Gly	Lys	Ala	Glu	Thr	Ser	Glu	Gly	Ser
65					70					75					80
Gly	Ser	Ala	Pro	Ala	Val	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Lys	Gln	Arg
				85					90					95	
Arg	Ser	Ile	Ile	Arg	Asp	Arg	Gly	Pro	Met	Tyr	Asp	Asp	Pro	Thr	Leu
				100				105					110		
Pro	Glu	Gly	Trp	Thr	Arg	Lys	Leu	Lys	Gln	Arg	Lys	Ser	Gly	Arg	Ser
		115					120					125			
Ala	Gly	Lys	Tyr	Asp	Val	Tyr	Leu	Ile	Asn	Pro	Gln	Gly	Lys	Ala	Phe
	130						135				140				
Arg	Ser	Lys	Val	Glu	Leu	Ile	Ala	Tyr	Phe	Glu	Lys	Val	Gly	Asp	Thr
145				150						155					160
Ser	Leu	Asp	Pro	Asn	Asp	Phe	Asp	Phe	Thr	Val	Thr	Gly	Arg	Gly	Ser
				165					170					175	
Pro	Ser	Arg	Arg	Glu	Gln	Lys	Pro	Pro	Lys	Lys	Pro	Lys	Ser	Pro	Lys
		180							185				190		
Ala	Pro	Gly	Thr	Gly	Arg	Gly	Arg	Gly	Arg	Pro	Lys	Gly	Ser	Gly	Thr
		195					200					205			
Thr	Arg	Pro	Lys	Ala	Ala	Thr	Ser	Glu	Gly	Val	Gln	Val	Lys	Arg	Val
	210						215				220				
Leu	Glu	Lys	Ser	Pro	Gly	Lys	Leu	Leu	Val	Lys	Met	Pro	Phe	Gln	Thr
225				230						235					240
Ser	Pro	Gly	Gly	Lys	Ala	Glu	Gly	Gly	Gly	Ala	Thr	Thr	Ser	Thr	Gln
				245					250					255	
Val	Met	Val	Ile	Lys	Arg	Pro	Gly	Arg	Lys	Arg	Lys	Ala	Glu	Ala	Asp
		260						265					270		
Pro	Gln	Ala	Ile	Pro	Lys	Lys	Arg	Gly	Arg	Lys	Pro	Gly	Ser	Val	Val
		275						280				285			
Ala	Ala	Ala	Ala	Ala	Glu	Ala	Lys	Lys	Lys	Ala	Val	Lys	Glu	Ser	Ser
	290						295				300				
Ile	Arg	Ser	Val	Gln	Glu	Thr	Val	Leu	Pro	Ile	Lys	Lys	Arg	Lys	Thr

305 310 315 320

Arg Glu Thr Val Ser Ile Glu Val Lys Glu Val Val Lys Pro Leu Leu

325 330 335

Val Ser Thr Leu Gly Glu Lys Ser Gly Lys Gly Leu Lys Thr Cys Lys

340 345 350

Ser Pro Gly Arg Lys Ser Lys Glu Ser Ser Pro Lys Gly Arg Ser Ser

355 360 365

Ser Ala Ser Ser Pro Pro Lys Lys Glu His His His His His His His

370 375 380

Ser Glu Ser Pro Lys Ala Pro Val Pro Leu Leu Pro Pro Leu Pro Pro

385 390 395 400

Pro Pro Pro Glu Pro Glu Ser Ser Glu Asp Pro Thr Ser Pro Pro Glu

405 410 415

Pro Gln Asp Leu Ser Ser Ser Val Cys Lys Glu Glu Lys Met Pro Arg

420 425 430

Gly Gly Ser Leu Glu Ser Asp Gly Cys Pro Lys Glu Pro Ala Lys Thr

435 440 445

Gln Pro Ala Val Ala Thr Ala Ala Thr Ala Ala Glu Lys Tyr Lys His

450 455 460

Arg Gly Glu Gly Glu Arg Lys Asp Ile Val Ser Ser Ser Met Pro Arg

465 470 475 480

Pro Asn Arg Glu Glu Pro Val Asp Ser Arg Thr Pro Val Thr Glu Arg

485 490 495

Val Ser

<210> 4351

<211> 552

<212> PRT

<213> homo sapiens

<400> 4351

Met Arg Leu Leu Pro Leu Ala Pro Gly Arg Leu Arg Arg Gly Ser Pro

1	5	10	15
Arg His Leu Pro Ser Cys Ser Pro Ala Leu Leu Leu Val Leu Gly			
	20	25	30
Gly Cys Leu Gly Val Phe Gly Val Ala Ala Gly Thr Arg Arg Pro Asn			
	35	40	45
Val Val Leu Leu Leu Thr Asp Asp Gln Asp Glu Val Leu Gly Gly Met			
	50	55	60
Thr Pro Leu Lys Lys Thr Lys Ala Leu Ile Gly Glu Met Gly Met Thr			
65	70	75	80
Phe Ser Ser Ala Tyr Val Pro Ser Ala Leu Cys Cys Pro Ser Arg Ala			
	85	90	95
Ser Ile Leu Thr Gly Lys Tyr Pro His Asn His His Val Val Asn Asn			
	100	105	110
Thr Leu Glu Gly Asn Cys Ser Ser Lys Ser Trp Gln Lys Ile Gln Glu			
	115	120	125
Pro Asn Thr Phe Pro Ala Ile Leu Arg Ser Met Cys Gly Tyr Gln Thr			
130	135	140	
Phe Phe Ala Gly Lys Tyr Leu Asn Glu Tyr Gly Ala Pro Asp Ala Gly			
145	150	155	160
Gly Leu Glu His Val Pro Leu Gly Trp Ser Tyr Trp Tyr Ala Leu Glu			
	165	170	175
Lys Asn Ser Lys Tyr Tyr Asn Tyr Thr Leu Ser Ile Asn Gly Lys Ala			
	180	185	190
Arg Lys His Gly Glu Asn Tyr Ser Val Asp Tyr Leu Thr Asp Val Leu			
195	200	205	
Ala Asn Val Ser Leu Asp Phe Leu Asp Tyr Lys Ser Asn Phe Glu Pro			
210	215	220	
Phe Phe Met Met Ile Ala Thr Pro Ala Pro His Ser Pro Trp Thr Ala			
225	230	235	240
Ala Pro Gln Tyr Gln Lys Ala Phe Gln Asn Val Phe Ala Pro Arg Asn			
	245	250	255

Lys Asn Phe Asn Ile His Gly Thr Asn Lys His Trp Leu Ile Arg Gln

260 265 270

Ala Lys Thr Pro Met Thr Asn Ser Ser Ile Gln Phe Leu Asp Asn Ala

275 280 285

Phe Arg Lys Arg Trp Gln Thr Leu Leu Ser Val Asp Asp Leu Val Glu

290 295 300

Lys Leu Val Lys Arg Leu Glu Phe Thr Gly Glu Leu Asn Asn Thr Tyr

305 310 315 320

Ile Phe Tyr Thr Ser Asp Asn Gly Tyr His Thr Gly Gln Phe Ser Leu

325 330 335

Pro Ile Asp Lys Arg Gln Leu Tyr Glu Phe Asp Ile Lys Val Pro Leu

340 345 350

Leu Val Arg Gly Pro Gly Ile Lys Pro Asn Gln Thr Ser Lys Met Leu

355 360 365

Val Ala Asn Ile Asp Leu Gly Pro Thr Ile Leu Asp Ile Ala Gly Tyr

370 375 380

Asp Leu Asn Lys Thr Gln Met Asp Gly Met Ser Leu Leu Pro Ile Leu

385 390 395 400

Arg Gly Ala Ser Asn Leu Thr Trp Arg Ser Asp Val Leu Val Glu Tyr

405 410 415

Gln Gly Glu Gly Arg Asn Val Thr Asp Pro Thr Cys Pro Ser Leu Ser

420 425 430

Pro Gly Val Ser Gln Cys Phe Pro Asp Cys Val Cys Glu Asp Ala Tyr

435 440 445

Asn Asn Thr Tyr Ala Cys Val Arg Thr Met Ser Ala Leu Trp Asn Leu

450 455 460

Gln Tyr Cys Glu Phe Asp Asp Gln Glu Val Phe Val Glu Val Tyr Asn

465 470 475 480

Leu Thr Ala Asp Pro Asp Gln Ile Thr Asn Ile Ala Lys Thr Ile Asp

485 490 495

Pro Glu Leu Leu Gly Lys Met Asn Tyr Arg Leu Met Met Leu Gln Ser

500 505 510
Cys Ser Gly Pro Thr Cys Arg Thr Pro Gly Val Phe Asp Pro Gly Tyr

515 520 525
Arg Phe Asp Pro Arg Leu Met Phe Ser Asn Arg Gly Ser Val Arg Thr

530 535 540

Arg Arg Phe Ser Lys His Leu Leu

545 550

<210> 4352

<211> 207

<212> PRT

<213> homo sapiens

<400> 4352

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu

1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln

20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln

35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val

50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly

65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln

85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly

100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys

115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg

130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro

145 150 155 160
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 165 170 175
 His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 180 185 190
 Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205
 <210> 4353
 <211> 735
 <212> PRT
 <213> homo sapiens

 <400> 4353
 Met Glu Gly Ala Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu
 1 5 10 15
 Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
 20 25 30
 Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
 35 40 45
 Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
 50 55 60

 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
 65 70 75 80
 Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
 85 90 95
 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
 100 105 110
 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
 115 120 125

 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
 130 135 140
 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu
 145 150 155 160

Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
165 170 175

Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
180 185 190

His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
195 200 205

Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
210 215 220

Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
225 230 235 240

Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp
245 250 255

Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly
260 265 270

Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr
275 280 285

Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln
290 295 300

Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln
305 310 315 320

Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val
325 330 335

Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe
340 345 350

Ser Leu Gln Gln Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp
355 360 365

Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser
370 375 380

Ser Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu
385 390 395 400

Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn

405 410 415
 Asp Thr Glu Thr Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn
 420 425 430
 Asp Val Met Leu Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu
 435 440 445

 Ala Met Ser Pro Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser
 450 455 460
 Ser Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro
 465 470 475 480
 Asn Pro Glu Ser Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp
 485 490 495
 Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu
 500 505 510

 Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val
 515 520 525
 Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr
 530 535 540
 Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu
 545 550 555 560
 Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser
 565 570 575

 Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser
 580 585 590
 Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln
 595 600 605
 Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu
 610 615 620
 Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala
 625 630 635 640

 Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser
 645 650 655

Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala
660 665 670

Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro
675 680 685

Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu
690 695 700

Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg
705 710 715 720

Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Ile
725 730 735

<210> 4354

<211> 826

<212> PRT

<213> homo sapiens

<400> 4354

Met Glu Gly Ala Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu
1 5 10 15

Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
20 25 30

Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
35 40 45

Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
50 55 60

Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile
65 70 75 80

Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu
85 90 95

Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile
100 105 110

Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
115 120 125

Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met

130 135 140
 Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu

 145 150 155 160
 Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr

 165 170 175
 Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu

 180 185 190
 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro

 195 200 205
 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys

 210 215 220
 Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
 225 230 235 240
 Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp

 245 250 255
 Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly

 260 265 270
 Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr

 275 280 285
 Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln

 290 295 300
 Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln
 305 310 315 320
 Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val

 325 330 335
 Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe

 340 345 350
 Ser Leu Gln Gln Thr Glu Cys Val Leu Lys Pro Val Glu Ser Ser Asp

 355 360 365
 Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser

 370 375 380

Ser Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu
385 390 395 400
Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asn
405 410 415
Asp Thr Glu Thr Asp Asp Gln Gln Leu Glu Glu Val Pro Leu Tyr Asn
420 425 430
Asp Val Met Leu Pro Ser Pro Asn Glu Lys Leu Gln Asn Ile Asn Leu
435 440 445
Ala Met Ser Pro Leu Pro Thr Ala Glu Thr Pro Lys Pro Leu Arg Ser
450 455 460
Ser Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Pro
465 470 475 480
Asn Pro Glu Ser Leu Glu Leu Ser Phe Thr Met Pro Gln Ile Gln Asp
485 490 495
Gln Thr Pro Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu
500 505 510
Pro Asn Ser Pro Ser Glu Tyr Cys Phe Tyr Val Asp Ser Asp Met Val
515 520 525
Asn Glu Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr
530 535 540
Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu
545 550 555 560
Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser
565 570 575
Phe Asp Gln Leu Ser Pro Leu Glu Ser Ser Ser Ala Ser Pro Glu Ser
580 585 590
Ala Ser Pro Gln Ser Thr Val Thr Val Phe Gln Gln Thr Gln Ile Gln
595 600 605
Glu Pro Thr Ala Asn Ala Thr Thr Thr Thr Ala Thr Thr Asp Glu Leu
610 615 620
Lys Thr Val Thr Lys Asp Arg Met Glu Asp Ile Lys Ile Leu Ile Ala

625 630 635 640
 Ser Pro Ser Pro Thr His Ile His Lys Glu Thr Thr Ser Ala Thr Ser
 645 650 655
 Ser Pro Tyr Arg Asp Thr Gln Ser Arg Thr Ala Ser Pro Asn Arg Ala

 660 665 670
 Gly Lys Gly Val Ile Glu Gln Thr Glu Lys Ser His Pro Arg Ser Pro
 675 680 685
 Asn Val Leu Ser Val Ala Leu Ser Gln Arg Thr Thr Val Pro Glu Glu
 690 695 700
 Glu Leu Asn Pro Lys Ile Leu Ala Leu Gln Asn Ala Gln Arg Lys Arg
 705 710 715 720
 Lys Met Glu His Asp Gly Ser Leu Phe Gln Ala Val Gly Ile Gly Thr

 725 730 735
 Leu Leu Gln Gln Pro Asp Asp His Ala Ala Thr Thr Ser Leu Ser Trp
 740 745 750
 Lys Arg Val Lys Gly Cys Lys Ser Ser Glu Gln Asn Gly Met Glu Gln
 755 760 765
 Lys Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly
 770 775 780
 Gln Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys

 785 790 795 800
 Glu Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu
 805 810 815
 Glu Leu Leu Arg Ala Leu Asp Gln Val Asn
 820 825
 <210> 4355
 <211> 418
 <212> PRT
 <213> homo sapiens
 <400> 4355
 Met Gln Ala Leu Val Leu Leu Leu Cys Ile Gly Ala Leu Leu Gly His
 1 5 10 15

Ser Ser Cys Gln Asn Pro Ala Ser Pro Pro Glu Glu Gly Ser Pro Asp

20 25 30

Pro Asp Ser Thr Gly Ala Leu Val Glu Glu Glu Asp Pro Phe Phe Lys

35 40 45

Val Pro Val Asn Lys Leu Ala Ala Ala Val Ser Asn Phe Gly Tyr Asp

50 55 60

Leu Tyr Arg Val Arg Ser Ser Thr Ser Pro Thr Thr Asn Val Leu Leu

65 70 75 80

Ser Pro Leu Ser Val Ala Thr Ala Leu Ser Ala Leu Ser Leu Gly Ala

85 90 95

Glu Gln Arg Thr Glu Ser Ile Ile His Arg Ala Leu Tyr Tyr Asp Leu

100 105 110

Ile Ser Ser Pro Asp Ile His Gly Thr Tyr Lys Glu Leu Leu Asp Thr

115 120 125

Val Thr Ala Pro Gln Lys Asn Leu Lys Ser Ala Ser Arg Ile Val Phe

130 135 140

Glu Lys Lys Leu Arg Ile Lys Ser Ser Phe Val Ala Pro Leu Glu Lys

145 150 155 160

Ser Tyr Gly Thr Arg Pro Arg Val Leu Thr Gly Asn Pro Arg Leu Asp

165 170 175

Leu Gln Glu Ile Asn Asn Trp Val Gln Ala Gln Met Lys Gly Lys Leu

180 185 190

Ala Arg Ser Thr Lys Glu Ile Pro Asp Glu Ile Ser Ile Leu Leu Leu

195 200 205

Gly Val Ala His Phe Lys Gly Gln Trp Val Thr Lys Phe Asp Ser Arg

210 215 220

Lys Thr Ser Leu Glu Asp Phe Tyr Leu Asp Glu Glu Arg Thr Val Arg

225 230 235 240

Val Pro Met Met Ser Asp Pro Lys Ala Val Leu Arg Tyr Gly Leu Asp

245 250 255

Ser Asp Leu Ser Cys Lys Ile Ala Gln Leu Pro Leu Thr Gly Ser Met

260 265 270
Ser Ile Ile Phe Phe Leu Pro Leu Lys Val Thr Gln Asn Leu Thr Leu

275 280 285
Ile Glu Glu Ser Leu Thr Ser Glu Phe Ile His Asp Ile Asp Arg Glu

290 295 300
Leu Lys Thr Val Gln Ala Val Leu Thr Val Pro Lys Leu Lys Leu Ser

305 310 315 320
Tyr Glu Gly Glu Val Thr Lys Ser Leu Gln Glu Met Lys Leu Gln Ser

325 330 335
Leu Phe Asp Ser Pro Asp Phe Ser Lys Ile Thr Gly Lys Pro Ile Lys

340 345 350
Leu Thr Gln Val Glu His Arg Ala Gly Phe Glu Trp Asn Glu Asp Gly

355 360 365
Ala Gly Thr Thr Pro Ser Pro Gly Leu Gln Pro Ala His Leu Thr Phe

370 375 380
Pro Leu Asp Tyr His Leu Asn Gln Pro Phe Ile Phe Val Leu Arg Asp

385 390 395 400
Thr Asp Thr Gly Ala Leu Leu Phe Ile Gly Lys Ile Leu Asp Pro Arg

405 410 415
Gly Pro

<210> 4356

<211> 317

<212> PRT

<213> homo sapiens

<400> 4356

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu

1 5 10 15

Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln

20 25 30

Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg

35 40 45
 Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe
 50 55 60
 Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
 65 70 75 80
 Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
 85 90 95
 Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
 100 105 110

 Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp
 115 120 125
 Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
 130 135 140
 Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro
 145 150 155 160
 His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
 165 170 175

 Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
 180 185 190
 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 195 200 205
 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 210 215 220
 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 225 230 235 240

 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
 245 250 255
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 260 265 270
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 275 280 285

Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
290 295 300

His Asn Lys Cys Glu Cys Arg Cys Asp Lys Pro Arg Arg
305 310 315

<210> 4357
<211> 232
<212> PRT
<213> homo sapiens
<400> 4357

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
145 150 155 160

Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp
165 170 175

Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys
180 185 190
His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn
195 200 205
Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr
210 215 220
Cys Arg Cys Asp Lys Pro Arg Arg
225 230

<210> 4358

<211> 354

<212> PRT

<213> homo sapiens

<400> 4358

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu
1 5 10 15
Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln
20 25 30
Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg
35 40 45
Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe

50 55 60
Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
65 70 75 80
Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
85 90 95
Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
100 105 110
Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp

115 120 125
Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
130 135 140
Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro

145 150 155 160
 His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
 165 170 175
 Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu

 180 185 190
 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 195 200 205
 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 210 215 220
 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 225 230 235 240
 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser

 245 250 255
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 260 265 270
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 275 280 285
 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 290 295 300
 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu

 305 310 315 320
 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
 325 330 335
 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
 340 345 350
 Lys Met

<210> 4359

<211> 327

<212> PRT

<213> homo sapiens

<400> 4359

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu
1 5 10 15

Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln
20 25 30

Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg
35 40 45

Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe
50 55 60

Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
65 70 75 80

Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
85 90 95

Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
100 105 110

Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp
115 120 125

Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
130 135 140

Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro
145 150 155 160

His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
165 170 175

Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
180 185 190

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
195 200 205

Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
210 215 220

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
225 230 235 240

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser

245 250 255
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
260 265 270

Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
275 280 285

Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
290 295 300

His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
305 310 315 320

Lys Cys Asp Lys Pro Arg Arg
325

<210> 4360

<211> 395

<212> PRT

<213> homo sapiens

<400> 4360

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu
1 5 10 15

Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln
20 25 30

Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg
35 40 45

Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe
50 55 60

Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
65 70 75 80

Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
85 90 95

Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
100 105 110

Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp

115	120	125
Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly		
130	135	140
Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro		
145	150	155
160		
His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg		
165	170	175
Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu		
180	185	190
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro		
195	200	205
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met		
210	215	220
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp		
225	230	235
240		
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser		
245	250	255
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu		
260	265	270
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg		
275	280	285
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln		
290	295	300
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu		
305	310	315
320		
Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys		
325	330	335
Lys Ser Arg Tyr Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu		
340	345	350
Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser		
355	360	365

Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn
370 375 380

Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
385 390 395

<210> 4361

<211> 137

<212> PRT

<213> homo sapiens

<400> 4361

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Cys Asp Lys Pro Arg Arg
130 135

<210> 4362

<211> 412

<212> PRT

<213> homo sapiens

<400> 4362

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu
1 5 10 15
Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln
20 25 30
Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg
35 40 45
Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe
50 55 60
Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
65 70 75 80
Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
85 90 95
Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
100 105 110
Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp
115 120 125
Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
130 135 140
Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro
145 150 155 160
His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
165 170 175
Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
180 185 190
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
195 200 205
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
210 215 220
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
225 230 235 240
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser

245 250 255
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 260 265 270
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 275 280 285

 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 290 295 300
 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
 305 310 315 320
 Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys
 325 330 335
 Lys Ser Arg Tyr Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys
 340 345 350

 Leu Met Pro Trp Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser
 355 360 365
 Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys
 370 375 380
 Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu
 385 390 395 400
 Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 405 410

 <210> 4363

 <211> 191
 <212> PRT
 <213> homo sapiens
 <400> 4363

 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu

50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro

85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His

100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys

115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly

130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr

145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln

165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Ser Leu Thr Arg Lys Asp

180 185 190

<210> 4364

<211> 371

<212> PRT

<213> homo sapiens

<400> 4364

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu

1 5 10 15

Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln

20 25 30

Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg

35 40 45

Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe

50 55 60

Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
 65 70 75 80
 Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
 85 90 95
 Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
 100 105 110

 Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp
 115 120 125
 Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
 130 135 140
 Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro
 145 150 155 160
 His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
 165 170 175

 Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
 180 185 190
 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 195 200 205
 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 210 215 220
 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 225 230 235 240

 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
 245 250 255
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 260 265 270
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 275 280 285
 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 290 295 300

 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu

305 310 315 320
 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
 325 330 335
 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
 340 345 350
 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
 355 360 365

Pro Arg Arg

370

<210> 4365

<211> 389

<212> PRT

<213> homo sapiens

<400> 4365

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu
 1 5 10 15
 Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln
 20 25 30
 Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg
 35 40 45
 Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe

50

55

60

Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala
 65 70 75 80
 Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu
 85 90 95
 Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly
 100 105 110
 Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp

115

120

125

Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly
 130 135 140

Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro
 145 150 155 160
 His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg
 165 170 175
 Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu

 180 185 190
 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 195 200 205
 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 210 215 220
 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 225 230 235 240
 Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser

 245 250 255
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 260 265 270
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 275 280 285
 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 290 295 300
 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu

 305 310 315 320
 Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys
 325 330 335
 Lys Ser Arg Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe
 340 345 350
 Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser
 355 360 365
 Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys

 370 375 380
 Asp Lys Pro Arg Arg

385

<210> 4366

<211> 371

<212> PRT

<213> homo sapiens

<400> 4366

Met Thr Asp Arg Gln Thr Asp Thr Ala Pro Ser Pro Ser Tyr His Leu

1 5 10 15

Leu Pro Gly Arg Arg Arg Thr Val Asp Ala Ala Ala Ser Arg Gly Gln

20 25 30

Gly Pro Glu Pro Ala Pro Gly Gly Gly Val Glu Gly Val Gly Ala Arg

35 40 45

Gly Val Ala Leu Lys Leu Phe Val Gln Leu Leu Gly Cys Ser Arg Phe

50 55 60

Gly Gly Ala Val Val Arg Ala Gly Glu Ala Glu Pro Ser Gly Ala Ala

65 70 75 80

Arg Ser Ala Ser Ser Gly Arg Glu Glu Pro Gln Pro Glu Glu Gly Glu

85 90 95

Glu Glu Glu Glu Lys Glu Glu Glu Arg Gly Pro Gln Trp Arg Leu Gly

100 105 110

Ala Arg Lys Pro Gly Ser Trp Thr Gly Glu Ala Ala Val Cys Ala Asp

115 120 125

Ser Ala Pro Ala Ala Arg Ala Pro Gln Ala Leu Ala Arg Ala Ser Gly

130 135 140

Arg Gly Gly Arg Val Ala Arg Arg Gly Ala Glu Glu Ser Gly Pro Pro

145 150 155 160

His Ser Pro Ser Arg Arg Gly Ser Ala Ser Arg Ala Gly Pro Gly Arg

165 170 175

Ala Ser Glu Thr Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu

180 185 190

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro

195 200 205

Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
210 215 220
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
225 230 235 240
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
245 250 255
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
260 265 270
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
275 280 285
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
290 295 300
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
305 310 315 320
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
325 330 335
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
340 345 350
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Ser Leu Thr
355 360 365
Arg Lys Asp
370
<210> 4367
<211> 174
<212> PRT
<213> homo sapiens
<400> 4367
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln

35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu

50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro

85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His

100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys

115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly

130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr

145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Met

165 170

<210> 4368

<211> 191

<212> PRT

<213> homo sapiens

<400> 4368

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu

1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly

20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln

35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu

50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

65 70 75 80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys

 115 120 125
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140
Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
145 150 155 160
Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175
Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg

 180 185 190

<210> 4369

<211> 209

<212> PRT

<213> homo sapiens

<400> 4369

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Pro
145 150 155 160

Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro
165 170 175

Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala
180 185 190

Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg
195 200 205

Arg

<210> 4370

<211> 215

<212> PRT

<213> homo sapiens

<400> 4370

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro

85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His

100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys

115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val

130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr

145 150 155 160

Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His

165 170 175

Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr

180 185 190

Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys

195 200 205

Arg Cys Asp Lys Pro Arg Arg

210 215

<210> 4371

<211> 147

<212> PRT

<213> homo sapiens

<400> 4371

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu

1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly

20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln

35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu

50 55 60

Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu
65					70				75					80	
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro
				85					90					95	
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His
			100					105					110		
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys
	115						120					125			
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Cys	Asp	Lys
	130						135				140				
Pro	Arg	Arg													
145															
<210>	4372														
<211>	247														
<212>	PRT														
<213>	homo sapiens														
<400>	4372														
Met	Leu	Gln	Asn	Ser	Ala	Val	Leu	Leu	Val	Leu	Val	Ile	Ser	Ala	Ser
1			5					10					15		
Ala	Thr	His	Glu	Ala	Glu	Gln	Asn	Asp	Ser	Val	Ser	Pro	Arg	Lys	Ser
			20					25					30		
Arg	Val	Ala	Ala	Gln	Asn	Ser	Ala	Glu	Val	Val	Arg	Cys	Leu	Asn	Ser
		35					40					45			
Ala	Leu	Gln	Val	Gly	Cys	Gly	Ala	Phe	Ala	Cys	Leu	Glu	Asn	Ser	Thr
	50						55				60				
Cys	Asp	Thr	Asp	Gly	Met	Tyr	Asp	Ile	Cys	Lys	Ser	Phe	Leu	Tyr	Ser
65					70					75					80
Ala	Ala	Lys	Phe	Asp	Thr	Gln	Gly	Lys	Ala	Phe	Val	Lys	Glu	Ser	Leu
				85						90				95	
Lys	Cys	Ile	Ala	Asn	Gly	Val	Thr	Ser	Lys	Val	Phe	Leu	Ala	Ile	Arg
			100					105					110		
Arg	Cys	Ser	Thr	Phe	Gln	Arg	Met	Ile	Ala	Glu	Val	Gln	Glu	Glu	Cys

115 120 125
Tyr Ser Lys Leu Asn Val Cys Ser Ile Ala Lys Arg Asn Pro Glu Ala
130 135 140
Ile Thr Glu Val Val Gln Leu Pro Asn His Phe Ser Asn Arg Tyr Tyr
145 150 155 160

Asn Arg Leu Val Arg Ser Leu Leu Glu Cys Asp Glu Asp Thr Val Ser
165 170 175
Thr Ile Arg Asp Ser Leu Met Glu Lys Ile Gly Pro Asn Met Ala Ser
180 185 190
Leu Phe His Ile Leu Gln Thr Asp His Cys Ala Gln Thr His Pro Arg
195 200 205
Ala Asp Phe Asn Arg Arg Arg Thr Asn Glu Pro Gln Lys Leu Lys Val
210 215 220

Leu Leu Arg Asn Leu Arg Gly Glu Glu Asp Ser Pro Ser His Ile Lys
225 230 235 240
Arg Thr Ser His Glu Ser Ala
245

<210> 4373

<211> 151

<212> PRT

<213> homo sapiens

<400> 4373

Met Glu Arg Pro Glu Pro Glu Leu Ile Arg Gln Ser Trp Arg Ala Val
1 5 10 15
Ser Arg Ser Pro Leu Glu His Gly Thr Val Leu Phe Ala Arg Leu Phe
20 25 30

Ala Leu Glu Pro Asp Leu Leu Pro Leu Phe Gln Tyr Asn Cys Arg Gln
35 40 45
Phe Ser Ser Pro Glu Asp Cys Leu Ser Ser Pro Glu Phe Leu Asp His
50 55 60
Ile Arg Lys Val Met Leu Val Ile Asp Ala Ala Val Thr Asn Val Glu
65 70 75 80

Asp Leu Ser Ser Leu Glu Glu Tyr Leu Ala Ser Leu Gly Arg Lys His
 85 90 95

 Arg Ala Val Gly Val Lys Leu Ser Ser Phe Ser Thr Val Gly Glu Ser
 100 105 110
 Leu Leu Tyr Met Leu Glu Lys Cys Leu Gly Pro Ala Phe Thr Pro Ala
 115 120 125
 Thr Arg Ala Ala Trp Ser Gln Leu Tyr Gly Ala Val Val Gln Ala Met
 130 135 140
 Ser Arg Gly Trp Asp Gly Glu
 145 150
 <210> 4374
 <211> 589
 <212> PRT
 <213> homo sapiens

 <400> 4374
 Met Asp Leu Ile Asp Ile Leu Trp Arg Gln Asp Ile Asp Leu Gly Val
 1 5 10 15
 Ser Arg Glu Val Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu
 20 25 30
 Glu Lys Gln Lys Lys Leu Glu Lys Glu Arg Gln Glu Gln Leu Gln Lys
 35 40 45
 Glu Gln Glu Lys Ala Phe Phe Ala Gln Leu Gln Leu Asp Glu Glu Thr
 50 55 60

 Gly Glu Phe Leu Pro Ile Gln Pro Ala Gln His Ile Gln Ser Glu Thr
 65 70 75 80
 Ser Gly Ser Ala Asn Tyr Ser Gln Val Ala His Ile Pro Lys Ser Asp
 85 90 95
 Ala Leu Tyr Phe Asp Asp Cys Met Gln Leu Leu Ala Gln Thr Phe Pro
 100 105 110
 Phe Val Asp Asp Asn Glu Val Ser Ser Ala Thr Phe Gln Ser Leu Val
 115 120 125

Pro Asp Ile Pro Gly His Ile Glu Ser Pro Val Phe Ile Ala Thr Asn
 130 135 140
 Gln Ala Gln Ser Pro Glu Thr Ser Val Ala Gln Val Ala Pro Val Asp
 145 150 155 160
 Leu Asp Gly Met Gln Gln Asp Ile Glu Gln Val Trp Glu Glu Leu Leu
 165 170 175
 Ser Ile Pro Glu Leu Gln Cys Leu Asn Ile Glu Asn Asp Lys Leu Val
 180 185 190

 Glu Thr Thr Met Val Pro Ser Pro Glu Ala Lys Leu Thr Glu Val Asp
 195 200 205
 Asn Tyr His Phe Tyr Ser Ser Ile Pro Ser Met Glu Lys Glu Val Gly
 210 215 220
 Asn Cys Ser Pro His Phe Leu Asn Ala Phe Glu Asp Ser Phe Ser Ser
 225 230 235 240
 Ile Leu Ser Thr Glu Asp Pro Asn Gln Leu Thr Val Asn Ser Leu Asn
 245 250 255

 Ser Asp Ala Thr Val Asn Thr Asp Phe Gly Asp Glu Phe Tyr Ser Ala
 260 265 270
 Phe Ile Ala Glu Pro Ser Ile Ser Asn Ser Met Pro Ser Pro Ala Thr
 275 280 285
 Leu Ser His Ser Leu Ser Glu Leu Leu Asn Gly Pro Ile Asp Val Ser
 290 295 300
 Asp Leu Ser Leu Cys Lys Ala Phe Asn Gln Asn His Pro Glu Ser Thr
 305 310 315 320

 Ala Glu Phe Asn Asp Ser Asp Ser Gly Ile Ser Leu Asn Thr Ser Pro
 325 330 335
 Ser Val Ala Ser Pro Glu His Ser Val Glu Ser Ser Ser Tyr Gly Asp
 340 345 350
 Thr Leu Leu Gly Leu Ser Asp Ser Glu Val Glu Glu Leu Asp Ser Ala
 355 360 365
 Pro Gly Ser Val Lys Gln Asn Gly Pro Lys Thr Pro Val His Ser Ser

370 375 380
 Gly Asp Met Val Gln Pro Leu Ser Pro Ser Gln Gly Gln Ser Thr His
 385 390 395 400
 Val His Asp Ala Gln Cys Glu Asn Thr Pro Glu Lys Glu Leu Pro Val
 405 410 415
 Ser Pro Gly His Arg Lys Thr Pro Phe Thr Lys Asp Lys His Ser Ser
 420 425 430
 Arg Leu Glu Ala His Leu Thr Arg Asp Glu Leu Arg Ala Lys Ala Leu
 435 440 445

 His Ile Pro Phe Pro Val Glu Lys Ile Ile Asn Leu Pro Val Val Asp
 450 455 460
 Phe Asn Glu Met Met Ser Lys Glu Gln Phe Asn Glu Ala Gln Leu Ala
 465 470 475 480
 Leu Ile Arg Asp Ile Arg Arg Arg Gly Lys Asn Lys Val Ala Ala Gln
 485 490 495
 Asn Cys Arg Lys Arg Lys Leu Glu Asn Ile Val Glu Leu Glu Gln Asp
 500 505 510

 Leu Asp His Leu Lys Asp Glu Lys Glu Lys Leu Leu Lys Glu Lys Gly
 515 520 525
 Glu Asn Asp Lys Ser Leu His Leu Leu Lys Lys Gln Leu Ser Thr Leu
 530 535 540
 Tyr Leu Glu Val Phe Ser Met Leu Arg Asp Glu Asp Gly Lys Pro Tyr
 545 550 555 560
 Ser Pro Ser Glu Tyr Ser Leu Gln Gln Thr Arg Asp Gly Asn Val Phe
 565 570 575

 Leu Val Pro Lys Ser Lys Lys Pro Asp Val Lys Lys Asn
 580 585
 <210> 4375
 <211> 605
 <212> PRT
 <213> homo sapiens

<400> 4375

Met Met Asp Leu Glu Leu Pro Pro Pro Gly Leu Pro Ser Gln Gln Asp

1 5 10 15

Met Asp Leu Ile Asp Ile Leu Trp Arg Gln Asp Ile Asp Leu Gly Val

20 25 30

Ser Arg Glu Val Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu

35 40 45

Glu Lys Gln Lys Lys Leu Glu Lys Glu Arg Gln Glu Gln Leu Gln Lys

50 55 60

Glu Gln Glu Lys Ala Phe Phe Ala Gln Leu Gln Leu Asp Glu Glu Thr

65 70 75 80

Gly Glu Phe Leu Pro Ile Gln Pro Ala Gln His Ile Gln Ser Glu Thr

85 90 95

Ser Gly Ser Ala Asn Tyr Ser Gln Val Ala His Ile Pro Lys Ser Asp

100 105 110

Ala Leu Tyr Phe Asp Asp Cys Met Gln Leu Leu Ala Gln Thr Phe Pro

115 120 125

Phe Val Asp Asp Asn Glu Val Ser Ser Ala Thr Phe Gln Ser Leu Val

130 135 140

Pro Asp Ile Pro Gly His Ile Glu Ser Pro Val Phe Ile Ala Thr Asn

145 150 155 160

Gln Ala Gln Ser Pro Glu Thr Ser Val Ala Gln Val Ala Pro Val Asp

165 170 175

Leu Asp Gly Met Gln Gln Asp Ile Glu Gln Val Trp Glu Glu Leu Leu

180 185 190

Ser Ile Pro Glu Leu Gln Cys Leu Asn Ile Glu Asn Asp Lys Leu Val

195 200 205

Glu Thr Thr Met Val Pro Ser Pro Glu Ala Lys Leu Thr Glu Val Asp

210 215 220

Asn Tyr His Phe Tyr Ser Ser Ile Pro Ser Met Glu Lys Glu Val Gly

225 230 235 240

Asn Cys Ser Pro His Phe Leu Asn Ala Phe Glu Asp Ser Phe Ser Ser
 245 250 255
 Ile Leu Ser Thr Glu Asp Pro Asn Gln Leu Thr Val Asn Ser Leu Asn
 260 265 270
 Ser Asp Ala Thr Val Asn Thr Asp Phe Gly Asp Glu Phe Tyr Ser Ala
 275 280 285
 Phe Ile Ala Glu Pro Ser Ile Ser Asn Ser Met Pro Ser Pro Ala Thr
 290 295 300
 Leu Ser His Ser Leu Ser Glu Leu Leu Asn Gly Pro Ile Asp Val Ser
 305 310 315 320
 Asp Leu Ser Leu Cys Lys Ala Phe Asn Gln Asn His Pro Glu Ser Thr
 325 330 335
 Ala Glu Phe Asn Asp Ser Asp Ser Gly Ile Ser Leu Asn Thr Ser Pro
 340 345 350
 Ser Val Ala Ser Pro Glu His Ser Val Glu Ser Ser Ser Tyr Gly Asp
 355 360 365
 Thr Leu Leu Gly Leu Ser Asp Ser Glu Val Glu Glu Leu Asp Ser Ala
 370 375 380
 Pro Gly Ser Val Lys Gln Asn Gly Pro Lys Thr Pro Val His Ser Ser
 385 390 395 400
 Gly Asp Met Val Gln Pro Leu Ser Pro Ser Gln Gly Gln Ser Thr His
 405 410 415
 Val His Asp Ala Gln Cys Glu Asn Thr Pro Glu Lys Glu Leu Pro Val
 420 425 430
 Ser Pro Gly His Arg Lys Thr Pro Phe Thr Lys Asp Lys His Ser Ser
 435 440 445
 Arg Leu Glu Ala His Leu Thr Arg Asp Glu Leu Arg Ala Lys Ala Leu
 450 455 460
 His Ile Pro Phe Pro Val Glu Lys Ile Ile Asn Leu Pro Val Val Asp
 465 470 475 480
 Phe Asn Glu Met Met Ser Lys Glu Gln Phe Asn Glu Ala Gln Leu Ala

485 490 495
 Leu Ile Arg Asp Ile Arg Arg Arg Gly Lys Asn Lys Val Ala Ala Gln
 500 505 510
 Asn Cys Arg Lys Arg Lys Leu Glu Asn Ile Val Glu Leu Glu Gln Asp
 515 520 525
 Leu Asp His Leu Lys Asp Glu Lys Glu Lys Leu Leu Lys Glu Lys Gly
 530 535 540
 Glu Asn Asp Lys Ser Leu His Leu Leu Lys Lys Gln Leu Ser Thr Leu

545 550 555 560
 Tyr Leu Glu Val Phe Ser Met Leu Arg Asp Glu Asp Gly Lys Pro Tyr
 565 570 575
 Ser Pro Ser Glu Tyr Ser Leu Gln Gln Thr Arg Asp Gly Asn Val Phe
 580 585 590
 Leu Val Pro Lys Ser Lys Lys Pro Asp Val Lys Lys Asn
 595 600 605

<210> 4376

<211> 582

<212> PRT

<213> homo sapiens

<400> 4376

Met Asp Leu Ile Asp Ile Leu Trp Arg Gln Asp Ile Asp Leu Gly Val
 1 5 10 15
 Ser Arg Glu Val Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu
 20 25 30
 Glu Lys Gln Lys Lys Leu Glu Lys Glu Arg Gln Glu Gln Leu Gln Lys
 35 40 45
 Glu Gln Glu Lys Ala Phe Phe Ala Gln Leu Gln Leu Asp Glu Glu Thr
 50 55 60

Gly Glu Phe Leu Pro Ile Gln Pro Ala Gln His Ile Gln Ser Glu Thr
 65 70 75 80
 Ser Gly Ser Ala Asn Tyr Ser Gln Val Ala His Ile Pro Lys Ser Asp
 85 90 95

Ala Leu Tyr Phe Asp Asp Cys Met Gln Leu Leu Ala Gln Thr Phe Pro
100 105 110

Phe Val Asp Asp Asn Glu Ser Leu Val Pro Asp Ile Pro Gly His Ile
115 120 125

Glu Ser Pro Val Phe Ile Ala Thr Asn Gln Ala Gln Ser Pro Glu Thr
130 135 140

Ser Val Ala Gln Val Ala Pro Val Asp Leu Asp Gly Met Gln Gln Asp
145 150 155 160

Ile Glu Gln Val Trp Glu Glu Leu Leu Ser Ile Pro Glu Leu Gln Cys
165 170 175

Leu Asn Ile Glu Asn Asp Lys Leu Val Glu Thr Thr Met Val Pro Ser
180 185 190

Pro Glu Ala Lys Leu Thr Glu Val Asp Asn Tyr His Phe Tyr Ser Ser
195 200 205

Ile Pro Ser Met Glu Lys Glu Val Gly Asn Cys Ser Pro His Phe Leu
210 215 220

Asn Ala Phe Glu Asp Ser Phe Ser Ser Ile Leu Ser Thr Glu Asp Pro
225 230 235 240

Asn Gln Leu Thr Val Asn Ser Leu Asn Ser Asp Ala Thr Val Asn Thr
245 250 255

Asp Phe Gly Asp Glu Phe Tyr Ser Ala Phe Ile Ala Glu Pro Ser Ile
260 265 270

Ser Asn Ser Met Pro Ser Pro Ala Thr Leu Ser His Ser Leu Ser Glu
275 280 285

Leu Leu Asn Gly Pro Ile Asp Val Ser Asp Leu Ser Leu Cys Lys Ala
290 295 300

Phe Asn Gln Asn His Pro Glu Ser Thr Ala Glu Phe Asn Asp Ser Asp
305 310 315 320

Ser Gly Ile Ser Leu Asn Thr Ser Pro Ser Val Ala Ser Pro Glu His
325 330 335

Ser Val Glu Ser Ser Ser Tyr Gly Asp Thr Leu Leu Gly Leu Ser Asp

340	345	350	
Ser Glu Val Glu Glu Leu Asp Ser Ala Pro Gly Ser Val Lys Gln Asn			
355	360	365	
Gly Pro Lys Thr Pro Val His Ser Ser Gly Asp Met Val Gln Pro Leu			
370	375	380	
Ser Pro Ser Gln Gly Gln Ser Thr His Val His Asp Ala Gln Cys Glu			
385	390	395	400
Asn Thr Pro Glu Lys Glu Leu Pro Val Ser Pro Gly His Arg Lys Thr			
405	410	415	
Pro Phe Thr Lys Asp Lys His Ser Ser Arg Leu Glu Ala His Leu Thr			
420	425	430	
Arg Asp Glu Leu Arg Ala Lys Ala Leu His Ile Pro Phe Pro Val Glu			
435	440	445	
Lys Ile Ile Asn Leu Pro Val Val Asp Phe Asn Glu Met Met Ser Lys			
450	455	460	
Glu Gln Phe Asn Glu Ala Gln Leu Ala Leu Ile Arg Asp Ile Arg Arg			
465	470	475	480
Arg Gly Lys Asn Lys Val Ala Ala Gln Asn Cys Arg Lys Arg Lys Leu			
485	490	495	
Glu Asn Ile Val Glu Leu Glu Gln Asp Leu Asp His Leu Lys Asp Glu			
500	505	510	
Lys Glu Lys Leu Leu Lys Glu Lys Gly Glu Asn Asp Lys Ser Leu His			
515	520	525	
Leu Leu Lys Lys Gln Leu Ser Thr Leu Tyr Leu Glu Val Phe Ser Met			
530	535	540	
Leu Arg Asp Glu Asp Gly Lys Pro Tyr Ser Pro Ser Glu Tyr Ser Leu			
545	550	555	560
Gln Gln Thr Arg Asp Gly Asn Val Phe Leu Val Pro Lys Ser Lys Lys			
565	570	575	
Pro Asp Val Lys Lys Asn			
580			

<210> 4377

<211> 816

<212> PRT

<213> homo sapiens

<400> 4377

Met Ala Glu Pro Leu Lys Glu Glu Asp Gly Glu Asp Gly Ser Ala Glu

1 5 10 15

Pro Pro Gly Pro Val Lys Ala Glu Pro Ala His Thr Ala Ala Ser Val

20 25 30

Ala Ala Lys Asn Leu Ala Leu Leu Lys Ala Arg Ser Phe Asp Val Thr

35 40 45

Phe Asp Val Gly Asp Glu Tyr Glu Ile Ile Glu Thr Ile Gly Asn Gly

50 55 60

Ala Tyr Gly Val Val Ser Ser Ala Arg Arg Arg Leu Thr Gly Gln Gln

65 70 75 80

Val Ala Ile Lys Lys Ile Pro Asn Ala Phe Asp Val Val Thr Asn Ala

85 90 95

Lys Arg Thr Leu Arg Glu Leu Lys Ile Leu Lys His Phe Lys His Asp

100 105 110

Asn Ile Ile Ala Ile Lys Asp Ile Leu Arg Pro Thr Val Pro Tyr Gly

115 120 125

Glu Phe Lys Ser Val Tyr Val Val Leu Asp Leu Met Glu Ser Asp Leu

130 135 140

His Gln Ile Ile His Ser Ser Gln Pro Leu Thr Leu Glu His Val Arg

145 150 155 160

Tyr Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Met His Ser Ala

165 170 175

Gln Val Ile His Arg Asp Leu Lys Pro Ser Asn Leu Leu Val Asn Glu

180 185 190

Asn Cys Glu Leu Lys Ile Gly Asp Phe Gly Met Ala Arg Gly Leu Cys

195 200 205

Thr Ser Pro Ala Glu His Gln Tyr Phe Met Thr Glu Tyr Val Ala Thr

210 215 220
 Arg Trp Tyr Arg Ala Pro Glu Leu Met Leu Ser Leu His Glu Tyr Thr
 225 230 235 240

 Gln Ala Ile Asp Leu Trp Ser Val Gly Cys Ile Phe Gly Glu Met Leu
 245 250 255
 Ala Arg Arg Gln Leu Phe Pro Gly Lys Asn Tyr Val His Gln Leu Gln
 260 265 270
 Leu Ile Met Met Val Leu Gly Thr Pro Ser Pro Ala Val Ile Gln Ala
 275 280 285
 Val Gly Ala Glu Arg Val Arg Ala Tyr Ile Gln Ser Leu Pro Pro Arg
 290 295 300

 Gln Pro Val Pro Trp Glu Thr Val Tyr Pro Gly Ala Asp Arg Gln Ala
 305 310 315 320
 Leu Ser Leu Leu Gly Arg Met Leu Arg Phe Glu Pro Ser Ala Arg Ile
 325 330 335
 Ser Ala Ala Ala Ala Leu Arg His Pro Phe Leu Ala Lys Tyr His Asp
 340 345 350
 Pro Asp Asp Glu Pro Asp Cys Ala Pro Pro Phe Asp Phe Ala Phe Asp
 355 360 365

 Arg Glu Ala Leu Thr Arg Glu Arg Ile Lys Glu Ala Ile Val Ala Glu
 370 375 380
 Ile Glu Asp Phe His Ala Arg Arg Glu Gly Ile Arg Gln Gln Ile Arg
 385 390 395 400
 Phe Gln Pro Ser Leu Gln Pro Val Ala Ser Glu Pro Gly Cys Pro Asp
 405 410 415
 Val Glu Met Pro Ser Pro Trp Ala Pro Ser Gly Asp Cys Ala Met Glu
 420 425 430

 Ser Pro Pro Pro Ala Pro Pro Pro Cys Pro Gly Pro Ala Pro Asp Thr
 435 440 445
 Ile Asp Leu Thr Leu Gln Pro Pro Pro Pro Val Ser Glu Pro Ala Pro
 450 455 460

Pro Lys Lys Asp Gly Ala Ile Ser Asp Asn Thr Lys Ala Ala Leu Lys
465 470 475 480
Ala Ala Leu Leu Lys Ser Leu Arg Ser Arg Leu Arg Asp Gly Pro Ser
485 490 495

Ala Pro Leu Glu Ala Pro Glu Pro Arg Lys Pro Val Thr Ala Gln Glu
500 505 510
Arg Gln Arg Glu Arg Glu Glu Lys Arg Arg Arg Arg Gln Glu Arg Ala
515 520 525
Lys Glu Arg Glu Lys Arg Arg Gln Glu Arg Glu Arg Lys Glu Arg Gly
530 535 540
Ala Gly Ala Ser Gly Gly Pro Ser Thr Asp Pro Leu Ala Gly Leu Val
545 550 555 560

Leu Ser Asp Asn Asp Arg Ser Leu Leu Glu Arg Trp Thr Arg Met Ala
565 570 575
Arg Pro Ala Ala Pro Ala Leu Thr Ser Val Pro Ala Pro Ala Pro Ala
580 585 590
Pro Thr Pro Thr Pro Thr Pro Val Gln Pro Thr Ser Pro Pro Pro Gly
595 600 605
Pro Val Ala Gln Pro Thr Gly Pro Gln Pro Gln Ser Ala Gly Ser Thr
610 615 620

Ser Gly Pro Val Pro Gln Pro Ala Cys Pro Pro Pro Gly Pro Ala Pro
625 630 635 640
His Pro Thr Gly Pro Pro Gly Pro Ile Pro Val Pro Ala Pro Pro Gln
645 650 655
Ile Ala Thr Ser Thr Ser Leu Leu Ala Ala Gln Ser Leu Val Pro Pro
660 665 670
Pro Gly Leu Pro Gly Ser Ser Thr Pro Gly Val Leu Pro Tyr Phe Pro
675 680 685

Pro Gly Leu Pro Pro Pro Asp Ala Gly Gly Ala Pro Gln Ser Ser Met
690 695 700
Ser Glu Ser Pro Asp Val Asn Leu Val Thr Gln Gln Leu Ser Lys Ser

705 710 715 720
Gln Val Glu Asp Pro Leu Pro Pro Val Phe Ser Gly Thr Pro Lys Gly
725 730 735
Ser Gly Ala Gly Tyr Gly Val Gly Phe Asp Leu Glu Glu Phe Leu Asn
740 745 750

Gln Ser Phe Asp Met Gly Val Ala Asp Gly Pro Gln Asp Gly Gln Ala
755 760 765
Asp Ser Ala Ser Leu Ser Ala Ser Leu Leu Ala Asp Trp Leu Glu Gly
770 775 780
His Gly Met Asn Pro Ala Asp Ile Glu Ser Leu Gln Arg Glu Ile Gln
785 790 795 800
Met Asp Ser Pro Met Leu Leu Ala Asp Leu Pro Asp Leu Gln Asp Pro
805 810 815

<210> 4378

<211> 816

<212> PRT

<213> homo sapiens

<400> 4378

Met Ala Glu Pro Leu Lys Glu Glu Asp Gly Glu Asp Gly Ser Ala Glu
1 5 10 15
Pro Pro Gly Pro Val Lys Ala Glu Pro Ala His Thr Ala Ala Ser Val
20 25 30
Ala Ala Lys Asn Leu Ala Leu Leu Lys Ala Arg Ser Phe Asp Val Thr
35 40 45
Phe Asp Val Gly Asp Glu Tyr Glu Ile Ile Glu Thr Ile Gly Asn Gly
50 55 60
Ala Tyr Gly Val Val Ser Ser Ala Arg Arg Arg Leu Thr Gly Gln Gln
65 70 75 80
Val Ala Ile Lys Lys Ile Pro Asn Ala Phe Asp Val Val Thr Asn Ala
85 90 95
Lys Arg Thr Leu Arg Glu Leu Lys Ile Leu Lys His Phe Lys His Asp
100 105 110

Asn Ile Ile Ala Ile Lys Asp Ile Leu Arg Pro Thr Val Pro Tyr Gly

115 120 125

Glu Phe Lys Ser Val Tyr Val Val Leu Asp Leu Met Glu Ser Asp Leu

130 135 140

His Gln Ile Ile His Ser Ser Gln Pro Leu Thr Leu Glu His Val Arg

145 150 155 160

Tyr Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Met His Ser Ala

165 170 175

Gln Val Ile His Arg Asp Leu Lys Pro Ser Asn Leu Leu Val Asn Glu

180 185 190

Asn Cys Glu Leu Lys Ile Gly Asp Phe Gly Met Ala Arg Gly Leu Cys

195 200 205

Thr Ser Pro Ala Glu His Gln Tyr Phe Met Thr Glu Tyr Val Ala Thr

210 215 220

Arg Trp Tyr Arg Ala Pro Glu Leu Met Leu Ser Leu His Glu Tyr Thr

225 230 235 240

Gln Ala Ile Asp Leu Trp Ser Val Gly Cys Ile Phe Gly Glu Met Leu

245 250 255

Ala Arg Arg Gln Leu Phe Pro Gly Lys Asn Tyr Val His Gln Leu Gln

260 265 270

Leu Ile Met Met Val Leu Gly Thr Pro Ser Pro Ala Val Ile Gln Ala

275 280 285

Val Gly Ala Glu Arg Val Arg Ala Tyr Ile Gln Ser Leu Pro Pro Arg

290 295 300

Gln Pro Val Pro Trp Glu Thr Val Tyr Pro Gly Ala Asp Arg Gln Ala

305 310 315 320

Leu Ser Leu Leu Gly Arg Met Leu Arg Phe Glu Pro Ser Ala Arg Ile

325 330 335

Ser Ala Ala Ala Ala Leu Arg His Pro Phe Leu Ala Lys Tyr His Asp

340 345 350

Pro Asp Asp Glu Pro Asp Cys Ala Pro Pro Phe Asp Phe Ala Phe Asp

355 Arg Glu Ala Leu Thr Arg Glu Arg Ile Lys Glu Ala Ile Val Ala Glu
360 365

370 Ile Glu Asp Phe His Ala Arg Arg Glu Gly Ile Arg Gln Gln Ile Arg
385 390 395 400

Phe Gln Pro Ser Leu Gln Pro Val Ala Ser Glu Pro Gly Cys Pro Asp
405 410 415

Val Glu Met Pro Ser Pro Trp Ala Pro Ser Gly Asp Cys Ala Met Glu
420 425 430

Ser Pro Pro Pro Ala Pro Pro Pro Cys Pro Gly Pro Ala Pro Asp Thr

435 440 445
Ile Asp Leu Thr Leu Gln Pro Pro Pro Pro Val Ser Glu Pro Ala Pro

450 455 460
Pro Lys Lys Asp Gly Ala Ile Ser Asp Asn Thr Lys Ala Ala Leu Lys

465 470 475 480
Ala Ala Leu Leu Lys Ser Leu Arg Ser Arg Leu Arg Asp Gly Pro Ser

485 490 495
Ala Pro Leu Glu Ala Pro Glu Pro Arg Lys Pro Val Thr Ala Gln Glu

500 505 510
Arg Gln Arg Glu Arg Glu Glu Lys Arg Arg Arg Arg Gln Glu Arg Ala

515 520 525
Lys Glu Arg Glu Lys Arg Arg Gln Glu Arg Glu Arg Lys Glu Arg Gly

530 535 540
Ala Gly Ala Ser Gly Gly Pro Ser Thr Asp Pro Leu Ala Gly Leu Val

545 550 555 560
Leu Ser Asp Asn Asp Arg Ser Leu Leu Glu Arg Trp Thr Arg Met Ala

565 570 575
Arg Pro Ala Ala Pro Ala Leu Thr Ser Val Pro Ala Pro Ala Pro Ala

580 585 590
Pro Thr Pro Thr Pro Thr Pro Val Gln Pro Thr Ser Pro Pro Pro Gly

595 600 605

Pro Val Ala Gln Pro Thr Gly Pro Gln Pro Gln Ser Ala Gly Ser Thr

610 615 620

Ser Gly Pro Val Pro Gln Pro Ala Cys Pro Pro Pro Gly Pro Ala Pro

625 630 635 640

His Pro Thr Gly Pro Pro Gly Pro Ile Pro Val Pro Ala Pro Pro Gln

645 650 655

Ile Ala Thr Ser Thr Ser Leu Leu Ala Ala Gln Ser Leu Val Pro Pro

660 665 670

Pro Gly Leu Pro Gly Ser Ser Thr Pro Gly Val Leu Pro Tyr Phe Pro

675 680 685

Pro Gly Leu Pro Pro Pro Asp Ala Gly Gly Ala Pro Gln Ser Ser Met

690 695 700

Ser Glu Ser Pro Asp Val Asn Leu Val Thr Gln Gln Leu Ser Lys Ser

705 710 715 720

Gln Val Glu Asp Pro Leu Pro Pro Val Phe Ser Gly Thr Pro Lys Gly

725 730 735

Ser Gly Ala Gly Tyr Gly Val Gly Phe Asp Leu Glu Glu Phe Leu Asn

740 745 750

Gln Ser Phe Asp Met Gly Val Ala Asp Gly Pro Gln Asp Gly Gln Ala

755 760 765

Asp Ser Ala Ser Leu Ser Ala Ser Leu Leu Ala Asp Trp Leu Glu Gly

770 775 780

His Gly Met Asn Pro Ala Asp Ile Glu Ser Leu Gln Arg Glu Ile Gln

785 790 795 800

Met Asp Ser Pro Met Leu Leu Ala Asp Leu Pro Asp Leu Gln Asp Pro

805 810 815

<210> 4379

<211> 677

<212> PRT

<213> homo sapiens

<400> 4379

Met Glu Ser Asp Leu His Gln Ile Ile His Ser Ser Gln Pro Leu Thr
1 5 10 15
Leu Glu His Val Arg Tyr Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys
20 25 30
Tyr Met His Ser Ala Gln Val Ile His Arg Asp Leu Lys Pro Ser Asn
35 40 45
Leu Leu Val Asn Glu Asn Cys Glu Leu Lys Ile Gly Asp Phe Gly Met
50 55 60

Ala Arg Gly Leu Cys Thr Ser Pro Ala Glu His Gln Tyr Phe Met Thr
65 70 75 80
Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Met Leu Ser
85 90 95
Leu His Glu Tyr Thr Gln Ala Ile Asp Leu Trp Ser Val Gly Cys Ile
100 105 110
Phe Gly Glu Met Leu Ala Arg Arg Gln Leu Phe Pro Gly Lys Asn Tyr
115 120 125

Val His Gln Leu Gln Leu Ile Met Met Val Leu Gly Thr Pro Ser Pro
130 135 140
Ala Val Ile Gln Ala Val Gly Ala Glu Arg Val Arg Ala Tyr Ile Gln
145 150 155 160
Ser Leu Pro Pro Arg Gln Pro Val Pro Trp Glu Thr Val Tyr Pro Gly
165 170 175
Ala Asp Arg Gln Ala Leu Ser Leu Leu Gly Arg Met Leu Arg Phe Glu
180 185 190

Pro Ser Ala Arg Ile Ser Ala Ala Ala Ala Leu Arg His Pro Phe Leu
195 200 205
Ala Lys Tyr His Asp Pro Asp Asp Glu Pro Asp Cys Ala Pro Pro Phe
210 215 220
Asp Phe Ala Phe Asp Arg Glu Ala Leu Thr Arg Glu Arg Ile Lys Glu
225 230 235 240
Ala Ile Val Ala Glu Ile Glu Asp Phe His Ala Arg Arg Glu Gly Ile

Pro Gly Pro Ala Pro His Pro Thr Gly Pro Pro Gly Pro Ile Pro Val
500 505 510

Pro Ala Pro Pro Gln Ile Ala Thr Ser Thr Ser Leu Leu Ala Ala Gln
515 520 525

Ser Leu Val Pro Pro Pro Gly Leu Pro Gly Ser Ser Thr Pro Gly Val
530 535 540

Leu Pro Tyr Phe Pro Pro Gly Leu Pro Pro Pro Asp Ala Gly Gly Ala
545 550 555 560

Pro Gln Ser Ser Met Ser Glu Ser Pro Asp Val Asn Leu Val Thr Gln
565 570 575

Gln Leu Ser Lys Ser Gln Val Glu Asp Pro Leu Pro Pro Val Phe Ser
580 585 590

Gly Thr Pro Lys Gly Ser Gly Ala Gly Tyr Gly Val Gly Phe Asp Leu
595 600 605

Glu Glu Phe Leu Asn Gln Ser Phe Asp Met Gly Val Ala Asp Gly Pro
610 615 620

Gln Asp Gly Gln Ala Asp Ser Ala Ser Leu Ser Ala Ser Leu Leu Ala
625 630 635 640

Asp Trp Leu Glu Gly His Gly Met Asn Pro Ala Asp Ile Glu Ser Leu
645 650 655

Gln Arg Glu Ile Gln Met Asp Ser Pro Met Leu Leu Ala Asp Leu Pro
660 665 670

Asp Leu Gln Asp Pro
675

<210> 4380

<211> 816

<212> PRT

<213> homo sapiens

<400> 4380

Met Ala Glu Pro Leu Lys Glu Glu Asp Gly Glu Asp Gly Ser Ala Glu
1 5 10 15

Pro Pro Gly Pro Val Lys Ala Glu Pro Ala His Thr Ala Ala Ser Val
 20 25 30
 Ala Ala Lys Asn Leu Ala Leu Leu Lys Ala Arg Ser Phe Asp Val Thr
 35 40 45
 Phe Asp Val Gly Asp Glu Tyr Glu Ile Ile Glu Thr Ile Gly Asn Gly
 50 55 60
 Ala Tyr Gly Val Val Ser Ser Ala Arg Arg Arg Leu Thr Gly Gln Gln
 65 70 75 80

 Val Ala Ile Lys Lys Ile Pro Asn Ala Phe Asp Val Val Thr Asn Ala
 85 90 95
 Lys Arg Thr Leu Arg Glu Leu Lys Ile Leu Lys His Phe Lys His Asp
 100 105 110
 Asn Ile Ile Ala Ile Lys Asp Ile Leu Arg Pro Thr Val Pro Tyr Gly
 115 120 125
 Glu Phe Lys Ser Val Tyr Val Val Leu Asp Leu Met Glu Ser Asp Leu
 130 135 140

 His Gln Ile Ile His Ser Ser Gln Pro Leu Thr Leu Glu His Val Arg
 145 150 155 160
 Tyr Phe Leu Tyr Gln Leu Leu Arg Gly Leu Lys Tyr Met His Ser Ala
 165 170 175
 Gln Val Ile His Arg Asp Leu Lys Pro Ser Asn Leu Leu Val Asn Glu
 180 185 190
 Asn Cys Glu Leu Lys Ile Gly Asp Phe Gly Met Ala Arg Gly Leu Cys
 195 200 205

 Thr Ser Pro Ala Glu His Gln Tyr Phe Met Thr Glu Tyr Val Ala Thr
 210 215 220
 Arg Trp Tyr Arg Ala Pro Glu Leu Met Leu Ser Leu His Glu Tyr Thr
 225 230 235 240
 Gln Ala Ile Asp Leu Trp Ser Val Gly Cys Ile Phe Gly Glu Met Leu
 245 250 255
 Ala Arg Arg Gln Leu Phe Pro Gly Lys Asn Tyr Val His Gln Leu Gln

260	265	270
Leu Ile Met Met Val Leu Gly Thr Pro Ser Pro Ala Val Ile Gln Ala		
275	280	285
Val Gly Ala Glu Arg Val Arg Ala Tyr Ile Gln Ser Leu Pro Pro Arg		
290	295	300
Gln Pro Val Pro Trp Glu Thr Val Tyr Pro Gly Ala Asp Arg Gln Ala		
305	310	315
Leu Ser Leu Leu Gly Arg Met Leu Arg Phe Glu Pro Ser Ala Arg Ile		
325	330	335
Ser Ala Ala Ala Ala Leu Arg His Pro Phe Leu Ala Lys Tyr His Asp		
340	345	350
Pro Asp Asp Glu Pro Asp Cys Ala Pro Pro Phe Asp Phe Ala Phe Asp		
355	360	365
Arg Glu Ala Leu Thr Arg Glu Arg Ile Lys Glu Ala Ile Val Ala Glu		
370	375	380
Ile Glu Asp Phe His Ala Arg Arg Glu Gly Ile Arg Gln Gln Ile Arg		
385	390	395
Phe Gln Pro Ser Leu Gln Pro Val Ala Ser Glu Pro Gly Cys Pro Asp		
405	410	415
Val Glu Met Pro Ser Pro Trp Ala Pro Ser Gly Asp Cys Ala Met Glu		
420	425	430
Ser Pro Pro Pro Ala Pro Pro Pro Cys Pro Gly Pro Ala Pro Asp Thr		
435	440	445
Ile Asp Leu Thr Leu Gln Pro Pro Pro Pro Val Ser Glu Pro Ala Pro		
450	455	460
Pro Lys Lys Asp Gly Ala Ile Ser Asp Asn Thr Lys Ala Ala Leu Lys		
465	470	475
Ala Ala Leu Leu Lys Ser Leu Arg Ser Arg Leu Arg Asp Gly Pro Ser		
485	490	495
Ala Pro Leu Glu Ala Pro Glu Pro Arg Lys Pro Val Thr Ala Gln Glu		
500	505	510

Arg Gln Arg Glu Arg Glu Glu Lys Arg Arg Arg Arg Gln Glu Arg Ala
515 520 525

Lys Glu Arg Glu Lys Arg Arg Gln Glu Arg Glu Arg Lys Glu Arg Gly
530 535 540

Ala Gly Ala Ser Gly Gly Pro Ser Thr Asp Pro Leu Ala Gly Leu Val
545 550 555 560

Leu Ser Asp Asn Asp Arg Ser Leu Leu Glu Arg Trp Thr Arg Met Ala
565 570 575

Arg Pro Ala Ala Pro Ala Leu Thr Ser Val Pro Ala Pro Ala Pro Ala
580 585 590

Pro Thr Pro Thr Pro Thr Pro Val Gln Pro Thr Ser Pro Pro Pro Gly
595 600 605

Pro Val Ala Gln Pro Thr Gly Pro Gln Pro Gln Ser Ala Gly Ser Thr
610 615 620

Ser Gly Pro Val Pro Gln Pro Ala Cys Pro Pro Pro Gly Pro Ala Pro
625 630 635 640

His Pro Thr Gly Pro Pro Gly Pro Ile Pro Val Pro Ala Pro Pro Gln
645 650 655

Ile Ala Thr Ser Thr Ser Leu Leu Ala Ala Gln Ser Leu Val Pro Pro
660 665 670

Pro Gly Leu Pro Gly Ser Ser Thr Pro Gly Val Leu Pro Tyr Phe Pro
675 680 685

Pro Gly Leu Pro Pro Pro Asp Ala Gly Gly Ala Pro Gln Ser Ser Met
690 695 700

Ser Glu Ser Pro Asp Val Asn Leu Val Thr Gln Gln Leu Ser Lys Ser
705 710 715 720

Gln Val Glu Asp Pro Leu Pro Pro Val Phe Ser Gly Thr Pro Lys Gly
725 730 735

Ser Gly Ala Gly Tyr Gly Val Gly Phe Asp Leu Glu Glu Phe Leu Asn
740 745 750

Gln Ser Phe Asp Met Gly Val Ala Asp Gly Pro Gln Asp Gly Gln Ala

755 760 765
 Asp Ser Ala Ser Leu Ser Ala Ser Leu Leu Ala Asp Trp Leu Glu Gly
 770 775 780

His Gly Met Asn Pro Ala Asp Ile Glu Ser Leu Gln Arg Glu Ile Gln
 785 790 795 800
 Met Asp Ser Pro Met Leu Leu Ala Asp Leu Pro Asp Leu Gln Asp Pro
 805 810 815

<210> 4381

<211> 279

<212> PRT

<213> homo sapiens

<400> 4381

Met Glu Asn Ser Glu Lys Thr Glu Val Val Leu Leu Ala Cys Gly Ser
 1 5 10 15
 Phe Asn Pro Ile Thr Asn Met His Leu Arg Leu Phe Glu Leu Ala Lys

20 25 30
 Asp Tyr Met Asn Gly Thr Gly Arg Tyr Thr Val Val Lys Gly Ile Ile
 35 40 45
 Ser Pro Val Gly Asp Ala Tyr Lys Lys Lys Gly Leu Ile Pro Ala Tyr
 50 55 60
 His Arg Val Ile Met Ala Glu Leu Ala Thr Lys Asn Ser Lys Trp Val
 65 70 75 80
 Glu Val Asp Thr Trp Glu Ser Leu Gln Lys Glu Trp Lys Glu Thr Leu

85 90 95
 Lys Val Leu Arg His His Gln Glu Lys Leu Glu Ala Ser Asp Cys Asp
 100 105 110
 His Gln Gln Asn Ser Pro Thr Leu Glu Arg Pro Gly Arg Lys Arg Lys
 115 120 125
 Trp Thr Glu Thr Gln Asp Ser Ser Gln Lys Lys Ser Leu Glu Pro Lys
 130 135 140
 Thr Lys Ala Val Pro Lys Val Lys Leu Leu Cys Gly Ala Asp Leu Leu

145 150 155 160
 Glu Ser Phe Ala Val Pro Asn Leu Trp Lys Ser Glu Asp Ile Thr Gln
 165 170 175
 Ile Val Ala Asn Tyr Gly Leu Ile Cys Val Thr Arg Ala Gly Asn Asp
 180 185 190
 Ala Gln Lys Phe Ile Tyr Glu Ser Asp Val Leu Trp Lys His Arg Ser
 195 200 205
 Asn Ile His Val Val Asn Glu Trp Ile Ala Asn Asp Ile Ser Ser Thr

 210 215 220
 Lys Ile Arg Arg Ala Leu Arg Arg Gly Gln Ser Ile Arg Tyr Leu Val
 225 230 235 240
 Pro Asp Leu Val Gln Glu Tyr Ile Glu Lys His Asn Leu Tyr Ser Ser
 245 250 255
 Glu Ser Glu Asp Arg Asn Ala Gly Val Ile Leu Ala Pro Leu Gln Arg
 260 265 270
 Asn Thr Ala Glu Ala Lys Thr
 275

 <210> 4382
 <211> 241
 <212> PRT
 <213> homo sapiens
 <400> 4382
 Met Ser Met Leu Phe Tyr Thr Leu Ile Thr Ala Phe Leu Ile Gly Ile
 1 5 10 15
 Gln Ala Glu Pro His Ser Glu Ser Asn Val Pro Ala Gly His Thr Ile
 20 25 30
 Pro Gln Ala His Trp Thr Lys Leu Gln His Ser Leu Asp Thr Ala Leu
 35 40 45
 Arg Arg Ala Arg Ser Ala Pro Ala Ala Ala Ile Ala Ala Arg Val Ala

 50 55 60
 Gly Gln Thr Arg Asn Ile Thr Val Asp Pro Arg Leu Phe Lys Lys Arg
 65 70 75 80

Arg Leu Arg Ser Pro Arg Val Leu Phe Ser Thr Gln Pro Pro Arg Glu
85 90 95
Ala Ala Asp Thr Gln Asp Leu Asp Phe Glu Val Gly Gly Ala Ala Pro
100 105 110
Phe Asn Arg Thr His Arg Ser Lys Arg Ser Ser Ser His Pro Ile Phe
115 120 125
His Arg Gly Glu Phe Ser Val Cys Asp Ser Val Ser Val Trp Val Gly
130 135 140
Asp Lys Thr Thr Ala Thr Asp Ile Lys Gly Lys Glu Val Met Val Leu
145 150 155 160
Gly Glu Val Asn Ile Asn Asn Ser Val Phe Lys Gln Tyr Phe Phe Glu
165 170 175
Thr Lys Cys Arg Asp Pro Asn Pro Val Asp Ser Gly Cys Arg Gly Ile
180 185 190
Asp Ser Lys His Trp Asn Ser Tyr Cys Thr Thr Thr His Thr Phe Val
195 200 205
Lys Ala Leu Thr Met Asp Gly Lys Gln Ala Ala Trp Arg Phe Ile Arg
210 215 220
Ile Asp Thr Ala Cys Val Cys Val Leu Ser Arg Lys Ala Val Arg Arg
225 230 235 240
Ala

<210> 4383

<211> 743

<212> PRT

<213> homo sapiens

<400> 4383

Met Glu Ala Val Ala Val Ala Ala Ala Val Gly Val Leu Leu Leu Ala
1 5 10 15
Gly Ala Gly Gly Ala Ala Gly Asp Glu Ala Arg Glu Ala Ala Ala Val
20 25 30
Arg Ala Leu Val Ala Arg Leu Leu Gly Pro Gly Pro Ala Ala Asp Phe

35 40 45
 Ser Val Ser Val Glu Arg Ala Leu Ala Ala Lys Pro Gly Leu Asp Thr
 50 55 60

 Tyr Ser Leu Gly Gly Gly Gly Ala Ala Arg Val Arg Val Arg Gly Ser
 65 70 75 80
 Thr Gly Val Ala Ala Ala Ala Gly Leu His Arg Tyr Leu Arg Asp Phe
 85 90 95
 Cys Gly Cys His Val Ala Trp Ser Gly Ser Gln Leu Arg Leu Pro Arg
 100 105 110
 Pro Leu Pro Ala Val Pro Gly Glu Leu Thr Glu Ala Thr Pro Asn Arg
 115 120 125

 Tyr Arg Tyr Tyr Gln Asn Val Cys Thr Gln Ser Tyr Ser Phe Val Trp
 130 135 140
 Trp Asp Trp Ala Arg Trp Glu Arg Glu Ile Asp Trp Met Ala Leu Asn
 145 150 155 160
 Gly Ile Asn Leu Ala Leu Ala Trp Ser Gly Gln Glu Ala Ile Trp Gln
 165 170 175
 Arg Val Tyr Leu Ala Leu Gly Leu Thr Gln Ala Glu Ile Asn Glu Phe
 180 185 190

 Phe Thr Gly Pro Ala Phe Leu Ala Trp Gly Arg Met Gly Asn Leu His
 195 200 205
 Thr Trp Asp Gly Pro Leu Pro Pro Ser Trp His Ile Lys Gln Leu Tyr
 210 215 220
 Leu Gln His Arg Val Leu Asp Gln Met Arg Ser Phe Gly Met Thr Pro
 225 230 235 240
 Val Leu Pro Ala Phe Ala Gly His Val Pro Glu Ala Val Thr Arg Val
 245 250 255

 Phe Pro Gln Val Asn Val Thr Lys Met Gly Ser Trp Gly His Phe Asn
 260 265 270
 Cys Ser Tyr Ser Cys Ser Phe Leu Leu Ala Pro Glu Asp Pro Ile Phe
 275 280 285

Pro Ile Ile Gly Ser Leu Phe Leu Arg Glu Leu Ile Lys Glu Phe Gly
290 295 300

Thr Asp His Ile Tyr Gly Ala Asp Thr Phe Asn Glu Met Gln Pro Pro
305 310 315 320

Ser Ser Glu Pro Ser Tyr Leu Ala Ala Ala Thr Thr Ala Val Tyr Glu
325 330 335

Ala Met Thr Ala Val Asp Thr Glu Ala Val Trp Leu Leu Gln Gly Trp
340 345 350

Leu Phe Gln His Gln Pro Gln Phe Trp Gly Pro Ala Gln Ile Arg Ala
355 360 365

Val Leu Gly Ala Val Pro Arg Gly Arg Leu Leu Val Leu Asp Leu Phe
370 375 380

Ala Glu Ser Gln Pro Val Tyr Thr Arg Thr Ala Ser Phe Gln Gly Gln
385 390 395 400

Pro Phe Ile Trp Cys Met Leu His Asn Phe Gly Gly Asn His Gly Leu
405 410 415

Phe Gly Ala Leu Glu Ala Val Asn Gly Gly Pro Glu Ala Ala Arg Leu
420 425 430

Phe Pro Asn Ser Thr Met Val Gly Thr Gly Met Ala Pro Glu Gly Ile
435 440 445

Ser Gln Asn Glu Val Val Tyr Ser Leu Met Ala Glu Leu Gly Trp Arg
450 455 460

Lys Asp Pro Val Pro Asp Leu Ala Ala Trp Val Thr Ser Phe Ala Ala
465 470 475 480

Arg Arg Tyr Gly Val Ser His Pro Asp Ala Gly Ala Ala Trp Arg Leu
485 490 495

Leu Leu Arg Ser Val Tyr Asn Cys Ser Gly Glu Ala Cys Arg Gly His
500 505 510

Asn Arg Ser Pro Leu Val Arg Arg Pro Ser Leu Gln Met Asn Thr Ser
515 520 525

Ile Trp Tyr Asn Arg Ser Asp Val Phe Glu Ala Trp Arg Leu Leu Leu

530 535 540
 Thr Ser Ala Pro Ser Leu Ala Thr Ser Pro Ala Phe Arg Tyr Asp Leu
 545 550 555 560
 Leu Asp Leu Thr Arg Gln Ala Val Gln Glu Leu Val Ser Leu Tyr Tyr
 565 570 575

 Glu Glu Ala Arg Ser Ala Tyr Leu Ser Lys Glu Leu Ala Ser Leu Leu
 580 585 590
 Arg Ala Gly Gly Val Leu Ala Tyr Glu Leu Leu Pro Ala Leu Asp Glu
 595 600 605
 Val Leu Ala Ser Asp Ser Arg Phe Leu Leu Gly Ser Trp Leu Glu Gln
 610 615 620
 Ala Arg Ala Ala Ala Val Ser Glu Ala Glu Ala Asp Phe Tyr Glu Gln
 625 630 635 640

 Asn Ser Arg Tyr Gln Leu Thr Leu Trp Gly Pro Glu Gly Asn Ile Leu
 645 650 655
 Asp Tyr Ala Asn Lys Gln Leu Ala Gly Leu Val Ala Asn Tyr Tyr Thr
 660 665 670
 Pro Arg Trp Arg Leu Phe Leu Glu Ala Leu Val Asp Ser Val Ala Gln
 675 680 685
 Gly Ile Pro Phe Gln Gln His Gln Phe Asp Lys Asn Val Phe Gln Leu
 690 695 700

 Glu Gln Ala Phe Val Leu Ser Lys Gln Arg Tyr Pro Ser Gln Pro Arg
 705 710 715 720
 Gly Asp Thr Val Asp Leu Ala Lys Lys Ile Phe Leu Lys Tyr Tyr Pro
 725 730 735
 Arg Trp Val Ala Gly Ser Trp
 740

 <210> 4384
 <211> 449
 <212> PRT
 <213> homo sapiens
 <400> 4384

Met Met Lys Thr Leu Leu Leu Phe Val Gly Leu Leu Leu Thr Trp Glu
1 5 10 15

Ser Gly Gln Val Leu Gly Asp Gln Thr Val Ser Asp Asn Glu Leu Gln
20 25 30

Glu Met Ser Asn Gln Gly Ser Lys Tyr Val Asn Lys Glu Ile Gln Asn
35 40 45

Ala Val Asn Gly Val Lys Gln Ile Lys Thr Leu Ile Glu Lys Thr Asn
50 55 60

Glu Glu Arg Lys Thr Leu Leu Ser Asn Leu Glu Glu Ala Lys Lys Lys
65 70 75 80

Lys Glu Asp Ala Leu Asn Glu Thr Arg Glu Ser Glu Thr Lys Leu Lys
85 90 95

Glu Leu Pro Gly Val Cys Asn Glu Thr Met Met Ala Leu Trp Glu Glu
100 105 110

Cys Lys Pro Cys Leu Lys Gln Thr Cys Met Lys Phe Tyr Ala Arg Val
115 120 125

Cys Arg Ser Gly Ser Gly Leu Val Gly Arg Gln Leu Glu Glu Phe Leu
130 135 140

Asn Gln Ser Ser Pro Phe Tyr Phe Trp Met Asn Gly Asp Arg Ile Asp
145 150 155 160

Ser Leu Leu Glu Asn Asp Arg Gln Gln Thr His Met Leu Asp Val Met
165 170 175

Gln Asp His Phe Ser Arg Ala Ser Ser Ile Ile Asp Glu Leu Phe Gln
180 185 190

Asp Arg Phe Phe Thr Arg Glu Pro Gln Asp Thr Tyr His Tyr Leu Pro
195 200 205

Phe Ser Leu Pro His Arg Arg Pro His Phe Phe Phe Pro Lys Ser Arg
210 215 220

Ile Val Arg Ser Leu Met Pro Phe Ser Pro Tyr Glu Pro Leu Asn Phe
225 230 235 240

His Ala Met Phe Gln Pro Phe Leu Glu Met Ile His Glu Ala Gln Gln

245 250 255
Ala Met Asp Ile His Phe His Ser Pro Ala Phe Gln His Pro Pro Thr
260 265 270

Glu Phe Ile Arg Glu Gly Asp Asp Asp Arg Thr Val Cys Arg Glu Ile
275 280 285

Arg His Asn Ser Thr Gly Cys Leu Arg Met Lys Asp Gln Cys Asp Lys
290 295 300

Cys Arg Glu Ile Leu Ser Val Asp Cys Ser Thr Asn Asn Pro Ser Gln
305 310 315 320

Ala Lys Leu Arg Arg Glu Leu Asp Glu Ser Leu Gln Val Ala Glu Arg
325 330 335

Leu Thr Arg Lys Tyr Asn Glu Leu Leu Lys Ser Tyr Gln Trp Lys Met
340 345 350

Leu Asn Thr Ser Ser Leu Leu Glu Gln Leu Asn Glu Gln Phe Asn Trp
355 360 365

Val Ser Arg Leu Ala Asn Leu Thr Gln Gly Glu Asp Gln Tyr Tyr Leu
370 375 380

Arg Val Thr Thr Val Ala Ser His Thr Ser Asp Ser Asp Val Pro Ser
385 390 395 400

Gly Val Thr Glu Val Val Val Lys Leu Phe Asp Ser Asp Pro Ile Thr
405 410 415

Val Thr Val Pro Val Glu Val Ser Arg Lys Asn Pro Lys Phe Met Glu
420 425 430

Thr Val Ala Glu Lys Ala Leu Gln Glu Tyr Arg Lys Lys His Arg Glu
435 440 445

Glu

<210> 4385

<211> 750

<212> PRT

<213> homo sapiens

<400> 4385

Met Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro

1 5 10 15

Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser

20 25 30

Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu

35 40 45

Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys

50 55 60

Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys

65 70 75 80

Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val

85 90 95

Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp

100 105 110

Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu

115 120 125

Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile

130 135 140

Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu

145 150 155 160

Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln

165 170 175

Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn

180 185 190

Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp

195 200 205

Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu

210 215 220

Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu

225 230 235 240

Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile

245 250 255
Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu

260 265 270
Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala

275 280 285
Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr

290 295 300
Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro

305 310 315 320
Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile

325 330 335
Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu

340 345 350
Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln

355 360 365
Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser

370 375 380
Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly

385 390 395 400
Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn

405 410 415
Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe

420 425 430
Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg

435 440 445
Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu

450 455 460
Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile

465 470 475 480
Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu

485 490 495

Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile
 500 505 510
 Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu
 515 520 525
 Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala
 530 535 540
 Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu
 545 550 555 560
 Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly
 565 570 575
 Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp
 580 585 590
 Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr
 595 600 605
 Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr
 610 615 620
 Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
 625 630 635 640
 Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
 645 650 655
 Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu
 660 665 670
 Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu
 675 680 685
 Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val
 690 695 700
 Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile
 705 710 715 720
 Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
 725 730 735
 Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp

740 745 750

<210> 4386

<211> 750

<212> PRT

<213> homo sapiens

<400> 4386

Met Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro

1 5 10 15

Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser

20 25 30

Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu

35 40 45

Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys

50 55 60

Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys

65 70 75 80

Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val

85 90 95

Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp

100 105 110

Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu

115 120 125

Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile

130 135 140

Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu

145 150 155 160

Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln

165 170 175

Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn

180 185 190

Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp

195	200	205
Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu		
210	215	220
Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu		
225	230	235
Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile		
245	250	255
Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu		
260	265	270
Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala		
275	280	285
Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr		
290	295	300
Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro		
305	310	315
Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile		
325	330	335
Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu		
340	345	350
Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln		
355	360	365
Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser		
370	375	380
Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly		
385	390	395
Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn		
405	410	415
Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe		
420	425	430
Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg		
435	440	445

Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu
450 455 460

Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile
465 470 475 480

Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu
485 490 495

Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile
500 505 510

Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu
515 520 525

Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala
530 535 540

Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu
545 550 555 560

Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly
565 570 575

Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp
580 585 590

Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr
595 600 605

Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr
610 615 620

Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
625 630 635 640

Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
645 650 655

Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu
660 665 670

Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu
675 680 685

Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val

690 695 700
 Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile
 705 710 715 720

 Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
 725 730 735
 Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
 740 745 750
 <210> 4387
 <211> 750
 <212> PRT
 <213> homo sapiens
 <400> 4387
 Met Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro
 1 5 10 15
 Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser

 20 25 30
 Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu
 35 40 45
 Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys
 50 55 60
 Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys
 65 70 75 80
 Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val

 85 90 95
 Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp
 100 105 110
 Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu
 115 120 125
 Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile
 130 135 140
 Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu

145 150 155 160
 Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln
 165 170 175
 Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn
 180 185 190
 Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp
 195 200 205
 Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu

 210 215 220
 Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu
 225 230 235 240
 Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile
 245 250 255
 Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu
 260 265 270
 Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala

 275 280 285
 Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr
 290 295 300
 Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro
 305 310 315 320
 Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile
 325 330 335
 Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu

 340 345 350
 Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln
 355 360 365
 Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser
 370 375 380
 Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly
 385 390 395 400

Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn

405 410 415

Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe

420 425 430

Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg

435 440 445

Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu

450 455 460

Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile

465 470 475 480

Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu

485 490 495

Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile

500 505 510

Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu

515 520 525

Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala

530 535 540

Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu

545 550 555 560

Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly

565 570 575

Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp

580 585 590

Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr

595 600 605

Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr

610 615 620

Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn

625 630 635 640

Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly

645 650 655
Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu

660 665 670
Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu

675 680 685
Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val

690 695 700
Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile

705 710 715 720
Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg

725 730 735
Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp

740 745 750

<210> 4388

<211> 750

<212> PRT

<213> homo sapiens

<400> 4388

Met Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro

1 5 10 15

Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser

20 25 30

Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu

35 40 45

Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys

50 55 60

Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys

65 70 75 80

Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val

85 90 95

Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp

100 105 110
 Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu
 115 120 125
 Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile
 130 135 140
 Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu
 145 150 155 160

 Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln
 165 170 175
 Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn
 180 185 190
 Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp
 195 200 205
 Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu
 210 215 220

 Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu
 225 230 235 240
 Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile
 245 250 255
 Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu
 260 265 270
 Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala
 275 280 285

 Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr
 290 295 300
 Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro
 305 310 315 320
 Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile
 325 330 335
 Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu
 340 345 350

Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln
 355 360 365
 Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser
 370 375 380
 Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly
 385 390 395 400
 Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn
 405 410 415

 Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe
 420 425 430
 Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg
 435 440 445
 Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu
 450 455 460
 Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile
 465 470 475 480

 Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu
 485 490 495
 Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile
 500 505 510
 Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu
 515 520 525
 Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala
 530 535 540

 Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu
 545 550 555 560
 Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly
 565 570 575
 Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp
 580 585 590
 Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr

595 600 605
 Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr
 610 615 620
 Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
 625 630 635 640
 Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
 645 650 655
 Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu
 660 665 670

 Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu
 675 680 685
 Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val
 690 695 700
 Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile
 705 710 715 720
 Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
 725 730 735

 Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
 740 745 750

 <210> 4389
 <211> 480
 <212> PRT
 <213> homo sapiens
 <400> 4389

 Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro Asp Gln
 20 25 30
 Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser Phe Arg

 35 40 45
 Gln Tyr Ser Gly Tyr Leu Lys Gly Ser Gly Ser Lys His Leu His Tyr

50 55 60
 Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val Val Leu
 65 70 75 80
 Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Thr
 85 90 95
 Glu His Gly Pro Phe Leu Val Gln Pro Asp Gly Val Thr Leu Glu Tyr

 100 105 110
 Asn Pro Tyr Ser Trp Asn Leu Ile Ala Asn Val Leu Tyr Leu Glu Ser
 115 120 125
 Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr Ala Thr
 130 135 140
 Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln Asp Phe
 145 150 155 160
 Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu Thr Gly

 165 170 175
 Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu Val Met
 180 185 190
 Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn Gly Leu
 195 200 205
 Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala Tyr Tyr
 210 215 220
 His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr His Cys

 225 230 235 240
 Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu Glu Cys
 245 250 255
 Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser Gly Leu
 260 265 270
 Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro Ser His
 275 280 285
 Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly Asn Ile

 290 295 300

Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu Leu Arg
 305 310 315 320
 Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr Ala
 325 330 335
 Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn Ile
 340 345 350
 Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn Leu

 355 360 365
 Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys Leu
 370 375 380
 Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val Asp
 385 390 395 400
 Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu Asn
 405 410 415
 Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly Asp

 420 425 430
 Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His Ile Ala
 435 440 445
 Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp Lys Pro
 450 455 460
 Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln Pro Tyr
 465 470 475 480
 <210> 4390
 <211> 498
 <212> PRT
 <213> homo sapiens

 <400> 4390
 Met Thr Ser Ser Pro Arg Ala Pro Pro Gly Glu Gln Gly Arg Gly Gly
 1 5 10 15
 Ala Glu Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro

35	40	45	
Asp Gln Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser			
50	55	60	
Phe Arg Gln Tyr Ser Gly Tyr Leu Lys Gly Ser Gly Ser Lys His Leu			
65	70	75	80
His Tyr Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val			
85	90	95	
Val Leu Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu			
100	105	110	
Leu Thr Glu His Gly Pro Phe Leu Val Gln Pro Asp Gly Val Thr Leu			
115	120	125	
Glu Tyr Asn Pro Tyr Ser Trp Asn Leu Ile Ala Asn Val Leu Tyr Leu			
130	135	140	
Glu Ser Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr			
145	150	155	160
Ala Thr Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln			
165	170	175	
Asp Phe Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu			
180	185	190	
Thr Gly Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu			
195	200	205	
Val Met Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn			
210	215	220	
Gly Leu Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala			
225	230	235	240
Tyr Tyr His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr			
245	250	255	
His Cys Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu			
260	265	270	
Glu Cys Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser			
275	280	285	

Gly Leu Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro
 290 295 300
 Ser His Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly
 305 310 315 320

Asn Ile Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu
 325 330 335
 Leu Arg Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr
 340 345 350
 Thr Ala Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu
 355 360 365
 Asn Ile Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val
 370 375 380

Asn Leu Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu
 385 390 395 400
 Lys Leu Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp
 405 410 415
 Val Asp Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser
 420 425 430
 Leu Asn Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr
 435 440 445

Gly Asp Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His
 450 455 460
 Ile Ala Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp
 465 470 475 480
 Lys Pro Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln
 485 490 495
 Pro Tyr

<210> 4391

<211> 481

<212> PRT

<213> homo sapiens

<400> 4391

Met Thr Ser Ser Pro Arg Ala Pro Pro Gly Glu Gln Gly Arg Gly Gly

1 5 10 15

Ala Glu Met Ile Arg Ala Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu

20 25 30

Leu Leu Leu Leu Leu Val Ser Trp Ala Ser Arg Gly Glu Ala Ala Pro

35 40 45

Asp Gln Asp Glu Ile Gln Arg Leu Pro Gly Leu Ala Lys Gln Pro Ser

50 55 60

Phe Arg Gln Tyr Ser Gly Tyr Leu Lys Gly Ser Gly Ser Lys His Leu

65 70 75 80

His Tyr Trp Phe Val Glu Ser Gln Lys Asp Pro Glu Asn Ser Pro Val

85 90 95

Val Leu Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu

100 105 110

Leu Thr Glu His Gly Pro Phe Leu Ile Ala Asn Val Leu Tyr Leu Glu

115 120 125

Ser Pro Ala Gly Val Gly Phe Ser Tyr Ser Asp Asp Lys Phe Tyr Ala

130 135 140

Thr Asn Asp Thr Glu Val Ala Gln Ser Asn Phe Glu Ala Leu Gln Asp

145 150 155 160

Phe Phe Arg Leu Phe Pro Glu Tyr Lys Asn Asn Lys Leu Phe Leu Thr

165 170 175

Gly Glu Ser Tyr Ala Gly Ile Tyr Ile Pro Thr Leu Ala Val Leu Val

180 185 190

Met Gln Asp Pro Ser Met Asn Leu Gln Gly Leu Ala Val Gly Asn Gly

195 200 205

Leu Ser Ser Tyr Glu Gln Asn Asp Asn Ser Leu Val Tyr Phe Ala Tyr

210 215 220

Tyr His Gly Leu Leu Gly Asn Arg Leu Trp Ser Ser Leu Gln Thr His

225 230 235 240

Cys Cys Ser Gln Asn Lys Cys Asn Phe Tyr Asp Asn Lys Asp Leu Glu
 245 250 255
 Cys Val Thr Asn Leu Gln Glu Val Ala Arg Ile Val Gly Asn Ser Gly
 260 265 270
 Leu Asn Ile Tyr Asn Leu Tyr Ala Pro Cys Ala Gly Gly Val Pro Ser
 275 280 285
 His Phe Arg Tyr Glu Lys Asp Thr Val Val Val Gln Asp Leu Gly Asn
 290 295 300
 Ile Phe Thr Arg Leu Pro Leu Lys Arg Met Trp His Gln Ala Leu Leu
 305 310 315 320
 Arg Ser Gly Asp Lys Val Arg Met Asp Pro Pro Cys Thr Asn Thr Thr
 325 330 335
 Ala Ala Ser Thr Tyr Leu Asn Asn Pro Tyr Val Arg Lys Ala Leu Asn
 340 345 350
 Ile Pro Glu Gln Leu Pro Gln Trp Asp Met Cys Asn Phe Leu Val Asn
 355 360 365
 Leu Gln Tyr Arg Arg Leu Tyr Arg Ser Met Asn Ser Gln Tyr Leu Lys
 370 375 380
 Leu Leu Ser Ser Gln Lys Tyr Gln Ile Leu Leu Tyr Asn Gly Asp Val
 385 390 395 400
 Asp Met Ala Cys Asn Phe Met Gly Asp Glu Trp Phe Val Asp Ser Leu
 405 410 415
 Asn Gln Lys Met Glu Val Gln Arg Arg Pro Trp Leu Val Lys Tyr Gly
 420 425 430
 Asp Ser Gly Glu Gln Ile Ala Gly Phe Val Lys Glu Phe Ser His Ile
 435 440 445
 Ala Phe Leu Thr Ile Lys Gly Ala Gly His Met Val Pro Thr Asp Lys
 450 455 460
 Pro Leu Ala Ala Phe Thr Met Phe Ser Arg Phe Leu Asn Lys Gln Pro
 465 470 475 480
 Tyr

<210> 4392

<211> 306

<212> PRT

<213> homo sapiens

<400> 4392

Met Ala Ser Pro Gly Cys Leu Trp Leu Leu Ala Val Ala Leu Leu Pro

1 5 10 15

Trp Thr Cys Ala Ser Arg Ala Leu Gln His Leu Asp Pro Pro Ala Pro

20 25 30

Leu Pro Leu Val Ile Trp His Gly Met Gly Asp Ser Cys Cys Asn Pro

35 40 45

Leu Ser Met Gly Ala Ile Lys Lys Met Val Glu Lys Lys Ile Pro Gly

50 55 60

Ile Tyr Val Leu Ser Leu Glu Ile Gly Lys Thr Leu Met Glu Asp Val

65 70 75 80

Glu Asn Ser Phe Phe Leu Asn Val Asn Ser Gln Val Thr Thr Val Cys

85 90 95

Gln Ala Leu Ala Lys Asp Pro Lys Leu Gln Gln Gly Tyr Asn Ala Met

100 105 110

Gly Phe Ser Gln Gly Gly Gln Phe Leu Arg Ala Val Ala Gln Arg Cys

115 120 125

Pro Ser Pro Pro Met Ile Asn Leu Ile Ser Val Gly Gly Gln His Gln

130 135 140

Gly Val Phe Gly Leu Pro Arg Cys Pro Gly Glu Ser Ser His Ile Cys

145 150 155 160

Asp Phe Ile Arg Lys Thr Leu Asn Ala Gly Ala Tyr Ser Lys Val Val

165 170 175

Gln Glu Arg Leu Val Gln Ala Glu Tyr Trp His Asp Pro Ile Lys Glu

180 185 190

Asp Val Tyr Arg Asn His Ser Ile Phe Leu Ala Asp Ile Asn Gln Glu

195 200 205

Arg Gly Ile Asn Glu Ser Tyr Lys Lys Asn Leu Met Ala Leu Lys Lys
210 215 220

Phe Val Met Val Lys Phe Leu Asn Asp Ser Ile Val Asp Pro Val Asp
225 230 235 240

Ser Glu Trp Phe Gly Phe Tyr Arg Ser Gly Gln Ala Lys Glu Thr Ile
245 250 255

Pro Leu Gln Glu Thr Ser Leu Tyr Thr Gln Asp Arg Leu Gly Leu Lys
260 265 270

Glu Met Asp Asn Ala Gly Gln Leu Val Phe Leu Ala Thr Glu Gly Asp
275 280 285

His Leu Gln Leu Ser Glu Glu Trp Phe Tyr Ala His Ile Ile Pro Phe
290 295 300

Leu Gly

305

<210> 4393

<211> 203

<212> PRT

<213> homo sapiens

<400> 4393

Met Ala Ser Pro Gly Cys Leu Trp Leu Leu Ala Val Ala Leu Leu Pro
1 5 10 15

Trp Thr Cys Ala Ser Arg Ala Leu Gln His Leu Asp Pro Pro Ala Pro
20 25 30

Leu Pro Leu Val Ile Trp His Gly Met Gly Val Phe Gly Leu Pro Arg

35 40 45

Cys Pro Gly Glu Ser Ser His Ile Cys Asp Phe Ile Arg Lys Thr Leu
50 55 60

Asn Ala Gly Ala Tyr Ser Lys Val Val Gln Glu Arg Leu Val Gln Ala
65 70 75 80

Glu Tyr Trp His Asp Pro Ile Lys Glu Asp Val Tyr Arg Asn His Ser
85 90 95

Ile Phe Leu Ala Asp Ile Asn Gln Glu Arg Gly Ile Asn Glu Ser Tyr

100 105 110

Lys Lys Asn Leu Met Ala Leu Lys Lys Phe Val Met Val Lys Phe Leu

115 120 125

Asn Asp Ser Ile Val Asp Pro Val Asp Ser Glu Trp Phe Gly Phe Tyr

130 135 140

Arg Ser Gly Gln Ala Lys Glu Thr Ile Pro Leu Gln Glu Thr Ser Leu

145 150 155 160

Tyr Thr Gln Asp Arg Leu Gly Leu Lys Glu Met Asp Asn Ala Gly Gln

165 170 175

Leu Val Phe Leu Ala Thr Glu Gly Asp His Leu Gln Leu Ser Glu Glu

180 185 190

Trp Phe Tyr Ala His Ile Ile Pro Phe Leu Gly

195 200

<210> 4394

<211> 220

<212> PRT

<213> homo sapiens

<400> 4394

Met Gly Ala Ala Ala Arg Thr Leu Arg Leu Ala Leu Gly Leu Leu Leu

1 5 10 15

Leu Ala Thr Leu Leu Arg Pro Ala Asp Ala Cys Ser Cys Ser Pro Val

20 25 30

His Pro Gln Gln Ala Phe Cys Asn Ala Asp Val Val Ile Arg Ala Lys

35 40 45

Ala Val Ser Glu Lys Glu Val Asp Ser Gly Asn Asp Ile Tyr Gly Asn

50 55 60

Pro Ile Lys Arg Ile Gln Tyr Glu Ile Lys Gln Ile Lys Met Phe Lys

65 70 75 80

Gly Pro Glu Lys Asp Ile Glu Phe Ile Tyr Thr Ala Pro Ser Ser Ala

85 90 95

Val Cys Gly Val Ser Leu Asp Val Gly Gly Lys Lys Glu Tyr Leu Ile
100 105 110

Ala Gly Lys Ala Glu Gly Asp Gly Lys Met His Ile Thr Leu Cys Asp
115 120 125

Phe Ile Val Pro Trp Asp Thr Leu Ser Thr Thr Gln Lys Lys Ser Leu
130 135 140

Asn His Arg Tyr Gln Met Gly Cys Glu Cys Lys Ile Thr Arg Cys Pro

145 150 155 160

Met Ile Pro Cys Tyr Ile Ser Ser Pro Asp Glu Cys Leu Trp Met Asp
165 170 175

Trp Val Thr Glu Lys Asn Ile Asn Gly His Gln Ala Lys Phe Phe Ala
180 185 190

Cys Ile Lys Arg Ser Asp Gly Ser Cys Ala Trp Tyr Arg Gly Ala Ala
195 200 205

Pro Pro Lys Gln Glu Phe Leu Asp Ile Glu Asp Pro

210 215 220

<210> 4395

<211> 185

<212> PRT

<213> homo sapiens

<400> 4395

Met Arg Arg Met Arg Arg Met Trp Ala Thr Gln Gly Leu Ala Val Ala
1 5 10 15

Leu Ala Leu Ser Val Leu Pro Gly Ser Arg Ala Leu Arg Pro Gly Asp
20 25 30

Cys Glu Val Cys Ile Ser Tyr Leu Gly Arg Phe Tyr Gln Asp Leu Lys
35 40 45

Asp Arg Asp Val Thr Phe Ser Pro Ala Thr Ile Glu Asn Glu Leu Ile
50 55 60

Lys Phe Cys Arg Glu Ala Arg Gly Lys Glu Asn Arg Leu Cys Tyr Tyr
65 70 75 80

Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile Asn Glu Val Ser

85 90 95
Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile Cys Glu Lys Leu
100 105 110

Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr Asp Lys Gln Ile
115 120 125

Asp Leu Ser Thr Val Asp Leu Lys Lys Leu Arg Val Lys Glu Leu Lys
130 135 140

Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly Cys Ala Glu Lys
145 150 155 160

Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro Lys Tyr Ala Pro
165 170 175

Lys Ala Ala Ser Ala Arg Thr Asp Leu
180 185

<210> 4396

<211> 207

<212> PRT

<213> homo sapiens

<400> 4396

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
1 5 10 15

Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
20 25 30

Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
35 40 45

Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
50 55 60

Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
65 70 75 80

Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
85 90 95

His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu

100	105	110	
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp			
115	120	125	
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr			
130	135	140	
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Ile Pro Cys			
145	150	155	160
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln			
165	170	175	
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg			
180	185	190	
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala			
195	200	205	
<210> 4397			
<211> 585			
<212> PRT			
<213> homo sapiens			
<400> 4397			
Met Ala Ser Pro Gly Ser Gly Phe Trp Ser Phe Gly Ser Glu Asp Gly			
1	5	10	15
Ser Gly Asp Ser Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val			
20	25	30	
Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu			
35	40	45	
Tyr Gly Asp Ala Glu Lys Pro Ala Glu Ser Gly Gly Ser Gln Pro Pro			
50	55	60	
Arg Ala Ala Ala Arg Lys Ala Ala Cys Ala Cys Asp Gln Lys Pro Cys			
65	70	75	80
Ser Cys Ser Lys Val Asp Val Asn Tyr Ala Phe Leu His Ala Thr Asp			
85	90	95	
Leu Leu Pro Ala Cys Asp Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln			

100 105 110
 Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg
 115 120 125
 Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu
 130 135 140
 Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu

 145 150 155 160
 Met His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro
 165 170 175
 Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala
 180 185 190
 Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu
 195 200 205
 Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met

 210 215 220
 Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser
 225 230 235 240
 Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe
 245 250 255
 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
 260 265 270
 Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly

 275 280 285
 Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys
 290 295 300
 Asp Glu Arg Gly Lys Met Ile Pro Ser Asp Leu Glu Arg Arg Ile Leu
 305 310 315 320
 Glu Ala Lys Gln Lys Gly Phe Val Pro Phe Leu Val Ser Ala Thr Ala
 325 330 335
 Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp

 340 345 350

Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly
355 360 365

Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Ser Gly Val
370 375 380

Glu Arg Ala Asn Ser Val Thr Trp Asn Pro His Lys Met Met Gly Val
385 390 395 400

Pro Leu Gln Cys Ser Ala Leu Leu Val Arg Glu Glu Gly Leu Met Gln
405 410 415

Asn Cys Asn Gln Met His Ala Ser Tyr Leu Phe Gln Gln Asp Lys His
420 425 430

Tyr Asp Leu Ser Tyr Asp Thr Gly Asp Lys Ala Leu Gln Cys Gly Arg
435 440 445

His Val Asp Val Phe Lys Leu Trp Leu Met Trp Arg Ala Lys Gly Thr
450 455 460

Thr Gly Phe Glu Ala His Val Asp Lys Cys Leu Glu Leu Ala Glu Tyr
465 470 475 480

Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp
485 490 495

Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser
500 505 510

Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys
515 520 525

Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met
530 535 540

Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn Phe Phe Arg Met Val
545 550 555 560

Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu
565 570 575

Glu Ile Glu Arg Leu Gly Gln Asp Leu
580 585

<210> 4398

<211> 585

<212> PRT

<213> homo sapiens

<400> 4398

Met Ala Ser Pro Gly Ser Gly Phe Trp Ser Phe Gly Ser Glu Asp Gly

1 5 10 15
Ser Gly Asp Ser Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val

20 25 30
Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu

35 40 45
Tyr Gly Asp Ala Glu Lys Pro Ala Glu Ser Gly Gly Ser Gln Pro Pro

50 55 60
Arg Ala Ala Ala Arg Lys Ala Ala Cys Ala Cys Asp Gln Lys Pro Cys

65 70 75 80
Ser Cys Ser Lys Val Asp Val Asn Tyr Ala Phe Leu His Ala Thr Asp

85 90 95
Leu Leu Pro Ala Cys Asp Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln

100 105 110
Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg

115 120 125
Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu

130 135 140
Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu

145 150 155 160
Met His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro

165 170 175
Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala

180 185 190
Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu

195 200 205
Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met

210 215 220

Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser
 225 230 235 240
 Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe
 245 250 255
 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
 260 265 270
 Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly
 275 280 285
 Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys
 290 295 300
 Asp Glu Arg Gly Lys Met Ile Pro Ser Asp Leu Glu Arg Arg Ile Leu
 305 310 315 320
 Glu Ala Lys Gln Lys Gly Phe Val Pro Phe Leu Val Ser Ala Thr Ala
 325 330 335
 Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp
 340 345 350
 Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly
 355 360 365
 Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Ser Gly Val
 370 375 380
 Glu Arg Ala Asn Ser Val Thr Trp Asn Pro His Lys Met Met Gly Val
 385 390 395 400
 Pro Leu Gln Cys Ser Ala Leu Leu Val Arg Glu Glu Gly Leu Met Gln
 405 410 415
 Asn Cys Asn Gln Met His Ala Ser Tyr Leu Phe Gln Gln Asp Lys His
 420 425 430
 Tyr Asp Leu Ser Tyr Asp Thr Gly Asp Lys Ala Leu Gln Cys Gly Arg
 435 440 445
 His Val Asp Val Phe Lys Leu Trp Leu Met Trp Arg Ala Lys Gly Thr
 450 455 460
 Thr Gly Phe Glu Ala His Val Asp Lys Cys Leu Glu Leu Ala Glu Tyr

465 470 475 480
 Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp
 485 490 495
 Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser
 500 505 510
 Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys

 515 520 525
 Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met
 530 535 540
 Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn Phe Phe Arg Met Val
 545 550 555 560
 Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu
 565 570 575
 Glu Ile Glu Arg Leu Gly Gln Asp Leu
 580 585

 <210> 4399
 <211> 685
 <212> PRT
 <213> homo sapiens
 <400> 4399

 Met Ala Glu Trp Leu Leu Ser Ala Ser Trp Gln Arg Arg Ala Lys Ala
 1 5 10 15
 Met Thr Ala Ala Ala Gly Ser Ala Gly Arg Ala Ala Val Pro Leu Leu
 20 25 30
 Leu Cys Ala Leu Leu Ala Pro Gly Gly Ala Tyr Val Leu Asp Asp Ser
 35 40 45
 Asp Gly Leu Gly Arg Glu Phe Asp Gly Ile Gly Ala Val Ser Gly Gly

 50 55 60
 Gly Ala Thr Ser Arg Leu Leu Val Asn Tyr Pro Glu Pro Tyr Arg Ser
 65 70 75 80
 Gln Ile Leu Asp Tyr Leu Phe Lys Pro Asn Phe Gly Ala Ser Leu His
 85 90 95

Ile Leu Lys Val Glu Ile Gly Gly Asp Gly Gln Thr Thr Asp Gly Thr
100 105 110
Glu Pro Ser His Met His Tyr Ala Leu Asp Glu Asn Tyr Phe Arg Gly
115 120 125
Tyr Glu Trp Trp Leu Met Lys Glu Ala Lys Lys Arg Asn Pro Asn Ile
130 135 140
Thr Leu Ile Gly Leu Pro Trp Ser Phe Pro Gly Trp Leu Gly Lys Gly
145 150 155 160
Phe Asp Trp Pro Tyr Val Asn Leu Gln Leu Thr Ala Tyr Tyr Val Val
165 170 175
Thr Trp Ile Val Gly Ala Lys Arg Tyr His Asp Leu Asp Ile Asp Tyr
180 185 190
Ile Gly Ile Trp Asn Glu Arg Ser Tyr Asn Ala Asn Tyr Ile Lys Ile
195 200 205
Leu Arg Lys Met Leu Asn Tyr Gln Gly Leu Gln Arg Val Lys Ile Ile
210 215 220
Ala Ser Asp Asn Leu Trp Glu Ser Ile Ser Ala Ser Met Leu Leu Asp
225 230 235 240
Ala Glu Leu Phe Lys Val Val Asp Val Ile Gly Ala His Tyr Pro Gly
245 250 255
Thr His Ser Ala Lys Asp Ala Lys Leu Thr Gly Lys Lys Leu Trp Ser
260 265 270
Ser Glu Asp Phe Ser Thr Leu Asn Ser Asp Met Gly Ala Gly Cys Trp
275 280 285
Gly Arg Ile Leu Asn Gln Asn Tyr Ile Asn Gly Tyr Met Thr Ser Thr
290 295 300
Ile Ala Trp Asn Leu Val Ala Ser Tyr Tyr Glu Gln Leu Pro Tyr Gly
305 310 315 320
Arg Cys Gly Leu Met Thr Ala Gln Glu Pro Trp Ser Gly His Tyr Val
325 330 335
Val Glu Ser Pro Val Trp Val Ser Ala His Thr Thr Gln Phe Thr Gln

340 345 350
Pro Gly Trp Tyr Tyr Leu Lys Thr Val Gly His Leu Glu Lys Gly Gly

355 360 365
Ser Tyr Val Ala Leu Thr Asp Gly Leu Gly Asn Leu Thr Ile Ile Ile

370 375 380
Glu Thr Met Ser His Lys His Ser Lys Cys Ile Arg Pro Phe Leu Pro

385 390 395 400
Tyr Phe Asn Val Ser Gln Gln Phe Ala Thr Phe Val Leu Lys Gly Ser

405 410 415
Phe Ser Glu Ile Pro Glu Leu Gln Val Trp Tyr Thr Lys Leu Gly Lys

420 425 430
Thr Ser Glu Arg Phe Leu Phe Lys Gln Leu Asp Ser Leu Trp Leu Leu

435 440 445
Asp Ser Asp Gly Ser Phe Thr Leu Ser Leu His Glu Asp Glu Leu Phe

450 455 460
Thr Leu Thr Thr Leu Thr Thr Gly Arg Lys Gly Ser Tyr Pro Leu Pro

465 470 475 480
Pro Lys Ser Gln Pro Phe Pro Ser Thr Tyr Lys Asp Asp Phe Asn Val

485 490 495
Asp Tyr Pro Phe Phe Ser Glu Ala Pro Asn Phe Ala Asp Gln Thr Gly

500 505 510
Val Phe Glu Tyr Phe Thr Asn Ile Glu Asp Pro Gly Glu His His Phe

515 520 525
Thr Leu Arg Gln Val Leu Asn Gln Arg Pro Ile Thr Trp Ala Ala Asp

530 535 540
Ala Ser Asn Thr Ile Ser Ile Ile Gly Asp Tyr Asn Trp Thr Asn Leu

545 550 555 560
Thr Ile Lys Cys Asp Val Tyr Ile Glu Thr Pro Asp Thr Gly Gly Val

565 570 575
Phe Ile Ala Gly Arg Val Asn Lys Gly Gly Ile Leu Ile Arg Ser Ala

580 585 590

Arg Gly Ile Phe Phe Trp Ile Phe Ala Asn Gly Ser Tyr Arg Val Thr
595 600 605

Gly Asp Leu Ala Gly Trp Ile Ile Tyr Ala Leu Gly Arg Val Glu Val
610 615 620

Thr Ala Lys Lys Trp Tyr Thr Leu Thr Leu Thr Ile Lys Gly His Phe

625 630 635 640

Thr Ser Gly Met Leu Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro Val
645 650 655

Asn Phe Pro Lys Asn Gly Trp Ala Ala Ile Gly Thr His Ser Phe Glu
660 665 670

Phe Ala Gln Phe Asp Asn Phe Leu Val Glu Ala Thr Arg
675 680 685

<210> 4400

<211> 594

<212> PRT

<213> homo sapiens

<400> 4400

Met Ala Ser Ser Thr Pro Ser Ser Ser Ala Thr Ser Ser Asn Ala Gly
1 5 10 15

Ala Asp Pro Asn Thr Thr Asn Leu Arg Pro Thr Thr Tyr Asp Thr Trp
20 25 30

Cys Gly Val Ala His Gly Cys Thr Arg Lys Leu Gly Leu Lys Ile Cys
35 40 45

Gly Phe Leu Gln Arg Thr Asn Ser Leu Glu Glu Lys Ser Arg Leu Val
50 55 60

Ser Ala Phe Lys Glu Arg Gln Ser Ser Lys Asn Leu Leu Ser Cys Glu
65 70 75 80

Asn Ser Asp Arg Asp Ala Arg Phe Arg Arg Thr Glu Thr Asp Phe Ser
85 90 95

Asn Leu Phe Ala Arg Asp Leu Leu Pro Ala Lys Asn Gly Glu Glu Gln
100 105 110

Thr Val Gln Phe Leu Leu Glu Val Val Asp Ile Leu Leu Asn Tyr Val

115	120	125
Arg Lys Thr Phe Asp Arg Ser Thr Lys Val Leu Asp Phe His His Pro		
130	135	140
His Gln Leu Leu Glu Gly Met Glu Gly Phe Asn Leu Glu Leu Ser Asp		
145	150	155
His Pro Glu Ser Leu Glu Gln Ile Leu Val Asp Cys Arg Asp Thr Leu		
165	170	175
Lys Tyr Gly Val Arg Thr Gly His Pro Arg Phe Phe Asn Gln Leu Ser		
180	185	190
Thr Gly Leu Asp Ile Ile Gly Leu Ala Gly Glu Trp Leu Thr Ser Thr		
195	200	205
Ala Asn Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val Leu		
210	215	220
Met Glu Gln Ile Thr Leu Lys Lys Met Arg Glu Ile Val Gly Trp Ser		
225	230	235
Ser Lys Asp Gly Asp Gly Ile Phe Ser Pro Gly Gly Ala Ile Ser Asn		
245	250	255
Met Tyr Ser Ile Met Ala Ala Arg Tyr Lys Tyr Phe Pro Glu Val Lys		
260	265	270
Thr Lys Gly Met Ala Ala Val Pro Lys Leu Val Leu Phe Thr Ser Glu		
275	280	285
Gln Ser His Tyr Ser Ile Lys Lys Ala Gly Ala Ala Leu Gly Phe Gly		
290	295	300
Thr Asp Asn Val Ile Leu Ile Lys Cys Asn Glu Arg Gly Lys Ile Ile		
305	310	315
Pro Ala Asp Phe Glu Ala Lys Ile Leu Glu Ala Lys Gln Lys Gly Tyr		
325	330	335
Val Pro Phe Tyr Val Asn Ala Thr Ala Gly Thr Thr Val Tyr Gly Ala		
340	345	350
Phe Asp Pro Ile Gln Glu Ile Ala Asp Ile Cys Glu Lys Tyr Asn Leu		
355	360	365

Trp Leu His Val Asp Ala Ala Trp Gly Gly Gly Leu Leu Met Ser Arg

370

375

380

Lys His Arg His Lys Leu Asn Gly Ile Glu Arg Ala Asn Ser Val Thr

385

390

395

400

Trp Asn Pro His Lys Met Met Gly Val Leu Leu Gln Cys Ser Ala Ile

405

410

415

Leu Val Lys Glu Lys Gly Ile Leu Gln Gly Cys Asn Gln Met Cys Ala

420

425

430

Gly Tyr Leu Phe Gln Pro Asp Lys Gln Tyr Asp Val Ser Tyr Asp Thr

435

440

445

Gly Asp Lys Ala Ile Gln Cys Gly Arg His Val Asp Ile Phe Lys Phe

450

455

460

Trp Leu Met Trp Lys Ala Lys Gly Thr Val Gly Phe Glu Asn Gln Ile

465

470

475

480

Asn Lys Cys Leu Glu Leu Ala Glu Tyr Leu Tyr Ala Lys Ile Lys Asn

485

490

495

Arg Glu Glu Phe Glu Met Val Phe Asn Gly Glu Pro Glu His Thr Asn

500

505

510

Val Cys Phe Trp Tyr Ile Pro Gln Ser Leu Arg Gly Val Pro Asp Ser

515

520

525

Pro Gln Arg Arg Glu Lys Leu His Lys Val Ala Pro Lys Ile Lys Ala

530

535

540

Leu Met Met Glu Ser Gly Thr Thr Met Val Gly Tyr Gln Pro Gln Gly

545

550

555

560

Asp Lys Ala Asn Phe Phe Arg Met Val Ile Ser Asn Pro Ala Ala Thr

565

570

575

Gln Ser Asp Ile Asp Phe Leu Ile Glu Glu Ile Glu Arg Leu Gly Gln

580

585

590

Asp Leu

<210> 4401

<211> 224

<212> PRT

<213> homo sapiens

<400> 4401

Met Ala Ser Ser Thr Pro Ser Ser Ser Ala Thr Ser Ser Asn Ala Gly

1 5 10 15

Ala Asp Pro Asn Thr Thr Asn Leu Arg Pro Thr Thr Tyr Asp Thr Trp

20 25 30

Cys Gly Val Ala His Gly Cys Thr Arg Lys Leu Gly Leu Lys Ile Cys

35 40 45

Gly Phe Leu Gln Arg Thr Asn Ser Leu Glu Glu Lys Ser Arg Leu Val

50 55 60

Ser Ala Phe Lys Glu Arg Gln Ser Ser Lys Asn Leu Leu Ser Cys Glu

65 70 75 80

Asn Ser Asp Arg Asp Ala Arg Phe Arg Arg Thr Glu Thr Asp Phe Ser

85 90 95

Asn Leu Phe Ala Arg Asp Leu Leu Pro Ala Lys Asn Gly Glu Glu Gln

100 105 110

Thr Val Gln Phe Leu Leu Glu Val Val Asp Ile Leu Leu Asn Tyr Val

115 120 125

Arg Lys Thr Phe Asp Arg Ser Thr Lys Val Leu Asp Phe His His Pro

130 135 140

His Gln Leu Leu Glu Gly Met Glu Gly Phe Asn Leu Glu Leu Ser Asp

145 150 155 160

His Pro Glu Ser Leu Glu Gln Ile Leu Val Asp Cys Arg Asp Thr Leu

165 170 175

Lys Tyr Gly Val Arg Thr Gly His Pro Arg Phe Phe Asn Gln Leu Ser

180 185 190

Thr Gly Leu Asp Ile Ile Gly Leu Ala Gly Glu Trp Leu Thr Ser Thr

195 200 205

Ala Asn Thr Asn Met Pro Ser Asp Met Arg Glu Cys Trp Leu Leu Arg

210 215 220

<210> 4402

<211> 257

<212> PRT

<213> homo sapiens

<400> 4402

Met Ser Ile Leu Phe Tyr Val Ile Phe Leu Ala Tyr Leu Arg Gly Ile

1 5 10 15

Gln Gly Asn Asn Met Asp Gln Arg Ser Leu Pro Glu Asp Ser Leu Asn

20 25 30

Ser Leu Ile Ile Lys Leu Ile Gln Ala Asp Ile Leu Lys Asn Lys Leu

35 40 45

Ser Lys Gln Met Val Asp Val Lys Glu Asn Tyr Gln Ser Thr Leu Pro

50 55 60

Lys Ala Glu Ala Pro Arg Glu Pro Glu Arg Gly Gly Pro Ala Lys Ser

65 70 75 80

Ala Phe Gln Pro Val Ile Ala Met Asp Thr Glu Leu Leu Arg Gln Gln

85 90 95

Arg Arg Tyr Asn Ser Pro Arg Val Leu Leu Ser Asp Ser Thr Pro Leu

100 105 110

Glu Pro Pro Pro Leu Tyr Leu Met Glu Asp Tyr Val Gly Ser Pro Val

115 120 125

Val Ala Asn Arg Thr Ser Arg Arg Lys Arg Tyr Ala Glu His Lys Ser

130 135 140

His Arg Gly Glu Tyr Ser Val Cys Asp Ser Glu Ser Leu Trp Val Thr

145 150 155 160

Asp Lys Ser Ser Ala Ile Asp Ile Arg Gly His Gln Val Thr Val Leu

165 170 175

Gly Glu Ile Lys Thr Gly Asn Ser Pro Val Lys Gln Tyr Phe Tyr Glu

180 185 190

Thr Arg Cys Lys Glu Ala Arg Pro Val Lys Asn Gly Cys Arg Gly Ile

195 200 205

Asp Asp Lys His Trp Asn Ser Gln Cys Lys Thr Ser Gln Thr Tyr Val
 210 215 220
 Arg Ala Leu Thr Ser Glu Asn Asn Lys Leu Val Gly Trp Arg Trp Ile
 225 230 235 240
 Arg Ile Asp Thr Ser Cys Val Cys Ala Leu Ser Arg Lys Ile Gly Arg
 245 250 255

Thr

<210> 4403

<211> 270

<212> PRT

<213> homo sapiens

<400> 4403

Met Val Thr Phe Ala Thr Ile Leu Gln Val Asn Lys Val Met Ser Ile
 1 5 10 15
 Leu Phe Tyr Val Ile Phe Leu Ala Tyr Leu Arg Gly Ile Gln Gly Asn
 20 25 30
 Asn Met Asp Gln Arg Ser Leu Pro Glu Asp Ser Leu Asn Ser Leu Ile
 35 40 45
 Ile Lys Leu Ile Gln Ala Asp Ile Leu Lys Asn Lys Leu Ser Lys Gln

50 55 60
 Met Val Asp Val Lys Glu Asn Tyr Gln Ser Thr Leu Pro Lys Ala Glu
 65 70 75 80
 Ala Pro Arg Glu Pro Glu Arg Gly Gly Pro Ala Lys Ser Ala Phe Gln
 85 90 95
 Pro Val Ile Ala Met Asp Thr Glu Leu Leu Arg Gln Gln Arg Arg Tyr
 100 105 110

Asn Ser Pro Arg Val Leu Leu Ser Asp Ser Thr Pro Leu Glu Pro Pro
 115 120 125
 Pro Leu Tyr Leu Met Glu Asp Tyr Val Gly Ser Pro Val Val Ala Asn
 130 135 140
 Arg Thr Ser Arg Arg Lys Arg Tyr Ala Glu His Lys Ser His Arg Gly

145 150 155 160
 Glu Tyr Ser Val Cys Asp Ser Glu Ser Leu Trp Val Thr Asp Lys Ser
 165 170 175
 Ser Ala Ile Asp Ile Arg Gly His Gln Val Thr Val Leu Gly Glu Ile

 180 185 190
 Lys Thr Gly Asn Ser Pro Val Lys Gln Tyr Phe Tyr Glu Thr Arg Cys
 195 200 205
 Lys Glu Ala Arg Pro Val Lys Asn Gly Cys Arg Gly Ile Asp Asp Lys
 210 215 220
 His Trp Asn Ser Gln Cys Lys Thr Ser Gln Thr Tyr Val Arg Ala Leu
 225 230 235 240
 Thr Ser Glu Asn Asn Lys Leu Val Gly Trp Arg Trp Ile Arg Ile Asp

 245 250 255
 Thr Ser Cys Val Cys Ala Leu Ser Arg Lys Ile Gly Arg Thr
 260 265 270
 <210> 4404
 <211> 651
 <212> PRT
 <213> homo sapiens
 <400> 4404
 Met Ala Arg Gly Ser Ala Val Ala Trp Ala Ala Leu Gly Pro Leu Leu
 1 5 10 15
 Trp Gly Cys Ala Leu Gly Leu Gln Gly Gly Met Leu Tyr Pro Gln Glu
 20 25 30

 Ser Pro Ser Arg Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg
 35 40 45
 Ala Asp Phe Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr
 50 55 60
 Arg Arg Pro Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro
 65 70 75 80
 Ser Ser Phe Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val

85

90

95

Gly Trp Val Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp Thr

100

105

110

Gln Asp Leu Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala His Ser

115

120

125

Tyr Ala Ile Val Trp Val Asn Gly Val Asp Thr Leu Glu His Glu Gly

130

135

140

Gly Tyr Leu Pro Phe Glu Ala Asp Ile Ser Asn Leu Val Gln Val Gly

145

150

155

160

Pro Leu Pro Ser Arg Leu Arg Ile Thr Ile Ala Ile Asn Asn Thr Leu

165

170

175

Thr Pro Thr Thr Leu Pro Pro Gly Thr Ile Gln Tyr Leu Thr Asp Thr

180

185

190

Ser Lys Tyr Pro Lys Gly Tyr Phe Val Gln Asn Thr Tyr Phe Asp Phe

195

200

205

Phe Asn Tyr Ala Gly Leu Gln Arg Ser Val Leu Leu Tyr Thr Thr Pro

210

215

220

Thr Thr Tyr Ile Asp Asp Ile Thr Val Thr Thr Ser Val Glu Gln Asp

225

230

235

240

Ser Gly Leu Val Asn Tyr Gln Ile Ser Val Lys Gly Ser Asn Leu Phe

245

250

255

Lys Leu Glu Val Arg Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn

260

265

270

Gly Thr Gly Thr Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp

275

280

285

Trp Pro Tyr Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu

290

295

300

Val Gln Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr

305

310

315

320

Thr Leu Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe

325

330

335

Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His Glu
 340 345 350

Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu Val Lys
 355 360 365

Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe Arg Thr Ser
 370 375 380

His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met Cys Asp Arg Tyr Gly
 385 390 395 400

Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly Leu Ala Leu Pro Gln
 405 410 415

Phe Phe Asn Asn Val Ser Leu His His His Met Gln Val Met Glu Glu
 420 425 430

Val Val Arg Arg Asp Lys Asn His Pro Ala Val Val Met Trp Ser Val
 435 440 445

Ala Asn Glu Pro Ala Ser His Leu Glu Ser Ala Gly Tyr Tyr Leu Lys
 450 455 460

Met Val Ile Ala His Thr Lys Ser Leu Asp Pro Ser Arg Pro Val Thr
 465 470 475 480

Phe Val Ser Asn Ser Asn Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val
 485 490 495

Asp Val Ile Cys Leu Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly
 500 505 510

His Leu Glu Leu Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp
 515 520 525

Tyr Lys Lys Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu
 530 535 540

Thr Ile Ala Gly Phe His Gln Asp Pro Pro Leu Met Phe Thr Glu Glu
 545 550 555 560

Tyr Gln Lys Ser Leu Leu Glu Gln Tyr His Leu Gly Leu Asp Gln Lys
 565 570 575

Arg Arg Lys Tyr Val Val Gly Glu Leu Ile Trp Asn Phe Ala Asp Phe

580 585 590
Met Thr Glu Gln Ser Pro Thr Arg Val Leu Gly Asn Lys Lys Gly Ile
595 600 605

Phe Thr Arg Gln Arg Gln Pro Lys Ser Ala Ala Phe Leu Leu Arg Glu
610 615 620
Arg Tyr Trp Lys Ile Ala Asn Glu Thr Arg Tyr Pro His Ser Val Ala
625 630 635 640
Lys Ser Gln Cys Leu Glu Asn Ser Leu Phe Thr
645 650

<210> 4405

<211> 723

<212> PRT

<213> homo sapiens

<400> 4405

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
1 5 10 15

Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
20 25 30
Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
35 40 45
Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
50 55 60
Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
65 70 75 80

Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
85 90 95
Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
100 105 110
Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
115 120 125
Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys

130	135	140	
Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His			
145	150	155	160
Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg			
	165	170	175
Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg			
	180	185	190
Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr			
195	200	205	
Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly			
210	215	220	
Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe			
225	230	235	240
Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg			
	245	250	255
Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His			
260	265	270	
Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met			
275	280	285	
Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln			
290	295	300	
Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro			
305	310	315	320
Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro			
	325	330	335
Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro			
340	345	350	
Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg			
355	360	365	
Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln			
370	375	380	

Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln
385 390 395 400

Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp
405 410 415

Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu
420 425 430

Asn Tyr Cys Arg Asn Pro Asp Asp Ala His Gly Pro Trp Cys Tyr
435 440 445

Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys
450 455 460

Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile
465 470 475 480

Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr
485 490 495

Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His
500 505 510

Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg
515 520 525

Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly
530 535 540

Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu
545 550 555 560

Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu
565 570 575

Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile
580 585 590

Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser
595 600 605

Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu
610 615 620

Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His

625 630 635 640
His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala
 645 650 655

Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu
 660 665 670
Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro
 675 680 685
Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val
 690 695 700
Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val
705 710 715 720

Pro Gln Ser

<210> 4406

<211> 290

<212> PRT

<213> homo sapiens

<400> 4406

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu
1 5 10 15
Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
 20 25 30
Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
 35 40 45
Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val

 50 55 60
Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
65 70 75 80
Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
 85 90 95
Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
 100 105 110

Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys

115 120 125

Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys

130 135 140

Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His

145 150 155 160

Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr

165 170 175

Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser

180 185 190

Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu

195 200 205

Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp

210 215 220

His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro

225 230 235 240

His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp

245 250 255

Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr

260 265 270

Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys

275 280 285

Glu Thr

290

<210> 4407

<211> 210

<212> PRT

<213> homo sapiens

<400> 4407

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu

1 5 10 15

Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
 20 25 30
 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
 35 40 45
 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
 50 55 60
 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
 65 70 75 80

Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
 85 90 95
 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
 100 105 110
 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
 115 120 125
 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
 130 135 140

Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
 145 150 155 160
 Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
 165 170 175
 Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser
 180 185 190
 Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
 195 200 205

Gly Lys

210

<210> 4408

<211> 728

<212> PRT

<213> homo sapiens

<400> 4408

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu

1 5 10 15
 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
 20 25 30
 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
 35 40 45
 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val

 50 55 60
 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
 65 70 75 80
 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
 85 90 95
 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
 100 105 110
 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys

 115 120 125
 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
 130 135 140
 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
 145 150 155 160
 Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr
 165 170 175
 Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser

 180 185 190
 Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu
 195 200 205
 Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp
 210 215 220
 His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro
 225 230 235 240
 His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp

 245 250 255

Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr
 260 265 270
 Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys
 275 280 285
 Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu
 290 295 300
 Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile

 305 310 315 320
 Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu
 325 330 335
 His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn
 340 345 350
 Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr
 355 360 365
 Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp

 370 375 380
 Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met
 385 390 395 400
 Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp
 405 410 415
 Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala
 420 425 430
 Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Ala His

 435 440 445
 Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys
 450 455 460
 Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu
 465 470 475 480
 Asp His Pro Val Ile Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val
 485 490 495
 Asn Gly Ile Pro Thr Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg

500 505 510
Tyr Arg Asn Lys His Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp
515 520 525
Val Leu Thr Ala Arg Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr
530 535 540
Glu Ala Trp Leu Gly Ile His Asp Val His Gly Arg Gly Asp Glu Lys
545 550 555 560
Cys Lys Gln Val Leu Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly

565 570 575
Ser Asp Leu Val Leu Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp
580 585 590
Phe Val Ser Thr Ile Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu
595 600 605
Lys Thr Ser Cys Ser Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn
610 615 620
Tyr Asp Gly Leu Leu Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu

625 630 635 640
Lys Cys Ser Gln His His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu
645 650 655
Ile Cys Ala Gly Ala Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp
660 665 670
Tyr Gly Gly Pro Leu Val Cys Glu Gln His Lys Met Arg Met Val Leu
675 680 685
Gly Val Ile Val Pro Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly

690 695 700
Ile Phe Val Arg Val Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile
705 710 715 720
Leu Thr Tyr Lys Val Pro Gln Ser

725

<210> 4409

<211> 285

<212> PRT

<213> homo sapiens

<400> 4409

Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu

1 5 10 15

Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln

20 25 30

Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr

35 40 45

Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val

50 55 60

Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu

65 70 75 80

Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys

85 90 95

Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe

100 105 110

Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys

115 120 125

Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys

130 135 140

Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His

145 150 155 160

Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg

165 170 175

Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg

180 185 190

Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr

195 200 205

Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly

210 215 220

Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe

225 230 235 240
 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg
 245 250 255
 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His
 260 265 270
 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Glu Thr

 275 280 285
 <210> 4410
 <211> 410
 <212> PRT
 <213> homo sapiens
 <400> 4410
 Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala
 1 5 10 15
 Thr Gly Ala Thr Phe Pro Glu Glu Ala Ile Ala Asp Leu Ser Val Asn
 20 25 30
 Met Tyr Asn Arg Leu Arg Ala Thr Gly Glu Asp Glu Asn Ile Leu Phe
 35 40 45

 Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala
 50 55 60
 Gln Gly Ser Thr Gln Lys Glu Ile Arg His Ser Met Gly Tyr Asp Ser
 65 70 75 80
 Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met
 85 90 95
 Val Thr Ala Lys Glu Ser Gln Tyr Val Met Lys Ile Ala Asn Ser Leu
 100 105 110

 Phe Val Gln Asn Gly Phe His Val Asn Glu Glu Phe Leu Gln Met Met
 115 120 125
 Lys Lys Tyr Phe Asn Ala Ala Val Asn His Val Asp Phe Ser Gln Asn
 130 135 140
 Val Ala Val Ala Asn Tyr Ile Asn Lys Trp Val Glu Asn Asn Thr Asn
 145 150 155 160

Asn Leu Val Lys Asp Leu Val Ser Pro Arg Asp Phe Asp Ala Ala Thr
165 170 175

Tyr Leu Ala Leu Ile Asn Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser
180 185 190

Gln Phe Arg Pro Glu Asn Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp
195 200 205

Glu Ser Glu Val Gln Ile Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr
210 215 220

Tyr Gly Glu Phe Ser Asp Gly Ser Asn Glu Ala Gly Gly Ile Tyr Gln
225 230 235 240

Val Leu Glu Ile Pro Tyr Glu Gly Asp Glu Ile Ser Met Met Leu Val
245 250 255

Leu Ser Arg Gln Glu Val Pro Leu Ala Thr Leu Glu Pro Leu Val Lys
260 265 270

Ala Gln Leu Val Glu Glu Trp Ala Asn Ser Val Lys Lys Gln Lys Val
275 280 285

Glu Val Tyr Leu Pro Arg Phe Thr Val Glu Gln Glu Ile Asp Leu Lys
290 295 300

Asp Val Leu Lys Ala Leu Gly Ile Thr Glu Ile Phe Ile Lys Asp Ala
305 310 315 320

Asn Leu Thr Gly Leu Ser Asp Asn Lys Glu Ile Phe Leu Ser Lys Ala
325 330 335

Ile His Lys Ser Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
340 345 350

Ala Val Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro
355 360 365

Gln Val Ile Val Asp His Pro Phe Phe Phe Leu Ile Arg Asn Arg Arg
370 375 380

Thr Gly Thr Ile Leu Phe Met Gly Arg Val Met His Pro Glu Thr Met
385 390 395 400

Asn Thr Ser Gly His Asp Phe Glu Glu Leu

405 410

<210> 4411

<211> 410

<212> PRT

<213> homo sapiens

<400> 4411

Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala

1 5 10 15

Thr Gly Ala Thr Phe Pro Glu Glu Ala Ile Ala Asp Leu Ser Val Asn

20 25 30

Met Tyr Asn Arg Leu Arg Ala Thr Gly Glu Asp Glu Asn Ile Leu Phe

35 40 45

Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala

50 55 60

Gln Gly Ser Thr Gln Lys Glu Ile Arg His Ser Met Gly Tyr Asp Ser

65 70 75 80

Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met

85 90 95

Val Thr Ala Lys Glu Ser Gln Tyr Val Met Lys Ile Ala Asn Ser Leu

100 105 110

Phe Val Gln Asn Gly Phe His Val Asn Glu Glu Phe Leu Gln Met Met

115 120 125

Lys Lys Tyr Phe Asn Ala Ala Val Asn His Val Asp Phe Ser Gln Asn

130 135 140

Val Ala Val Ala Asn Tyr Ile Asn Lys Trp Val Glu Asn Asn Thr Asn

145 150 155 160

Asn Leu Val Lys Asp Leu Val Ser Pro Arg Asp Phe Asp Ala Ala Thr

165 170 175

Tyr Leu Ala Leu Ile Asn Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser

180 185 190

Gln Phe Arg Pro Glu Asn Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp

195 200 205
 Glu Ser Glu Val Gln Ile Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr
 210 215 220
 Tyr Gly Glu Phe Ser Asp Gly Ser Asn Glu Ala Gly Gly Ile Tyr Gln
 225 230 235 240
 Val Leu Glu Ile Pro Tyr Glu Gly Asp Glu Ile Ser Met Met Leu Val
 245 250 255
 Leu Ser Arg Gln Glu Val Pro Leu Ala Thr Leu Glu Pro Leu Val Lys
 260 265 270

 Ala Gln Leu Val Glu Glu Trp Ala Asn Ser Val Lys Lys Gln Lys Val
 275 280 285
 Glu Val Tyr Leu Pro Arg Phe Thr Val Glu Gln Glu Ile Asp Leu Lys
 290 295 300
 Asp Val Leu Lys Ala Leu Gly Ile Thr Glu Ile Phe Ile Lys Asp Ala
 305 310 315 320
 Asn Leu Thr Gly Leu Ser Asp Asn Lys Glu Ile Phe Leu Ser Lys Ala
 325 330 335

 Ile His Lys Ser Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
 340 345 350
 Ala Val Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro
 355 360 365
 Gln Val Ile Val Asp His Pro Phe Phe Phe Leu Ile Arg Asn Arg Arg
 370 375 380
 Thr Gly Thr Ile Leu Phe Met Gly Arg Val Met His Pro Glu Thr Met
 385 390 395 400

 Asn Thr Ser Gly His Asp Phe Glu Glu Leu
 405 410

 <210> 4412
 <211> 211
 <212> PRT
 <213> homo sapiens

<400> 4412

Met Gln Ser Ala Met Phe Leu Ala Val Gln His Asp Cys Arg Pro Met

1 5 10 15

Asp Lys Ser Ala Gly Ser Gly His Lys Ser Glu Glu Lys Arg Glu Lys

20 25 30

Met Lys Arg Thr Leu Leu Lys Asp Trp Lys Thr Arg Leu Ser Tyr Phe

35 40 45

Leu Gln Asn Ser Ser Thr Pro Gly Lys Pro Lys Thr Gly Lys Lys Ser

50 55 60

Lys Gln Gln Ala Phe Ile Lys Pro Ser Pro Glu Glu Ala Gln Leu Trp

65 70 75 80

Ser Glu Ala Phe Asp Glu Leu Leu Ala Ser Lys Tyr Gly Leu Ala Ala

85 90 95

Phe Arg Ala Phe Leu Lys Ser Glu Phe Cys Glu Glu Asn Ile Glu Phe

100 105 110

Trp Leu Ala Cys Glu Asp Phe Lys Lys Thr Lys Ser Pro Gln Lys Leu

115 120 125

Ser Ser Lys Ala Arg Lys Ile Tyr Thr Asp Phe Ile Glu Lys Glu Ala

130 135 140

Pro Lys Glu Ile Asn Ile Asp Phe Gln Thr Lys Thr Leu Ile Ala Gln

145 150 155 160

Asn Ile Gln Glu Ala Thr Ser Gly Cys Phe Thr Thr Ala Gln Lys Arg

165 170 175

Val Tyr Ser Leu Met Glu Asn Asn Ser Tyr Pro Arg Phe Leu Glu Ser

180 185 190

Glu Phe Tyr Gln Asp Leu Cys Lys Lys Pro Gln Ile Thr Thr Glu Pro

195 200 205

His Ala Thr

210

<210> 4413

<211> 97

<212> PRT

<213> homo sapiens

<400> 4413

Met Leu Gly Asn Lys Arg Leu Gly Leu Ser Gly Leu Thr Leu Ala Leu

1 5 10 15

Ser Leu Leu Val Cys Leu Gly Ala Leu Ala Glu Ala Tyr Pro Ser Lys

20 25 30

Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala Arg Tyr

35 40 45

Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr

50 55 60

Gly Lys Arg Ser Ser Pro Glu Thr Leu Ile Ser Asp Leu Leu Met Arg

65 70 75 80

Glu Ser Thr Glu Asn Val Pro Arg Thr Arg Leu Glu Asp Pro Ala Met

85 90 95

Trp

<210> 4414

<211> 309

<212> PRT

<213> homo sapiens

<400> 4414

Met Val Gly Phe Lys Ala Thr Asp Val Pro Pro Thr Ala Thr Val Lys

1 5 10 15

Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe

20 25 30

Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln

35 40 45

Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly

50 55 60

Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn

65 70 75 80

Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg

85 90 95
 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
 100 105 110

His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
 115 120 125

Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
 130 135 140

Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg Tyr Gln Ser Thr Val
 145 150 155 160

Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
 165 170 175

Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
 180 185 190

Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
 195 200 205

Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
 210 215 220

Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
 225 230 235 240

Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
 245 250 255

Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
 260 265 270

Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
 275 280 285

Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser
 290 295 300

Arg Glu Ala Pro Phe

305

<210> 4415

<211> 116

<212> PRT

<213> homo sapiens

<400> 4415

Met Leu Ser Cys Arg Leu Gln Cys Ala Leu Ala Ala Leu Ser Ile Val

1 5 10 15

Leu Ala Leu Gly Cys Val Thr Gly Ala Pro Ser Asp Pro Arg Leu Arg

20 25 30

Gln Phe Leu Gln Lys Ser Leu Ala Ala Ala Ala Gly Lys Gln Glu Leu

35 40 45

Ala Lys Tyr Phe Leu Ala Glu Leu Leu Ser Glu Pro Asn Gln Thr Glu

50 55 60

Asn Asp Ala Leu Glu Pro Glu Asp Leu Ser Gln Ala Ala Glu Gln Asp

65 70 75 80

Glu Met Arg Leu Glu Leu Gln Arg Ser Ala Asn Ser Asn Pro Ala Met

85 90 95

Ala Pro Arg Glu Arg Lys Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr

100 105 110

Phe Thr Ser Cys

115

<210> 4416

<211> 502

<212> PRT

<213> homo sapiens

<400> 4416

Met Ser Cys Pro Val Pro Ala Cys Cys Ala Leu Leu Leu Val Leu Gly

1 5 10 15

Leu Cys Arg Ala Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp

20 25 30

Gly Gly Phe Glu Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro

35 40 45

His Leu Asp Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe

50 55 60

Thr	Ser	Val	Ser	Ser	Cys	Ser	Pro	Ser	Arg	Ala	Ser	Leu	Leu	Thr	Gly
65				70				75				80			
Leu	Pro	Gln	His	Gln	Asn	Gly	Met	Tyr	Gly	Leu	His	Gln	Asp	Val	His
85				90				95							
His	Phe	Asn	Ser	Phe	Asp	Lys	Val	Arg	Ser	Leu	Pro	Leu	Leu	Leu	Ser
100				105				110							
Gln	Ala	Gly	Val	Arg	Thr	Gly	Ile	Ile	Gly	Lys	Lys	His	Val	Gly	Pro
115				120				125							
Glu	Thr	Val	Tyr	Pro	Phe	Asp	Phe	Ala	Tyr	Thr	Glu	Glu	Asn	Gly	Ser
130				135				140							
Val	Leu	Gln	Val	Gly	Arg	Asn	Ile	Thr	Arg	Ile	Lys	Leu	Leu	Val	Arg
145				150				155				160			
Lys	Phe	Leu	Gln	Thr	Gln	Asp	Asp	Arg	Pro	Phe	Phe	Leu	Tyr	Val	Ala
165				170				175							
Phe	His	Asp	Pro	His	Arg	Cys	Gly	His	Ser	Gln	Pro	Gln	Tyr	Gly	Thr
180				185				190							
Phe	Cys	Glu	Lys	Phe	Gly	Asn	Gly	Glu	Ser	Gly	Met	Gly	Arg	Ile	Pro
195				200				205							
Asp	Trp	Thr	Pro	Gln	Ala	Tyr	Asp	Pro	Leu	Asp	Val	Leu	Val	Pro	Tyr
210				215				220							
Phe	Val	Pro	Asn	Thr	Pro	Ala	Ala	Arg	Ala	Asp	Leu	Ala	Ala	Gln	Tyr
225				230				235				240			
Thr	Thr	Val	Gly	Arg	Met	Asp	Gln	Gly	Val	Gly	Leu	Val	Leu	Gln	Glu
245				250				255							
Leu	Arg	Asp	Ala	Gly	Val	Leu	Asn	Asp	Thr	Leu	Val	Ile	Phe	Thr	Ser
260				265				270							
Asp	Asn	Gly	Ile	Pro	Phe	Pro	Ser	Gly	Arg	Thr	Asn	Leu	Tyr	Trp	Pro
275				280				285							
Gly	Thr	Ala	Glu	Pro	Leu	Leu	Val	Ser	Ser	Pro	Glu	His	Pro	Lys	Arg
290				295				300							
Trp	Gly	Gln	Val	Ser	Glu	Ala	Tyr	Val	Ser	Leu	Leu	Asp	Leu	Thr	Pro

305 310 315 320
 Thr Ile Leu Asp Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe
 325 330 335
 Gly Ser Lys Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu
 340 345 350
 Glu Ala Glu Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His
 355 360 365
 Glu Val Thr Met Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe

 370 375 380
 Arg Leu Val His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln
 385 390 395 400
 Asp Phe Tyr Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr
 405 410 415
 Ala Gly Gln Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr
 420 425 430
 Arg Ala Arg Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr

 435 440 445
 Gln Asn Leu Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu
 450 455 460
 Arg Asp Gln Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val
 465 470 475 480
 Cys Ala Pro Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln
 485 490 495
 Pro Leu His Asn Glu Leu

500

<210> 4417

<211> 502

<212> PRT

<213> homo sapiens

<400> 4417

Met Leu Ala Ala Met Gly Ser Leu Ala Ala Ala Leu Trp Ala Val Val

1 5 10 15

His Pro Arg Thr Leu Leu Leu Gly Thr Val Ala Phe Leu Leu Ala Ala
 20 25 30
 Asp Phe Leu Lys Arg Arg Arg Pro Lys Asn Tyr Pro Pro Gly Pro Trp
 35 40 45
 Arg Leu Pro Phe Leu Gly Asn Phe Phe Leu Val Asp Phe Glu Gln Ser
 50 55 60
 His Leu Glu Val Gln Leu Phe Val Lys Lys Tyr Gly Asn Leu Phe Ser
 65 70 75 80
 Leu Glu Leu Gly Asp Ile Ser Ala Val Leu Ile Thr Gly Leu Pro Leu
 85 90 95
 Ile Lys Glu Ala Leu Ile His Met Asp Gln Asn Phe Gly Asn Arg Pro
 100 105 110
 Val Thr Pro Met Arg Glu His Ile Phe Lys Lys Asn Gly Leu Ile Met
 115 120 125
 Ser Ser Gly Gln Ala Trp Lys Glu Gln Arg Arg Phe Thr Leu Thr Ala
 130 135 140
 Leu Arg Asn Phe Gly Leu Gly Lys Lys Ser Leu Glu Glu Arg Ile Gln
 145 150 155 160
 Glu Glu Ala Gln His Leu Thr Glu Ala Ile Lys Glu Glu Asn Gly Gln
 165 170 175
 Pro Phe Asp Pro His Phe Lys Ile Asn Asn Ala Val Ser Asn Ile Ile
 180 185 190
 Cys Ser Ile Thr Phe Gly Glu Arg Phe Glu Tyr Gln Asp Ser Trp Phe
 195 200 205
 Gln Gln Leu Leu Lys Leu Leu Asp Glu Val Thr Tyr Leu Glu Ala Ser
 210 215 220
 Lys Thr Cys Gln Leu Tyr Asn Val Phe Pro Trp Ile Met Lys Phe Leu
 225 230 235 240
 Pro Gly Pro His Gln Thr Leu Phe Ser Asn Trp Lys Lys Leu Lys Leu
 245 250 255
 Phe Val Ser His Met Ile Asp Lys His Arg Lys Asp Trp Asn Pro Ala

260	265	270	
Glu Thr Arg Asp Phe Ile Asp Ala Tyr Leu Lys Glu Met Ser Lys His			
275	280	285	
Thr Gly Asn Pro Thr Ser Ser Phe His Glu Glu Asn Leu Ile Cys Ser			
290	295	300	
Thr Leu Asp Leu Phe Phe Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu			
305	310	315	320
Arg Trp Ala Leu Leu Tyr Met Ala Leu Tyr Pro Glu Ile Gln Glu Lys			
325	330	335	
Val Gln Ala Glu Ile Asp Arg Val Ile Gly Gln Gly Gln Gln Pro Ser			
340	345	350	
Thr Ala Ala Arg Glu Ser Met Pro Tyr Thr Asn Ala Val Ile His Glu			
355	360	365	
Val Gln Arg Met Gly Asn Ile Ile Pro Leu Asn Val Pro Arg Glu Val			
370	375	380	
Thr Val Asp Thr Thr Leu Ala Gly Tyr His Leu Pro Lys Gly Thr Met			
385	390	395	400
Ile Leu Thr Asn Leu Thr Ala Leu His Arg Asp Pro Thr Glu Trp Ala			
405	410	415	
Thr Pro Asp Thr Phe Asn Pro Asp His Phe Leu Glu Asn Gly Gln Phe			
420	425	430	
Lys Lys Arg Glu Ala Phe Met Pro Phe Ser Ile Gly Lys Arg Ala Cys			
435	440	445	
Leu Gly Glu Gln Leu Ala Arg Thr Glu Leu Phe Ile Phe Phe Thr Ser			
450	455	460	
Leu Met Gln Lys Phe Thr Phe Arg Pro Pro Asn Asn Glu Lys Leu Ser			
465	470	475	480
Leu Lys Phe Arg Met Gly Ile Thr Ile Ser Pro Val Ser His Arg Leu			
485	490	495	
Cys Ala Val Pro Gln Val			
500			

<210> 4418

<211> 193

<212> PRT

<213> homo sapiens

<400> 4418

Met Gln Ser Leu Met Gln Ala Pro Leu Leu Ile Ala Leu Gly Leu Leu

1 5 10 15

Leu Ala Ala Pro Ala Gln Ala His Leu Lys Lys Pro Ser Gln Leu Ser

20 25 30

Ser Phe Ser Trp Asp Asn Cys Asp Glu Gly Lys Asp Pro Ala Val Ile

35 40 45

Arg Ser Leu Thr Leu Glu Pro Asp Pro Ile Ile Val Pro Gly Asn Val

50 55 60

Thr Leu Ser Val Met Gly Ser Thr Ser Val Pro Leu Ser Ser Pro Leu

65 70 75 80

Lys Val Asp Leu Val Leu Glu Lys Glu Val Ala Gly Leu Trp Ile Lys

85 90 95

Ile Pro Cys Thr Asp Tyr Ile Gly Ser Cys Thr Phe Glu His Phe Cys

100 105 110

Asp Val Leu Asp Met Leu Ile Pro Thr Gly Glu Pro Cys Pro Glu Pro

115 120 125

Leu Arg Thr Tyr Gly Leu Pro Cys His Cys Pro Phe Lys Glu Gly Thr

130 135 140

Tyr Ser Leu Pro Lys Ser Glu Phe Val Val Pro Asp Leu Glu Leu Pro

145 150 155 160

Ser Trp Leu Thr Thr Gly Asn Tyr Arg Ile Glu Ser Val Leu Ser Ser

165 170 175

Ser Gly Lys Arg Leu Gly Cys Ile Lys Ile Ala Ala Ser Leu Lys Gly

180 185 190

Ile

<210> 4419

<211> 186

<212> PRT

<213> homo sapiens

<400> 4419

Met Gln Ser Leu Met Gln Ala Pro Leu Leu Ile Ala Leu Gly Leu Leu

1 5 10 15

Leu Ala Ala Pro Ala Gln Ala His Leu Lys Lys Pro Ser Gln Leu Ser

20 25 30

Ser Phe Ser Trp Asp Asn Cys Asp Glu Gly Lys Asp Pro Ala Val Ile

35 40 45

Arg Ser Leu Thr Leu Glu Pro Asp Pro Ile Ile Val Pro Gly Asn Val

50 55 60

Thr Leu Ser Val Met Gly Ser Thr Ser Val Pro Leu Ser Ser Pro Leu

65 70 75 80

Lys Val Asp Leu Val Leu Glu Lys Glu Val Ala Gly Leu Trp Ile Lys

85 90 95

Ile Pro Cys Thr Asp Tyr Ile Gly Ser Cys Thr Phe Glu His Phe Cys

100 105 110

Asp Val Leu Asp Met Leu Ile Pro Thr Gly Glu Pro Cys Pro Glu Pro

115 120 125

Leu Arg Thr Tyr Gly Leu Pro Cys His Cys Pro Phe Ser Ser Val Leu

130 135 140

Cys Leu Pro Arg Pro Asn Ser His Ser Leu Pro Pro Phe Asn Pro Leu

145 150 155 160

Ser Thr Val Ser Pro Leu Pro Ser Leu Lys Ile Ile Leu Tyr His Leu

165 170 175

His Phe Arg Leu Gly Gln Ala Ala Leu Thr

180 185

<210> 4420

<211> 529

<212> PRT

<213> homo sapiens

<400> 4420

Met Thr Ser Ser Arg Leu Trp Phe Ser Leu Leu Leu Ala Ala Ala Phe

1 5 10 15

Ala Gly Arg Ala Thr Ala Leu Trp Pro Trp Pro Gln Asn Phe Gln Thr

20 25 30

Ser Asp Gln Arg Tyr Val Leu Tyr Pro Asn Asn Phe Gln Phe Gln Tyr

35 40 45

Asp Val Ser Ser Ala Ala Gln Pro Gly Cys Ser Val Leu Asp Glu Ala

50 55 60

Phe Gln Arg Tyr Arg Asp Leu Leu Phe Gly Ser Gly Ser Trp Pro Arg

65 70 75 80

Pro Tyr Leu Thr Gly Lys Arg His Thr Leu Glu Lys Asn Val Leu Val

85 90 95

Val Ser Val Val Thr Pro Gly Cys Asn Gln Leu Pro Thr Leu Glu Ser

100 105 110

Val Glu Asn Tyr Thr Leu Thr Ile Asn Asp Asp Gln Cys Leu Leu Leu

115 120 125

Ser Glu Thr Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln

130 135 140

Leu Val Trp Lys Ser Ala Glu Gly Thr Phe Phe Ile Asn Lys Thr Glu

145 150 155 160

Ile Glu Asp Phe Pro Arg Phe Pro His Arg Gly Leu Leu Leu Asp Thr

165 170 175

Ser Arg His Tyr Leu Pro Leu Ser Ser Ile Leu Asp Thr Leu Asp Val

180 185 190

Met Ala Tyr Asn Lys Leu Asn Val Phe His Trp His Leu Val Asp Asp

195 200 205

Pro Ser Phe Pro Tyr Glu Ser Phe Thr Phe Pro Glu Leu Met Arg Lys

210 215 220

Gly Ser Tyr Asn Pro Val Thr His Ile Tyr Thr Ala Gln Asp Val Lys

225 230 235 240

Glu Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Ala Glu
 245 250 255
 Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Pro Gly Ile Pro Gly
 260 265 270
 Leu Leu Thr Pro Cys Tyr Ser Gly Ser Glu Pro Ser Gly Thr Phe Gly
 275 280 285
 Pro Val Asn Pro Ser Leu Asn Asn Thr Tyr Glu Phe Met Ser Thr Phe
 290 295 300

 Phe Leu Glu Val Ser Ser Val Phe Pro Asp Phe Tyr Leu His Leu Gly
 305 310 315 320
 Gly Asp Glu Val Asp Phe Thr Cys Trp Lys Ser Asn Pro Glu Ile Gln
 325 330 335
 Asp Phe Met Arg Lys Lys Gly Phe Gly Glu Asp Phe Lys Gln Leu Glu
 340 345 350
 Ser Phe Tyr Ile Gln Thr Leu Leu Asp Ile Val Ser Ser Tyr Gly Lys
 355 360 365

 Gly Tyr Val Val Trp Gln Glu Val Phe Asp Asn Lys Val Lys Ile Gln
 370 375 380
 Pro Asp Thr Ile Ile Gln Val Trp Arg Glu Asp Ile Pro Val Asn Tyr
 385 390 395 400
 Met Lys Glu Leu Glu Leu Val Thr Lys Ala Gly Phe Arg Ala Leu Leu
 405 410 415
 Ser Ala Pro Trp Tyr Leu Asn Arg Ile Ser Tyr Gly Pro Asp Trp Lys
 420 425 430

 Asp Phe Tyr Ile Val Glu Pro Leu Ala Phe Glu Gly Thr Pro Glu Gln
 435 440 445
 Lys Ala Leu Val Ile Gly Gly Glu Ala Cys Met Trp Gly Glu Tyr Val
 450 455 460
 Asp Asn Thr Asn Leu Val Pro Arg Leu Trp Pro Arg Ala Gly Ala Val
 465 470 475 480
 Ala Glu Arg Leu Trp Ser Asn Lys Leu Thr Ser Asp Leu Thr Phe Ala

485 490 495

Tyr Glu Arg Leu Ser His Phe Arg Cys Glu Leu Leu Arg Arg Gly Val

500 505 510

Gln Ala Gln Pro Leu Asn Val Gly Phe Cys Glu Gln Glu Phe Glu Gln

515 520 525

Thr

<210> 4421

<211> 223

<212> PRT

<213> homo sapiens

<400> 4421

Met Gln Leu Lys Pro Met Glu Ile Asn Pro Glu Met Leu Asn Lys Val

1 5 10 15

Leu Ser Arg Leu Gly Val Ala Gly Gln Trp Arg Phe Val Asp Val Leu

20 25 30

Gly Leu Glu Glu Glu Ser Leu Gly Ser Val Pro Ala Pro Ala Cys Ala

35 40 45

Leu Leu Leu Leu Phe Pro Leu Thr Ala Gln His Glu Asn Phe Arg Lys

50 55 60

Lys Gln Ile Glu Glu Leu Lys Gly Gln Glu Val Ser Pro Lys Val Tyr

65 70 75 80

Phe Met Lys Gln Thr Ile Gly Asn Ser Cys Gly Thr Ile Gly Leu Ile

85 90 95

His Ala Val Ala Asn Asn Gln Asp Lys Leu Gly Phe Glu Asp Gly Ser

100 105 110

Val Leu Lys Gln Phe Leu Ser Glu Thr Glu Lys Met Ser Pro Glu Asp

115 120 125

Arg Ala Lys Cys Phe Glu Lys Asn Glu Ala Ile Gln Ala Ala His Asp

130 135 140

Ala Val Ala Gln Glu Gly Gln Cys Arg Val Asp Asp Lys Val Asn Phe

145 150 155 160
His Phe Ile Leu Phe Asn Asn Val Asp Gly His Leu Tyr Glu Leu Asp
 165 170 175
Gly Arg Met Pro Phe Pro Val Asn His Gly Ala Ser Ser Glu Asp Thr
 180 185 190
Leu Leu Lys Asp Ala Ala Lys Val Cys Arg Glu Phe Thr Glu Arg Glu
 195 200 205
Gln Gly Glu Val Arg Phe Ser Ala Val Ala Leu Cys Lys Ala Ala

210 215 220
<210> 4422
<211> 556
<212> PRT
<213> homo sapiens
<400> 4422

Met Glu Leu Cys Gly Leu Gly Leu Pro Arg Pro Pro Met Leu Leu Ala
1 5 10 15
Leu Leu Leu Ala Thr Leu Leu Ala Ala Met Leu Ala Leu Leu Thr Gln
 20 25 30
Val Ala Leu Val Val Gln Val Ala Glu Ala Ala Arg Ala Pro Ser Val
 35 40 45

Ser Ala Lys Pro Gly Pro Ala Leu Trp Pro Leu Pro Leu Ser Val Lys
50 55 60
Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser
65 70 75 80
His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu
 85 90 95
Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His
 100 105 110

His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu
115 120 125
Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser
130 135 140

Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu
145 150 155 160
Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser
165 170 175

Gln Leu Val Tyr Gln Asp Ser Tyr Gly Thr Phe Thr Ile Asn Glu Ser
180 185 190
Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp
195 200 205
Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp
210 215 220
Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp
225 230 235 240

Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn
245 250 255
Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg
260 265 270
Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu
275 280 285
Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Lys Gly Gln Lys Asp
290 295 300

Leu Leu Thr Pro Cys Tyr Ser Arg Gln Asn Lys Leu Asp Ser Phe Gly
305 310 315 320
Pro Ile Asn Pro Thr Leu Asn Thr Thr Tyr Ser Phe Leu Thr Thr Phe
325 330 335
Phe Lys Glu Ile Ser Glu Val Phe Pro Asp Gln Phe Ile His Leu Gly
340 345 350
Gly Asp Glu Val Glu Phe Lys Cys Trp Glu Ser Asn Pro Lys Ile Gln
355 360 365

Asp Phe Met Arg Gln Lys Gly Phe Gly Thr Asp Phe Lys Lys Leu Glu
370 375 380
Ser Phe Tyr Ile Gln Lys Val Leu Asp Ile Ile Ala Thr Ile Asn Lys

385 390 395 400
 Gly Ser Ile Val Trp Gln Glu Val Phe Asp Asp Lys Ala Lys Leu Ala
 405 410 415
 Pro Gly Thr Ile Val Glu Val Trp Lys Asp Ser Ala Tyr Pro Glu Glu
 420 425 430

 Leu Ser Arg Val Thr Ala Ser Gly Phe Pro Val Ile Leu Ser Ala Pro
 435 440 445
 Trp Tyr Leu Asp Leu Ile Ser Tyr Gly Gln Asp Trp Arg Lys Tyr Tyr
 450 455 460
 Lys Val Glu Pro Leu Asp Phe Gly Gly Thr Gln Lys Gln Lys Gln Leu
 465 470 475 480
 Phe Ile Gly Gly Glu Ala Cys Leu Trp Gly Glu Tyr Val Asp Ala Thr
 485 490 495

 Asn Leu Thr Pro Arg Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg
 500 505 510
 Leu Trp Ser Ser Lys Asp Val Arg Asp Met Asp Asp Ala Tyr Asp Arg
 515 520 525
 Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln
 530 535 540
 Pro Leu Tyr Ala Gly Tyr Cys Asn His Glu Asn Met
 545 550 555
 <210> 4423

 <211> 581
 <212> PRT
 <213> homo sapiens
 <400> 4423

 Met Ala Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala
 1 5 10 15
 Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly
 20 25 30
 Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp
 35 40 45

Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro

50

55

60

Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg

65

70

75

80

Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys

85

90

95

Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu

100

105

110

Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile

115

120

125

Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp

130

135

140

Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln

145

150

155

160

Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro

165

170

175

Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro

180

185

190

Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala

195

200

205

Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile

210

215

220

Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu

225

230

235

240

Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val

245

250

255

Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro

260

265

270

Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu

275

280

285

Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His

290 295 300
 Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn

 305 310 315 320
 Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro
 325 330 335
 Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His
 340 345 350
 Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile
 355 360 365
 Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp

 370 375 380
 Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe
 385 390 395 400
 Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro
 405 410 415
 Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser
 420 425 430
 Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly

 435 440 445
 Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg
 450 455 460
 Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro
 465 470 475 480
 Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys
 485 490 495
 Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp

 500 505 510
 Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val
 515 520 525
 Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu
 530 535 540

Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala
545 550 555 560
Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser
565 570 575
Trp Arg Ala Ala Leu
580
<210> 4424
<211> 256
<212> PRT
<213> homo sapiens
<400> 4424
Met Ala Ala Ala Val Gly Arg Leu Leu Arg Ala Ser Val Ala Arg His
1 5 10 15
Val Ser Ala Ile Pro Trp Gly Ile Ser Ala Thr Ala Ala Leu Arg Pro
20 25 30
Ala Ala Cys Gly Arg Thr Ser Leu Thr Asn Leu Leu Cys Ser Gly Ser
35 40 45
Ser Gln Ala Lys Leu Phe Ser Thr Ser Ser Ser Cys His Ala Pro Ala
50 55 60
Val Thr Gln His Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn Gly
65 70 75 80
Glu Phe Lys Asp Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu Val
85 90 95
Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
100 105 110
Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys Glu
115 120 125
Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp Ile
130 135 140
Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Ala Leu
145 150 155 160

Leu Ser Asp Leu Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu Leu

165 170 175

Glu Gly Ser Gly Leu Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro Asn

180 185 190

Gly Val Ile Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg Ser

195 200 205

Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Tyr Val Glu Thr

210 215 220

His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Asp Ser Pro Thr Ile

225 230 235 240

Lys Pro Ser Pro Ala Ala Ser Lys Glu Tyr Phe Gln Lys Val Asn Gln

245 250 255

<210> 4425

<211> 199

<212> PRT

<213> homo sapiens

<400> 4425

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys

1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser

20 25 30

Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe

35 40 45

Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu

50 55 60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser

65 70 75 80

His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly

85 90 95

Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile

100 105 110

Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
115 120 125
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
130 135 140
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145 150 155 160

Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
165 170 175
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
180 185 190
Glu Tyr Phe Ser Lys Gln Lys
195

<210> 4426

<211> 199

<212> PRT

<213> homo sapiens

<400> 4426

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
20 25 30
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
35 40 45
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
50 55 60
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65 70 75 80

His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
85 90 95
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
100 105 110
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg

115 120 125
 Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
 130 135 140

Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
 145 150 155 160
 Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
 165 170 175
 Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
 180 185 190

Glu Tyr Phe Ser Lys Gln Lys
 195

<210> 4427

<211> 199

<212> PRT

<213> homo sapiens

<400> 4427

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
 1 5 10 15
 Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
 20 25 30
 Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
 35 40 45
 Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
 50 55 60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
 65 70 75 80
 His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
 85 90 95
 Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
 100 105 110
 Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg

115 120 125
 Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
 130 135 140
 Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
 145 150 155 160
 Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
 165 170 175
 Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
 180 185 190

 Glu Tyr Phe Ser Lys Gln Lys
 195
 <210> 4428
 <211> 546
 <212> PRT
 <213> homo sapiens
 <400> 4428
 Met Pro Gly Phe Leu Val Arg Ile Leu Pro Leu Leu Leu Val Leu Leu
 1 5 10 15
 Leu Leu Gly Pro Thr Arg Gly Leu Arg Asn Ala Thr Gln Arg Met Phe
 20 25 30
 Glu Ile Asp Tyr Ser Arg Asp Ser Phe Leu Lys Asp Gly Gln Pro Phe
 35 40 45

 Arg Tyr Ile Ser Gly Ser Ile His Tyr Ser Arg Val Pro Arg Phe Tyr
 50 55 60
 Trp Lys Asp Arg Leu Leu Lys Met Lys Met Ala Gly Leu Asn Ala Ile
 65 70 75 80
 Gln Thr Leu Pro Gly Ser Cys Gly Gln Val Val Gly Ser Pro Ser Ala
 85 90 95
 Gln Asp Glu Ala Ser Pro Leu Ser Glu Trp Arg Ala Ser Tyr Asn Ser
 100 105 110

 Ala Gly Ser Asn Ile Thr Asp Ala Phe Leu Ser Gln Arg Lys Cys Glu

115	120	125	
Pro Lys Gly Pro Leu Ile Asn Ser Glu Phe Tyr Thr Gly Trp Leu Asp			
130	135	140	
His Trp Gly Gln Pro His Ser Thr Ile Lys Thr Glu Ala Val Ala Ser			
145	150	155	160
Ser Leu Tyr Asp Ile Leu Ala Arg Gly Ala Ser Val Asn Leu Tyr Met			
165	170	175	
Phe Ile Gly Gly Thr Asn Phe Ala Tyr Trp Asn Gly Ala Asn Ser Pro			
180	185	190	
Tyr Ala Ala Gln Pro Thr Ser Tyr Asp Tyr Asp Ala Pro Leu Ser Glu			
195	200	205	
Ala Gly Asp Leu Thr Glu Lys Tyr Phe Ala Leu Arg Asn Ile Ile Gln			
210	215	220	
Lys Phe Glu Lys Val Pro Glu Gly Pro Ile Pro Pro Ser Thr Pro Lys			
225	230	235	240
Phe Ala Tyr Gly Lys Val Thr Leu Glu Lys Leu Lys Thr Val Gly Ala			
245	250	255	
Ala Leu Asp Ile Leu Cys Pro Ser Gly Pro Ile Lys Ser Leu Tyr Pro			
260	265	270	
Leu Thr Phe Ile Gln Val Lys Gln His Tyr Gly Phe Val Leu Tyr Arg			
275	280	285	
Thr Thr Leu Pro Gln Asp Cys Ser Asn Pro Ala Pro Leu Ser Ser Pro			
290	295	300	
Leu Asn Gly Val His Asp Arg Ala Tyr Val Ala Val Asp Gly Ile Pro			
305	310	315	320
Gln Gly Val Leu Glu Arg Asn Asn Val Ile Thr Leu Asn Ile Thr Gly			
325	330	335	
Lys Ala Gly Ala Thr Leu Asp Leu Leu Val Glu Asn Met Gly Arg Val			
340	345	350	
Asn Tyr Gly Ala Tyr Ile Asn Asp Phe Lys Gly Leu Val Ser Asn Leu			
355	360	365	

Thr Leu Ser Ser Asn Ile Leu Thr Asp Trp Thr Ile Phe Pro Leu Asp

370 375 380

Thr Glu Asp Ala Val Arg Ser His Leu Gly Gly Trp Gly His Arg Asp

385 390 395 400

Ser Gly His His Asp Glu Ala Trp Ala His Asn Ser Ser Asn Tyr Thr

405 410 415

Leu Pro Ala Phe Tyr Met Gly Asn Phe Ser Ile Pro Ser Gly Ile Pro

420 425 430

Asp Leu Pro Gln Asp Thr Phe Ile Gln Phe Pro Gly Trp Thr Lys Gly

435 440 445

Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr Trp Pro Ala Arg

450 455 460

Gly Pro Gln Leu Thr Leu Phe Val Pro Gln His Ile Leu Met Thr Ser

465 470 475 480

Ala Pro Asn Thr Ile Thr Val Leu Glu Leu Glu Trp Ala Pro Cys Ser

485 490 495

Ser Asp Asp Pro Glu Leu Cys Ala Val Thr Phe Val Asp Arg Pro Val

500 505 510

Ile Gly Ser Ser Val Thr Tyr Asp His Pro Ser Lys Pro Val Glu Lys

515 520 525

Arg Leu Met Pro Pro Pro Pro Gln Lys Asn Lys Asp Ser Trp Leu Asp

530 535 540

His Val

545

<210> 4429

<211> 647

<212> PRT

<213> homo sapiens

<400> 4429

Met Phe Glu Ile Asp Tyr Ser Arg Asp Ser Phe Leu Lys Asp Gly Gln

1 5 10 15

Pro Phe Arg Tyr Ile Ser Gly Ser Ile His Tyr Ser Arg Val Pro Arg

20 25 30
 Phe Tyr Trp Lys Asp Arg Leu Leu Lys Met Lys Met Ala Gly Leu Asn
 35 40 45
 Ala Ile Gln Thr Tyr Val Pro Trp Asn Phe His Glu Pro Trp Pro Gly
 50 55 60
 Gln Tyr Gln Phe Ser Glu Asp His Asp Val Glu Tyr Phe Leu Arg Leu

 65 70 75 80
 Ala His Glu Leu Gly Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile
 85 90 95
 Cys Ala Glu Trp Glu Met Gly Gly Leu Pro Ala Trp Leu Leu Glu Lys
 100 105 110
 Glu Ser Ile Leu Leu Arg Ser Ser Asp Pro Asp Tyr Leu Ala Ala Val
 115 120 125
 Asp Lys Trp Leu Gly Val Leu Leu Pro Lys Met Lys Pro Leu Leu Tyr

 130 135 140
 Gln Asn Gly Gly Pro Val Ile Thr Val Gln Val Glu Asn Glu Tyr Gly
 145 150 155 160
 Ser Tyr Phe Ala Cys Asp Phe Asp Tyr Leu Arg Phe Leu Gln Lys Arg
 165 170 175
 Phe Arg His His Leu Gly Asp Asp Val Val Leu Phe Thr Thr Asp Gly
 180 185 190
 Ala His Lys Thr Phe Leu Lys Cys Gly Ala Leu Gln Gly Leu Tyr Thr

 195 200 205
 Thr Val Asp Phe Gly Thr Gly Ser Asn Ile Thr Asp Ala Phe Leu Ser
 210 215 220
 Gln Arg Lys Cys Glu Pro Lys Gly Pro Leu Ile Asn Ser Glu Phe Tyr
 225 230 235 240
 Thr Gly Trp Leu Asp His Trp Gly Gln Pro His Ser Thr Ile Lys Thr
 245 250 255
 Glu Ala Val Ala Ser Ser Leu Tyr Asp Ile Leu Ala Arg Gly Ala Ser

 260 265 270

Val Asn Leu Tyr Met Phe Ile Gly Gly Thr Asn Phe Ala Tyr Trp Asn
275 280 285

Gly Ala Asn Ser Pro Tyr Ala Ala Gln Pro Thr Ser Tyr Asp Tyr Asp
290 295 300

Ala Pro Leu Ser Glu Ala Gly Asp Leu Thr Glu Lys Tyr Phe Ala Leu
305 310 315 320

Arg Asn Ile Ile Gln Lys Phe Glu Lys Val Pro Glu Gly Pro Ile Pro
325 330 335

Pro Ser Thr Pro Lys Phe Ala Tyr Gly Lys Val Thr Leu Glu Lys Leu
340 345 350

Lys Thr Val Gly Ala Ala Leu Asp Ile Leu Cys Pro Ser Gly Pro Ile
355 360 365

Lys Ser Leu Tyr Pro Leu Thr Phe Ile Gln Val Lys Gln His Tyr Gly
370 375 380

Phe Val Leu Tyr Arg Thr Thr Leu Pro Gln Asp Cys Ser Asn Pro Ala
385 390 395 400

Pro Leu Ser Ser Pro Leu Asn Gly Val His Asp Arg Ala Tyr Val Ala
405 410 415

Val Asp Gly Ile Pro Gln Gly Val Leu Glu Arg Asn Asn Val Ile Thr
420 425 430

Leu Asn Ile Thr Gly Lys Ala Gly Ala Thr Leu Asp Leu Leu Val Glu
435 440 445

Asn Met Gly Arg Val Asn Tyr Gly Ala Tyr Ile Asn Asp Phe Lys Gly
450 455 460

Leu Val Ser Asn Leu Thr Leu Ser Ser Asn Ile Leu Thr Asp Trp Thr
465 470 475 480

Ile Phe Pro Leu Asp Thr Glu Asp Ala Val Arg Ser His Leu Gly Gly
485 490 495

Trp Gly His Arg Asp Ser Gly His His Asp Glu Ala Trp Ala His Asn
500 505 510

Ser Ser Asn Tyr Thr Leu Pro Ala Phe Tyr Met Gly Asn Phe Ser Ile

515 520 525
Pro Ser Gly Ile Pro Asp Leu Pro Gln Asp Thr Phe Ile Gln Phe Pro
530 535 540
Gly Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg
545 550 555 560
Tyr Trp Pro Ala Arg Gly Pro Gln Leu Thr Leu Phe Val Pro Gln His
565 570 575
Ile Leu Met Thr Ser Ala Pro Asn Thr Ile Thr Val Leu Glu Leu Glu

580 585 590
Trp Ala Pro Cys Ser Ser Asp Asp Pro Glu Leu Cys Ala Val Thr Phe
595 600 605
Val Asp Arg Pro Val Ile Gly Ser Ser Val Thr Tyr Asp His Pro Ser
610 615 620
Lys Pro Val Glu Lys Arg Leu Met Pro Pro Pro Pro Gln Lys Asn Lys
625 630 635 640
Asp Ser Trp Leu Asp His Val
645

<210> 4430

<211> 677

<212> PRT

<213> homo sapiens

<400> 4430

Met Pro Gly Phe Leu Val Arg Ile Leu Pro Leu Leu Leu Val Leu Leu
1 5 10 15
Leu Leu Gly Pro Thr Arg Gly Leu Arg Asn Ala Thr Gln Arg Met Phe
20 25 30
Glu Ile Asp Tyr Ser Arg Asp Ser Phe Leu Lys Asp Gly Gln Pro Phe
35 40 45
Arg Tyr Ile Ser Gly Ser Ile His Tyr Ser Arg Val Pro Arg Phe Tyr

50 55 60
Trp Lys Asp Arg Leu Leu Lys Met Lys Met Ala Gly Leu Asn Ala Ile
65 70 75 80

Gln Thr Tyr Val Pro Trp Asn Phe His Glu Pro Trp Pro Gly Gln Tyr
85 90 95
Gln Phe Ser Glu Asp His Asp Val Glu Tyr Phe Leu Arg Leu Ala His
100 105 110
Glu Leu Gly Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala
115 120 125
Glu Trp Glu Met Gly Gly Leu Pro Ala Trp Leu Leu Glu Lys Glu Ser
130 135 140
Ile Leu Leu Arg Ser Ser Asp Pro Asp Tyr Leu Ala Ala Val Asp Lys
145 150 155 160
Trp Leu Gly Val Leu Leu Pro Lys Met Lys Pro Leu Leu Tyr Gln Asn
165 170 175
Gly Gly Pro Val Ile Thr Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr
180 185 190
Phe Ala Cys Asp Phe Asp Tyr Leu Arg Phe Leu Gln Lys Arg Phe Arg
195 200 205
His His Leu Gly Asp Asp Val Val Leu Phe Thr Thr Asp Gly Ala His
210 215 220
Lys Thr Phe Leu Lys Cys Gly Ala Leu Gln Gly Leu Tyr Thr Thr Val
225 230 235 240
Asp Phe Gly Thr Gly Ser Asn Ile Thr Asp Ala Phe Leu Ser Gln Arg
245 250 255
Lys Cys Glu Pro Lys Gly Pro Leu Ile Asn Ser Glu Phe Tyr Thr Gly
260 265 270
Trp Leu Asp His Trp Gly Gln Pro His Ser Thr Ile Lys Thr Glu Ala
275 280 285
Val Ala Ser Ser Leu Tyr Asp Ile Leu Ala Arg Gly Ala Ser Val Asn
290 295 300
Leu Tyr Met Phe Ile Gly Gly Thr Asn Phe Ala Tyr Trp Asn Gly Ala
305 310 315 320
Asn Ser Pro Tyr Ala Ala Gln Pro Thr Ser Tyr Asp Tyr Asp Ala Pro

325 330 335
 Leu Ser Glu Ala Gly Asp Leu Thr Glu Lys Tyr Phe Ala Leu Arg Asn
 340 345 350
 Ile Ile Gln Lys Phe Glu Lys Val Pro Glu Gly Pro Ile Pro Pro Ser
 355 360 365
 Thr Pro Lys Phe Ala Tyr Gly Lys Val Thr Leu Glu Lys Leu Lys Thr

 370 375 380
 Val Gly Ala Ala Leu Asp Ile Leu Cys Pro Ser Gly Pro Ile Lys Ser
 385 390 395 400
 Leu Tyr Pro Leu Thr Phe Ile Gln Val Lys Gln His Tyr Gly Phe Val
 405 410 415
 Leu Tyr Arg Thr Thr Leu Pro Gln Asp Cys Ser Asn Pro Ala Pro Leu
 420 425 430
 Ser Ser Pro Leu Asn Gly Val His Asp Arg Ala Tyr Val Ala Val Asp

 435 440 445
 Gly Ile Pro Gln Gly Val Leu Glu Arg Asn Asn Val Ile Thr Leu Asn
 450 455 460
 Ile Thr Gly Lys Ala Gly Ala Thr Leu Asp Leu Leu Val Glu Asn Met
 465 470 475 480
 Gly Arg Val Asn Tyr Gly Ala Tyr Ile Asn Asp Phe Lys Gly Leu Val
 485 490 495
 Ser Asn Leu Thr Leu Ser Ser Asn Ile Leu Thr Asp Trp Thr Ile Phe

 500 505 510
 Pro Leu Asp Thr Glu Asp Ala Val Arg Ser His Leu Gly Gly Trp Gly
 515 520 525
 His Arg Asp Ser Gly His His Asp Glu Ala Trp Ala His Asn Ser Ser
 530 535 540
 Asn Tyr Thr Leu Pro Ala Phe Tyr Met Gly Asn Phe Ser Ile Pro Ser
 545 550 555 560
 Gly Ile Pro Asp Leu Pro Gln Asp Thr Phe Ile Gln Phe Pro Gly Trp

 565 570 575

Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr Trp
580 585 590

Pro Ala Arg Gly Pro Gln Leu Thr Leu Phe Val Pro Gln His Ile Leu
595 600 605

Met Thr Ser Ala Pro Asn Thr Ile Thr Val Leu Glu Leu Glu Trp Ala
610 615 620

Pro Cys Ser Ser Asp Asp Pro Glu Leu Cys Ala Val Thr Phe Val Asp

625 630 635 640

Arg Pro Val Ile Gly Ser Ser Val Thr Tyr Asp His Pro Ser Lys Pro
645 650 655

Val Glu Lys Arg Leu Met Pro Pro Pro Pro Gln Lys Asn Lys Asp Ser
660 665 670

Trp Leu Asp His Val
675

<210> 4431

<211> 563

<212> PRT

<213> homo sapiens

<400> 4431

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu Ser

1 5 10 15

Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr Leu Pro
20 25 30

Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu Glu Leu Ser
35 40 45

Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg Leu Ser Glu Leu
50 55 60

Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln Tyr Gly Lys Tyr Leu

65 70 75 80

Thr Leu Glu Asn Val Ala Asp Leu Val Arg Pro Ser Pro Leu Thr Leu
85 90 95

His Thr Val Gln Lys Trp Leu Leu Ala Ala Gly Ala Gln Lys Cys His

100	105	110	
Ser Val Ile Thr Gln Asp Phe Leu Thr Cys Trp Leu Ser Ile Arg Gln			
115	120	125	
Ala Glu Leu Leu Leu Pro Gly Ala Glu Phe His His Tyr Val Gly Gly			
130	135	140	
Pro Thr Glu Thr His Val Val Arg Ser Pro His Pro Tyr Gln Leu Pro			
145	150	155	160
Gln Ala Leu Ala Pro His Val Asp Phe Val Gly Gly Leu His Arg Phe			
165	170	175	
Pro Pro Thr Ser Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly			
180	185	190	
Thr Val Gly Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg			
195	200	205	
Tyr Asn Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser			
210	215	220	
Gln Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu			
225	230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala Ser			
245	250	255	
Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly Ile Glu			
260	265	270	
Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala Asn Ile Ser			
275	280	285	
Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly Gln Glu Pro Phe			
290	295	300	
Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser Ala Leu Pro His Val			
305	310	315	320
His Thr Val Ser Tyr Gly Asp Asp Glu Asp Ser Leu Ser Ser Ala Tyr			
325	330	335	
Ile Gln Arg Val Asn Thr Glu Leu Met Lys Ala Ala Ala Arg Gly Leu			
340	345	350	

Thr Leu Leu Phe Ala Ser Gly Asp Ser Gly Ala Gly Cys Trp Ser Val
355 360 365
Ser Gly Arg His Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr
370 375 380
Val Thr Thr Val Gly Gly Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr
385 390 395 400
Asn Glu Ile Val Asp Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe
405 410 415
Pro Arg Pro Ser Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser
420 425 430
Ser Pro His Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala
435 440 445
Tyr Pro Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn
450 455 460
Arg Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
465 470 475 480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser Gly
485 490 495
Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln His Gly
500 505 510
Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser Cys Leu Asp
515 520 525
Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp Asp Pro
530 535 540
Val Thr Gly Trp Gly Thr Pro Asn Phe Pro Ala Leu Leu Lys Thr Leu
545 550 555 560
Leu Asn Pro

<210> 4432

<211> 147

<212> PRT

<213> homo sapiens

<400> 4432

Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
1 5 10 15

Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
20 25 30

Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
35 40 45

Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
50 55 60

Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Ser Ile Lys Ala Ile
65 70 75 80

Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
85 90 95

Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
100 105 110

Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
115 120 125

Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
130 135 140

Arg Arg Pro

145

<210> 4433

<211> 147

<212> PRT

<213> homo sapiens

<400> 4433

Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
1 5 10 15

Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
20 25 30

Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
35 40 45

Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys

50 55 60

Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Ser Ile Lys Ala Ile

65 70 75 80

Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser

85 90 95

Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro

100 105 110

Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val

115 120 125

Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe

130 135 140

Arg Arg Pro

145

<210> 4434

<211> 288

<212> PRT

<213> homo sapiens

<400> 4434

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1 5 10 15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20 25 30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35 40 45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp

85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
100 105 110
Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115 120 125
Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130 135 140
Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165 170 175
Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180 185 190
Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
195 200 205
Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
210 215 220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225 230 235 240
Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
245 250 255
Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
260 265 270
Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
275 280 285

<210> 4435

<211> 640

<212> PRT

<213> homo sapiens

<400> 4435

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15
Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser

20 25 30
 Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45
 Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser

 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95
 Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr

 115 120 125
 Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
 145 150 155 160
 Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 165 170 175
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

 180 185 190
 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
 195 200 205
 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
 210 215 220
 Val Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln
 225 230 235 240
 Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val

 245 250 255
 Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys
 260 265 270

Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn
 275 280 285
 Met Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu
 290 295 300
 Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser

 305 310 315 320
 Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His
 325 330 335
 Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser
 340 345 350
 His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His
 355 360 365
 Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro

 370 375 380
 Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu
 385 390 395 400
 Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg
 405 410 415
 Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala
 420 425 430
 Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro

 435 440 445
 Pro Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro
 450 455 460
 Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu
 465 470 475 480
 Val Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln
 485 490 495
 Gln Phe Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu

 500 505 510
 Pro Ala Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr

515 520 525
 Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser
 530 535 540
 Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu
 545 550 555 560
 Glu Val Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu

 565 570 575
 Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln
 580 585 590
 Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala
 595 600 605
 Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile
 610 615 620
 Gln Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val

 625 630 635 640
 <210> 4436
 <211> 177
 <212> PRT
 <213> homo sapiens
 <400> 4436
 Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15
 Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45

 Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His
130 135 140

Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly
145 150 155 160

Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys
165 170 175

Lys

<210> 4437

<211> 459

<212> PRT

<213> homo sapiens

<400> 4437

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr

115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu

130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr

145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr

165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

195 200 205

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

210 215 220

Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val

225 230 235 240

Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met

245 250 255

Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His

260 265 270

Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn

275 280 285

Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln

290 295 300

Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile

305 310 315 320

Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser

325 330 335

Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp

340 345 350

Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile

355 360 365
Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly

370 375 380
Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser
385 390 395 400
Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro
405 410 415
His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala
420 425 430
His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg

435 440 445
Ser Ser Ser Ile Pro His Leu Gly Phe Ile Leu

450 455

<210> 4438

<211> 207

<212> PRT

<213> homo sapiens

<400> 4438

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15
Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30
Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala

35 40 45
Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60
Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80
Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95
Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys

100 105 110
Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125
Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His
130 135 140
Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly
145 150 155 160
Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys

165 170 175
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
180 185 190

Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
195 200 205

<210> 4439

<211> 462

<212> PRT

<213> homo sapiens

<400> 4439

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125
 Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140

 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
 145 150 155 160
 Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 165 170 175
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
 180 185 190
 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
 195 200 205

 Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
 210 215 220
 Val Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln
 225 230 235 240
 Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val
 245 250 255
 Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys
 260 265 270

 Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn
 275 280 285
 Met Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu
 290 295 300
 Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser
 305 310 315 320
 Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His
 325 330 335

 Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser
 340 345 350
 His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His

355 360 365
 Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro
 370 375 380
 Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu
 385 390 395 400

Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg
 405 410 415
 Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg Arg
 420 425 430
 Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala Thr
 435 440 445
 His Leu Arg Ser Ser Ser Ile Pro His Leu Gly Phe Ile Leu
 450 455 460

<210> 4440

<211> 422

<212> PRT

<213> homo sapiens

<400> 4440

Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1 5 10 15
 Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
 20 25 30
 Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
 35 40 45
 Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser

50 55 60
 Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
 65 70 75 80
 Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
 85 90 95
 Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
 100 105 110

Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro

115 120 125

Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro

130 135 140

Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr

145 150 155 160

Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys

165 170 175

Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala

180 185 190

Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe

195 200 205

Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg

210 215 220

Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val

225 230 235 240

Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu

245 250 255

Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys

260 265 270

Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn

275 280 285

Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln

290 295 300

Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala

305 310 315 320

Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp

325 330 335

Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr

340 345 350

Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys

355 360 365
Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser

370 375 380
Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp
385 390 395 400
Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
405 410 415
Phe Leu Ser Leu Pro Glu

420

<210> 4441

<211> 607

<212> PRT

<213> homo sapiens

<400> 4441

Met Gly Lys Gly Arg Ala Gly Arg Val Gly Thr Thr Ala Leu Pro Pro

1 5 10 15
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
20 25 30
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys
35 40 45
Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn
50 55 60
Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys

65 70 75 80
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys
85 90 95
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn
100 105 110
Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser
115 120 125
Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys

130	135	140	
Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met			
145	150	155	160
Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn			
	165	170	175
Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr			
	180	185	190
Lys His Leu Gly Ile Glu Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys			
	195	200	205
Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly			
	210	215	220
Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys			
225	230	235	240
Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met			
	245	250	255
Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn			
	260	265	270
Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu			
	275	280	285
His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr			
	290	295	300
Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His			
305	310	315	320
Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser			
	325	330	335
Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr			
	340	345	350
Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys			
	355	360	365
Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp			
370	375	380	

Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg

385 390 395 400

Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro

405 410 415

Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser

420 425 430

Met Ala Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val

435 440 445

Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln

450 455 460

Phe Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro

465 470 475 480

Ala Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln

485 490 495

Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg

500 505 510

Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu

515 520 525

Val Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr

530 535 540

Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn

545 550 555 560

Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp

565 570 575

Ser Arg Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln

580 585 590

Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val

595 600 605

<210> 4442

<211> 308

<212> PRT

<213> homo sapiens

<400> 4442

Met Gln Ile Pro Lys His Ile Ser Ile Glu Asp Ile Thr Ala Thr Ser

1 5 10 15

Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu

20 25 30

Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu

35 40 45

Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly

50 55 60

Ala Arg Cys Thr Glu Asn Val Pro Met Lys Val Gln Asn Gln Glu Lys

65 70 75 80

Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys

85 90 95

Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys

100 105 110

Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu

115 120 125

Arg Ser Glu Arg Asn Asn Met Met Asn Ile Ala Asn Gly Pro His His

130 135 140

Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser

145 150 155 160

Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr

165 170 175

Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr Thr

180 185 190

Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu Ser

195 200 205

Ile Leu Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu Asn

210 215 220

Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly

225 230 235 240
 Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu
 245 250 255
 Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg His Asn Leu
 260 265 270
 Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln
 275 280 285

 Ile Gln Leu Ser Ala Thr His Leu Arg Ser Ser Ser Ile Pro His Leu
 290 295 300
 Gly Phe Ile Leu
 305
 <210> 4443
 <211> 645
 <212> PRT
 <213> homo sapiens
 <400> 4443
 Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15
 Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala

 35 40 45
 Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95
 Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys

 100 105 110
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140
 Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
 145 150 155 160
 Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 165 170 175
 Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
 180 185 190
 Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
 195 200 205
 Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
 210 215 220
 Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala
 225 230 235 240
 Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile
 245 250 255
 Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr
 260 265 270
 Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg
 275 280 285
 Ser Glu Arg Asn Asn Met Met Asn Ile Ala Asn Gly Pro His His Pro
 290 295 300
 Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys
 305 310 315 320
 Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser
 325 330 335
 Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val
 340 345 350
 Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile
 355 360 365
 Leu Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser

370 375 380
 Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr
 385 390 395 400
 Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr
 405 410 415
 Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala

 420 425 430
 Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe His Thr Pro Ser
 435 440 445
 Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val Ser Ser Met
 450 455 460
 Thr Val Ser Met Pro Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu
 465 470 475 480
 Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe

 485 490 495
 Asp His His Pro Gln Gln Phe Ser Ser Phe His His Asn Pro Ala His
 500 505 510
 Asp Ser Asn Ser Leu Pro Ala Ser Pro Leu Arg Ile Val Glu Asp Glu
 515 520 525
 Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys
 530 535 540
 Lys Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His

 545 550 555 560
 Ile Ala Asn Arg Leu Glu Val Asp Ser Asn Thr Ser Ser Gln Ser Ser
 565 570 575
 Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro
 580 585 590
 Phe Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro
 595 600 605
 Ala Phe Arg Leu Ala Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe Ser

 610 615 620

Thr Gln Glu Glu Ile Gln Ala Arg Leu Ser Ser Val Ile Ala Asn Gln
625 630 635 640
Asp Pro Ile Ala Val
645
<210> 4444
<211> 624
<212> PRT
<213> homo sapiens
<400> 4444
Met Gly Lys Gly Arg Ala Gly Arg Val Gly Thr Thr Ala Leu Pro Pro
1 5 10 15
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu
20 25 30
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys
35 40 45
Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn
50 55 60
Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys
65 70 75 80
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys
85 90 95
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn
100 105 110
Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val Ser
115 120 125
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn Thr
130 135 140
Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys
145 150 155 160
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe
165 170 175
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro

180 185 190
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe
195 200 205
Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala Glu Glu Leu Tyr Gln

210 215 220
Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val
225 230 235 240
Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys
245 250 255
Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn
260 265 270
Met Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu

275 280 285
Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser
290 295 300
Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His
305 310 315 320
Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser
325 330 335
His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His

340 345 350
Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro
355 360 365
Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu
370 375 380
Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg
385 390 395 400
Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala

405 410 415
Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro
420 425 430

Pro Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro
435 440 445
Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu
450 455 460
Val Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln
465 470 475 480
Gln Phe Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu
485 490 495
Pro Ala Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr
500 505 510
Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser
515 520 525
Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu
530 535 540
Glu Val Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu
545 550 555 560
Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln
565 570 575
Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala
580 585 590
Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile
595 600 605
Gln Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val
610 615 620
<210> 4445
<211> 420
<212> PRT
<213> homo sapiens
<400> 4445
Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15
Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser

20	25	30
Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala		
35	40	45
Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser		
50	55	60
Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys		
65	70	75
Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu		
85	90	95
Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys		
100	105	110
Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr		
115	120	125
Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu		
130	135	140
Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr		
145	150	155
Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr		
165	170	175
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn		
180	185	190
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr		
195	200	205
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr		
210	215	220
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val		
225	230	235
Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met		
245	250	255
Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His		
260	265	270

Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn
 275 280 285

 Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln
 290 295 300
 Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile
 305 310 315 320
 Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser
 325 330 335
 Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp
 340 345 350

 Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile
 355 360 365
 Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly
 370 375 380
 Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser
 385 390 395 400
 Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro
 405 410 415

 His Ser Glu Arg
 420
 <210> 4446
 <211> 637
 <212> PRT
 <213> homo sapiens
 <400> 4446
 Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15
 Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser

50

55

60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys

65

70

75

80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu

85

90

95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys

100

105

110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr

115

120

125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu

130

135

140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr

145

150

155

160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr

165

170

175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

180

185

190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

195

200

205

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr

210

215

220

Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val

225

230

235

240

Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met

245

250

255

Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His

260

265

270

Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn

275

280

285

Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln

290 295 300
 Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile

 305 310 315 320
 Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser
 325 330 335
 Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp
 340 345 350
 Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile
 355 360 365
 Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly

 370 375 380
 Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser
 385 390 395 400
 Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro
 405 410 415
 His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser
 420 425 430
 Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu

 435 440 445
 Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala
 450 455 460
 Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro
 465 470 475 480
 Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser
 485 490 495
 Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser

 500 505 510
 Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr
 515 520 525
 Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala
 530 535 540

Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp
 545 550 555 560
 Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp

565 570 575
 Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu
 580 585 590
 Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg
 595 600 605
 Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala Arg
 610 615 620
 Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val

625 630 635

<210> 4447

<211> 241

<212> PRT

<213> homo sapiens

<400> 4447

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15
 Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95
 Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125
Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140
Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
145 150 155 160
Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180 185 190
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
195 200 205
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
210 215 220
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
225 230 235 240

Glu

<210> 4448

<211> 296

<212> PRT

<213> homo sapiens

<400> 4448

Met Glu Ile Tyr Ser Pro Asp Met Ser Glu Val Ala Ala Glu Arg Ser
1 5 10 15
Ser Ser Pro Ser Thr Gln Leu Ser Ala Asp Pro Ser Leu Asp Gly Leu
20 25 30
Pro Ala Ala Glu Asp Met Pro Glu Pro Gln Thr Glu Asp Gly Arg Thr
35 40 45
Pro Gly Leu Val Gly Leu Ala Val Pro Cys Cys Ala Cys Leu Glu Ala
50 55 60

Glu Arg Leu Arg Gly Cys Leu Asn Ser Glu Lys Ile Cys Ile Val Pro

65 70 75 80
 Ile Leu Ala Cys Leu Val Ser Leu Cys Leu Cys Ile Ala Gly Leu Lys
 85 90 95
 Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro Thr His Leu
 100 105 110
 Asp Pro Gly Gly Leu Gly Gln Asp Pro Ile Ile Ser Leu Asp Ala Thr

 115 120 125
 Ala Ala Ser Ala Val Trp Val Ser Ser Glu Ala Tyr Thr Ser Pro Val
 130 135 140
 Ser Arg Ala Gln Ser Glu Ser Glu Val Gln Val Thr Val Gln Gly Asp
 145 150 155 160
 Lys Ala Val Val Ser Phe Glu Pro Ser Ala Ala Pro Thr Pro Lys Asn
 165 170 175
 Arg Ile Phe Ala Phe Ser Phe Leu Pro Ser Thr Ala Pro Ser Phe Pro

 180 185 190
 Ser Pro Thr Arg Asn Pro Glu Val Arg Thr Pro Lys Ser Ala Thr Gln
 195 200 205
 Pro Gln Thr Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr
 210 215 220
 Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys
 225 230 235 240
 Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp

 245 250 255
 Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr
 260 265 270
 Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
 275 280 285
 Thr Pro Phe Leu Ser Leu Pro Glu
 290 295
 <210> 4449
 <211> 194
 <212> PRT

<213> homo sapiens

<400> 4449

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys

1 5 10 15
Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45
Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys

65 70 75 80
Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95
Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110
Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125
Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu

130 135 140
Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser
145 150 155 160
His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
 165 170 175
Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 180 185 190
Cys Lys

<210> 4450

<211> 211

<212> PRT

<213> homo sapiens

<400> 4450

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys

1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser

20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala

35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser

50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys

65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu

85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys

100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr

115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu

130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr

145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr

165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn

180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr

195 200 205

Leu Cys Lys

210

<210> 4451

<211> 590

<212> PRT

<213> homo sapiens

<400> 4451

Met Gly Lys Gly Arg Ala Gly Arg Val Gly Thr Thr Ala Leu Pro Pro

1 5 10 15

Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu

20 25 30

Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys

35 40 45

Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn

50 55 60

Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys

65 70 75 80

Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys

85 90 95

Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn

100 105 110

Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala

115 120 125

Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val

130 135 140

Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu

145 150 155 160

Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys

165 170 175

His Leu Gly Ile Glu Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg

180 185 190

Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile

195 200 205

Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu

210 215 220

His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met
 225 230 235 240
 Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val
 245 250 255
 Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His
 260 265 270
 Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr
 275 280 285

 Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser
 290 295 300
 Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val
 305 310 315 320
 Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly
 325 330 335
 Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn
 340 345 350

 Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser
 355 360 365
 Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met
 370 375 380
 Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser
 385 390 395 400
 Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser Met
 405 410 415

 Ala Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr
 420 425 430
 Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe
 435 440 445
 Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala
 450 455 460
 Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu

465 470 475 480

Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg

485 490 495

Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val

500 505 510

Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu

515 520 525

Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro

530 535 540

Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser

545 550 555 560

Arg Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala

565 570 575

Arg Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val

580 585 590

<210> 4452

<211> 462

<212> PRT

<213> homo sapiens

<400> 4452

Met Gln Leu Arg Lys Met Gln Thr Val Lys Lys Glu Gln Ala Ser Leu

1 5 10 15

Asp Ala Ser Ser Asn Val Asp Lys Met Met Val Leu Asn Ser Ala Leu

20 25 30

Thr Glu Val Ser Glu Asp Ser Thr Thr Gly Glu Glu Leu Leu Leu Ser

35 40 45

Glu Gly Ser Val Gly Lys Asn Lys Ser Ser Ala Cys Arg Arg Lys Arg

50 55 60

Glu Phe Ile Pro Asp Glu Lys Lys Asp Ala Met Tyr Trp Glu Lys Arg

65 70 75 80

Arg Lys Asn Asn Glu Ala Ala Lys Arg Ser Arg Glu Lys Arg Arg Leu

85	90	95	
Asn Asp Leu Val Leu Glu Asn Lys Leu Ile Ala Leu Gly Glu Glu Asn			
100	105	110	
Ala Thr Leu Lys Ala Glu Leu Leu Ser Leu Lys Leu Lys Phe Gly Leu			
115	120	125	
Ile Ser Ser Thr Ala Tyr Ala Gln Glu Ile Gln Lys Leu Ser Asn Ser			
130	135	140	
Thr Ala Val Tyr Phe Gln Asp Tyr Gln Thr Ser Lys Ser Asn Val Ser			
145	150	155	160
Ser Phe Val Asp Glu His Glu Pro Ser Met Val Ser Ser Ser Cys Ile			
165	170	175	
Ser Val Ile Lys His Ser Pro Gln Ser Ser Leu Ser Asp Val Ser Glu			
180	185	190	
Val Ser Ser Val Glu His Thr Gln Glu Ser Ser Val Gln Gly Ser Cys			
195	200	205	
Arg Ser Pro Glu Asn Lys Phe Gln Ile Ile Lys Gln Glu Pro Met Glu			
210	215	220	
Leu Glu Ser Tyr Thr Arg Glu Pro Arg Asp Asp Arg Gly Ser Tyr Thr			
225	230	235	240
Ala Ser Ile Tyr Gln Asn Tyr Met Gly Asn Ser Phe Ser Gly Tyr Ser			
245	250	255	
His Ser Pro Pro Leu Leu Gln Val Asn Arg Ser Ser Ser Asn Ser Pro			
260	265	270	
Arg Thr Ser Glu Thr Asp Asp Gly Val Val Gly Lys Ser Ser Asp Gly			
275	280	285	
Glu Asp Glu Gln Gln Val Pro Lys Gly Pro Ile His Ser Pro Val Glu			
290	295	300	
Leu Lys His Val His Ala Thr Val Val Lys Val Pro Glu Val Asn Ser			
305	310	315	320
Ser Ala Leu Pro His Lys Leu Arg Ile Lys Ala Lys Ala Met Gln Ile			
325	330	335	

Lys Val Glu Ala Phe Asp Asn Glu Phe Glu Ala Thr Gln Lys Leu Ser
 340 345 350
 Ser Pro Ile Asp Met Thr Ser Lys Arg His Phe Glu Leu Glu Lys His
 355 360 365
 Ser Ala Pro Ser Met Val His Ser Ser Leu Thr Pro Phe Ser Val Gln
 370 375 380
 Val Thr Asn Ile Gln Asp Trp Ser Leu Lys Ser Glu His Trp His Gln

 385 390 395 400
 Lys Glu Leu Ser Gly Lys Thr Gln Asn Ser Phe Lys Thr Gly Val Val
 405 410 415
 Glu Met Lys Asp Ser Gly Tyr Lys Val Ser Asp Pro Glu Asn Leu Tyr
 420 425 430
 Leu Lys Gln Gly Ile Ala Asn Leu Ser Ala Glu Val Val Ser Leu Lys
 435 440 445
 Arg Leu Ile Ala Thr Gln Pro Ile Ser Ala Ser Asp Ser Gly

 450 455 460
 <210> 4453
 <211> 1011
 <212> PRT
 <213> homo sapiens
 <400> 4453
 Met Gly Ala Tyr Ala Arg Ala Ser Gly Val Cys Ala Arg Gly Cys Leu
 1 5 10 15
 Asp Ser Ala Gly Pro Trp Thr Met Ser Arg Ala Leu Arg Pro Pro Leu
 20 25 30
 Pro Pro Leu Cys Phe Phe Leu Leu Leu Leu Ala Ala Ala Gly Ala Arg
 35 40 45

 Ala Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn
 50 55 60
 Val His Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr
 65 70 75 80
 Val Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly

85	90	95	
Val Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro			
100	105	110	
Thr Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp			
115	120	125	
His Gln Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg			
130	135	140	
Gln Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu			
145	150	155	160
Ala Ala Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr Leu Gly Leu			
165	170	175	
Arg Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro Arg Val Ala			
180	185	190	
Trp His Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe			
195	200	205	
Ala Gln Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln			
210	215	220	
Asp Lys Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg			
225	230	235	240
Ala Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val			
245	250	255	
Leu Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu			
260	265	270	
Cys Val Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn			
275	280	285	
Ala Lys Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly			
290	295	300	
Arg Tyr Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe			
305	310	315	320
Gln Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile			
325	330	335	

Arg Leu Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu
 340 345 350
 Tyr Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu
 355 360 365

 Thr Trp Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro
 370 375 380
 His Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg
 385 390 395 400
 Tyr Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu
 405 410 415
 Ala Leu Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp
 420 425 430

 Ser Ala Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala
 435 440 445
 Val Ser Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln
 450 455 460
 Leu Ala Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu
 465 470 475 480
 Ala Arg Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu
 485 490 495

 Asn Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val
 500 505 510
 Ile Val Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg Leu
 515 520 525
 Pro Val Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly Arg Thr
 530 535 540
 Val Pro Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser Gln Ala His
 545 550 555 560

 Pro Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser
 565 570 575
 Thr Tyr Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln Ala Arg Ala

580 585 590
 Pro Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu Thr Ile Glu
 595 600 605
 Asn Glu His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly Leu Leu Met
 610 615 620

 Glu Ile Met Asn Met Asn Gln Gln Leu Leu Leu Pro Val Arg Gln Thr
 625 630 635 640
 Phe Phe Trp Tyr Asn Ala Ser Ile Gly Asp Asn Glu Ser Asp Gln Ala
 645 650 655
 Ser Gly Ala Tyr Ile Phe Arg Pro Asn Gln Gln Lys Pro Leu Pro Val
 660 665 670
 Ser Arg Trp Ala Gln Ile His Leu Val Lys Thr Pro Leu Val Gln Glu
 675 680 685

 Val His Gln Asn Phe Ser Ala Trp Cys Ser Gln Val Val Arg Leu Tyr
 690 695 700
 Pro Gly Gln Arg His Leu Glu Leu Glu Trp Ser Val Gly Pro Ile Pro
 705 710 715 720
 Val Gly Asp Thr Trp Gly Lys Glu Val Ile Ser Arg Phe Asp Thr Pro
 725 730 735
 Leu Glu Thr Lys Gly Arg Phe Tyr Thr Asp Ser Asn Gly Arg Glu Ile
 740 745 750

 Leu Glu Arg Arg Arg Asp Tyr Arg Pro Thr Trp Lys Leu Asn Gln Thr
 755 760 765
 Glu Pro Val Ala Gly Asn Tyr Tyr Pro Val Asn Thr Arg Ile Tyr Ile
 770 775 780
 Thr Asp Gly Asn Met Gln Leu Thr Val Leu Thr Asp Arg Ser Gln Gly
 785 790 795 800
 Gly Ser Ser Leu Arg Asp Gly Ser Leu Glu Leu Met Val His Arg Arg
 805 810 815

 Leu Leu Lys Asp Asp Gly Arg Gly Val Ser Glu Pro Leu Met Glu Asn
 820 825 830

Gly Ser Gly Ala Trp Val Arg Gly Arg His Leu Val Leu Leu Asp Thr

835 840 845

Ala Gln Ala Ala Ala Ala Gly His Arg Leu Leu Ala Glu Gln Glu Val

850 855 860

Leu Ala Pro Gln Val Val Leu Ala Pro Gly Gly Gly Ala Ala Tyr Asn

865 870 875 880

Leu Gly Ala Pro Pro Arg Thr Gln Phe Ser Gly Leu Arg Arg Asp Leu

885 890 895

Pro Pro Ser Val His Leu Leu Thr Leu Ala Ser Trp Gly Pro Glu Met

900 905 910

Val Leu Leu Arg Leu Glu His Gln Phe Ala Val Gly Glu Asp Ser Gly

915 920 925

Arg Asn Leu Ser Ala Pro Val Thr Leu Asn Leu Arg Asp Leu Phe Ser

930 935 940

Thr Phe Thr Ile Thr Arg Leu Gln Glu Thr Thr Leu Val Ala Asn Gln

945 950 955 960

Leu Arg Glu Ala Ala Ser Arg Leu Lys Trp Thr Thr Asn Thr Gly Pro

965 970 975

Thr Pro His Gln Thr Pro Tyr Gln Leu Asp Pro Ala Asn Ile Thr Leu

980 985 990

Glu Pro Met Glu Ile Arg Thr Phe Leu Ala Ser Val Gln Trp Lys Glu

995 1000 1005

Val Asp Gly

1010

<210> 4454

<211> 516

<212> PRT

<213> homo sapiens

<400> 4454

Met Glu Pro Ala Val Ser Leu Ala Val Cys Ala Leu Leu Phe Leu Leu

1 5 10 15

Trp Val Arg Leu Lys Gly Leu Glu Phe Val Leu Ile His Gln Arg Trp

20 25 30
 Val Phe Val Cys Leu Phe Leu Leu Pro Leu Ser Leu Ile Phe Asp Ile
 35 40 45
 Tyr Tyr Tyr Val Arg Ala Trp Val Val Phe Lys Leu Ser Ser Ala Pro

 50 55 60
 Arg Leu His Glu Gln Arg Val Arg Asp Ile Gln Lys Gln Val Arg Glu
 65 70 75 80
 Trp Lys Glu Gln Gly Ser Lys Thr Phe Met Cys Thr Gly Arg Pro Gly
 85 90 95
 Trp Leu Thr Val Ser Leu Arg Val Gly Lys Tyr Lys Lys Thr His Lys
 100 105 110
 Asn Ile Met Ile Asn Leu Met Asp Ile Leu Glu Val Asp Thr Lys Lys

 115 120 125
 Gln Ile Val Arg Val Glu Pro Leu Val Thr Met Gly Gln Val Thr Ala
 130 135 140
 Leu Leu Thr Ser Ile Gly Trp Thr Leu Pro Val Leu Pro Glu Leu Asp
 145 150 155 160
 Asp Leu Thr Val Gly Gly Leu Ile Met Gly Thr Gly Ile Glu Ser Ser
 165 170 175
 Ser His Lys Tyr Gly Leu Phe Gln His Ile Cys Thr Ala Tyr Glu Leu

 180 185 190
 Val Leu Ala Asp Gly Ser Phe Val Arg Cys Thr Pro Ser Glu Asn Ser
 195 200 205
 Asp Leu Phe Tyr Ala Val Pro Trp Ser Cys Gly Thr Leu Gly Phe Leu
 210 215 220
 Val Ala Ala Glu Ile Arg Ile Ile Pro Ala Lys Lys Tyr Val Lys Leu
 225 230 235 240
 Arg Phe Glu Pro Val Arg Gly Leu Glu Ala Ile Cys Ala Lys Phe Thr

 245 250 255
 His Glu Ser Gln Arg Gln Glu Asn His Phe Val Glu Gly Leu Leu Tyr
 260 265 270

Ser Leu Asp Glu Ala Val Ile Met Thr Gly Val Met Thr Asp Glu Ala
 275 280 285
 Glu Pro Ser Lys Leu Asn Ser Ile Gly Asn Tyr Tyr Lys Pro Trp Phe
 290 295 300
 Phe Lys His Val Glu Asn Tyr Leu Lys Thr Asn Arg Glu Gly Leu Glu

 305 310 315 320
 Tyr Ile Pro Leu Arg His Tyr Tyr His Arg His Thr Arg Ser Ile Phe
 325 330 335
 Trp Glu Leu Gln Asp Ile Ile Pro Phe Gly Asn Asn Pro Ile Phe Arg
 340 345 350
 Tyr Leu Phe Gly Trp Met Val Pro Pro Lys Ile Ser Leu Leu Lys Leu
 355 360 365
 Thr Gln Gly Glu Thr Leu Arg Lys Leu Tyr Glu Gln His His Val Val

 370 375 380
 Gln Asp Met Leu Val Pro Met Lys Cys Leu Gln Gln Ala Leu His Thr
 385 390 395 400
 Phe Gln Asn Asp Ile His Val Tyr Pro Ile Trp Leu Cys Pro Phe Ile
 405 410 415
 Leu Pro Ser Gln Pro Gly Leu Val His Pro Lys Gly Asn Glu Ala Glu
 420 425 430
 Leu Tyr Ile Asp Ile Gly Ala Tyr Gly Glu Pro Arg Val Lys His Phe

 435 440 445
 Glu Ala Arg Ser Cys Met Arg Gln Leu Glu Lys Phe Val Arg Ser Val
 450 455 460
 His Gly Phe Gln Met Leu Tyr Ala Asp Cys Tyr Met Asn Arg Glu Glu
 465 470 475 480
 Phe Trp Glu Met Phe Asp Gly Ser Leu Tyr His Lys Leu Arg Glu Lys
 485 490 495
 Leu Gly Cys Gln Asp Ala Phe Pro Glu Val Tyr Asp Lys Ile Cys Lys

 500 505 510
 Ala Ala Arg His

515

<210> 4455

<211> 480

<212> PRT

<213> homo sapiens

<400> 4455

Met Asn Ala Ser Glu Phe Arg Arg Arg Gly Lys Glu Met Val Asp Tyr

1 5 10 15

Val Ala Asn Tyr Met Glu Gly Ile Glu Gly Arg Gln Val Tyr Pro Asp

20 25 30

Val Glu Pro Gly Tyr Leu Arg Pro Leu Ile Pro Ala Ala Ala Pro Gln

35 40 45

Glu Pro Asp Thr Phe Glu Asp Ile Ile Asn Asp Val Glu Lys Ile Ile

50 55 60

Met Pro Gly Val Thr His Trp His Ser Pro Tyr Phe Phe Ala Tyr Phe

65 70 75 80

Pro Thr Ala Ser Ser Tyr Pro Ala Met Leu Ala Asp Met Leu Cys Gly

85 90 95

Ala Ile Gly Cys Ile Gly Phe Ser Trp Ala Ala Ser Pro Ala Cys Thr

100 105 110

Glu Leu Glu Thr Val Met Met Asp Trp Leu Gly Lys Met Leu Glu Leu

115 120 125

Pro Lys Ala Phe Leu Asn Glu Lys Ala Gly Glu Gly Gly Gly Val Ile

130 135 140

Gln Gly Ser Ala Ser Glu Ala Thr Leu Val Ala Leu Leu Ala Ala Arg

145 150 155 160

Thr Lys Val Ile His Arg Leu Gln Ala Ala Ser Pro Glu Leu Thr Gln

165 170 175

Ala Ala Ile Met Glu Lys Leu Val Ala Tyr Ser Ser Asp Gln Ala His

180 185 190

Ser Ser Val Glu Arg Ala Gly Leu Ile Gly Gly Val Lys Leu Lys Ala

195 200 205

Ile Pro Ser Asp Gly Asn Phe Ala Met Arg Ala Ser Ala Leu Gln Glu
210 215 220

Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Met Val
225 230 235 240

Ala Thr Leu Gly Thr Thr Thr Cys Cys Ser Phe Asp Asn Leu Leu Glu
245 250 255

Val Gly Pro Ile Cys Asn Lys Glu Asp Ile Trp Leu His Val Asp Ala
260 265 270

Ala Tyr Ala Gly Ser Ala Phe Ile Cys Pro Glu Phe Arg His Leu Leu
275 280 285

Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys Trp
290 295 300

Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Lys Arg Thr
305 310 315 320

Asp Leu Thr Gly Ala Phe Arg Leu Asp Pro Thr Tyr Leu Lys His Ser
325 330 335

His Gln Asp Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Ile Pro
340 345 350

Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg Met
355 360 365

Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln Leu
370 375 380

Ser His Glu Phe Glu Ser Leu Val Arg Gln Asp Pro Arg Phe Glu Ile
385 390 395 400

Cys Val Glu Val Ile Leu Gly Leu Val Cys Phe Arg Leu Lys Gly Ser
405 410 415

Asn Lys Val Asn Glu Ala Leu Leu Gln Arg Ile Asn Ser Ala Lys Lys
420 425 430

Ile His Leu Val Pro Cys His Leu Arg Asp Lys Phe Val Leu Arg Phe
435 440 445

Ala Ile Cys Ser Arg Thr Val Glu Ser Ala His Val Gln Arg Ala Trp

450 455 460
 Glu His Ile Lys Glu Leu Ala Ala Asp Val Leu Arg Ala Glu Arg Glu
 465 470 475 480
 <210> 4456
 <211> 480
 <212> PRT
 <213> homo sapiens
 <400> 4456

Met Asn Ala Ser Glu Phe Arg Arg Arg Gly Lys Glu Met Val Asp Tyr

1 5 10 15
 Val Ala Asn Tyr Met Glu Gly Ile Glu Gly Arg Gln Val Tyr Pro Asp
 20 25 30
 Val Glu Pro Gly Tyr Leu Arg Pro Leu Ile Pro Ala Ala Ala Pro Gln
 35 40 45
 Glu Pro Asp Thr Phe Glu Asp Ile Ile Asn Asp Val Glu Lys Ile Ile
 50 55 60
 Met Pro Gly Val Thr His Trp His Ser Pro Tyr Phe Phe Ala Tyr Phe

65 70 75 80
 Pro Thr Ala Ser Ser Tyr Pro Ala Met Leu Ala Asp Met Leu Cys Gly
 85 90 95
 Ala Ile Gly Cys Ile Gly Phe Ser Trp Ala Ala Ser Pro Ala Cys Thr
 100 105 110
 Glu Leu Glu Thr Val Met Met Asp Trp Leu Gly Lys Met Leu Glu Leu
 115 120 125
 Pro Lys Ala Phe Leu Asn Glu Lys Ala Gly Glu Gly Gly Gly Val Ile

130 135 140
 Gln Gly Ser Ala Ser Glu Ala Thr Leu Val Ala Leu Leu Ala Ala Arg
 145 150 155 160
 Thr Lys Val Ile His Arg Leu Gln Ala Ala Ser Pro Glu Leu Thr Gln
 165 170 175
 Ala Ala Ile Met Glu Lys Leu Val Ala Tyr Ser Ser Asp Gln Ala His
 180 185 190

Ser Ser Val Glu Arg Ala Gly Leu Ile Gly Gly Val Lys Leu Lys Ala

195 200 205

Ile Pro Ser Asp Gly Asn Phe Ala Met Arg Ala Ser Ala Leu Gln Glu

210 215 220

Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Met Val

225 230 235 240

Ala Thr Leu Gly Thr Thr Thr Cys Cys Ser Phe Asp Asn Leu Leu Glu

245 250 255

Val Gly Pro Ile Cys Asn Lys Glu Asp Ile Trp Leu His Val Asp Ala

260 265 270

Ala Tyr Ala Gly Ser Ala Phe Ile Cys Pro Glu Phe Arg His Leu Leu

275 280 285

Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys Trp

290 295 300

Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Lys Arg Thr

305 310 315 320

Asp Leu Thr Gly Ala Phe Arg Leu Asp Pro Thr Tyr Leu Lys His Ser

325 330 335

His Gln Asp Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Ile Pro

340 345 350

Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg Met

355 360 365

Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln Leu

370 375 380

Ser His Glu Phe Glu Ser Leu Val Arg Gln Asp Pro Arg Phe Glu Ile

385 390 395 400

Cys Val Glu Val Ile Leu Gly Leu Val Cys Phe Arg Leu Lys Gly Ser

405 410 415

Asn Lys Val Asn Glu Ala Leu Leu Gln Arg Ile Asn Ser Ala Lys Lys

420 425 430

Ile His Leu Val Pro Cys His Leu Arg Asp Lys Phe Val Leu Arg Phe

435 440 445
Ala Ile Cys Ser Arg Thr Val Glu Ser Ala His Val Gln Arg Ala Trp

450 455 460
Glu His Ile Lys Glu Leu Ala Ala Asp Val Leu Arg Ala Glu Arg Glu
465 470 475 480

<210> 4457

<211> 209

<212> PRT

<213> homo sapiens

<400> 4457

Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp

1 5 10 15

Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys

20 25 30

Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu

35 40 45

Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg

50 55 60

Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe

65 70 75 80

Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp

85 90 95

Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met Gly

100 105 110

Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser

115 120 125

Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala

130 135 140

Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys

145 150 155 160

Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala Leu

165 170 175
Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys Lys Pro Leu Asp
180 185 190
Gly Glu Tyr Phe Thr Leu Gln Asp Gln Thr Ser Phe Gln Lys Glu Asn
195 200 205
Cys

<210> 4458

<211> 214

<212> PRT

<213> homo sapiens

<400> 4458

Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp

1 5 10 15
Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys
20 25 30
Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu
35 40 45
Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg
50 55 60
Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe

65 70 75 80
Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp
85 90 95
Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met Gly
100 105 110
Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser
115 120 125
Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala

130 135 140
Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys
145 150 155 160

Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala Leu
165 170 175
Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys Lys Pro Leu Asp
180 185 190
Gly Glu Tyr Phe Thr Leu Gln Met Leu Leu Asp Leu Arg Trp Cys Tyr
195 200 205
Phe Leu Ile Asn Ser Ser
210
<210> 4459
<211> 346
<212> PRT
<213> homo sapiens
<400> 4459
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
1 5 10 15
Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
20 25 30
Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
35 40 45
Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
50 55 60
Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
65 70 75 80
Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
85 90 95
Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
100 105 110
Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
115 120 125
Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
130 135 140
Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met

145 150 155 160
Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys

165 170 175
Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln

180 185 190
His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp

195 200 205
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu

210 215 220
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser

225 230 235 240
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr

245 250 255
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val

260 265 270
Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn

275 280 285
Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr

290 295 300
Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys

305 310 315 320
Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Met Leu Leu Asp Leu

325 330 335
Arg Trp Cys Tyr Phe Leu Ile Asn Ser Ser

340 345
<210> 4460

<211> 393
<212> PRT

<213> homo sapiens
<400> 4460

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln

1	5	10	15
Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu			
	20	25	30
Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp			
	35	40	45
Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro			
	50	55	60
Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro			
65	70	75	80
Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser			
	85	90	95
Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly			
	100	105	110
Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro			
	115	120	125
Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln			
130	135	140	
Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met			
145	150	155	160
Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys			
	165	170	175
Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln			
	180	185	190
His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp			
195	200	205	
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu			
	210	215	220
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser			
225	230	235	240
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr			
	245	250	255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val

260 265 270
Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
275 280 285
Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
290 295 300
Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305 310 315 320
Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu

325 330 335
Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
340 345 350
Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
355 360 365
Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
370 375 380
Phe Lys Thr Glu Gly Pro Asp Ser Asp
385 390

<210> 4461

<211> 261

<212> PRT

<213> homo sapiens

<400> 4461

Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp
1 5 10 15
Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys
20 25 30
Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu
35 40 45
Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg

50

55

60

Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe
65 70 75 80
Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp
85 90 95
Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met Gly
100 105 110
Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser
115 120 125
Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala
130 135 140
Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys
145 150 155 160
Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala Leu
165 170 175
Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys Lys Pro Leu Asp
180 185 190
Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu Met
195 200 205
Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly
210 215 220
Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys
225 230 235 240
Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu
245 250 255
Gly Pro Asp Ser Asp
260
<210> 4462
<211> 341
<212> PRT
<213> homo sapiens
<400> 4462
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln

1 5 10 15
 Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
 20 25 30
 Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp

 35 40 45
 Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
 50 55 60
 Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro
 65 70 75 80
 Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
 85 90 95
 Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly

 100 105 110
 Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
 115 120 125
 Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
 130 135 140
 Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
 145 150 155 160
 Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys

 165 170 175
 Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
 180 185 190
 His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
 195 200 205
 Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
 210 215 220
 Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser

 225 230 235 240
 Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
 245 250 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
275 280 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr

290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Asp Gln Thr Ser Phe
325 330 335

Gln Lys Glu Asn Cys

340

<210> 4463

<211> 393

<212> PRT

<213> homo sapiens

<400> 4463

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln

1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
20 25 30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro

65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser
85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro

115 120 125
 Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln

 130 135 140
 Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
 145 150 155 160
 Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
 165 170 175
 Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
 180 185 190
 His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp

 195 200 205
 Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu
 210 215 220
 Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
 225 230 235 240
 Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
 245 250 255
 Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val

 260 265 270
 Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
 275 280 285
 Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
 290 295 300
 Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
 305 310 315 320
 Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu

 325 330 335
 Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
 340 345 350
 Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
 355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
 370 375 380
 Phe Lys Thr Glu Gly Pro Asp Ser Asp
 385 390

 <210> 4464
 <211> 1102
 <212> PRT
 <213> homo sapiens
 <400> 4464
 Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
 1 5 10 15
 Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
 20 25 30
 Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
 35 40 45
 Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr

 50 55 60
 Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
 65 70 75 80
 Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
 85 90 95
 His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
 100 105 110
 Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe

 115 120 125
 His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
 130 135 140
 Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
 145 150 155 160
 Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
 165 170 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val

180 185 190
Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
195 200 205
Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
210 215 220
Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225 230 235 240
Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly

245 250 255
His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
260 265 270
Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
275 280 285
Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
290 295 300
Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn

305 310 315 320
Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
325 330 335
Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
340 345 350
Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
355 360 365
Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln

370 375 380
Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385 390 395 400
Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
405 410 415
Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala

420 425 430
Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile

435 440 445
Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His

450 455 460
Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr

465 470 475 480
Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg

485 490 495
Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu

500 505 510
Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala

515 520 525
Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr

530 535 540
Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr

545 550 555 560
Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala

565 570 575
Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys

580 585 590
Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser

595 600 605
Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys

610 615 620
Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala

625 630 635 640
His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val

645 650 655
Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr

660 665 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
675 680 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
690 695 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705 710 715 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
725 730 735

Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
740 745 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
755 760 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
770 775 780

Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785 790 795 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
805 810 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
820 825 830

Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
835 840 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
850 855 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865 870 875 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
885 890 895

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
900 905 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp

915 920 925
 Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
 930 935 940
 Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp

 945 950 955 960
 Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
 965 970 975
 Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
 980 985 990
 Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser
 995 1000 1005
 Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg

 1010 1015 1020
 Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly
 1025 1030 1035
 Phe Trp Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn
 1040 1045 1050
 Asp Glu Arg Leu Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr
 1055 1060 1065
 Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Asn Met Thr Asp Gly

 1070 1075 1080
 Val Ala Glu Pro Met His Gly Ser Leu Ala Gly Val Lys Leu Ser
 1085 1090 1095
 Ser Gln Gln Ala
 1100
 <210> 4465
 <211> 1102
 <212> PRT
 <213> homo sapiens
 <400> 4465
 Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
 1 5 10 15

Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
20 25 30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
35 40 45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
50 55 60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65 70 75 80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
85 90 95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
100 105 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
115 120 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
130 135 140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145 150 155 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
165 170 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
180 185 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
195 200 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
210 215 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225 230 235 240

Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
245 250 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala

260	265	270
Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly		
275	280	285
Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val		
290	295	300
Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn		
305	310	315
Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser		
325	330	335
Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly		
340	345	350
Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln		
355	360	365
Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln		
370	375	380
Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser		
385	390	395
Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln		
405	410	415
Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala		
420	425	430
Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile		
435	440	445
Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His		
450	455	460
Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr		
465	470	475
Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg		
485	490	495
Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu		
500	505	510

Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
 515 520 525
 Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
 530 535 540

 Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
 545 550 555 560
 Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
 565 570 575
 Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
 580 585 590
 Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
 595 600 605

 Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
 610 615 620
 Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
 625 630 635 640
 His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
 645 650 655
 Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
 660 665 670

 Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
 675 680 685
 Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
 690 695 700
 Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
 705 710 715 720
 Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
 725 730 735

 Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
 740 745 750
 Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys

755 760 765
 Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
 770 775 780
 Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
 785 790 795 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
 805 810 815
 Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
 820 825 830
 Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
 835 840 845
 His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
 850 855 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
 865 870 875 880
 Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
 885 890 895
 Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
 900 905 910
 Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
 915 920 925

Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
 930 935 940
 Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
 945 950 955 960
 Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
 965 970 975
 Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
 980 985 990

Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser
 995 1000 1005

Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg
 1010 1015 1020
 Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly
 1025 1030 1035
 Phe Trp Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn
 1040 1045 1050

Asp Glu Arg Leu Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr
 1055 1060 1065
 Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Asn Met Thr Asp Gly
 1070 1075 1080
 Val Ala Glu Pro Met His Gly Ser Leu Ala Gly Val Lys Leu Ser
 1085 1090 1095

Ser Gln Gln Ala
 1100

<210> 4466

<211> 597

<212> PRT

<213> homo sapiens

<400> 4466

Met Ala Glu Gly Ser Ala Val Ser Asp Pro Gln His Ala Ala Arg Leu

1 5 10 15
 Leu Arg Ala Leu Ser Ser Phe Arg Glu Glu Ser Arg Phe Cys Asp Ala
 20 25 30
 His Leu Val Leu Asp Gly Glu Glu Ile Pro Val Gln Lys Asn Ile Leu
 35 40 45
 Ala Ala Ala Ser Pro Tyr Ile Arg Thr Lys Leu Asn Tyr Asn Pro Pro
 50 55 60
 Lys Asp Asp Gly Ser Thr Tyr Lys Ile Glu Leu Glu Gly Ile Ser Val

65 70 75 80
 Met Val Met Arg Glu Ile Leu Asp Tyr Ile Phe Ser Gly Gln Ile Arg
 85 90 95
 Leu Asn Glu Asp Thr Ile Gln Asp Val Val Gln Ala Ala Asp Leu Leu

100	105	110	
Leu Leu Thr Asp Leu Lys Thr Leu Cys Cys Glu Phe Leu Glu Gly Cys			
115	120	125	
Ile Ala Ala Glu Asn Cys Ile Gly Ile Arg Asp Phe Ala Leu His Tyr			
130	135	140	
Cys Leu His His Val His Tyr Leu Ala Thr Glu Tyr Leu Glu Thr His			
145	150	155	160
Phe Arg Asp Val Ser Ser Thr Glu Glu Phe Leu Glu Leu Ser Pro Gln			
165	170	175	
Lys Leu Lys Glu Val Ile Ser Leu Glu Lys Leu Asn Val Gly Asn Glu			
180	185	190	
Arg Tyr Val Phe Glu Ala Val Ile Arg Trp Ile Ala His Asp Thr Glu			
195	200	205	
Ile Arg Lys Val His Met Lys Asp Val Met Ser Ala Leu Trp Val Ser			
210	215	220	
Gly Leu Asp Ser Ser Tyr Leu Arg Glu Gln Met Leu Asn Glu Pro Leu			
225	230	235	240
Val Arg Glu Ile Val Lys Glu Cys Ser Asn Ile Pro Leu Ser Gln Pro			
245	250	255	
Gln Gln Gly Glu Ala Met Leu Ala Asn Phe Lys Pro Arg Gly Tyr Ser			
260	265	270	
Glu Cys Ile Val Thr Val Gly Gly Glu Glu Arg Val Ser Arg Lys Pro			
275	280	285	
Thr Ala Ala Met Arg Cys Met Cys Pro Leu Tyr Asp Pro Asn Arg Gln			
290	295	300	
Leu Trp Ile Glu Leu Ala Pro Leu Ser Met Pro Arg Ile Asn His Gly			
305	310	315	320
Val Leu Ser Ala Glu Gly Phe Leu Phe Val Phe Gly Gly Gln Asp Glu			
325	330	335	
Asn Lys Gln Thr Leu Ser Ser Gly Glu Lys Tyr Asp Pro Asp Ala Asn			
340	345	350	

Thr Trp Thr Ala Leu Pro Pro Met Asn Glu Ala Arg His Asn Phe Gly
 355 360 365
 Ile Val Glu Ile Asp Gly Met Leu Tyr Ile Leu Gly Gly Glu Asp Gly
 370 375 380
 Glu Lys Glu Leu Ile Ser Met Glu Cys Tyr Asp Ile Tyr Ser Lys Thr

 385 390 395 400
 Trp Thr Lys Gln Pro Asp Leu Thr Met Val Arg Lys Ile Gly Cys Tyr
 405 410 415
 Ala Ala Met Lys Lys Lys Ile Tyr Ala Met Gly Gly Gly Ser Tyr Gly
 420 425 430
 Lys Leu Phe Glu Ser Val Glu Cys Tyr Asp Pro Arg Thr Gln Gln Trp
 435 440 445
 Thr Ala Ile Cys Pro Leu Lys Glu Arg Arg Phe Gly Ala Val Ala Cys

 450 455 460
 Gly Val Ala Met Glu Leu Tyr Val Phe Gly Gly Val Arg Ser Arg Glu
 465 470 475 480
 Asp Ala Gln Gly Ser Glu Met Val Thr Cys Lys Ser Glu Phe Tyr His
 485 490 495
 Asp Glu Phe Lys Arg Trp Ile Tyr Leu Asn Asp Gln Asn Leu Cys Ile
 500 505 510
 Pro Ala Ser Ser Ser Phe Val Tyr Gly Ala Val Pro Ile Gly Ala Ser

 515 520 525
 Ile Tyr Val Ile Gly Asp Leu Asp Thr Gly Thr Asn Tyr Asp Tyr Val
 530 535 540
 Arg Glu Phe Lys Arg Ser Thr Gly Thr Trp His His Thr Lys Pro Leu
 545 550 555 560
 Leu Pro Ser Asp Leu Arg Arg Thr Gly Cys Ala Ala Leu Arg Ile Ala
 565 570 575
 Asn Cys Lys Leu Phe Arg Leu Gln Leu Gln Gln Gly Leu Phe Arg Ile

 580 585 590
 Arg Val His Ser Pro

595

<210> 4467

<211> 123

<212> PRT

<213> homo sapiens

<400> 4467

Met Ala Arg Gly Ser Ala Leu Leu Leu Ala Ser Leu Leu Leu Ala Ala

1 5 10 15

Ala Leu Ser Ala Ser Ala Gly Leu Trp Ser Pro Ala Lys Glu Lys Arg

 20 25 30

Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Pro His Ala Val

 35 40 45

Gly Asn His Arg Ser Phe Ser Asp Lys Asn Gly Leu Thr Ser Lys Arg

 50 55 60

Glu Leu Arg Pro Glu Asp Asp Met Lys Pro Gly Ser Phe Asp Arg Ser

65 70 75 80

Ile Pro Glu Asn Asn Ile Met Arg Thr Ile Ile Glu Phe Leu Ser Phe

 85 90 95

Leu His Leu Lys Glu Ala Gly Ala Leu Asp Arg Leu Leu Asp Leu Pro

 100 105 110

Ala Ala Ala Ser Ser Glu Asp Ile Glu Arg Ser

 115 120

<210> 4468

<211> 294

<212> PRT

<213> homo sapiens

<400> 4468

Met Ala Met Ser Ser Gly Gly Ser Gly Gly Gly Val Pro Glu Gln Glu

1 5 10 15

Asp Ser Val Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp

 20 25 30

Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala

35 40 45
 Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly
 50 55 60
 Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser
 65 70 75 80
 Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp
 85 90 95
 Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr

 100 105 110
 Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr
 115 120 125
 Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro
 130 135 140
 Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu
 145 150 155 160
 Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro

 165 170 175
 Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser
 180 185 190
 Phe Leu Pro Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly
 195 200 205
 Lys Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro Pro
 210 215 220
 Pro Pro His Leu Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro

 225 230 235 240
 Pro Ile Ile Pro Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp
 245 250 255
 Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr
 260 265 270
 His Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Gln Lys Glu Gly Arg
 275 280 285
 Cys Ser His Ser Leu Asn

290

<210> 4469

<211> 250

<212> PRT

<213> homo sapiens

<400> 4469

Met Ala Met Ser Ser Gly Gly Ser Gly Gly Gly Val Pro Glu Gln Glu

1 5 10 15

Asp Ser Val Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp

20 25 30

Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala

35 40 45

Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly

50 55 60

Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser

65 70 75 80

Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp

85 90 95

Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr

100 105 110

Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr

115 120 125

Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro

130 135 140

Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu

145 150 155 160

Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro

165 170 175

Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser

180 185 190

Phe Leu Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly

195 200 205
 Lys Ile Ile Pro Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp
 210 215 220
 Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr
 225 230 235 240
 His Thr Gly Tyr Tyr Met Glu Met Leu Ala
 245 250

<210> 4470

<211> 262

<212> PRT

<213> homo sapiens

<400> 4470

Met Ala Met Ser Ser Gly Gly Ser Gly Gly Gly Val Pro Glu Gln Glu
 1 5 10 15
 Asp Ser Val Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp
 20 25 30
 Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala
 35 40 45
 Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly

50 55 60
 Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser
 65 70 75 80
 Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp
 85 90 95
 Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr
 100 105 110
 Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr

115 120 125
 Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro
 130 135 140
 Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu
 145 150 155 160

Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro
165 170 175
Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser
180 185 190
Phe Leu Pro Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly
195 200 205
Lys Ile Ile Pro Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp
210 215 220
Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr
225 230 235 240
His Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Gln Lys Glu Gly Arg
245 250 255
Cys Ser His Ser Leu Asn
260
<210> 4471
<211> 294
<212> PRT
<213> homo sapiens
<400> 4471
Met Ala Met Ser Ser Gly Gly Ser Gly Gly Gly Val Pro Glu Gln Glu
1 5 10 15
Asp Ser Val Leu Phe Arg Arg Gly Thr Gly Gln Ser Asp Asp Ser Asp
20 25 30
Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala
35 40 45
Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly
50 55 60
Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser
65 70 75 80
Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp
85 90 95

Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr

100 105 110

Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr

115 120 125

Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro

130 135 140

Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu

145 150 155 160

Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro

165 170 175

Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser

180 185 190

Phe Leu Pro Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly

195 200 205

Lys Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro

210 215 220

Pro Pro His Leu Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro

225 230 235 240

Pro Ile Ile Pro Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp

245 250 255

Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr

260 265 270

His Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Gln Lys Glu Gly Arg

275 280 285

Cys Ser His Ser Leu Asn

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<210> 4472

<211> 1515

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding GRA16

<400> 4472

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gaagggaag aggattttca gtacacgacg tctccttggg tgattccacc tgacggatta	180
gtcagtcggc gacttgctga ggaacctcct agaaagcgct tgcgaaaaac aaacaaatca	240
gatcgtgact cagattctgc tcaaggttcc aggacgactt ctctggcag tctgggcggt	300
tttggtgcaa cagttgggagc tgttgccact ccgcgaatac ggagtggtgt tgtggcgtcg	360
gaggcgatcc gaggtacaat ttggaggagg ccagggtgaag tcgaaagcac ctgaaagctt	420
cgtagaacca ggcttcaata ttacaaaaca gatggagatg gcttgcaggc gaacaggctt	480
tcatcgacag gggaacgatc aggaatatcg catggggcgc agtctctggc aatgcgcca	540
aggacaatgg gacaaacaat gaaatctttg gagagctcat gggattcgga tccactcgaa	600
ggaacatcac gggattggca atatgtacca acgagtgaga cagctgcttc gcccggcctt	660
accggccttg gagggattgg tagaaagttt gccctctttt acgtacgaga taggaaattt	720
gacttacttc aatttgtgaa tctgacgagg agcaagaaac agaaactctt aatgtcatca	780
aagagccctt cgctcagaag gctcctcatg aacgacatgg cccaggaatg ggctctagga	840
atattgcaga tcgcgttgca gggacgacaa agagctctgc aggttccca caccacgca	900
actacagaac ccgaagtgg tactgacggc actagtaaata cgctcggaaga cgaagcaaca	960
cgcgccagtg agggcaacgc ttccgtcaac cagacatccc ccgccgcgtc atatccgca	1020
cggccctctt ccgacgaagg gcaggacagc ggacgtagaa agtgttcaaa gcgaagtcg	1080
tctcgtctcg tacagaacgc tcctcttttt ctgaaggatg atagtcattc actgaaggac	1140
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<210> 4473

<211> 2465

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of GRA16_5'UTR

<400> 4473

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 ccgtc 2465

<210> 4474

<211> 27

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding HA tag

<400> 4474

taccctacg acgtcccga ctacgcg 27

<210> 4475

<211> 693

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding HXGPRT

<400> 4475

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 tacattgaca aaatcctcct ccctgggtgga ttggtcaagg acagagtga gaagttggcg 180
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gacaacagca caggccagct caccgtcttg agcgacgact tgtcaatctt tcgacacaag 420
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cgctgaaag ccgtcggtcc caagtcgatg agaatcgcca ccctcgctga gaagcgaca 540
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<210> 4476
<211> 1506
<212> DNA
<213> Artificial Sequence
<220><223> Nucleic Acid sequence encoding MeCP2
<400> 4476

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aagccactga agtttaagaa ggcgaagaaa gacaagaagg aggacaaaga aggcaagcat 180
gagccactac aaccttcagc ccaccattct gcagagccag cagaggcagg caaagcagaa 240
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cggcgctcca ttatccgtga ccggggacct atgtatgatg accccacctt gcctgaaggt 360
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agctga 1506

<210> 4477
<211> 1506
<212> DNA
<213> Artificial Sequence
<220><223> Nucleic Acid sequence encoding MECP2_codon_optimized
<400> 4477

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ggggaagagg aacgacttga ggagaaatct gaagaccagg acctccagg cctgagagac 120
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gaacctctgc agcgtctgc ccaccactcg gccgaaccgg ccgaagccgg caaggccgag 240
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aaagtgggag acacatctct ggaccgaac gacttcgact tcaccgtgac tggacgggc 540
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tcctga	1506
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<211> 1237	
<212> DNA	
<213> Artificial Sequence	
<220><223> Nucleic Acid sequence encoding PARK2	
<400> 4478	
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gagtgtgtcc tgcagatggg gggcgtgtta tgccccgcc ctggctgtgg agcggggctg 1080
ctgccggagc ctgaccagag gaaagtcacc tgcgaagggg gcaatggcct gggctgtggg 1140
tatggacaac gaagaacaaa ataagctgcc tcagggagaa gtgagtgcct cattcaatac 1200
atcgttcaag gaaaagtcac tggtagcaaa gctatag 1237

<210> 4479

<211> 885

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding SMN1

<400> 4479

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aaagcatatg ataaagctgt ggcttcattt aagcatgctc taaagaatgg tgacatttgt 180
gaaacttcgg gtaaaccaaa aaccacacct aaaagaaaac ctgctaagaa gaataaaagc 240
caaaagaaga atactgcagc ttccttacia cagtggaaag ttggggacaa atgttctgcc 300
atttggtcag aagacggttg catttaccac gctaccattg cttcaattga ttttaagaga 360

gaaacctgtg ttgtggttta cactggatat ggaaatagag aggagcaaaa tctgtccgat 420
ctactttccc caatctgtga agtagctaata aatatagaac aaaatgctca agagaatgag 480
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gataacatca agcccaaatac tgctccatgg aactcttttc tccctccacc acccccatg 600
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ggaagtatgt taatttcatg gtacatgagt ggctatcata ctggctatta tatgggtttt 840
agacaaaatc aaaaagaagg aaggtgctca cattccttaa attaa 885

<210> 4480

<211> 33

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding TAT

<400> 4480

tatggacgga agaagcggcg acagcgacga cga 33

<210> 4481

<211> 735

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding Toxofilin

<400> 4481

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ctgctgaccg catccgaatc ggtccagctt tctgaaggca tgaagaggct cagcatgaga 120

ggaagaagtc ccagcccgaa aaggggaaga ttcgagagtg gagacgaagg gacatctaca 180

atgtcgccct ccgtcgacg acgccaacag gaactagggc tgctccgtcc ggaagagagg 240

ctcattgcgg gtcaagccaa agcagcggcg ctacagactg tccatcaatt aggagcagtt 300

gtctttaccc cagagcaagc taaagccgca ctgctagacg aaattctcag agccacgcaa 360

aatttgacc tcaggaagta cgagaatctc aacacggagc acaaaaaggc ctatgaacaa 420

gtccagaggg atctttcgca actgagtcg gaaacgaagg ctttgctcat tgaaaatcag 480

aggaaggaga aaaccctact tgaaaaggcg agaaagctct tccaaagacg ccactaccac 540

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gcattacaat caggtgctgt gaagactgcg atccaaagag ccaacgagca gtacaacgtc 660

gctgaggaag acaagaactt taacaggaa cagcatgcat cacaactgaa aaaggtaggc 720

gctatgccct cgtcg 735

<210> 4482

<211> 1116

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of Toxofilin_5'UTR

<400>

> 4482

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ctttggactt cggtggtcgg cactgacgct ttgctagccc tcgcctttgg cgacattcag 120

cacccttgtc tggaccaagc cttttccca cgagcacagc cgactggcac cagacgagtg 180

tatggtatct ctacgaacaa cagcacgccg ttactcctcg aggaaagaga cacttttaaa 240

gaacagagaa aacgtctcga gaagattctg cgggcggctt caccgtgct gcctttctgc 300

gccatttaga acaaggtgtt cgccacctcg tttatggctt atccggcctt ctgcttcaaa 360

aggaaaggcg acccctgcta gcgaccagtc ttgtttcttt gccaaaggcg acctgcacgt 420

caaaacccaa acatcatttg ctcggggtaa aatctgtcgc ggactgtcta cagcaaatac 480

gtgtctttct ctgaaacacc agcgaccttg acaagccaca cgcggtcgc cctagaccgg 540

ctgtctgcga gtctgcaaac ggcagttagc cgaagcga aaaccaatcag gcacagcgct 600

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tctatttcg ggaattccaa gtcaagacgc atgtcaagt accaaggcgt cgacgcgtcg 1080

aactctgtga aagccttcca cttgtaactg gtcaac 1116

<210> 4483

<211> 942

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding ASPA

<400> 4483

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ggtcacaaag acagtgaaga ttccatgac attatttttg acctcacaa caccacctct 360

aacatggggt gcactcttat tcttgaggat tccaggaata acttttaat tcagatgttt 420

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gctatcatcc atcctaattc gcaggatcaa gactggaaac cactgcatcc tggggatccc 780
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<210> 4484
<211> 1833
<212> DNA
<213> Artificial Sequence
<220><223> Nucleic Acid sequence encoding DHFR-TS_cDNA
<400> 4484

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<210> 4489

<211> 609

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence encoding GDNF

<400> 4489

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gactcaaata tgccagagga ttatcctgat cagttcgtat atgtcatgga ttttattcaa	180
gccaccatta aaagactgaa aaggtcacca gataaacaata tggcagtgct tcctagaaga	240
gagcggaatc ggcaggctgc agctgccaac ccagagaatt ccagaggaaa aggtcggaga	300
ggccagaggg gcaaaaaccg gggttgtgtc ttaactgcaa tacatttaaa tgtcactgac	360
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gatgcagctg agacaacgta cgacaaaata ttgaaaaact tatccagaaa tagaaggctg	480
gtgagtgaca aagtagggca ggcattgttc agaccatcg cctttgatga tgacctgtcg	540
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<210> 4490

<211> 12

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of Gly_linker

<400> 4490

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<210> 4491

<211> 428

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of GRA2_3'UTR

<400> 4491

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ttaagcatcg ttttcgaatg cagtcgtgt atcagttgtg cgcggaagga cactgcttca	180

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ccttgtgagt gtgtctggga tgcaagtttt tgggtgtcgt tgatttcgcc agcttatgac 360
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cagtcgac 428

<210> 4492
<211> 451
<212> DNA
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<220><223> Nucleic Acid sequence of DHFR-TS_5'UTR
<400> 4492

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atctgactgc cgtgcgcgaa aatgacgcca tttttgggaa aatcggggaa cttcattctt 180
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<210> 4493
<211> 743
<212> DNA
<213> Artificial Sequence
<220><223> Nucleic Acid sequence of DHFR-TS_3'UTR
<400> 4493

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<210> 4494

<211> 102

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of TALE Monomer templates pNN

<400> 4494

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<210> 4495

<211> 102

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of TALE Monomer templates pHD

<400> 4495

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<210> 4496

<211> 3782

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of pTALE-TF (NI)

<400> 4496

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tcgggattga gagctgcgga tgcaccaccc ccaacatgc gggaggccgt caccgctgcc 240

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cccgcagcgc aagtagattt gagaactttg ggatattcac agcagcagca ggaaaagatc 360

aagcccaaag tgaggctgac agtcgcgcag catcacgaag cgctgggtggg tcatgggttt 420

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aa 3782

<210> 4497

<211> 3782

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of pTALE-TF (NG)

<400> 4497

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<210> 4498
<211> 3782
<212> DNA
<213> Artificial Sequence
<220><223> Nucleic Acid sequence of pTALE-TF (NN)
<400> 4498

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<220><223> Nucleic Acid sequence of TALE NH monomer

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<211> 8

<212> DNA

<213> Artificial Sequence

<220><223> Nucleic Acid sequence of target sequence

<400> 4505

tacgtacg 8

<210> 4506

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<223> Hygromycin

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<223> SV40_pA_Signal

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<222> (6069)..(6917)

<223> Ampicillin (complement strand)

<400> 4506

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Ile Trp Asp Asp Thr Ala Leu Ile Lys Ala Tyr Asp Lys Ala Val Ala

35 40 45

Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly

50 55 60

Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser

65 70 75 80

Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp

85 90 95

Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr

100 105 110

Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr

115 120 125

Gly Tyr Gly Asn Arg Glu Glu Gln Asn Leu Ser Asp Leu Leu Ser Pro

130 135 140

Ile Cys Glu Val Ala Asn Asn Ile Glu Gln Asn Ala Gln Glu Asn Glu

145 150 155 160

Asn Glu Ser Gln Val Ser Thr Asp Glu Ser Glu Asn Ser Arg Ser Pro

165 170 175

Gly Asn Lys Ser Asp Asn Ile Lys Pro Lys Ser Ala Pro Trp Asn Ser

180 185 190

Phe Leu Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly

195 200 205

Lys Pro Gly Leu Lys Phe Asn Gly Pro Pro Pro Pro Pro Pro Pro

210 215 220

Pro Pro His Leu Leu Ser Cys Trp Leu Pro Pro Phe Pro Ser Gly Pro

225 230 235 240

Pro Ile Ile Pro Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp

245 250 255

Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr

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His Thr Gly Tyr Tyr Met Glu Met Leu Ala

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Ser Phe Lys His Ala Leu Lys Asn Gly Asp Ile Cys Glu Thr Ser Gly

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Lys Pro Lys Thr Thr Pro Lys Arg Lys Pro Ala Lys Lys Asn Lys Ser

65 70 75 80

Gln Lys Lys Asn Thr Ala Ala Ser Leu Gln Gln Trp Lys Val Gly Asp

85 90 95

Lys Cys Ser Ala Ile Trp Ser Glu Asp Gly Cys Ile Tyr Pro Ala Thr

100 105 110

Ile Ala Ser Ile Asp Phe Lys Arg Glu Thr Cys Val Val Val Tyr Thr

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Phe Leu Pro Pro Pro Pro Pro Met Pro Gly Pro Arg Leu Gly Pro Gly
195 200 205
Lys Ile Ile Pro Pro Pro Pro Pro Ile Cys Pro Asp Ser Leu Asp Asp
210 215 220
Ala Asp Ala Leu Gly Ser Met Leu Ile Ser Trp Tyr Met Ser Gly Tyr
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His Thr Gly Tyr Tyr Met Gly Phe Arg Gln Asn Gln Lys Glu Gly Arg
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Cys Ser His Ser Leu Asn
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 Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
 195 200 205
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 225 230 235 240
 Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
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 Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
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Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
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Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
405 410 415

Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
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35 40 45

Pro Ala Trp Ser Leu Gln Ala Gly Arg Leu Phe Ser Thr Gln Thr Ala
50 55 60

Glu Asp Lys Glu Glu Pro Leu His Ser Ile Ile Ser Ser Thr Glu Ser
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Val Gln Gly Ser Thr Ser Lys His Glu Phe Gln Ala Glu Thr Lys Lys

85

90

95

Leu Leu Asp Ile Val Ala Arg Ser Leu Tyr Ser Glu Lys Glu Val Phe

100

105

110

Ile Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Glu Lys Leu Arg

115

120

125

His Lys Leu Val Ser Asp Gly Gln Ala Leu Pro Glu Met Glu Ile His

130

135

140

Leu Gln Thr Asn Ala Glu Lys Gly Thr Ile Thr Ile Gln Asp Thr Gly

145

150

155

160

Ile Gly Met Thr Gln Glu Glu Leu Val Ser Asn Leu Gly Thr Ile Ala

165

170

175

Arg Ser Gly Ser Lys Ala Phe Leu Asp Ala Leu Gln Asn Gln Ala Glu

180

185

190

Ala Ser Ser Lys Ile Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala

195

200

205

Phe Met Val Ala Asp Arg Val Glu Val Tyr Ser Arg Ser Ala Ala Pro

210

215

220

Gly Ser Leu Gly Tyr Gln Trp Leu Ser Asp Gly Ser Gly Val Phe Glu

225

230

235

240

Ile Ala Glu Ala Ser Gly Val Arg Thr Gly Thr Lys Ile Ile Ile His

245

250

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Leu Lys Ser Asp Cys Lys Glu Phe Ser Ser Glu Ala Arg Val Arg Asp

260

265

270

Val Val Thr Lys Tyr Ser Asn Phe Val Ser Phe Pro Leu Tyr Leu Asn

275

280

285

Gly Arg Arg Met Asn Thr Leu Gln Ala Ile Trp Met Met Asp Pro Lys

290

295

300

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305

310

315

320

Ala His Asp Lys Pro Arg Tyr Thr Leu His Tyr Lys Thr Asp Ala Pro

325

330

335

Leu Asn Ile Arg Ser Ile Phe Tyr Val Pro Asp Met Lys Pro Ser Met
340 345 350

Phe Asp Val Ser Arg Glu Leu Gly Ser Ser Val Ala Leu Tyr Ser Arg
355 360 365

Lys Val Leu Ile Gln Thr Lys Ala Thr Asp Ile Leu Pro Lys Trp Leu
370 375 380

Arg Phe Ile Arg Gly Val Val Asp Ser Glu Asp Ile Pro Leu Asn Leu
385 390 395 400

Ser Arg Glu Leu Leu Gln Glu Ser Ala Leu Ile Arg Lys Leu Arg Asp
405 410 415

Val Leu Gln Gln Arg Leu Ile Lys Phe Phe Ile Asp Gln Ser Lys Lys
420 425 430

Asp Ala Glu Lys Tyr Ala Lys Phe Phe Glu Asp Tyr Gly Leu Phe Met
435 440 445

Arg Glu Gly Ile Val Thr Ala Thr Glu Gln Glu Val Lys Glu Asp Ile
450 455 460

Ala Lys Leu Leu Arg Tyr Glu Ser Ser Ala Leu Pro Ser Gly Gln Leu
465 470 475 480

Thr Ser Leu Ser Glu Tyr Ala Ser Arg Met Arg Ala Gly Thr Arg Asn
485 490 495

Ile Tyr Tyr Leu Cys Ala Pro Asn Arg His Leu Ala Glu His Ser Pro
500 505 510

Tyr Tyr Glu Ala Met Lys Lys Lys Asp Thr Glu Val Leu Phe Cys Phe
515 520 525

Glu Gln Phe Asp Glu Leu Thr Leu Leu His Leu Arg Glu Phe Asp Lys
530 535 540

Lys Lys Leu Ile Ser Val Glu Thr Asp Ile Val Val Asp His Tyr Lys
545 550 555 560

Glu Glu Lys Phe Glu Asp Arg Ser Pro Ala Ala Glu Cys Leu Ser Glu
565 570 575

Lys Glu Thr Glu Glu Leu Met Ala Trp Met Arg Asn Val Leu Gly Ser

580 585 590
 Arg Val Thr Asn Val Lys Val Thr Leu Arg Leu Asp Thr His Pro Ala
 595 600 605

Met Val Thr Val Leu Glu Met Gly Ala Ala Arg His Phe Leu Arg Met
 610 615 620
 Gln Gln Leu Ala Lys Thr Gln Glu Glu Arg Ala Gln Leu Leu Gln Pro
 625 630 635 640
 Thr Leu Glu Ile Asn Pro Arg His Ala Leu Ile Lys Lys Leu Asn Gln
 645 650 655
 Leu Arg Ala Ser Glu Pro Gly Leu Ala Gln Leu Leu Val Asp Gln Ile
 660 665 670

Tyr Glu Asn Ala Met Ile Ala Ala Gly Leu Val Asp Asp Pro Arg Ala
 675 680 685
 Met Val Gly Arg Leu Asn Glu Leu Leu Val Lys Ala Leu Glu Arg His
 690 695 700

<210> 4514

<211> 115

<212> PRT

<213> homo sapiens

<400> 4514

Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val
 1 5 10 15
 Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro

20 25 30
 Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys
 35 40 45
 Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys
 50 55 60
 Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Ser Trp
 65 70 75 80
 Ala Glu Gly Asn Leu Ala Pro His Pro Arg Ser Pro Ala Leu Gln Pro

	85	90	95
Gln Gln Ser Thr Ala Ala Gly Leu Arg Leu Ser Thr Gly Pro Ala Ala			
	100	105	110
Ala Gln Pro			
	115		
<210> 4515			
<211> 194			
<212> PRT			
<213> homo sapiens			
<400> 4515			
Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val			
1 5 10 15			
Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro			
20 25 30			
Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys			
35 40 45			
Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys			
50 55 60			
Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly			
65 70 75 80			
Thr Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser			
85 90 95			
Ile Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly			
100 105 110			
Arg Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr			
115 120 125			
Gln Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His			
130 135 140			
Ser Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln			
145 150 155 160			
Arg His Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu			
165 170 175			

Pro Pro Thr Gln Glu Ala Leu Pro Ser Ser His Ser Ser Pro Gln Gln
180 185 190

Gln Gly

<210> 4516

<211> 194

<212> PRT

<213> homo sapiens

<400> 4516

Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val

1 5 10 15

Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro

20 25 30

Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys

35 40 45

Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys

50 55 60

Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly

65 70 75 80

Thr Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser

85 90 95

Ile Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly

100 105 110

Arg Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr

115 120 125

Gln Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His

130 135 140

Ser Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln

145 150 155 160

Arg His Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu

165 170 175

Pro Pro Thr Gln Glu Ala Leu Pro Ser Ser His Ser Ser Pro Gln Gln

180 185 190

Gln Gly

<210> 4517

<211> 194

<212> PRT

<213> homo sapiens

<400> 4517

Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val

1 5 10 15

Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro

20 25 30

Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys

35 40 45

Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys

50 55 60

Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly

65 70 75 80

Thr Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser

85 90 95

Ile Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly

100 105 110

Arg Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr

115 120 125

Gln Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His

130 135 140

Ser Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln

145 150 155 160

Arg His Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu

165 170 175

Pro Pro Thr Gln Glu Ala Leu Pro Ser Ser His Ser Ser Pro Gln Gln

180 185 190

Gln Gly

<210> 4518

<211> 194

<212> PRT

<213> homo sapiens

<400> 4518

Met Thr Met Arg His Asn Trp Thr Pro Asp Leu Ser Pro Leu Trp Val

1	5	10	15
Leu Leu Leu Cys Ala His Val Val Thr Leu Leu Val Arg Ala Thr Pro			
20	25	30	
Val Ser Gln Thr Thr Thr Ala Ala Thr Ala Ser Val Arg Ser Thr Lys			
35	40	45	
Asp Pro Cys Pro Ser Gln Pro Pro Val Phe Pro Ala Ala Lys Gln Cys			
50	55	60	
Pro Ala Leu Glu Val Thr Trp Pro Glu Val Glu Val Pro Leu Asn Gly			

65	70	75	80
Thr Leu Ser Leu Ser Cys Val Ala Cys Ser Arg Phe Pro Asn Phe Ser			
85	90	95	
Ile Leu Tyr Trp Leu Gly Asn Gly Ser Phe Ile Glu His Leu Pro Gly			
100	105	110	
Arg Leu Trp Glu Gly Ser Thr Ser Arg Glu Arg Gly Ser Thr Gly Thr			
115	120	125	
Gln Leu Cys Lys Ala Leu Val Leu Glu Gln Leu Thr Pro Ala Leu His			

130	135	140
Ser Thr Asn Phe Ser Cys Val Leu Val Asp Pro Glu Gln Val Val Gln		
145	150	155
Arg His Val Val Leu Ala Gln Leu Trp Ala Gly Leu Arg Ala Thr Leu		
165	170	175
Pro Pro Thr Gln Glu Ala Leu Pro Ser Ser His Ser Ser Pro Gln Gln		
180	185	190
Gln Gly		

<210> 4519

<211> 224

<212> PRT

<213> homo sapiens

<400> 4519

Met Pro Gly Gly Leu Leu Leu Gly Asp Val Ala Pro Asn Phe Glu Ala

1 5 10 15

Asn Thr Thr Val Gly Arg Ile Arg Phe His Asp Phe Leu Gly Asp Ser

20 25 30

Trp Gly Ile Leu Phe Ser His Pro Arg Asp Phe Thr Pro Val Cys Thr

35 40 45

Thr Glu Leu Gly Arg Ala Ala Lys Leu Ala Pro Glu Phe Ala Lys Arg

50 55 60

Asn Val Lys Leu Ile Ala Leu Ser Ile Asp Ser Val Glu Asp His Leu

65 70 75 80

Ala Trp Ser Lys Asp Ile Asn Ala Tyr Asn Cys Glu Glu Pro Thr Glu

85 90 95

Lys Leu Pro Phe Pro Ile Ile Asp Asp Arg Asn Arg Glu Leu Ala Ile

100 105 110

Leu Leu Gly Met Leu Asp Pro Ala Glu Lys Asp Glu Lys Gly Met Pro

115 120 125

Val Thr Ala Arg Val Val Phe Val Phe Gly Pro Asp Lys Lys Leu Lys

130 135 140

Leu Ser Ile Leu Tyr Pro Ala Thr Thr Gly Arg Asn Phe Asp Glu Ile

145 150 155 160

Leu Arg Val Val Ile Ser Leu Gln Leu Thr Ala Glu Lys Arg Val Ala

165 170 175

Thr Pro Val Asp Trp Lys Asp Gly Asp Ser Val Met Val Leu Pro Thr

180 185 190

Ile Pro Glu Glu Glu Ala Lys Lys Leu Phe Pro Lys Gly Val Phe Thr

195 200 205
Lys Glu Leu Pro Ser Gly Lys Lys Tyr Leu Arg Tyr Thr Pro Gln Pro
210 215 220

<210> 4520

<211> 105

<212> PRT

<213> homo sapiens

<400> 4520

Met Val Lys Gln Ile Glu Ser Lys Thr Ala Phe Gln Glu Ala Leu Asp
1 5 10 15

Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys
20 25 30

Gly Pro Cys Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
35 40 45

Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp
50 55 60

Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
65 70 75 80

Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
85 90 95

Leu Glu Ala Thr Ile Asn Glu Leu Val
100 105

<210> 4521

<211> 952

<212> PRT

<213> homo sapiens

<400> 4521

Met Gly Val Arg His Pro Pro Cys Ser His Arg Leu Leu Ala Val Cys
1 5 10 15

Ala Leu Val Ser Leu Ala Thr Ala Ala Leu Leu Gly His Ile Leu Leu
20 25 30

His Asp Phe Leu Leu Val Pro Arg Glu Leu Ser Gly Ser Ser Pro Val

35	40	45	
Leu Glu Glu Thr His Pro Ala His Gln Gln Gly Ala Ser Arg Pro Gly			
50	55	60	
Pro Arg Asp Ala Gln Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr			
65	70	75	80
Gln Cys Asp Val Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys			
85	90	95	
Ala Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro			
100	105	110	
Ala Lys Gln Gly Leu Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe			
115	120	125	
Phe Pro Pro Ser Tyr Pro Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser			
130	135	140	
Glu Met Gly Tyr Thr Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe			
145	150	155	160
Pro Lys Asp Ile Leu Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu			
165	170	175	
Asn Arg Leu His Phe Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu			
180	185	190	
Val Pro Leu Glu Thr Pro His Val His Ser Arg Ala Pro Ser Pro Leu			
195	200	205	
Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val Ile Val Arg Arg			
210	215	220	
Gln Leu Asp Gly Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe			
225	230	235	240
Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr			
245	250	255	
Ile Thr Gly Leu Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser			
260	265	270	
Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly			
275	280	285	

Ala Asn Leu Tyr Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly
290 295 300

Gly Ser Ala His Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val
305 310 315 320

Val Leu Gln Pro Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile
325 330 335

Leu Asp Val Tyr Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln
340 345 350

Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly
355 360 365

Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr
370 375 380

Arg Gln Val Val Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val
385 390 395 400

Gln Trp Asn Asp Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe
405 410 415

Asn Lys Asp Gly Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His
420 425 430

Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser
435 440 445

Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg
450 455 460

Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val
465 470 475 480

Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu
485 490 495

Ala Trp Trp Glu Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe
500 505 510

Asp Gly Met Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly
515 520 525

Ser Glu Asp Gly Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val

530 535 540
 Pro Gly Val Val Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser
 545 550 555 560
 Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly
 565 570 575
 Leu Thr Glu Ala Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly
 580 585 590
 Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg
 595 600 605

 Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu
 610 615 620
 Ala Ser Ser Val Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro
 625 630 635 640
 Leu Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu
 645 650 655
 Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg
 660 665 670

 Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser
 675 680 685
 Glu Pro Ala Gln Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala
 690 695 700
 Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly
 705 710 715 720
 Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser
 725 730 735

 Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile
 740 745 750
 Thr Pro Val Leu Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro
 755 760 765
 Leu Gly Thr Trp Tyr Asp Leu Gln Thr Val Pro Val Glu Ala Leu Gly
 770 775 780

Ser Leu Pro Pro Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser
785 790 795 800

Glu Gly Gln Trp Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val
805 810 815

His Leu Arg Ala Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr
820 825 830

Thr Thr Glu Ser Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr
835 840 845

Lys Gly Gly Glu Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser
850 855 860

Leu Glu Val Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala
865 870 875 880

Arg Asn Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly
885 890 895

Ala Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala
900 905 910

Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr
915 920 925

Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly
930 935 940

Glu Gln Phe Leu Val Ser Trp Cys
945 950

<210> 4522

<211> 952

<212> PRT

<213> homo sapiens

<400> 4522

Met Gly Val Arg His Pro Pro Cys Ser His Arg Leu Leu Ala Val Cys
1 5 10 15

Ala Leu Val Ser Leu Ala Thr Ala Ala Leu Leu Gly His Ile Leu Leu
20 25 30

His Asp Phe Leu Leu Val Pro Arg Glu Leu Ser Gly Ser Ser Pro Val
 35 40 45
 Leu Glu Glu Thr His Pro Ala His Gln Gln Gly Ala Ser Arg Pro Gly
 50 55 60
 Pro Arg Asp Ala Gln Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr
 65 70 75 80
 Gln Cys Asp Val Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys
 85 90 95

 Ala Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro
 100 105 110
 Ala Lys Gln Gly Leu Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe
 115 120 125
 Phe Pro Pro Ser Tyr Pro Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser
 130 135 140
 Glu Met Gly Tyr Thr Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe
 145 150 155 160

 Pro Lys Asp Ile Leu Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu
 165 170 175
 Asn Arg Leu His Phe Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu
 180 185 190
 Val Pro Leu Glu Thr Pro His Val His Ser Arg Ala Pro Ser Pro Leu
 195 200 205
 Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val Ile Val Arg Arg
 210 215 220

 Gln Leu Asp Gly Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe
 225 230 235 240
 Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr
 245 250 255
 Ile Thr Gly Leu Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser
 260 265 270
 Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly

275 280 285
 Ala Asn Leu Tyr Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly
 290 295 300
 Gly Ser Ala His Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val
 305 310 315 320
 Val Leu Gln Pro Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile
 325 330 335
 Leu Asp Val Tyr Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln
 340 345 350

 Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly
 355 360 365
 Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr
 370 375 380
 Arg Gln Val Val Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val
 385 390 395 400
 Gln Trp Asn Asp Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe
 405 410 415

 Asn Lys Asp Gly Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His
 420 425 430
 Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser
 435 440 445
 Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg
 450 455 460
 Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val
 465 470 475 480

 Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu
 485 490 495
 Ala Trp Trp Glu Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe
 500 505 510
 Asp Gly Met Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly
 515 520 525

Ser Glu Asp Gly Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val
530 535 540

Pro Gly Val Val Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser
545 550 555 560

Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly
565 570 575

Leu Thr Glu Ala Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly
580 585 590

Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg
595 600 605

Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu
610 615 620

Ala Ser Ser Val Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro
625 630 635 640

Leu Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu
645 650 655

Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg
660 665 670

Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser
675 680 685

Glu Pro Ala Gln Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala
690 695 700

Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly
705 710 715 720

Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser
725 730 735

Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile
740 745 750

Thr Pro Val Leu Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro
755 760 765

Leu Gly Thr Trp Tyr Asp Leu Gln Thr Val Pro Val Glu Ala Leu Gly

770 775 780
 Ser Leu Pro Pro Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser
 785 790 795 800

Glu Gly Gln Trp Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val
 805 810 815
 His Leu Arg Ala Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr
 820 825 830
 Thr Thr Glu Ser Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr
 835 840 845
 Lys Gly Gly Glu Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser
 850 855 860

Leu Glu Val Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala
 865 870 875 880
 Arg Asn Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly
 885 890 895
 Ala Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala
 900 905 910
 Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr
 915 920 925

Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly
 930 935 940

Glu Gln Phe Leu Val Ser Trp Cys
 945 950

<210> 4523

<211> 952

<212> PRT

<213> homo sapiens

<400> 4523

Met Gly Val Arg His Pro Pro Cys Ser His Arg Leu Leu Ala Val Cys
 1 5 10 15

Ala Leu Val Ser Leu Ala Thr Ala Ala Leu Leu Gly His Ile Leu Leu

20	25	30	
His Asp Phe Leu Leu Val Pro Arg Glu Leu Ser Gly Ser Ser Pro Val			
35	40	45	
Leu Glu Glu Thr His Pro Ala His Gln Gln Gly Ala Ser Arg Pro Gly			
50	55	60	
Pro Arg Asp Ala Gln Ala His Pro Gly Arg Pro Arg Ala Val Pro Thr			
65	70	75	80
Gln Cys Asp Val Pro Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys			
85	90	95	
Ala Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys Cys Tyr Ile Pro			
100	105	110	
Ala Lys Gln Gly Leu Gln Gly Ala Gln Met Gly Gln Pro Trp Cys Phe			
115	120	125	
Phe Pro Pro Ser Tyr Pro Ser Tyr Lys Leu Glu Asn Leu Ser Ser Ser			
130	135	140	
Glu Met Gly Tyr Thr Ala Thr Leu Thr Arg Thr Thr Pro Thr Phe Phe			
145	150	155	160
Pro Lys Asp Ile Leu Thr Leu Arg Leu Asp Val Met Met Glu Thr Glu			
165	170	175	
Asn Arg Leu His Phe Thr Ile Lys Asp Pro Ala Asn Arg Arg Tyr Glu			
180	185	190	
Val Pro Leu Glu Thr Pro His Val His Ser Arg Ala Pro Ser Pro Leu			
195	200	205	
Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val Ile Val Arg Arg			
210	215	220	
Gln Leu Asp Gly Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe			
225	230	235	240
Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln Tyr			
245	250	255	
Ile Thr Gly Leu Ala Glu His Leu Ser Pro Leu Met Leu Ser Thr Ser			
260	265	270	

Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Leu Ala Pro Thr Pro Gly
275 280 285

Ala Asn Leu Tyr Gly Ser His Pro Phe Tyr Leu Ala Leu Glu Asp Gly
290 295 300

Gly Ser Ala His Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val
305 310 315 320

Val Leu Gln Pro Ser Pro Ala Leu Ser Trp Arg Ser Thr Gly Gly Ile
325 330 335

Leu Asp Val Tyr Ile Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln
340 345 350

Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly
355 360 365

Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Thr
370 375 380

Arg Gln Val Val Glu Asn Met Thr Arg Ala His Phe Pro Leu Asp Val
385 390 395 400

Gln Trp Asn Asp Leu Asp Tyr Met Asp Ser Arg Arg Asp Phe Thr Phe
405 410 415

Asn Lys Asp Gly Phe Arg Asp Phe Pro Ala Met Val Gln Glu Leu His
420 425 430

Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser
435 440 445

Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg
450 455 460

Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val
465 470 475 480

Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn Pro Thr Ala Leu
485 490 495

Ala Trp Trp Glu Asp Met Val Ala Glu Phe His Asp Gln Val Pro Phe
500 505 510

Asp Gly Met Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly

515	520	525	
Ser Glu Asp Gly Cys Pro Asn Asn Glu Leu Glu Asn Pro Pro Tyr Val			
530	535	540	
Pro Gly Val Val Gly Gly Thr Leu Gln Ala Ala Thr Ile Cys Ala Ser			
545	550	555	560
Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly			
565	570	575	
Leu Thr Glu Ala Ile Ala Ser His Arg Ala Leu Val Lys Ala Arg Gly			
580	585	590	
Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg			
595	600	605	
Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser Trp Glu Gln Leu			
610	615	620	
Ala Ser Ser Val Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro			
625	630	635	640
Leu Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asn Thr Ser Glu Glu			
645	650	655	
Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg			
660	665	670	
Asn His Asn Ser Leu Leu Ser Leu Pro Gln Glu Pro Tyr Ser Phe Ser			
675	680	685	
Glu Pro Ala Gln Gln Ala Met Arg Lys Ala Leu Thr Leu Arg Tyr Ala			
690	695	700	
Leu Leu Pro His Leu Tyr Thr Leu Phe His Gln Ala His Val Ala Gly			
705	710	715	720
Glu Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro Lys Asp Ser Ser			
725	730	735	
Thr Trp Thr Val Asp His Gln Leu Leu Trp Gly Glu Ala Leu Leu Ile			
740	745	750	
Thr Pro Val Leu Gln Ala Gly Lys Ala Glu Val Thr Gly Tyr Phe Pro			
755	760	765	

Leu Gly Thr Trp Tyr Asp Leu Gln Thr Val Pro Val Glu Ala Leu Gly
770 775 780

Ser Leu Pro Pro Pro Pro Ala Ala Pro Arg Glu Pro Ala Ile His Ser
785 790 795 800

Glu Gly Gln Trp Val Thr Leu Pro Ala Pro Leu Asp Thr Ile Asn Val
805 810 815

His Leu Arg Ala Gly Tyr Ile Ile Pro Leu Gln Gly Pro Gly Leu Thr
820 825 830

Thr Thr Glu Ser Arg Gln Gln Pro Met Ala Leu Ala Val Ala Leu Thr
835 840 845

Lys Gly Gly Glu Ala Arg Gly Glu Leu Phe Trp Asp Asp Gly Glu Ser
850 855 860

Leu Glu Val Leu Glu Arg Gly Ala Tyr Thr Gln Val Ile Phe Leu Ala
865 870 875 880

Arg Asn Asn Thr Ile Val Asn Glu Leu Val Arg Val Thr Ser Glu Gly
885 890 895

Ala Gly Leu Gln Leu Gln Lys Val Thr Val Leu Gly Val Ala Thr Ala
900 905 910

Pro Gln Gln Val Leu Ser Asn Gly Val Pro Val Ser Asn Phe Thr Tyr
915 920 925

Ser Pro Asp Thr Lys Val Leu Asp Ile Cys Val Ser Leu Leu Met Gly
930 935 940

Glu Gln Phe Leu Val Ser Trp Cys
945 950

<210> 4524

<211> 105

<212> PRT

<213> homo sapiens

<400> 4524

Met Phe Thr Cys Trp Trp Ser Tyr Leu Arg Ser Thr Leu Ala Ala Val
1 5 10 15

Pro Gly Glu Ala Ser Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro

20 25 30

Pro Ala Lys Leu Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu

35 40 45

Asp Gly Gly Gln Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe

50 55 60

Asn Ala Pro Phe Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln

65 70 75 80

Gln His Ser Gln Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu

85 90 95

Glu Ala Lys Glu Ala Pro Ala Asp Lys

100 105

<210> 4525

<211> 104

<212> PRT

<213> homo sapiens

<400> 4525

Met Phe Thr Cys Trp Trp Ser Tyr Leu Arg Ser Thr Leu Ala Ala Val

1 5 10 15

Pro Gly Glu Ala Ser Arg Val Gln Arg Lys Glu Ser Lys Lys Pro Pro

20 25 30

Ala Lys Leu Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp

35 40 45

Gly Gly Gln Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn

50 55 60

Ala Pro Phe Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln

65 70 75 80

His Ser Gln Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu

85 90 95

Ala Lys Glu Ala Pro Ala Asp Lys

100

<210> 4526

<211> 116

<212> PRT

<213>

homo sapiens

<400> 4526

Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Gly Met Leu

1 5 10 15

Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His

20 25 30

Gln Arg Val Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu Gln

35 40 45

Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln Ala

50 55 60

Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe Asp

65 70 75 80

Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln Ala

85 90 95

Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu Ala

100 105 110

Pro Ala Asp Lys

115

<210> 4527

<211> 117

<212> PRT

<213> homo sapiens

<400> 4527

Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Gly Met Leu

1 5 10 15

Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His

20 25 30

Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro Ala Lys Leu

35 40 45

Gln Pro Arg Ala Leu Ala Gly Trp Leu Arg Pro Glu Asp Gly Gly Gln

50 55 60

Ala Glu Gly Ala Glu Asp Glu Leu Glu Val Arg Phe Asn Ala Pro Phe

65 70 75 80
Asp Val Gly Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln

85 90 95
Ala Leu Gly Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu
100 105 110

Ala Pro Ala Asp Lys
115

<210> 4528

<211> 66

<212> PRT

<213> homo sapiens

<400> 4528

Met Phe Thr Cys Trp Trp Ser Tyr Leu Arg Ser Thr Leu Ala Ala Val

1 5 10 15
Pro Gly Glu Ala Ser Arg Val Gln Phe Asn Ala Pro Phe Asp Val Gly

20 25 30
Ile Lys Leu Ser Gly Val Gln Tyr Gln Gln His Ser Gln Ala Leu Gly
35 40 45

Lys Phe Leu Gln Asp Ile Leu Trp Glu Glu Ala Lys Glu Ala Pro Ala
50 55 60

Asp Lys

65

<210> 4529

<211> 204

<212> PRT

<213> homo sapiens

<400> 4529

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln

1 5 10 15
Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro
20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu

35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys

50 55 60

Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu

65 70 75 80

Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser

85 90 95

Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu

100 105 110

Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu

115 120 125

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala

130 135 140

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu

145 150 155 160

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg

165 170 175

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu

180 185 190

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro

195 200

<210> 4530

<211> 171

<212> PRT

<213> homo sapiens

<400> 4530

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln

1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro

20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu

35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys

50 55 60

Leu Val Ser Glu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe

65 70 75 80

Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu

85 90 95

Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr

100 105 110

Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln

115 120 125

Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg

130 135 140

Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val

145 150 155 160

Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro

165 170

<210> 4531

<211> 207

<212> PRT

<213> homo sapiens

<400> 4531

Met Ala Gly Pro Ala Thr Gln Ser Pro Met Lys Leu Met Ala Leu Gln

1 5 10 15

Leu Leu Leu Trp His Ser Ala Leu Trp Thr Val Gln Glu Ala Thr Pro

20 25 30

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu

35 40 45

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys

50 55 60

Leu Val Ser Glu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
 65 70 75 80
 Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
 85 90 95
 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 100 105 110
 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile

 115 120 125
 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
 130 135 140
 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
 145 150 155 160
 Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
 165 170 175
 Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser

 180 185 190
 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 195 200 205
 <210> 4532
 <211> 875
 <212> PRT
 <213> homo sapiens
 <400> 4532
 Met Glu Lys Leu His Gln Cys Tyr Trp Lys Ser Gly Glu Pro Gln Ser
 1 5 10 15
 Asp Asp Ile Glu Ala Ser Arg Met Lys Arg Ala Ala Ala Lys His Leu
 20 25 30

 Ile Glu Arg Tyr Tyr His Gln Leu Thr Glu Gly Cys Gly Asn Glu Ala
 35 40 45
 Cys Thr Asn Glu Phe Cys Ala Ser Cys Pro Thr Phe Leu Arg Met Asp
 50 55 60
 Asn Asn Ala Ala Ala Ile Lys Ala Leu Glu Leu Tyr Lys Ile Asn Ala

65	70	75	80
Lys Leu Cys Asp Pro His Pro Ser Lys Lys Gly Ala Ser Ser Ala Tyr			
	85	90	95
Leu Glu Asn Ser Lys Gly Ala Pro Asn Asn Ser Cys Ser Glu Ile Lys			
	100	105	110
Met Asn Lys Lys Gly Ala Arg Ile Asp Phe Lys Asp Val Thr Tyr Leu			
	115	120	125
Thr Glu Glu Lys Val Tyr Glu Ile Leu Glu Leu Cys Arg Glu Arg Glu			
	130	135	140
Asp Tyr Ser Pro Leu Ile Arg Val Ile Gly Arg Val Phe Ser Ser Ala			
145	150	155	160
Glu Ala Leu Val Gln Ser Phe Arg Lys Val Lys Gln His Thr Lys Glu			
	165	170	175
Glu Leu Lys Ser Leu Gln Ala Lys Asp Glu Asp Lys Asp Glu Asp Glu			
	180	185	190
Lys Glu Lys Ala Ala Cys Ser Ala Ala Ala Met Glu Glu Asp Ser Glu			
	195	200	205
Ala Ser Ser Ser Arg Ile Gly Asp Ser Ser Gln Gly Asp Asn Asn Leu			
	210	215	220
Gln Lys Leu Gly Pro Asp Asp Val Ser Val Asp Ile Asp Ala Ile Arg			
225	230	235	240
Arg Val Tyr Thr Arg Leu Leu Ser Asn Glu Lys Ile Glu Thr Ala Phe			
	245	250	255
Leu Asn Ala Leu Val Tyr Leu Ser Pro Asn Val Glu Cys Asp Leu Thr			
	260	265	270
Tyr His Asn Val Tyr Ser Arg Asp Pro Asn Tyr Leu Asn Leu Phe Ile			
	275	280	285
Ile Val Met Glu Asn Arg Asn Leu His Ser Pro Glu Tyr Leu Glu Met			
	290	295	300
Ala Leu Pro Leu Phe Cys Lys Ala Met Ser Lys Leu Pro Leu Ala Ala			
305	310	315	320

Gln Gly Lys Leu Ile Arg Leu Trp Ser Lys Tyr Asn Ala Asp Gln Ile
325 330 335

Arg Arg Met Met Glu Thr Phe Gln Gln Leu Ile Thr Tyr Lys Val Ile
340 345 350

Ser Asn Glu Phe Asn Ser Arg Asn Leu Val Asn Asp Asp Asp Ala Ile
355 360 365

Val Ala Ala Ser Lys Cys Leu Lys Met Val Tyr Tyr Ala Asn Val Val
370 375 380

Gly Gly Glu Val Asp Thr Asn His Asn Glu Glu Asp Asp Glu Glu Pro
385 390 395 400

Ile Pro Glu Ser Ser Glu Leu Thr Leu Gln Glu Leu Leu Gly Glu Glu
405 410 415

Arg Arg Asn Lys Lys Gly Pro Arg Val Asp Pro Leu Glu Thr Glu Leu
420 425 430

Gly Val Lys Thr Leu Asp Cys Arg Lys Pro Leu Ile Pro Phe Glu Glu
435 440 445

Phe Ile Asn Glu Pro Leu Asn Glu Val Leu Glu Met Asp Lys Asp Tyr
450 455 460

Thr Phe Phe Lys Val Glu Thr Glu Asn Lys Phe Ser Phe Met Thr Cys
465 470 475 480

Pro Phe Ile Leu Asn Ala Val Thr Lys Asn Leu Gly Leu Tyr Tyr Asp
485 490 495

Asn Arg Ile Arg Met Tyr Ser Glu Arg Arg Ile Thr Val Leu Tyr Ser
500 505 510

Leu Val Gln Gly Gln Gln Leu Asn Pro Tyr Leu Arg Leu Lys Val Arg
515 520 525

Arg Asp His Ile Ile Asp Asp Ala Leu Val Arg Leu Glu Met Ile Ala
530 535 540

Met Glu Asn Pro Ala Asp Leu Lys Lys Gln Leu Tyr Val Glu Phe Glu
545 550 555 560

Gly Glu Gln Gly Val Asp Glu Gly Gly Val Ser Lys Glu Phe Phe Gln

565 570 575
 Leu Val Val Glu Glu Ile Phe Asn Pro Asp Ile Gly Met Phe Thr Tyr
 580 585 590
 Asp Glu Ser Thr Lys Leu Phe Trp Phe Asn Pro Ser Ser Phe Glu Thr
 595 600 605

 Glu Gly Gln Phe Thr Leu Ile Gly Ile Val Leu Gly Leu Ala Ile Tyr
 610 615 620
 Asn Asn Cys Ile Leu Asp Val His Phe Pro Met Val Val Tyr Arg Lys
 625 630 635 640
 Leu Met Gly Lys Lys Gly Thr Phe Arg Asp Leu Gly Asp Ser His Pro
 645 650 655
 Val Leu Tyr Gln Ser Leu Lys Asp Leu Leu Glu Tyr Glu Gly Asn Val
 660 665 670

 Glu Asp Asp Met Met Ile Thr Phe Gln Ile Ser Gln Thr Asp Leu Phe
 675 680 685
 Gly Asn Pro Met Met Tyr Asp Leu Lys Glu Asn Gly Asp Lys Ile Pro
 690 695 700
 Ile Thr Asn Glu Asn Arg Lys Glu Phe Val Asn Leu Tyr Ser Asp Tyr
 705 710 715 720
 Ile Leu Asn Lys Ser Val Glu Lys Gln Phe Lys Ala Phe Arg Arg Gly
 725 730 735

 Phe His Met Val Thr Asn Glu Ser Pro Leu Lys Tyr Leu Phe Arg Pro
 740 745 750
 Glu Glu Ile Glu Leu Leu Ile Cys Gly Ser Arg Asn Leu Asp Phe Gln
 755 760 765
 Ala Leu Glu Glu Thr Thr Glu Tyr Asp Gly Gly Tyr Thr Arg Asp Ser
 770 775 780
 Val Leu Ile Arg Glu Phe Trp Glu Ile Val His Ser Phe Thr Asp Glu
 785 790 795 800

 Gln Lys Arg Leu Phe Leu Gln Phe Thr Thr Gly Thr Asp Arg Ala Pro
 805 810 815

Val Gly Gly Leu Gly Lys Leu Lys Met Ile Ile Ala Lys Asn Gly Pro
820 825 830

Asp Thr Glu Arg Leu Pro Thr Ser His Thr Cys Phe Asn Val Leu Leu
835 840 845

Leu Pro Glu Tyr Ser Ser Lys Glu Lys Leu Lys Glu Arg Leu Leu Lys
850 855 860

Ala Ile Thr Tyr Ala Lys Gly Phe Gly Met Leu
865 870 875

<210> 4533

<211> 872

<212> PRT

<213> homo sapiens

<400> 4533

Met Ala Thr Ala Cys Lys Arg Ser Gly Glu Pro Gln Ser Asp Asp Ile
1 5 10 15

Glu Ala Ser Arg Met Lys Arg Ala Ala Ala Lys His Leu Ile Glu Arg
20 25 30

Tyr Tyr His Gln Leu Thr Glu Gly Cys Gly Asn Glu Ala Cys Thr Asn
35 40 45

Glu Phe Cys Ala Ser Cys Pro Thr Phe Leu Arg Met Asp Asn Asn Ala
50 55 60

Ala Ala Ile Lys Ala Leu Glu Leu Tyr Lys Ile Asn Ala Lys Leu Cys
65 70 75 80

Asp Pro His Pro Ser Lys Lys Gly Ala Ser Ser Ala Tyr Leu Glu Asn
85 90 95

Ser Lys Gly Ala Pro Asn Asn Ser Cys Ser Glu Ile Lys Met Asn Lys
100 105 110

Lys Gly Ala Arg Ile Asp Phe Lys Asp Val Thr Tyr Leu Thr Glu Glu
115 120 125

Lys Val Tyr Glu Ile Leu Glu Leu Cys Arg Glu Arg Glu Asp Tyr Ser
130 135 140

Pro Leu Ile Arg Val Ile Gly Arg Val Phe Ser Ser Ala Glu Ala Leu

145 150 155 160
 Val Gln Ser Phe Arg Lys Val Lys Gln His Thr Lys Glu Glu Leu Lys
 165 170 175

 Ser Leu Gln Ala Lys Asp Glu Asp Lys Asp Glu Asp Glu Lys Glu Lys
 180 185 190
 Ala Ala Cys Ser Ala Ala Ala Met Glu Glu Asp Ser Glu Ala Ser Ser
 195 200 205
 Ser Arg Ile Gly Asp Ser Ser Gln Gly Asp Asn Asn Leu Gln Lys Leu
 210 215 220
 Gly Pro Asp Asp Val Ser Val Asp Ile Asp Ala Ile Arg Arg Val Tyr
 225 230 235 240

 Thr Arg Leu Leu Ser Asn Glu Lys Ile Glu Thr Ala Phe Leu Asn Ala
 245 250 255
 Leu Val Tyr Leu Ser Pro Asn Val Glu Cys Asp Leu Thr Tyr His Asn
 260 265 270
 Val Tyr Ser Arg Asp Pro Asn Tyr Leu Asn Leu Phe Ile Ile Val Met
 275 280 285
 Glu Asn Arg Asn Leu His Ser Pro Glu Tyr Leu Glu Met Ala Leu Pro
 290 295 300

 Leu Phe Cys Lys Ala Met Ser Lys Leu Pro Leu Ala Ala Gln Gly Lys
 305 310 315 320
 Leu Ile Arg Leu Trp Ser Lys Tyr Asn Ala Asp Gln Ile Arg Arg Met
 325 330 335
 Met Glu Thr Phe Gln Gln Leu Ile Thr Tyr Lys Val Ile Ser Asn Glu
 340 345 350
 Phe Asn Ser Arg Asn Leu Val Asn Asp Asp Asp Ala Ile Val Ala Ala
 355 360 365

 Ser Lys Cys Leu Lys Met Val Tyr Tyr Ala Asn Val Val Gly Gly Glu
 370 375 380
 Val Asp Thr Asn His Asn Glu Glu Asp Asp Glu Glu Pro Ile Pro Glu
 385 390 395 400

Ser Ser Glu Leu Thr Leu Gln Glu Leu Leu Gly Glu Glu Arg Arg Asn
405 410 415

Lys Lys Gly Pro Arg Val Asp Pro Leu Glu Thr Glu Leu Gly Val Lys
420 425 430

Thr Leu Asp Cys Arg Lys Pro Leu Ile Pro Phe Glu Glu Phe Ile Asn
435 440 445

Glu Pro Leu Asn Glu Val Leu Glu Met Asp Lys Asp Tyr Thr Phe Phe
450 455 460

Lys Val Glu Thr Glu Asn Lys Phe Ser Phe Met Thr Cys Pro Phe Ile
465 470 475 480

Leu Asn Ala Val Thr Lys Asn Leu Gly Leu Tyr Tyr Asp Asn Arg Ile
485 490 495

Arg Met Tyr Ser Glu Arg Arg Ile Thr Val Leu Tyr Ser Leu Val Gln
500 505 510

Gly Gln Gln Leu Asn Pro Tyr Leu Arg Leu Lys Val Arg Arg Asp His
515 520 525

Ile Ile Asp Asp Ala Leu Val Arg Leu Glu Met Ile Ala Met Glu Asn
530 535 540

Pro Ala Asp Leu Lys Lys Gln Leu Tyr Val Glu Phe Glu Gly Glu Gln
545 550 555 560

Gly Val Asp Glu Gly Gly Val Ser Lys Glu Phe Phe Gln Leu Val Val
565 570 575

Glu Glu Ile Phe Asn Pro Asp Ile Gly Met Phe Thr Tyr Asp Glu Ser
580 585 590

Thr Lys Leu Phe Trp Phe Asn Pro Ser Ser Phe Glu Thr Glu Gly Gln
595 600 605

Phe Thr Leu Ile Gly Ile Val Leu Gly Leu Ala Ile Tyr Asn Asn Cys
610 615 620

Ile Leu Asp Val His Phe Pro Met Val Val Tyr Arg Lys Leu Met Gly
625 630 635 640

Lys Lys Gly Thr Phe Arg Asp Leu Gly Asp Ser His Pro Val Leu Tyr

645	650	655	
Gln Ser Leu Lys Asp Leu Leu Glu Tyr Glu Gly Asn Val Glu Asp Asp			
660	665	670	
Met Met Ile Thr Phe Gln Ile Ser Gln Thr Asp Leu Phe Gly Asn Pro			
675	680	685	
Met Met Tyr Asp Leu Lys Glu Asn Gly Asp Lys Ile Pro Ile Thr Asn			
690	695	700	
Glu Asn Arg Lys Glu Phe Val Asn Leu Tyr Ser Asp Tyr Ile Leu Asn			
705	710	715	720
Lys Ser Val Glu Lys Gln Phe Lys Ala Phe Arg Arg Gly Phe His Met			
725	730	735	
Val Thr Asn Glu Ser Pro Leu Lys Tyr Leu Phe Arg Pro Glu Glu Ile			
740	745	750	
Glu Leu Leu Ile Cys Gly Ser Arg Asn Leu Asp Phe Gln Ala Leu Glu			
755	760	765	
Glu Thr Thr Glu Tyr Asp Gly Gly Tyr Thr Arg Asp Ser Val Leu Ile			
770	775	780	
Arg Glu Phe Trp Glu Ile Val His Ser Phe Thr Asp Glu Gln Lys Arg			
785	790	795	800
Leu Phe Leu Gln Phe Thr Thr Gly Thr Asp Arg Ala Pro Val Gly Gly			
805	810	815	
Leu Gly Lys Leu Lys Met Ile Ile Ala Lys Asn Gly Pro Asp Thr Glu			
820	825	830	
Arg Leu Pro Thr Ser His Thr Cys Phe Asn Val Leu Leu Leu Pro Glu			
835	840	845	
Tyr Ser Ser Lys Glu Lys Leu Lys Glu Arg Leu Leu Lys Ala Ile Thr			
850	855	860	
Tyr Ala Lys Gly Phe Gly Met Leu			
865	870		
<210>	4534		
<211>	852		
<212>	PRT		

<213>

homo sapiens

<400> 4534

Met Lys Arg Ala Ala Ala Lys His Leu Ile Glu Arg Tyr Tyr His Gln

1 5 10 15

Leu Thr Glu Gly Cys Gly Asn Glu Ala Cys Thr Asn Glu Phe Cys Ala

20 25 30

Ser Cys Pro Thr Phe Leu Arg Met Asp Asn Asn Ala Ala Ala Ile Lys

35 40 45

Ala Leu Glu Leu Tyr Lys Ile Asn Ala Lys Leu Cys Asp Pro His Pro

50 55 60

Ser Lys Lys Gly Ala Ser Ser Ala Tyr Leu Glu Asn Ser Lys Gly Ala

65 70 75 80

Pro Asn Asn Ser Cys Ser Glu Ile Lys Met Asn Lys Lys Gly Ala Arg

85 90 95

Ile Asp Phe Lys Asp Val Thr Tyr Leu Thr Glu Glu Lys Val Tyr Glu

100 105 110

Ile Leu Glu Leu Cys Arg Glu Arg Glu Asp Tyr Ser Pro Leu Ile Arg

115 120 125

Val Ile Gly Arg Val Phe Ser Ser Ala Glu Ala Leu Val Gln Ser Phe

130 135 140

Arg Lys Val Lys Gln His Thr Lys Glu Glu Leu Lys Ser Leu Gln Ala

145 150 155 160

Lys Asp Glu Asp Lys Asp Glu Asp Glu Lys Glu Lys Ala Ala Cys Ser

165 170 175

Ala Ala Ala Met Glu Glu Asp Ser Glu Ala Ser Ser Ser Arg Ile Gly

180 185 190

Asp Ser Ser Gln Gly Asp Asn Asn Leu Gln Lys Leu Gly Pro Asp Asp

195 200 205

Val Ser Val Asp Ile Asp Ala Ile Arg Arg Val Tyr Thr Arg Leu Leu

210 215 220

Ser Asn Glu Lys Ile Glu Thr Ala Phe Leu Asn Ala Leu Val Tyr Leu

225 230 235 240
 Ser Pro Asn Val Glu Cys Asp Leu Thr Tyr His Asn Val Tyr Ser Arg
 245 250 255

 Asp Pro Asn Tyr Leu Asn Leu Phe Ile Ile Val Met Glu Asn Arg Asn
 260 265 270
 Leu His Ser Pro Glu Tyr Leu Glu Met Ala Leu Pro Leu Phe Cys Lys
 275 280 285
 Ala Met Ser Lys Leu Pro Leu Ala Ala Gln Gly Lys Leu Ile Arg Leu
 290 295 300
 Trp Ser Lys Tyr Asn Ala Asp Gln Ile Arg Arg Met Met Glu Thr Phe
 305 310 315 320

 Gln Gln Leu Ile Thr Tyr Lys Val Ile Ser Asn Glu Phe Asn Ser Arg
 325 330 335
 Asn Leu Val Asn Asp Asp Asp Ala Ile Val Ala Ala Ser Lys Cys Leu
 340 345 350
 Lys Met Val Tyr Tyr Ala Asn Val Val Gly Gly Glu Val Asp Thr Asn
 355 360 365
 His Asn Glu Glu Asp Asp Glu Glu Pro Ile Pro Glu Ser Ser Glu Leu
 370 375 380

 Thr Leu Gln Glu Leu Leu Gly Glu Glu Arg Arg Asn Lys Lys Gly Pro
 385 390 395 400
 Arg Val Asp Pro Leu Glu Thr Glu Leu Gly Val Lys Thr Leu Asp Cys
 405 410 415
 Arg Lys Pro Leu Ile Pro Phe Glu Glu Phe Ile Asn Glu Pro Leu Asn
 420 425 430
 Glu Val Leu Glu Met Asp Lys Asp Tyr Thr Phe Phe Lys Val Glu Thr
 435 440 445

 Glu Asn Lys Phe Ser Phe Met Thr Cys Pro Phe Ile Leu Asn Ala Val
 450 455 460
 Thr Lys Asn Leu Gly Leu Tyr Tyr Asp Asn Arg Ile Arg Met Tyr Ser
 465 470 475 480

Glu Arg Arg Ile Thr Val Leu Tyr Ser Leu Val Gln Gly Gln Gln Leu
 485 490 495
 Asn Pro Tyr Leu Arg Leu Lys Val Arg Arg Asp His Ile Ile Asp Asp
 500 505 510

 Ala Leu Val Arg Leu Glu Met Ile Ala Met Glu Asn Pro Ala Asp Leu
 515 520 525
 Lys Lys Gln Leu Tyr Val Glu Phe Glu Gly Glu Gln Gly Val Asp Glu
 530 535 540
 Gly Gly Val Ser Lys Glu Phe Phe Gln Leu Val Val Glu Glu Ile Phe
 545 550 555 560
 Asn Pro Asp Ile Gly Met Phe Thr Tyr Asp Glu Ser Thr Lys Leu Phe
 565 570 575

 Trp Phe Asn Pro Ser Ser Phe Glu Thr Glu Gly Gln Phe Thr Leu Ile
 580 585 590
 Gly Ile Val Leu Gly Leu Ala Ile Tyr Asn Asn Cys Ile Leu Asp Val
 595 600 605
 His Phe Pro Met Val Val Tyr Arg Lys Leu Met Gly Lys Lys Gly Thr
 610 615 620
 Phe Arg Asp Leu Gly Asp Ser His Pro Val Leu Tyr Gln Ser Leu Lys
 625 630 635 640

 Asp Leu Leu Glu Tyr Glu Gly Asn Val Glu Asp Asp Met Met Ile Thr
 645 650 655
 Phe Gln Ile Ser Gln Thr Asp Leu Phe Gly Asn Pro Met Met Tyr Asp
 660 665 670
 Leu Lys Glu Asn Gly Asp Lys Ile Pro Ile Thr Asn Glu Asn Arg Lys
 675 680 685
 Glu Phe Val Asn Leu Tyr Ser Asp Tyr Ile Leu Asn Lys Ser Val Glu
 690 695 700

 Lys Gln Phe Lys Ala Phe Arg Arg Gly Phe His Met Val Thr Asn Glu
 705 710 715 720
 Ser Pro Leu Lys Tyr Leu Phe Arg Pro Glu Glu Ile Glu Leu Leu Ile

725 730 735
 Cys Gly Ser Arg Asn Leu Asp Phe Gln Ala Leu Glu Glu Thr Thr Glu
 740 745 750
 Tyr Asp Gly Gly Tyr Thr Arg Asp Ser Val Leu Ile Arg Glu Phe Trp
 755 760 765

 Glu Ile Val His Ser Phe Thr Asp Glu Gln Lys Arg Leu Phe Leu Gln
 770 775 780
 Phe Thr Thr Gly Thr Asp Arg Ala Pro Val Gly Gly Leu Gly Lys Leu
 785 790 795 800
 Lys Met Ile Ile Ala Lys Asn Gly Pro Asp Thr Glu Arg Leu Pro Thr
 805 810 815
 Ser His Thr Cys Phe Asn Val Leu Leu Leu Pro Glu Tyr Ser Ser Lys
 820 825 830

 Glu Lys Leu Lys Glu Arg Leu Leu Lys Ala Ile Thr Tyr Ala Lys Gly
 835 840 845
 Phe Gly Met Leu
 850
 <210> 4535
 <211> 745
 <212> PRT
 <213> homo sapiens
 <400> 4535
 Met Pro Val Leu Ser Arg Pro Arg Pro Trp Arg Gly Asn Thr Leu Lys
 1 5 10 15
 Arg Thr Ala Val Leu Leu Ala Leu Ala Ala Tyr Gly Ala His Lys Val
 20 25 30
 Tyr Pro Leu Val Arg Gln Cys Leu Ala Pro Ala Arg Gly Leu Gln Ala

 35 40 45
 Pro Ala Gly Glu Pro Thr Gln Glu Ala Ser Gly Val Ala Ala Ala Lys
 50 55 60
 Ala Gly Met Asn Arg Val Phe Leu Gln Arg Leu Leu Trp Leu Leu Arg
 65 70 75 80

Leu Leu Phe Pro Arg Val Leu Cys Arg Glu Thr Gly Leu Leu Ala Leu
 85 90 95
 His Ser Ala Ala Leu Val Ser Arg Thr Phe Leu Ser Val Tyr Val Ala
 100 105 110
 Arg Leu Asp Gly Arg Leu Ala Arg Cys Ile Val Arg Lys Asp Pro Arg
 115 120 125
 Ala Phe Gly Trp Gln Leu Leu Gln Trp Leu Leu Ile Ala Leu Pro Ala
 130 135 140
 Thr Phe Val Asn Ser Ala Ile Arg Tyr Leu Glu Gly Gln Leu Ala Leu
 145 150 155 160
 Ser Phe Arg Ser Arg Leu Val Ala His Ala Tyr Arg Leu Tyr Phe Ser
 165 170 175
 Gln Gln Thr Tyr Tyr Arg Val Ser Asn Met Asp Gly Arg Leu Arg Asn
 180 185 190
 Pro Asp Gln Ser Leu Thr Glu Asp Val Val Ala Phe Ala Ala Ser Val
 195 200 205
 Ala His Leu Tyr Ser Asn Leu Thr Lys Pro Leu Leu Asp Val Ala Val
 210 215 220
 Thr Ser Tyr Thr Leu Leu Arg Ala Ala Arg Ser Arg Gly Ala Gly Thr
 225 230 235 240
 Ala Trp Pro Ser Ala Ile Ala Gly Leu Val Val Phe Leu Thr Ala Asn
 245 250 255
 Val Leu Arg Ala Phe Ser Pro Lys Phe Gly Glu Leu Val Ala Glu Glu
 260 265 270
 Ala Arg Arg Lys Gly Glu Leu Arg Tyr Met His Ser Arg Val Val Ala
 275 280 285
 Asn Ser Glu Glu Ile Ala Phe Tyr Gly Gly His Glu Val Glu Leu Ala
 290 295 300
 Leu Leu Gln Arg Ser Tyr Gln Asp Leu Ala Ser Gln Ile Asn Leu Ile
 305 310 315 320
 Leu Leu Glu Arg Leu Trp Tyr Val Met Leu Glu Gln Phe Leu Met Lys

325 330 335
 Tyr Val Trp Ser Ala Ser Gly Leu Leu Met Val Ala Val Pro Ile Ile
 340 345 350
 Thr Ala Thr Gly Tyr Ser Glu Ser Asp Ala Glu Ala Val Lys Lys Ala

 355 360 365
 Ala Leu Glu Lys Lys Glu Glu Glu Leu Val Ser Glu Arg Thr Glu Ala
 370 375 380
 Phe Thr Ile Ala Arg Asn Leu Leu Thr Ala Ala Ala Asp Ala Ile Glu
 385 390 395 400
 Arg Ile Met Ser Ser Tyr Lys Glu Val Thr Glu Leu Ala Gly Tyr Thr
 405 410 415
 Ala Arg Val His Glu Met Phe Gln Val Phe Glu Asp Val Gln Arg Cys

 420 425 430
 His Phe Lys Arg Pro Arg Glu Leu Glu Asp Ala Gln Ala Gly Ser Gly
 435 440 445
 Thr Ile Gly Arg Ser Gly Val Arg Val Glu Gly Pro Leu Lys Ile Arg
 450 455 460
 Gly Gln Val Val Asp Val Glu Gln Gly Ile Ile Cys Glu Asn Ile Pro
 465 470 475 480
 Ile Val Thr Pro Ser Gly Glu Val Val Val Ala Ser Leu Asn Ile Arg

 485 490 495
 Val Glu Glu Gly Met His Leu Leu Ile Thr Gly Pro Asn Gly Cys Gly
 500 505 510
 Lys Ser Ser Leu Phe Arg Ile Leu Gly Gly Leu Trp Pro Thr Tyr Gly
 515 520 525
 Gly Val Leu Tyr Lys Pro Pro Pro Gln Arg Met Phe Tyr Ile Pro Gln
 530 535 540
 Arg Pro Tyr Met Ser Val Gly Ser Leu Arg Asp Gln Val Ile Tyr Pro

 545 550 555 560
 Asp Ser Val Glu Asp Met Gln Arg Lys Gly Tyr Ser Glu Gln Asp Leu
 565 570 575

Glu Ala Ile Leu Asp Val Val His Leu His His Ile Leu Gln Arg Glu
580 585 590
Gly Gly Trp Glu Ala Met Cys Asp Trp Lys Asp Val Leu Ser Gly Gly
595 600 605
Glu Lys Gln Arg Ile Gly Met Ala Arg Met Phe Tyr His Arg Pro Lys
610 615 620
Tyr Ala Leu Leu Asp Glu Cys Thr Ser Ala Val Ser Ile Asp Val Glu
625 630 635 640
Gly Lys Ile Phe Gln Ala Ala Lys Asp Ala Gly Ile Ala Leu Leu Ser
645 650 655
Ile Thr His Arg Pro Ser Leu Trp Lys Tyr His Thr His Leu Leu Gln
660 665 670
Phe Asp Gly Glu Gly Gly Trp Lys Phe Glu Lys Leu Asp Ser Ala Ala
675 680 685
Arg Leu Ser Leu Thr Glu Glu Lys Gln Arg Leu Glu Gln Gln Leu Ala
690 695 700
Gly Ile Pro Lys Met Gln Arg Arg Leu Gln Glu Leu Cys Gln Ile Leu
705 710 715 720
Gly Glu Ala Val Ala Pro Ala His Val Pro Ala Pro Ser Pro Gln Gly
725 730 735
Pro Gly Gly Leu Gln Gly Ala Ser Thr
740 745

<210> 4536

<211> 133

<212> PRT

<213> homo sapiens

<400> 4536

Met Arg Lys His Val Leu Ala Ala Ser Phe Ser Met Leu Ser Leu Leu
1 5 10 15
Val Ile Met Gly Asp Thr Asp Ser Lys Thr Asp Ser Ser Phe Ile Met
20 25 30
Asp Ser Asp Pro Arg Arg Cys Met Arg His His Tyr Val Asp Ser Ile

35 40 45
Ser His Pro Leu Tyr Lys Cys Ser Ser Lys Met Val Leu Leu Ala Arg

50 55 60
Cys Glu Gly His Cys Ser Gln Ala Ser Arg Ser Glu Pro Leu Val Ser
65 70 75 80
Phe Ser Thr Val Leu Lys Gln Pro Phe Arg Ser Ser Cys His Cys Cys
85 90 95
Arg Pro Gln Thr Ser Lys Leu Lys Ala Leu Arg Leu Arg Cys Ser Gly
100 105 110
Gly Met Arg Leu Thr Ala Thr Tyr Arg Tyr Ile Leu Ser Cys His Cys

115 120 125
Glu Glu Cys Asn Ser
130

<210> 4537

<211> 528

<212> PRT

<213> homo sapiens

<400> 4537

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1 5 10 15
Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Val Arg
20 25 30
Gly Gln Gly Ala Pro Gly Pro Ser Leu Thr Gly Ser Pro Trp Pro Gly

35 40 45
Thr Ala Ala Pro Ala Ala Ser Tyr Thr Pro Thr Pro Arg Ser Pro Arg
50 55 60
Phe Ile Gly Arg Arg Gln Ser Leu Ile Glu Asp Ala Arg Lys Glu Arg
65 70 75 80
Glu Ala Ala Val Ala Ala Ala Ala Ala Val Pro Ser Glu Pro Gly
85 90 95
Asp Pro Leu Glu Ala Val Ala Phe Glu Glu Lys Glu Gly Lys Ala Val

100	105	110	
Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu Ser			
115	120	125	
Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His Leu			
130	135	140	
Glu Thr Arg Pro Ala Gln Arg Pro Arg Ala Gly Gly Pro His Leu Glu			
145	150	155	160
Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu Leu			
165	170	175	
Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly Pro			
180	185	190	
Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys His			
195	200	205	
His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro Gly			
210	215	220	
Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu Ile			
225	230	235	240
Ala Phe Gln Tyr Arg His Gly Asp Pro Ile Pro Arg Val Glu Tyr Thr			
245	250	255	
Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys Gly			
260	265	270	
Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala Leu			
275	280	285	
Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu			
290	295	300	
Asp Val Ser Arg Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu Arg Pro			
305	310	315	320
Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala Phe			
325	330	335	
Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro Met			
340	345	350	

His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val Pro

355 360 365
Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly Leu

370 375 380
Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr Leu

385 390 395 400
Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu Val

405 410 415
Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu His

420 425 430
Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala Ala

435 440 445
Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe Val

450 455 460
Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala Ser

465 470 475 480
Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu Ala

485 490 495
Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu Gly

500 505 510
Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile Gly

515 520 525
<210> 4538

<211> 524
<212> PRT

<213> homo sapiens
<400> 4538

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg
1 5 10 15

Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Gly Ala
20 25 30

Pro Gly Pro Ser Leu Thr Gly Ser Pro Trp Pro Gly Thr Ala Ala Pro
35 40 45

Ala Ala Ser Tyr Thr Pro Thr Pro Arg Ser Pro Arg Phe Ile Gly Arg
50 55 60

Arg Gln Ser Leu Ile Glu Asp Ala Arg Lys Glu Arg Glu Ala Ala Val
65 70 75 80

Ala Ala Ala Ala Ala Ala Val Pro Ser Glu Pro Gly Asp Pro Leu Glu
85 90 95

Ala Val Ala Phe Glu Glu Lys Glu Gly Lys Ala Val Leu Asn Leu Leu
100 105 110

Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu Ser Arg Ala Val Lys
115 120 125

Val Phe Glu Thr Phe Glu Ala Lys Ile His His Leu Glu Thr Arg Pro
130 135 140

Ala Gln Arg Pro Arg Ala Gly Gly Pro His Leu Glu Tyr Phe Val Arg
145 150 155 160

Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu Leu Ser Gly Val Arg
165 170 175

Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly Pro Lys Val Pro Trp
180 185 190

Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys His His Leu Val Thr
195 200 205

Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro Gly Phe Ser Asp Gln
210 215 220

Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu Ile Ala Phe Gln Tyr
225 230 235 240

Arg His Gly Asp Pro Ile Pro Arg Val Glu Tyr Thr Ala Glu Glu Ile
245 250 255

Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys Gly Leu Tyr Ala Thr
260 265 270

His Ala Cys Gly Glu His Leu Glu Ala Phe Ala Leu Leu Glu Arg Phe

275	280	285	
Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu Glu Asp Val Ser Arg			
290	295	300	
Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu Arg Pro Val Ala Gly Leu			
305	310	315	320
Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala Phe Arg Val Phe Gln			
325	330	335	
Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro Met His Ser Pro Glu			
340	345	350	
Pro Asp Cys Cys His Glu Leu Leu Gly His Val Pro Met Leu Ala Asp			
355	360	365	
Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly Leu Ala Ser Leu Gly			
370	375	380	
Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr Leu Tyr Trp Phe Thr			
385	390	395	400
Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu Val Lys Ala Tyr Gly			
405	410	415	
Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu His Cys Leu Ser Glu			
420	425	430	
Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala Ala Ala Val Gln Pro			
435	440	445	
Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe Val Ser Glu Ser Phe			
450	455	460	
Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala Ser Arg Ile Gln Arg			
465	470	475	480
Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu Ala Ile Asp Val Leu			
485	490	495	
Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu Gly Val Gln Asp Glu			
500	505	510	
Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile Gly			
515	520		

<210> 4539

<211> 497

<212> PRT

<213> homo sapiens

<400> 4539

Met Pro Thr Pro Asp Ala Thr Thr Pro Gln Ala Lys Gly Phe Arg Arg

1 5 10 15

Ala Val Ser Glu Leu Asp Ala Lys Gln Ala Glu Ala Ile Met Ser Pro

20 25 30

Arg Phe Ile Gly Arg Arg Gln Ser Leu Ile Glu Asp Ala Arg Lys Glu

35 40 45

Arg Glu Ala Ala Val Ala Ala Ala Ala Ala Val Pro Ser Glu Pro

50 55 60

Gly Asp Pro Leu Glu Ala Val Ala Phe Glu Glu Lys Glu Gly Lys Ala

65 70 75 80

Val Leu Asn Leu Leu Phe Ser Pro Arg Ala Thr Lys Pro Ser Ala Leu

85 90 95

Ser Arg Ala Val Lys Val Phe Glu Thr Phe Glu Ala Lys Ile His His

100 105 110

Leu Glu Thr Arg Pro Ala Gln Arg Pro Arg Ala Gly Gly Pro His Leu

115 120 125

Glu Tyr Phe Val Arg Leu Glu Val Arg Arg Gly Asp Leu Ala Ala Leu

130 135 140

Leu Ser Gly Val Arg Gln Val Ser Glu Asp Val Arg Ser Pro Ala Gly

145 150 155 160

Pro Lys Val Pro Trp Phe Pro Arg Lys Val Ser Glu Leu Asp Lys Cys

165 170 175

His His Leu Val Thr Lys Phe Asp Pro Asp Leu Asp Leu Asp His Pro

180 185 190

Gly Phe Ser Asp Gln Val Tyr Arg Gln Arg Arg Lys Leu Ile Ala Glu

195 200 205

Ile Ala Phe Gln Tyr Arg His Gly Asp Pro Ile Pro Arg Val Glu Tyr
 210 215 220
 Thr Ala Glu Glu Ile Ala Thr Trp Lys Glu Val Tyr Thr Thr Leu Lys
 225 230 235 240
 Gly Leu Tyr Ala Thr His Ala Cys Gly Glu His Leu Glu Ala Phe Ala
 245 250 255
 Leu Leu Glu Arg Phe Ser Gly Tyr Arg Glu Asp Asn Ile Pro Gln Leu
 260 265 270
 Glu Asp Val Ser Arg Phe Leu Lys Glu Arg Thr Gly Phe Gln Leu Arg
 275 280 285
 Pro Val Ala Gly Leu Leu Ser Ala Arg Asp Phe Leu Ala Ser Leu Ala
 290 295 300
 Phe Arg Val Phe Gln Cys Thr Gln Tyr Ile Arg His Ala Ser Ser Pro
 305 310 315 320
 Met His Ser Pro Glu Pro Asp Cys Cys His Glu Leu Leu Gly His Val
 325 330 335
 Pro Met Leu Ala Asp Arg Thr Phe Ala Gln Phe Ser Gln Asp Ile Gly
 340 345 350
 Leu Ala Ser Leu Gly Ala Ser Asp Glu Glu Ile Glu Lys Leu Ser Thr
 355 360 365
 Leu Tyr Trp Phe Thr Val Glu Phe Gly Leu Cys Lys Gln Asn Gly Glu
 370 375 380
 Val Lys Ala Tyr Gly Ala Gly Leu Leu Ser Ser Tyr Gly Glu Leu Leu
 385 390 395 400
 His Cys Leu Ser Glu Glu Pro Glu Ile Arg Ala Phe Asp Pro Glu Ala
 405 410 415
 Ala Ala Val Gln Pro Tyr Gln Asp Gln Thr Tyr Gln Ser Val Tyr Phe
 420 425 430
 Val Ser Glu Ser Phe Ser Asp Ala Lys Asp Lys Leu Arg Ser Tyr Ala
 435 440 445
 Ser Arg Ile Gln Arg Pro Phe Ser Val Lys Phe Asp Pro Tyr Thr Leu

450 455 460
 Ala Ile Asp Val Leu Asp Ser Pro Gln Ala Val Arg Arg Ser Leu Glu
 465 470 475 480
 Gly Val Gln Asp Glu Leu Asp Thr Leu Ala His Ala Leu Ser Ala Ile
 485 490 495

Gly

<210> 4540

<211> 250

<212> PRT

<213> homo sapiens

<400> 4540

Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
 1 5 10 15
 Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
 20 25 30
 Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
 35 40 45
 Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
 50 55 60

Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
 65 70 75 80
 Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
 85 90 95
 Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
 100 105 110
 Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
 115 120 125

Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
 130 135 140
 Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
 145 150 155 160

Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
165 170 175
Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
180 185 190
Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
195 200 205
Thr His Met Cys Met Val Met Arg Gly Val Gln Lys Met Asn Ser Lys
210 215 220
Thr Val Thr Ser Thr Met Leu Gly Val Phe Arg Glu Asp Pro Lys Thr
225 230 235 240
Arg Glu Glu Phe Leu Thr Leu Ile Arg Ser
245 250
<210> 4541
<211> 233
<212>
> PRT
<213> homo sapiens
<400> 4541
Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
1 5 10 15
Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
20 25 30
Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
35 40 45
Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
50 55 60
Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
65 70 75 80
Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
85 90 95
Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
100 105 110
Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu

115 120 125
 Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
 130 135 140
 Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
 145 150 155 160
 Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
 165 170 175
 Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
 180 185 190

 Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
 195 200 205
 Thr Lys Ser Asn Lys Tyr Asn Lys Gly Leu Ser Pro Leu Leu Ser Ser
 210 215 220
 Cys His Leu Phe Val Ala Ile Leu Lys
 225 230
 <210> 4542
 <211> 213
 <212> PRT
 <213> homo sapiens
 <400> 4542
 Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
 1 5 10 15

 Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
 20 25 30
 Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
 35 40 45
 Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
 50 55 60
 Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
 65 70 75 80

 Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp

85 90 95
 Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
 100 105 110
 Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
 115 120 125
 Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
 130 135 140

 Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
 145 150 155 160
 Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
 165 170 175
 Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
 180 185 190
 Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
 195 200 205

 Thr Ser Ala Glu Pro
 210
 <210> 4543
 <211> 250
 <212> PRT
 <213> homo sapiens
 <400> 4543
 Met Glu Lys Gly Pro Val Arg Ala Pro Ala Glu Lys Pro Arg Gly Ala
 1 5 10 15
 Arg Cys Ser Asn Gly Phe Pro Glu Arg Asp Pro Pro Arg Pro Gly Pro
 20 25 30
 Ser Arg Pro Ala Glu Lys Pro Pro Arg Pro Glu Ala Lys Ser Ala Gln
 35 40 45

 Pro Ala Asp Gly Trp Lys Gly Glu Arg Pro Arg Ser Glu Glu Asp Asn
 50 55 60
 Glu Leu Asn Leu Pro Asn Leu Ala Ala Ala Tyr Ser Ser Ile Leu Ser
 65 70 75 80

Ser Leu Gly Glu Asn Pro Gln Arg Gln Gly Leu Leu Lys Thr Pro Trp
85 90 95
Arg Ala Ala Ser Ala Met Gln Phe Phe Thr Lys Gly Tyr Gln Glu Thr
100 105 110
Ile Ser Asp Val Leu Asn Asp Ala Ile Phe Asp Glu Asp His Asp Glu
115 120 125
Met Val Ile Val Lys Asp Ile Asp Met Phe Ser Met Cys Glu His His
130 135 140
Leu Val Pro Phe Val Gly Lys Val His Ile Gly Tyr Leu Pro Asn Lys
145 150 155 160
Gln Val Leu Gly Leu Ser Lys Leu Ala Arg Ile Val Glu Ile Tyr Ser
165 170 175
Arg Arg Leu Gln Val Gln Glu Arg Leu Thr Lys Gln Ile Ala Val Ala
180 185 190
Ile Thr Glu Ala Leu Arg Pro Ala Gly Val Gly Val Val Val Glu Ala
195 200 205
Thr His Met Cys Met Val Met Arg Gly Val Gln Lys Met Asn Ser Lys
210 215 220
Thr Val Thr Ser Thr Met Leu Gly Val Phe Arg Glu Asp Pro Lys Thr
225 230 235 240
Arg Glu Glu Phe Leu Thr Leu Ile Arg Ser
245 250
<210> 4544
<211> 205
<212> PRT
<213> homo sapiens
<400> 4544
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
20 25 30
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile

35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
 85 90 95
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
 100 105 110

 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125
 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175

 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190
 Gly Gly Trp Val Gly Ala Leu Gly Asp Val Ser Leu Gly
 195 200 205
 <210> 4545
 <211> 239
 <212> PRT
 <213> homo sapiens
 <400> 4545
 Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15
 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30
 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile

35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr

 85 90 95
 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
 100 105 110
 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
 115 120 125
 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
 130 135 140
 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu

 145 150 155 160
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190
 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
 195 200 205
 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala

 210 215 220
 Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
 225 230 235
 <210> 4546
 <211> 434
 <212> PRT
 <213> homo sapiens
 <400> 4546
 Met Ser Ile Glu Lys Ile Trp Ala Arg Glu Ile Leu Asp Ser Arg Gly
 1 5 10 15

Asn Pro Thr Val Glu Val Asp Leu Tyr Thr Ala Lys Gly Leu Phe Arg
 20 25 30

 Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu
 35 40 45
 Leu Arg Asp Gly Asp Lys Gln Arg Tyr Leu Gly Lys Gly Val Leu Lys
 50 55 60
 Ala Val Asp His Ile Asn Ser Thr Ile Ala Pro Ala Leu Ile Ser Ser
 65 70 75 80
 Gly Leu Ser Val Val Glu Gln Glu Lys Leu Asp Asn Leu Met Leu Glu
 85 90 95

 Leu Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu
 100 105 110
 Gly Val Ser Leu Ala Val Cys Lys Ala Gly Ala Ala Glu Arg Glu Leu
 115 120 125
 Pro Leu Tyr Arg His Ile Ala Gln Leu Ala Gly Asn Ser Asp Leu Ile
 130 135 140
 Leu Pro Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly
 145 150 155 160

 Asn Lys Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Glu
 165 170 175
 Ser Phe Arg Asp Ala Met Arg Leu Gly Ala Glu Val Tyr His Thr Leu
 180 185 190
 Lys Gly Val Ile Lys Asp Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly
 195 200 205
 Asp Glu Gly Gly Phe Ala Pro Asn Ile Leu Glu Asn Ser Glu Ala Leu
 210 215 220

 Glu Leu Val Lys Glu Ala Ile Asp Lys Ala Gly Tyr Thr Glu Lys Ile
 225 230 235 240
 Val Ile Gly Met Asp Val Ala Ala Ser Glu Phe Tyr Arg Asp Gly Lys
 245 250 255
 Tyr Asp Leu Asp Phe Lys Ser Pro Thr Asp Pro Ser Arg Tyr Ile Thr

260 265 270
 Gly Asp Gln Leu Gly Ala Leu Tyr Gln Asp Phe Val Arg Asp Tyr Pro
 275 280 285

Val Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Ala Ala Trp
 290 295 300
 Ser Lys Phe Thr Ala Asn Val Gly Ile Gln Ile Val Gly Asp Asp Leu
 305 310 315 320
 Thr Val Thr Asn Pro Lys Arg Ile Glu Arg Ala Val Glu Glu Lys Ala
 325 330 335
 Cys Asn Cys Leu Leu Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu
 340 345 350

Ala Ile Gln Ala Cys Lys Leu Ala Gln Glu Asn Gly Trp Gly Val Met
 355 360 365
 Val Ser His Arg Ser Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu
 370 375 380
 Val Val Gly Leu Cys Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg
 385 390 395 400
 Ser Glu Arg Leu Ala Lys Tyr Asn Gln Leu Met Arg Ile Glu Glu Glu
 405 410 415

Leu Gly Asp Glu Ala Arg Phe Ala Gly His Asn Phe Arg Asn Pro Ser
 420 425 430
 Val Leu

<210> 4547

<211> 193

<212> PRT

<213> homo sapiens

<400> 4547

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
 1 5 10 15
 Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu

35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu

50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg

65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu

85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser

100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly

115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu

130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile

145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

180 185 190

Arg

<210> 4548

<211> 536

<212> PRT

<213> homo sapiens

<400> 4548

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser

1 5 10 15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln

20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
50 55 60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
65 70 75 80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
210 215 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225 230 235 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
245 250 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu

275 280 285
 Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300
 Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320
 Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335
 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350

 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365
 Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380
 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400
 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415

 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430
 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445
 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480

 Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495
 Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510
 Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp Arg Arg Gln

530

535

<210> 4549

<211> 487

<212> PRT

<213>

homo sapiens

<400> 4549

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser

1

5

10

15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln

20

25

30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe

35

40

45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser

50

55

60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu

65

70

75

80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln

85

90

95

Ala Asn His Thr Gly Thr Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro

100

105

110

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr

115

120

125

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr

130

135

140

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg

145

150

155

160

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys

165

170

175

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly

180

185

190

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
 195 200 205
 Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
 210 215 220
 Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
 225 230 235 240
 Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
 245 250 255

 Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
 260 265 270
 Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
 275 280 285
 Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
 290 295 300
 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
 305 310 315 320

 Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
 325 330 335
 Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
 340 345 350
 Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
 355 360 365
 Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
 370 375 380

 Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
 385 390 395 400
 Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
 405 410 415
 Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
 420 425 430
 Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val

[illegible]

145	150	155	160
Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp			
	165	170	175
Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp			
	180	185	190
Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln			
	195	200	205
Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu			
	210	215	220
Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro			
225	230	235	240
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu			
	245	250	255
Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu			
	260	265	270
Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu			
	275	280	285
Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly			
	290	295	300
Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu			
305	310	315	320
Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr			
	325	330	335
Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr			
	340	345	350
Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg			
	355	360	365
Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser			
	370	375	380
Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met			
385	390	395	400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
405 410 415
Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
420 425 430
Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
435 440 445
Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
465 470 475 480
Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
485 490 495
Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
500 505 510
Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
515 520 525

His Thr Tyr Leu Trp Arg Arg Gln
530 535

<210> 4551

<211> 449

<212> PRT

<213> homo sapiens

<400> 4551

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
1 5 10 15
Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
20 25 30
Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
35 40 45

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
50 55 60
Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe

65	70	75	80
Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu			
	85	90	95
His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu			
	100	105	110
Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala			
	115	120	125
Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn			
	130	135	140
Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr			
145	150	155	160
Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys			
	165	170	175
Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu			
	180	185	190
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln			
	195	200	205
Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr			
	210	215	220
His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu			
225	230	235	240
Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr			
	245	250	255
Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala			
	260	265	270
Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu			
	275	280	285
Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val			
	290	295	300
Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile			
305	310	315	320

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
325 330 335
Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
340 345 350
Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
355 360 365

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
370 375 380
Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
385 390 395 400
Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
405 410 415
Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
420 425 430

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
435 440 445

Gln

<210> 4552

<211> 536

<212> PRT

<213> homo sapiens

<400> 4552

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
1 5 10 15
Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
20 25 30
Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
35 40 45
Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
50 55 60
Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu

65			70					75					80				
Ser	Thr	Arg	Ser	Gly	Arg	Arg	Met	Glu	Leu	Ser	Met	Gly	Pro	Ile	Gln		
			85					90					95				
Ala	Asn	His	Thr	Gly	Thr	Gly	Leu	Leu	Leu	Thr	Leu	Gln	Pro	Glu	Gln		
			100					105					110				
Lys	Phe	Gln	Lys	Val	Lys	Gly	Phe	Gly	Gly	Ala	Met	Thr	Asp	Ala	Ala		
			115					120					125				
Ala	Leu	Asn	Ile	Leu	Ala	Leu	Ser	Pro	Pro	Ala	Gln	Asn	Leu	Leu	Leu		
			130					135					140				
Lys	Ser	Tyr	Phe	Ser	Glu	Glu	Gly	Ile	Gly	Tyr	Asn	Ile	Ile	Arg	Val		
			145					150					155				
Pro	Met	Ala	Ser	Cys	Asp	Phe	Ser	Ile	Arg	Thr	Tyr	Thr	Tyr	Ala	Asp		
			165					170					175				
Thr	Pro	Asp	Asp	Phe	Gln	Leu	His	Asn	Phe	Ser	Leu	Pro	Glu	Glu	Asp		
			180					185					190				
Thr	Lys	Leu	Lys	Ile	Pro	Leu	Ile	His	Arg	Ala	Leu	Gln	Leu	Ala	Gln		
			195					200					205				
Arg	Pro	Val	Ser	Leu	Leu	Ala	Ser	Pro	Trp	Thr	Ser	Pro	Thr	Trp	Leu		
			210					215					220				
Lys	Thr	Asn	Gly	Ala	Val	Asn	Gly	Lys	Gly	Ser	Leu	Lys	Gly	Gln	Pro		
			225					230					235				
Gly	Asp	Ile	Tyr	His	Gln	Thr	Trp	Ala	Arg	Tyr	Phe	Val	Lys	Phe	Leu		
			245					250					255				
Asp	Ala	Tyr	Ala	Glu	His	Lys	Leu	Gln	Phe	Trp	Ala	Val	Thr	Ala	Glu		
			260					265					270				
Asn	Glu	Pro	Ser	Ala	Gly	Leu	Leu	Ser	Gly	Tyr	Pro	Phe	Gln	Cys	Leu		
			275					280					285				
Gly	Phe	Thr	Pro	Glu	His	Gln	Arg	Asp	Phe	Ile	Ala	Arg	Asp	Leu	Gly		
			290					295					300				
Pro	Thr	Leu	Ala	Asn	Ser	Thr	His	His	Asn	Val	Arg	Leu	Leu	Met	Leu		
			305					310					315				
			320					325					330				

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335
 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350
 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365
 Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380
 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400
 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415
 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430
 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445
 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480
 Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495
 Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510
 Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525
 His Thr Tyr Leu Trp Arg Arg Gln
 530 535
 <210> 4553
 <211> 346
 <212> PRT
 <213> homo sapiens

<400> 4553

Met Ala Arg Lys Ser Asn Leu Pro Val Leu Leu Val Pro Phe Leu Leu

1 5 10 15

Cys Gln Ala Leu Val Arg Cys Ser Ser Pro Leu Pro Leu Val Val Asn

20 25 30

Thr Trp Pro Phe Lys Asn Ala Thr Glu Ala Ala Trp Arg Ala Leu Ala

35 40 45

Ser Gly Gly Ser Ala Leu Asp Ala Val Glu Ser Gly Cys Ala Met Cys

50 55 60

Glu Arg Glu Gln Cys Asp Gly Ser Val Gly Phe Gly Gly Ser Pro Asp

65 70 75 80

Glu Leu Gly Glu Thr Thr Leu Asp Ala Met Ile Met Asp Gly Thr Thr

85 90 95

Met Asp Val Gly Ala Val Gly Asp Leu Arg Arg Ile Lys Asn Ala Ile

100 105 110

Gly Val Ala Arg Lys Val Leu Glu His Thr Thr His Thr Leu Leu Val

115 120 125

Gly Glu Ser Ala Thr Thr Phe Ala Gln Ser Met Gly Phe Ile Asn Glu

130 135 140

Asp Leu Ser Thr Thr Ala Ser Gln Ala Leu His Ser Asp Trp Leu Ala

145 150 155 160

Arg Asn Cys Gln Pro Asn Tyr Trp Arg Asn Val Ile Pro Asp Pro Ser

165 170 175

Lys Tyr Cys Gly Pro Tyr Lys Pro Pro Gly Ile Leu Lys Gln Asp Ile

180 185 190

Pro Ile His Lys Glu Thr Glu Asp Asp Arg Gly His Asp Thr Ile Gly

195 200 205

Met Val Val Ile His Lys Thr Gly His Ile Ala Ala Gly Thr Ser Thr

210 215 220

Asn Gly Ile Lys Phe Lys Ile His Gly Arg Val Gly Asp Ser Pro Ile

225 230 235 240

Pro Gly Ala Gly Ala Tyr Ala Asp Asp Thr Ala Gly Ala Ala Ala Ala
245 250 255

Thr Gly Asn Gly Asp Ile Leu Met Arg Phe Leu Pro Ser Tyr Gln Ala
260 265 270

Val Glu Tyr Met Arg Arg Gly Glu Asp Pro Thr Ile Ala Cys Gln Lys
275 280 285

Val Ile Ser Arg Ile Gln Lys His Phe Pro Glu Phe Phe Gly Ala Val
290 295 300

Ile Cys Ala Asn Val Thr Gly Ser Tyr Gly Ala Ala Cys Asn Lys Leu
305 310 315 320

Ser Thr Phe Thr Gln Phe Ser Phe Met Val Tyr Asn Ser Glu Lys Asn
325 330 335

Gln Pro Thr Glu Glu Lys Val Asp Cys Ile
340 345

<210> 4554
<211> 336
<212> PRT
<213> homo sapiens
<400> 4554

Met Ala Arg Lys Ser Asn Leu Pro Val Leu Leu Val Pro Phe Leu Leu
1 5 10 15

Cys Gln Ala Leu Val Arg Cys Ser Ser Pro Leu Pro Leu Val Val Asn
20 25 30

Thr Trp Pro Phe Lys Asn Ala Thr Glu Ala Ala Trp Arg Ala Leu Ala
35 40 45

Ser Gly Gly Ser Ala Leu Asp Ala Val Glu Ser Gly Cys Ala Met Cys
50 55 60

Glu Arg Glu Gln Cys Asp Gly Ser Val Gly Phe Gly Gly Ser Pro Asp
65 70 75 80

Glu Leu Gly Glu Thr Thr Leu Asp Ala Met Ile Met Asp Gly Thr Thr
85 90 95

Met Asp Val Gly Ala Val Gly Asp Leu Arg Arg Ile Lys Asn Ala Ile

100 105 110

Gly Val Ala Arg Lys Val Leu Glu His Thr Thr His Thr Leu Leu Val

115 120 125

Gly Glu Ser Ala Thr Thr Phe Ala Gln Ser Met Gly Phe Ile Asn Glu

130 135 140

Asp Leu Ser Thr Thr Ala Ser Gln Ala Leu His Ser Asp Trp Leu Ala

145 150 155 160

Arg Asn Cys Gln Pro Asn Tyr Trp Arg Asn Val Ile Pro Asp Pro Ser

165 170 175

Lys Tyr Cys Gly Pro Tyr Lys Pro Pro Gly Ile Leu Lys Gln Asp Ile

180 185 190

Pro Ile His Lys Glu Thr Glu Asp Asp Arg Gly His Asp Thr Ile Gly

195 200 205

Met Val Val Ile His Lys Thr Gly His Ile Ala Ala Gly Thr Ser Thr

210 215 220

Asn Gly Asp Ser Pro Ile Pro Gly Ala Gly Ala Tyr Ala Asp Asp Thr

225 230 235 240

Ala Gly Ala Ala Ala Ala Thr Gly Asn Gly Asp Ile Leu Met Arg Phe

245 250 255

Leu Pro Ser Tyr Gln Ala Val Glu Tyr Met Arg Arg Gly Glu Asp Pro

260 265 270

Thr Ile Ala Cys Gln Lys Val Ile Ser Arg Ile Gln Lys His Phe Pro

275 280 285

Glu Phe Phe Gly Ala Val Ile Cys Ala Asn Val Thr Gly Ser Tyr Gly

290 295 300

Ala Ala Cys Asn Lys Leu Ser Thr Phe Thr Gln Phe Ser Phe Met Val

305 310 315 320

Tyr Asn Ser Glu Lys Asn Gln Pro Thr Glu Glu Lys Val Asp Cys Ile

325 330 335

<210> 4555

<211> 1118

<212> PRT

<213> homo sapiens

<400> 4555

Met Ser Val Glu Ala Tyr Gly Pro Ser Ser Gln Thr Leu Thr Phe Leu

1 5 10 15

Asp Thr Glu Glu Ala Glu Leu Leu Gly Ala Asp Thr Gln Gly Ser Glu

20 25 30

Phe Glu Phe Thr Asp Phe Thr Leu Pro Ser Gln Thr Gln Thr Pro Pro

35 40 45

Gly Gly Pro Gly Gly Pro Gly Gly Gly Gly Ala Gly Gly Pro Gly Gly

50 55 60

Ala Gly Ala Gly Ala Ala Ala Gly Gln Leu Asp Ala Gln Val Gly Pro

65 70 75 80

Glu Gly Ile Leu Gln Asn Gly Ala Val Asp Asp Ser Val Ala Lys Thr

85 90 95

Ser Gln Leu Leu Ala Glu Leu Asn Phe Glu Glu Asp Glu Glu Asp Thr

100 105 110

Tyr Tyr Thr Lys Asp Leu Pro Ile His Ala Cys Ser Tyr Cys Gly Ile

115 120 125

His Asp Pro Ala Cys Val Val Tyr Cys Asn Thr Ser Lys Lys Trp Phe

130 135 140

Cys Asn Gly Arg Gly Asn Thr Ser Gly Ser His Ile Val Asn His Leu

145 150 155 160

Val Arg Ala Lys Cys Lys Glu Val Thr Leu His Lys Asp Gly Pro Leu

165 170 175

Gly Glu Thr Val Leu Glu Cys Tyr Asn Cys Gly Cys Arg Asn Val Phe

180 185 190

Leu Leu Gly Phe Ile Pro Ala Lys Ala Asp Ser Val Val Val Leu Leu

195 200 205

Cys Arg Gln Pro Cys Ala Ser Gln Ser Ser Leu Lys Asp Ile Asn Trp

210	215	220	
Asp Ser Ser Gln Trp Gln Pro Leu Ile Gln Asp Arg Cys Phe Leu Ser			
225	230	235	240
Trp Leu Val Lys Ile Pro Ser Glu Gln Glu Gln Leu Arg Ala Arg Gln			
	245	250	255
Ile Thr Ala Gln Gln Ile Asn Lys Leu Glu Glu Leu Trp Lys Glu Asn			
	260	265	270
Pro Ser Ala Thr Leu Glu Asp Leu Glu Lys Pro Gly Val Asp Glu Glu			
	275	280	285
Pro Gln His Val Leu Leu Arg Tyr Glu Asp Ala Tyr Gln Tyr Gln Asn			
	290	295	300
Ile Phe Gly Pro Leu Val Lys Leu Glu Ala Asp Tyr Asp Lys Lys Leu			
305	310	315	320
Lys Glu Ser Gln Thr Gln Asp Asn Ile Thr Val Arg Trp Asp Leu Gly			
	325	330	335
Leu Asn Lys Lys Arg Ile Ala Tyr Phe Thr Leu Pro Lys Thr Asp Ser			
	340	345	350
Asp Met Arg Leu Met Gln Gly Asp Glu Ile Cys Leu Arg Tyr Lys Gly			
	355	360	365
Asp Leu Ala Pro Leu Trp Lys Gly Ile Gly His Val Ile Lys Val Pro			
	370	375	380
Asp Asn Tyr Gly Asp Glu Ile Ala Ile Glu Leu Arg Ser Ser Val Gly			
385	390	395	400
Ala Pro Val Glu Val Thr His Asn Phe Gln Val Asp Phe Val Trp Lys			
	405	410	415
Ser Thr Ser Phe Asp Arg Met Gln Ser Ala Leu Lys Thr Phe Ala Val			
	420	425	430
Asp Glu Thr Ser Val Ser Gly Tyr Ile Tyr His Lys Leu Leu Gly His			
	435	440	445
Glu Val Glu Asp Val Ile Ile Lys Cys Gln Leu Pro Lys Arg Phe Thr			
	450	455	460

Ala Gln Gly Leu Pro Asp Leu Asn His Ser Gln Val Tyr Ala Val Lys
465 470 475 480
Thr Val Leu Gln Arg Pro Leu Ser Leu Ile Gln Gly Pro Pro Gly Thr
485 490 495
Gly Lys Thr Val Thr Ser Ala Thr Ile Val Tyr His Leu Ala Arg Gln
500 505 510
Gly Asn Gly Pro Val Leu Val Cys Ala Pro Ser Asn Ile Ala Val Asp
515 520 525

Gln Leu Thr Glu Lys Ile His Gln Thr Gly Leu Lys Val Val Arg Leu
530 535 540
Cys Ala Lys Ser Arg Glu Ala Ile Asp Ser Pro Val Ser Phe Leu Ala
545 550 555 560
Leu His Asn Gln Ile Arg Asn Met Asp Ser Met Pro Glu Leu Gln Lys
565 570 575
Leu Gln Gln Leu Lys Asp Glu Thr Gly Glu Leu Ser Ser Ala Asp Glu
580 585 590

Lys Arg Tyr Arg Ala Leu Lys Arg Thr Ala Glu Arg Glu Leu Leu Met
595 600 605
Asn Ala Asp Val Ile Cys Cys Thr Cys Val Gly Ala Gly Asp Pro Arg
610 615 620
Leu Ala Lys Met Gln Phe Arg Ser Ile Leu Ile Asp Glu Ser Thr Gln
625 630 635 640
Ala Thr Glu Pro Glu Cys Met Val Pro Val Val Leu Gly Ala Lys Gln
645 650 655

Leu Ile Leu Val Gly Asp His Cys Gln Leu Gly Pro Val Val Met Cys
660 665 670
Lys Lys Ala Ala Lys Ala Gly Leu Ser Gln Ser Leu Phe Glu Arg Leu
675 680 685
Val Val Leu Gly Ile Arg Pro Ile Arg Leu Gln Val Gln Tyr Arg Met
690 695 700
His Pro Ala Leu Ser Ala Phe Pro Ser Asn Ile Phe Tyr Glu Gly Ser

705						710						715						720	
Leu	Gln	Asn	Gly	Val	Thr	Ala	Ala	Asp	Arg	Val	Lys	Lys	Gly	Phe	Asp				
					725					730					735				
Phe	Gln	Trp	Pro	Gln	Pro	Asp	Lys	Pro	Met	Phe	Phe	Tyr	Val	Thr	Gln				
					740					745					750				
Gly	Gln	Glu	Glu	Ile	Ala	Ser	Ser	Gly	Thr	Ser	Tyr	Leu	Asn	Arg	Thr				
					755					760					765				
Glu	Ala	Ala	Asn	Val	Glu	Lys	Ile	Thr	Thr	Lys	Leu	Leu	Lys	Ala	Gly				
					770					775					780				
Ala	Lys	Pro	Asp	Gln	Ile	Gly	Ile	Ile	Thr	Pro	Tyr	Glu	Gly	Gln	Arg				
					790					795					800				
Ser	Tyr	Leu	Val	Gln	Tyr	Met	Gln	Phe	Ser	Gly	Ser	Leu	His	Thr	Lys				
					805					810					815				
Leu	Tyr	Gln	Glu	Val	Glu	Ile	Ala	Ser	Val	Asp	Ala	Phe	Gln	Gly	Arg				
					820					825					830				
Glu	Lys	Asp	Phe	Ile	Ile	Leu	Ser	Cys	Val	Arg	Ala	Asn	Glu	His	Gln				
					835					840					845				
Gly	Ile	Gly	Phe	Leu	Asn	Asp	Pro	Arg	Arg	Leu	Asn	Val	Ala	Leu	Thr				
					855					860									
Arg	Ala	Arg	Tyr	Gly	Val	Ile	Ile	Val	Gly	Asn	Pro	Lys	Ala	Leu	Ser				
					870					875					880				
Lys	Gln	Pro	Leu	Trp	Asn	His	Leu	Leu	Asn	Tyr	Tyr	Lys	Glu	Gln	Lys				
					885					890					895				
Val	Leu	Val	Glu	Gly	Pro	Leu	Asn	Asn	Leu	Arg	Glu	Ser	Leu	Met	Gln				
					900					905					910				
Phe	Ser	Lys	Pro	Arg	Lys	Leu	Val	Asn	Thr	Ile	Asn	Pro	Gly	Ala	Arg				
					920					925									
Phe	Met	Thr	Thr	Ala	Met	Tyr	Asp	Ala	Arg	Glu	Ala	Ile	Ile	Pro	Gly				
					935					940									
Ser	Val	Tyr	Asp	Arg	Ser	Ser	Gln	Gly	Arg	Pro	Ser	Ser	Met	Tyr	Phe				
					950					955					960				

Gln Thr His Asp Gln Ile Gly Met Ile Ser Ala Gly Pro Ser His Val
965 970 975

Ala Ala Met Asn Ile Pro Ile Pro Phe Asn Leu Val Met Pro Pro Met
980 985 990

Pro Pro Pro Gly Tyr Phe Gly Gln Ala Asn Gly Pro Ala Ala Gly Arg
995 1000 1005

Gly Thr Pro Lys Gly Lys Thr Gly Arg Gly Gly Arg Gln Lys Asn
1010 1015 1020

Arg Phe Gly Leu Pro Gly Pro Ser Gln Thr Asn Leu Pro Asn Ser
1025 1030 1035

Gln Ala Ser Gln Asp Val Ala Ser Gln Pro Phe Ser Gln Gly Ala
1040 1045 1050

Leu Thr Gln Gly Tyr Ile Ser Met Ser Gln Pro Ser Gln Met Ser
1055 1060 1065

Gln Pro Gly Leu Ser Gln Pro Glu Leu Ser Gln Asp Ser Tyr Leu
1070 1075 1080

Gly Asp Glu Phe Lys Ser Gln Ile Asp Val Ala Leu Ser Gln Asp
1085 1090 1095

Ser Thr Tyr Gln Gly Glu Arg Ala Tyr Gln His Gly Gly Val Thr
1100 1105 1110

Gly Leu Ser Gln Tyr
1115

<210> 4556

<211> 526

<212> PRT

<213> homo sapiens

<400> 4556

Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
1 5 10 15

Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
20 25 30

Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
 35 40 45
 Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
 50 55 60
 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
 65 70 75 80
 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
 85 90 95

 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
 100 105 110
 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
 115 120 125
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
 130 135 140
 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
 145 150 155 160

 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
 165 170 175
 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
 180 185 190
 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
 195 200 205
 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
 210 215 220

 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
 225 230 235 240
 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
 245 250 255
 Met His Met Asp Gln Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe
 260 265 270
 Cys Asp Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys

275	280	285
Val Ala Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile		
290	295	300
Lys Lys His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys		
305	310	315
Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr		
325	330	335
Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro		
340	345	350
Lys Ser Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser		
355	360	365
Ser Ile Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys		
370	375	380
Ser Met Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val		
385	390	395
His Val Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys		
405	410	415
Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln		
420	425	430
Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro		
435	440	445
Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu		
450	455	460
Ile Glu Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys		
465	470	475
Ile Gly Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys		
485	490	495
Cys Ile Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala		
500	505	510
Gln Cys Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn		
515	520	525

<210> 4557

<211> 524

<212> PRT

<213> homo sapiens

<400> 4557

Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala

1 5 10 15
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp

20 25 30
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys

35 40 45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp

50 55 60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn

65 70 75 80
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp

85 90 95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser

100 105 110
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro

115 120 125
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His

130 135 140
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro

145 150 155 160
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro

165 170 175
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys

180 185 190
Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile

195 200 205

Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
210 215 220
His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
225 230 235 240
Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
245 250 255
Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp
260 265 270
Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala
275 280 285
Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys
290 295 300
His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe
305 310 315 320
Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys
325 330 335
Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser
340 345 350
Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile
355 360 365
Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met
370 375 380
Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val
385 390 395 400
Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val
405 410 415
Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile
420 425 430
Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln
435 440 445
Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu

450 455 460
 Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly
 465 470 475 480
 Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile
 485 490 495
 Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys
 500 505 510
 Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn

515 520
 <210> 4558
 <211> 527
 <212> PRT
 <213> homo sapiens
 <400> 4558

Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
 1 5 10 15
 Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
 20 25 30
 Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
 35 40 45

Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
 50 55 60
 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
 65 70 75 80
 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
 85 90 95
 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
 100 105 110

Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
 115 120 125
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
 130 135 140

Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
 145 150 155 160
 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
 165 170 175

 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
 180 185 190
 Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
 195 200 205
 Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
 210 215 220
 His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
 225 230 235 240

 Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
 245 250 255
 Met His Met Gln Asp Gln Gln Pro Lys Glu Ile Cys Ala Leu Val Gly
 260 265 270
 Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala
 275 280 285
 Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro
 290 295 300

 Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val
 305 310 315 320
 Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
 325 330 335
 Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu
 340 345 350
 Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly
 355 360 365

 Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val
 370 375 380
 Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr

385 390 395 400
 Val His Val Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys
 405 410 415
 Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys
 420 425 430

 Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp
 435 440 445
 Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val
 450 455 460
 Leu Ile Glu Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu
 465 470 475 480
 Lys Ile Gly Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu
 485 490 495

 Lys Cys Ile Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala
 500 505 510
 Ala Gln Cys Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn
 515 520 525

 <210> 4559
 <211> 346
 <212> PRT
 <213> homo sapiens
 <400> 4559

 Met Ala Met Val Ser Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn
 1 5 10 15
 Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro

 20 25 30
 Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val
 35 40 45
 Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr
 50 55 60
 Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile
 65 70 75 80

Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu

85 90 95

Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu

100 105 110

Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys

115 120 125

Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg

130 135 140

Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu

145 150 155 160

Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe

165 170 175

Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe

180 185 190

Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu

195 200 205

Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile

210 215 220

Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr

225 230 235 240

Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu

245 250 255

Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr

260 265 270

Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly

275 280 285

Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser

290 295 300

Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly

305 310 315 320

Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu

325 330 335
Lys Ile Leu Val Ala Leu Cys Gly Gly Asn
340 345

<210> 4560

<211> 158

<212> PRT

<213> homo sapiens

<400> 4560

Met Gly Lys Ile Ser Ser Leu Pro Thr Gln Leu Phe Lys Cys Cys Phe
1 5 10 15
Cys Asp Phe Leu Lys Val Lys Met His Thr Met Ser Ser Ser His Leu
20 25 30
Phe Tyr Leu Ala Leu Cys Leu Leu Thr Phe Thr Ser Ser Ala Thr Ala
35 40 45
Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe

50 55 60
Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
65 70 75 80
Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
85 90 95
Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
100 105 110
Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp

115 120 125
Met Pro Lys Thr Gln Lys Tyr Gln Pro Pro Ser Thr Asn Lys Asn Thr
130 135 140
Lys Ser Gln Arg Arg Lys Gly Ser Thr Phe Glu Glu Arg Lys
145 150 155

<210> 4561

<211> 137

<212> PRT

<213> homo sapiens

<400> 4561

Met Ile Thr Pro Thr Val Lys Met His Thr Met Ser Ser Ser His Leu
1 5 10 15

Phe Tyr Leu Ala Leu Cys Leu Leu Thr Phe Thr Ser Ser Ala Thr Ala
20 25 30

Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
35 40 45

Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
50 55 60

Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
65 70 75 80

Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
85 90 95

Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
100 105 110

Met Pro Lys Thr Gln Lys Glu Val His Leu Lys Asn Ala Ser Arg Gly
115 120 125

Ser Ala Gly Asn Lys Asn Tyr Arg Met
130 135

<210> 4562

<211> 153

<212> PRT

<213> homo sapiens

<400> 4562

Met Gly Lys Ile Ser Ser Leu Pro Thr Gln Leu Phe Lys Cys Cys Phe
1 5 10 15

Cys Asp Phe Leu Lys Val Lys Met His Thr Met Ser Ser Ser His Leu
20 25 30

Phe Tyr Leu Ala Leu Cys Leu Leu Thr Phe Thr Ser Ser Ala Thr Ala
35 40 45

Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe

50 55 60
 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
 65 70 75 80
 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
 85 90 95
 Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu Met Tyr Cys Ala Pro Leu
 100 105 110
 Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
 115 120 125

 Met Pro Lys Thr Gln Lys Glu Val His Leu Lys Asn Ala Ser Arg Gly
 130 135 140
 Ser Ala Gly Asn Lys Asn Tyr Arg Met
 145 150
 <210> 4563
 <211> 200
 <212> PRT
 <213> homo sapiens
 <400> 4563
 Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30

 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Ala Ser
 50 55 60
 Ala Leu Ser Leu Ser Ser Ser Thr Ser Thr Trp Pro Glu Gly Leu Asp
 65 70 75 80
 Ala Thr Ala Arg Ala Pro Pro Ala Leu Val Val Thr Ala Asn Ile Gly
 85 90 95

 Gln Ala Gly Gly Ser Ser Ser Arg Gln Phe Arg Gln Arg Ala Leu Gly

100 105 110
Thr Ser Asp Ser Pro Val Leu Phe Ile His Cys Pro Gly Ala Ala Gly
115 120 125
Thr Ala Gln Gly Leu Glu Tyr Arg Gly Arg Arg Val Thr Thr Glu Leu
130 135 140
Val Trp Glu Glu Val Asp Ser Ser Pro Gln Pro Gln Gly Ser Glu Ser
145 150 155 160

Leu Pro Ala Gln Pro Pro Ala Gln Pro Ala Pro Gln Pro Glu Pro Gln
165 170 175
Gln Ala Arg Glu Pro Ser Pro Glu Val Ser Cys Cys Gly Leu Trp Pro
180 185 190
Arg Arg Pro Gln Arg Ser Gln Asn
195 200

<210> 4564

<211> 180

<212> PRT

<213> homo sapiens

<400> 4564

Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu Thr Phe Leu
1 5 10 15

Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu
20 25 30
Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
35 40 45
Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
50 55 60
Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
65 70 75 80

Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
85 90 95
Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
100 105 110

Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
115 120 125

Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
130 135 140

Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
145 150 155 160

Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
165 170 175

Ser Asn Arg Lys
180

<210> 4565

<211> 180

<212> PRT

<213> homo sapiens

<400> 4565

Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu Thr Phe Leu
1 5 10 15

Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu
20 25 30

Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
35 40 45

Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
50 55 60

Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
65 70 75 80

Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
85 90 95

Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
100 105 110

Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
115 120 125

Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys

130 135 140
Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala

145 150 155 160
Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala

165 170 175
Ser Asn Arg Lys

180

<210> 4566

<211> 236

<212> PRT

<213> homo sapiens

<400> 4566

Met Val Ser Pro Asp Pro Gln Ile Ile Val Val Ala Pro Glu Thr Glu

1 5 10 15

Leu Ala Ser Met Gln Val Gln Arg Thr Glu Asp Gly Val Thr Ile Ile

20 25 30

Gln Ile Phe Trp Val Gly Arg Lys Gly Glu Leu Leu Arg Arg Thr Pro

35 40 45

Val Ser Ser Ala Met Gln Thr Pro Met Gly Ile Pro Met Gly Lys Ser

50 55 60

Met Leu Val Leu Leu Thr Phe Leu Ala Phe Ala Ser Cys Cys Ile Ala

65 70 75 80

Ala Tyr Arg Pro Ser Glu Thr Leu Cys Gly Gly Glu Leu Val Asp Thr

85 90 95

Leu Gln Phe Val Cys Gly Asp Arg Gly Phe Tyr Phe Ser Arg Pro Ala

100 105 110

Ser Arg Val Ser Arg Arg Ser Arg Gly Ile Val Glu Glu Cys Cys Phe

115 120 125

Arg Ser Cys Asp Leu Ala Leu Leu Glu Thr Tyr Cys Ala Thr Pro Ala

130 135 140

Lys Ser Glu Arg Asp Val Ser Thr Pro Pro Thr Val Leu Pro Asp Asn

145 150 155 160

Phe Pro Arg Tyr Pro Val Gly Lys Phe Phe Gln Tyr Asp Thr Trp Lys

 165 170 175

Gln Ser Thr Gln Arg Leu Arg Arg Gly Leu Pro Ala Leu Leu Arg Ala

 180 185 190

Arg Arg Gly His Val Leu Ala Lys Glu Leu Glu Ala Phe Arg Glu Ala

 195 200 205

Lys Arg His Arg Pro Leu Ile Ala Leu Pro Thr Gln Asp Pro Ala His

 210 215 220

Gly Gly Ala Pro Pro Glu Met Ala Ser Asn Arg Lys

225 230 235

<210> 4567

<211> 110

<212> PRT

<213> homo sapiens

<400> 4567

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu

1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly

 20 25 30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe

 35 40 45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly

 50 55 60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu

65 70 75 80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys

 85 90 95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

 100 105 110

<210> 4568

<211> 437

<212> PRT

<213> homo sapiens

<400> 4568

Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu

1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys

20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys

35 40 45

Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln

50 55 60

Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met

65 70 75 80

Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu

85 90 95

Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu

100 105 110

Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg

115 120 125

Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn

130 135 140

Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly

145 150 155 160

Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu

165 170 175

Thr Gln Glu Phe Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys

180 185 190

Glu Thr Ser Val Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile

195 200 205

Thr Cys Ile Thr Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln

210 215 220

Cys Asn Ser Arg His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys
 225 230 235 240
 Val Thr Arg Leu Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly

 245 250 255
 Tyr Ser Leu Pro Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu
 260 265 270
 Leu His His Phe Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln
 275 280 285
 Gln Tyr Gly Ala Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys
 290 295 300
 Pro Arg Pro Gly Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg

 305 310 315 320
 Lys Val Thr Cys Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe
 325 330 335
 Cys Arg Glu Cys Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val
 340 345 350
 Phe Glu Ala Ser Gly Thr Thr Thr Gln Ala Tyr Arg Val Asp Glu Arg
 355 360 365
 Ala Ala Glu Gln Ala Arg Trp Glu Ala Ala Ser Lys Glu Thr Ile Lys

 370 375 380
 Lys Thr Thr Lys Pro Cys Pro Arg Cys His Val Pro Val Glu Lys Asn
 385 390 395 400
 Gly Gly Cys Met His Met Lys Cys Pro Gln Pro Gln Cys Arg Leu Glu
 405 410 415
 Trp Cys Trp Asn Cys Gly Cys Glu Trp Asn Arg Val Cys Met Gly Asp
 420 425 430
 His Trp Phe Asp Val
 435
 <210
 > 4569
 <211> 316
 <212> PRT

<213> homo sapiens

<400> 4569

Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu

1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys

20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys

35 40 45

Glu Leu Arg Asn Asp Trp Thr Val Gln Glu Phe Phe Phe Lys Cys Gly

50 55 60

Ala His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile

65 70 75 80

Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg

85 90 95

Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu

100 105 110

Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe

115 120 125

Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val Ala Gly Cys

130 135 140

Pro Asn Ser Leu Ile Lys Glu Leu His His Phe Arg Ile Leu Gly Glu

145 150 155 160

Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala Glu Glu Cys Val Leu

165 170 175

Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly Cys Gly Ala Gly Leu

180 185 190

Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys Glu Gly Gly Asn Gly

195 200 205

Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys Lys Glu Ala Tyr His

210 215 220

Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser Gly Thr Thr Thr Gln

225 230 235 240

Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln Ala Arg Trp Glu Ala

245 250 255

Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys Pro Cys Pro Arg Cys

260 265 270

His Val Pro Val Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro

275 280 285

Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp

290 295 300

Asn Arg Val Cys Met Gly Asp His Trp Phe Asp Val

305 310 315

<210> 4570

<211> 465

<212> PRT

<213> homo sapiens

<400> 4570

Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu

1 5 10 15

Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys

20 25 30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys

35 40 45

Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln

50 55 60

Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met

65 70 75 80

Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu

85 90 95

Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu

100 105 110

Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg

115 120 125

Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn
 130 135 140
 Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly
 145 150 155 160
 Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu
 165 170 175

 Thr Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met
 180 185 190
 Ser Gly Glu Cys Gln Ser Pro His Cys Pro Gly Thr Ser Ala Glu Phe
 195 200 205
 Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Glu Thr Ser Val
 210 215 220
 Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr
 225 230 235 240

 Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg
 245 250 255
 His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu
 260 265 270
 Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro
 275 280 285
 Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu Leu His His Phe
 290 295 300

 Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala
 305 310 315 320
 Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly
 325 330 335
 Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys
 340 345 350
 Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys
 355 360 365

 Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser

370 375 380
 Gly Thr Thr Thr Gln Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln
 385 390 395 400
 Ala Arg Trp Glu Ala Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys
 405 410 415
 Pro Cys Pro Arg Cys His Val Pro Val Glu Lys Asn Gly Gly Cys Met
 420 425 430

 His Met Lys Cys Pro Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn
 435 440 445
 Cys Gly Cys Glu Trp Asn Arg Val Cys Met Gly Asp His Trp Phe Asp
 450 455 460
 Val
 465
 <210> 4571
 <211> 466
 <212> PRT
 <213> homo sapiens
 <400> 4571
 Met Arg Ala Pro Gly Met Arg Ser Arg Pro Ala Gly Pro Ala Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Phe Leu Gly Ala Ala Glu Ser Val Arg Arg Ala Gln

 20 25 30
 Pro Pro Arg Arg Tyr Thr Pro Asp Trp Pro Ser Leu Asp Ser Arg Pro
 35 40 45
 Leu Pro Ala Trp Phe Asp Glu Ala Lys Phe Gly Val Phe Ile His Trp
 50 55 60
 Gly Val Phe Ser Val Pro Ala Trp Gly Ser Glu Trp Phe Trp Trp His
 65 70 75 80
 Trp Gln Gly Glu Gly Arg Pro Gln Tyr Gln Arg Phe Met Arg Asp Asn

 85 90 95
 Tyr Pro Pro Gly Phe Ser Tyr Ala Asp Phe Gly Pro Gln Phe Thr Ala
 100 105 110

Arg Phe Phe His Pro Glu Glu Trp Ala Asp Leu Phe Gln Ala Ala Gly
 115 120 125
 Ala Lys Tyr Val Val Leu Thr Thr Lys His His Glu Gly Phe Thr Asn
 130 135 140
 Trp Pro Ser Pro Val Ser Trp Asn Trp Asn Ser Lys Asp Val Gly Pro

 145 150 155 160
 His Arg Asp Leu Val Gly Glu Leu Gly Thr Ala Leu Arg Lys Arg Asn
 165 170 175
 Ile Arg Tyr Gly Leu Tyr His Ser Leu Leu Glu Trp Phe His Pro Leu
 180 185 190
 Tyr Leu Leu Asp Lys Lys Asn Gly Phe Lys Thr Gln His Phe Val Ser
 195 200 205
 Ala Lys Thr Met Pro Glu Leu Tyr Asp Leu Val Asn Ser Tyr Lys Pro

 210 215 220
 Asp Leu Ile Trp Ser Asp Gly Glu Trp Glu Cys Pro Asp Thr Tyr Trp
 225 230 235 240
 Asn Ser Thr Asn Phe Leu Ser Trp Leu Tyr Asn Asp Ser Pro Val Lys
 245 250 255
 Asp Glu Val Val Val Asn Asp Arg Trp Gly Gln Asn Cys Ser Cys His
 260 265 270
 His Gly Gly Tyr Tyr Asn Cys Glu Asp Lys Phe Lys Pro Gln Ser Leu

 275 280 285
 Pro Asp His Lys Trp Glu Met Cys Thr Ser Ile Asp Lys Phe Ser Trp
 290 295 300
 Gly Tyr Arg Arg Asp Met Ala Leu Ser Asp Val Thr Glu Glu Ser Glu
 305 310 315 320
 Ile Ile Ser Glu Leu Val Gln Thr Val Ser Leu Gly Gly Asn Tyr Leu
 325 330 335
 Leu Asn Ile Gly Pro Thr Lys Asp Gly Leu Ile Val Pro Ile Phe Gln

 340 345 350
 Glu Arg Leu Leu Ala Val Gly Lys Trp Leu Ser Ile Asn Gly Glu Ala

355 360 365
 Ile Tyr Ala Ser Lys Pro Trp Arg Val Gln Trp Glu Lys Asn Thr Thr
 370 375 380
 Ser Val Trp Tyr Thr Ser Lys Gly Ser Ala Val Tyr Ala Ile Phe Leu
 385 390 395 400
 His Trp Pro Glu Asn Gly Val Leu Asn Leu Glu Ser Pro Ile Thr Thr

 405 410 415
 Ser Thr Thr Lys Ile Thr Met Leu Gly Ile Gln Gly Asp Leu Lys Trp
 420 425 430
 Ser Thr Asp Pro Asp Lys Gly Leu Phe Ile Ser Leu Pro Gln Leu Pro
 435 440 445
 Pro Ser Ala Val Pro Ala Glu Phe Ala Trp Thr Ile Lys Leu Thr Gly
 450 455 460
 Val Lys
 465
 <210> 4572
 <211> 452

 <212> PRT
 <213> homo sapiens
 <400> 4572
 Met Phe Asp Ile Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys
 1 5 10 15
 Phe Ala Lys Glu Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His
 20 25 30
 Lys Phe Ile Ala Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr
 35 40 45
 Thr Gln Asn Ile Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile

 50 55 60
 Ile Gln Cys His Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys
 65 70 75 80
 Tyr Lys Val Asp Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val
 85 90 95

Val Pro Arg Cys Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met
100 105 110
Lys Pro Glu Ile Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His
115 120 125
Arg Ala Met Lys Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile
130 135 140
Gly Ser Ser Leu Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile
145 150 155 160
Pro His Glu Val Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His
165 170 175
Leu His Phe Asp Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn
180 185 190
Glu Leu Cys His Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn
195 200 205
Pro Val Lys Leu Ser Glu Ile Thr Glu Lys Pro Pro Arg Thr Gln Lys
210 215 220
Glu Leu Ala Tyr Leu Ser Glu Leu Pro Pro Thr Pro Leu His Val Ser
225 230 235 240
Glu Asp Ser Ser Ser Pro Glu Arg Thr Ser Pro Pro Asp Ser Ser Val
245 250 255
Ile Val Thr Leu Leu Asp Gln Ala Ala Lys Ser Asn Asp Asp Leu Asp
260 265 270
Val Ser Glu Ser Lys Gly Cys Met Glu Glu Lys Pro Gln Glu Val Gln
275 280 285
Thr Ser Arg Asn Val Glu Ser Ile Ala Glu Gln Met Glu Asn Pro Asp
290 295 300
Leu Lys Asn Val Gly Ser Ser Thr Gly Glu Lys Asn Glu Arg Thr Ser
305 310 315 320
Val Ala Gly Thr Val Arg Lys Cys Trp Pro Asn Arg Val Ala Lys Glu
325 330 335
Gln Ile Ser Arg Arg Leu Asp Gly Asn Gln Tyr Leu Phe Leu Pro Pro

340 345 350
 Asn Arg Tyr Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp
 355 360 365
 Asp Val Leu Ser Ser Ser Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr

370 375 380
 Cys Gln Ser Pro Ser Leu Glu Glu Pro Met Glu Asp Glu Ser Glu Ile
 385 390 395 400
 Glu Glu Phe Tyr Asn Gly Leu Glu Asp Glu Pro Asp Val Pro Glu Arg
 405 410 415
 Ala Gly Gly Ala Gly Phe Gly Thr Asp Gly Asp Asp Gln Glu Ala Ile
 420 425 430
 Asn Glu Ala Ile Ser Val Lys Gln Glu Val Thr Asp Met Asn Tyr Pro

435 440 445
 Ser Asn Lys Ser

450
 <210> 4573
 <211> 747
 <212> PRT
 <213> homo sapiens
 <400> 4573

Met Ala Asp Glu Ala Ala Leu Ala Leu Gln Pro Gly Gly Ser Pro Ser
 1 5 10 15
 Ala Ala Gly Ala Asp Arg Glu Ala Ala Ser Ser Pro Ala Gly Glu Pro
 20 25 30
 Leu Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Glu Arg Ser Pro
 35 40 45

Gly Glu Pro Gly Gly Ala Ala Pro Glu Arg Glu Val Pro Ala Ala Ala
 50 55 60
 Arg Gly Cys Pro Gly Ala Ala Ala Ala Leu Trp Arg Glu Ala Glu
 65 70 75 80
 Ala Glu Ala Ala Ala Ala Gly Gly Glu Gln Glu Ala Gln Ala Thr Ala
 85 90 95

Ala Ala Gly Glu Gly Asp Asn Gly Pro Gly Leu Gln Gly Pro Ser Arg
100 105 110

Glu Pro Pro Leu Ala Asp Asn Leu Tyr Asp Glu Asp Asp Asp Asp Glu
115 120 125

Gly Glu Glu Glu Glu Glu Ala Ala Ala Ala Ala Ile Gly Tyr Arg Asp
130 135 140

Asn Leu Leu Phe Gly Asp Glu Ile Ile Thr Asn Gly Phe His Ser Cys
145 150 155 160

Glu Ser Asp Glu Glu Asp Arg Ala Ser His Ala Ser Ser Ser Asp Trp
165 170 175

Thr Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe Val Gln Gln His Leu
180 185 190

Met Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys Asp Leu Leu Pro Glu
195 200 205

Thr Ile Pro Pro Pro Glu Leu Asp Asp Met Thr Leu Trp Gln Ile Val
210 215 220

Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp Ile
225 230 235 240

Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys Ile
245 250 255

Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro Asp
260 265 270

Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe Pro
275 280 285

Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg Lys
290 295 300

Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly Gln
305 310 315 320

Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys Glu
325 330 335

Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu Gln

340 345 350
 Val Ala Gly Ile Gln Arg Ile Ile Gln Cys His Gly Ser Phe Ala Thr
 355 360 365

 Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val Arg
 370 375 380
 Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro Ala
 385 390 395 400
 Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly Glu
 405 410 415
 Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp Glu
 420 425 430

 Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro Val
 435 440 445
 Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu Ile
 450 455 460
 Asn Arg Glu Pro Leu Pro His Leu His Phe Asp Val Glu Leu Leu Gly
 465 470 475 480
 Asp Cys Asp Val Ile Ile Asn Glu Leu Cys His Arg Leu Gly Gly Glu
 485 490 495

 Tyr Ala Lys Leu Cys Cys Asn Pro Val Lys Leu Ser Glu Ile Thr Glu
 500 505 510
 Lys Pro Pro Arg Thr Gln Lys Glu Leu Ala Tyr Leu Ser Glu Leu Pro
 515 520 525
 Pro Thr Pro Leu His Val Ser Glu Asp Ser Ser Ser Pro Glu Arg Thr
 530 535 540
 Ser Pro Pro Asp Ser Ser Val Ile Val Thr Leu Leu Asp Gln Ala Ala
 545 550 555 560

 Lys Ser Asn Asp Asp Leu Asp Val Ser Glu Ser Lys Gly Cys Met Glu
 565 570 575
 Glu Lys Pro Gln Glu Val Gln Thr Ser Arg Asn Val Glu Ser Ile Ala
 580 585 590

Glu Gln Met Glu Asn Pro Asp Leu Lys Asn Val Gly Ser Ser Thr Gly
595 600 605

Glu Lys Asn Glu Arg Thr Ser Val Ala Gly Thr Val Arg Lys Cys Trp
610 615 620

Pro Asn Arg Val Ala Lys Glu Gln Ile Ser Arg Arg Leu Asp Gly Asn
625 630 635 640

Gln Tyr Leu Phe Leu Pro Pro Asn Arg Tyr Ile Phe His Gly Ala Glu
645 650 655

Val Tyr Ser Asp Ser Glu Asp Asp Val Leu Ser Ser Ser Ser Cys Gly
660 665 670

Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser Pro Ser Leu Glu Glu Pro
675 680 685

Met Glu Asp Glu Ser Glu Ile Glu Glu Phe Tyr Asn Gly Leu Glu Asp
690 695 700

Glu Pro Asp Val Pro Glu Arg Ala Gly Gly Ala Gly Phe Gly Thr Asp
705 710 715 720

Gly Asp Asp Gln Glu Ala Ile Asn Glu Ala Ile Ser Val Lys Gln Glu
725 730 735

Val Thr Asp Met Asn Tyr Pro Ser Asn Lys Ser
740 745

<210> 4574

<211> 189

<212> PRT

<213> homo sapiens

<400> 4574

Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu
1 5 10 15

Met Glu Thr Val Ile Pro Val Asp Val Met Arg Arg Ala Gly Ile Lys
20 25 30

Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg
35 40 45

Asp Val Val Ile Cys Pro Asp Ala Ser Leu Glu Asp Ala Lys Lys Glu

50 55 60

Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln

65 70 75 80

Asn Leu Ser Glu Ser Ala Ala Val Lys Glu Ile Leu Lys Glu Gln Glu

85 90 95

Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu

100 105 110

Leu Ala His Glu Ile Gly Phe Gly Ser Lys Val Thr Thr His Pro Leu

115 120 125

Ala Lys Asp Lys Met Met Asn Gly Gly His Tyr Thr Tyr Ser Glu Asn

130 135 140

Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr

145 150 155 160

Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Asn Gly Lys Glu

165 170 175

Val Ala Ala Gln Val Lys Ala Pro Leu Val Leu Lys Asp

180 185

<210> 4575

<211> 189

<212> PRT

<213> homo sapiens

<400> 4575

Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu

1 5 10 15

Met Glu Thr Val Ile Pro Val Asp Val Met Arg Arg Ala Gly Ile Lys

20 25 30

Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg

35 40 45

Asp Val Val Ile Cys Pro Asp Ala Ser Leu Glu Asp Ala Lys Lys Glu

50 55 60

Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln
65 70 75 80
Asn Leu Ser Glu Ser Ala Ala Val Lys Glu Ile Leu Lys Glu Gln Glu
85 90 95
Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu
100 105 110

Leu Ala His Glu Ile Gly Phe Gly Ser Lys Val Thr Thr His Pro Leu
115 120 125
Ala Lys Asp Lys Met Met Asn Gly Gly His Tyr Thr Tyr Ser Glu Asn
130 135 140
Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr
145 150 155 160
Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Asn Gly Lys Glu
165 170 175

Val Ala Ala Gln Val Lys Ala Pro Leu Val Leu Lys Asp
180 185

<210> 4576

<211> 339

<212> PRT

<213> homo sapiens

<400> 4576

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp
1 5 10 15
His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn
20 25 30
Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

35 40 45
Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser
50 55 60
Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys
65 70 75 80
Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu

85 90 95
 Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser
 100 105 110
 Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
 115 120 125
 Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
 130 135 140
 Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
 145 150 155 160
 Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
 165 170 175
 Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
 180 185 190
 Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
 195 200 205
 Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
 210 215 220
 Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
 225 230 235 240
 Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
 245 250 255
 Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
 260 265 270
 Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
 275 280 285
 Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
 290 295 300
 Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln
 305 310 315 320
 Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly
 325 330 335

Gly Asp Asp

<210> 4577

<211> 339

<212> PRT

<213> homo sapiens

<400> 4577

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp

1 5 10 15

His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn

20 25 30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser

50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys

65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu

85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser

100 105 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu

115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn

130 135 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile

145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys

165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp

180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr

195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His

210 215 220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met

225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe

245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp

260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu

275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg

290 295 300

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln

305 310 315 320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly

325 330 335

Gly Asp Asp

<210> 4578

<211> 357

<212> PRT

<213> homo sapiens

<400> 4578

Met Gly Arg Gln Leu Ala Gly Cys Gly Asp Ala Gly Lys Lys Ala Ser

1 5 10 15

Phe Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu

20 25 30

Gly Asp His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr

35 40 45

Thr Asn Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile

50 55 60
 Lys Thr Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn
 65 70 75 80
 Arg Ser Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg
 85 90 95
 Thr Lys Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His
 100 105 110
 Leu Glu Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp

 115 120 125
 Ala Ser Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp
 130 135 140
 Ser Leu Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu
 145 150 155 160
 Ile Asn Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp
 165 170 175
 Ile Ile Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu

 180 185 190
 Ala Lys Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu
 195 200 205
 Ile Asp Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys
 210 215 220
 Gly Thr Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val
 225 230 235 240
 Pro His Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr

 245 250 255
 Asp Met Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn
 260 265 270
 Ala Phe Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe
 275 280 285
 Ala Asp Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys
 290 295 300

Val Leu Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys

305 310 315 320

Ile Arg Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr

325 330 335

Ile Gln Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu

340 345 350

Cys Gly Gly Asp Asp

355

<210> 4579

<211> 339

<212> PRT

<213> homo sapiens

<400> 4579

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp

1 5 10 15

His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn

20 25 30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser

50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys

65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu

85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser

100 105 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu

115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn

130 135 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
 145 150 155 160
 Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
 165 170 175
 Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
 180 185 190
 Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr

 195 200 205
 Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
 210 215 220
 Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
 225 230 235 240
 Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
 245 250 255
 Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp

 260 265 270
 Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
 275 280 285
 Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
 290 295 300
 Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln
 305 310 315 320
 Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly

 325 330 335
 Gly Asp Asp

<210> 4580

<211> 180

<212> PRT

<213> homo sapiens

<400> 4580

Met Lys Ser Ile Tyr Phe Val Ala Gly Leu Phe Val Met Leu Val Gln

1 5 10 15
 Gly Ser Trp Gln Arg Ser Leu Gln Asp Thr Glu Glu Lys Ser Arg Ser
 20 25 30
 Phe Ser Ala Ser Gln Ala Asp Pro Leu Ser Asp Pro Asp Gln Met Asn
 35 40 45

Glu Asp Lys Arg His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys
 50 55 60
 Tyr Leu Asp Ser Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn
 65 70 75 80
 Thr Lys Arg Asn Arg Asn Asn Ile Ala Lys Arg His Asp Glu Phe Glu
 85 90 95
 Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu
 100 105 110

Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 115 120 125
 Arg Arg Asp Phe Pro Glu Glu Val Ala Ile Val Glu Glu Leu Gly Arg
 130 135 140
 Arg His Ala Asp Gly Ser Phe Ser Asp Glu Met Asn Thr Ile Leu Asp
 145 150 155 160
 Asn Leu Ala Ala Arg Asp Phe Ile Asn Trp Leu Ile Gln Thr Lys Ile
 165 170 175

Thr Asp Arg Lys
 180

<210> 4581

<211> 167

<212> PRT

<213> homo sapiens

<400> 4581

Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
 1 5 10 15
 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30

Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45
Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
50 55 60
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
65 70 75 80
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
85 90 95
Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
100 105 110
Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
115 120 125
Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
130 135 140
Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
145 150 155 160
Leu Asp Leu Ser Pro Gly Cys
165
<210> 4582
<211> 455
<212> PRT
<213> homo sapiens
<400> 4582
Met Asp Ala Ala Leu Lys Arg Ser Arg Ser Glu Glu Pro Ala Glu Ile
1 5 10 15
Leu Pro Pro Ala Arg Asp Glu Glu Glu Glu Glu Glu Gly Met Glu
20 25 30
Gln Gly Leu Glu Glu Glu Glu Glu Val Asp Pro Arg Ile Gln Gly Glu
35 40 45
Leu Glu Lys Leu Asn Gln Ser Thr Asp Asp Ile Asn Arg Arg Glu Thr
50 55 60

Glu Leu Glu Asp Ala Arg Gln Lys Phe Arg Ser Val Leu Val Glu Ala

65 70 75 80

Thr Val Lys Leu Asp Glu Leu Val Lys Lys Ile Gly Lys Ala Val Glu

85 90 95

Asp Ser Lys Pro Tyr Trp Glu Ala Arg Arg Val Ala Arg Gln Ala Gln

100 105 110

Leu Glu Ala Gln Lys Ala Thr Gln Asp Phe Gln Arg Ala Thr Glu Val

115 120 125

Leu Arg Ala Ala Lys Glu Thr Ile Ser Leu Ala Glu Gln Arg Leu Leu

130 135 140

Glu Asp Asp Lys Arg Gln Phe Asp Ser Ala Trp Gln Glu Met Leu Asn

145 150 155 160

His Ala Thr Gln Arg Val Met Glu Ala Glu Gln Thr Lys Thr Arg Ser

165 170 175

Glu Leu Val His Lys Glu Thr Ala Ala Arg Tyr Asn Ala Ala Met Gly

180 185 190

Arg Met Arg Gln Leu Glu Lys Lys Leu Lys Arg Ala Ile Asn Lys Ser

195 200 205

Lys Pro Tyr Phe Glu Leu Lys Ala Lys Tyr Tyr Val Gln Leu Glu Gln

210 215 220

Leu Lys Lys Thr Val Asp Asp Leu Gln Ala Lys Leu Thr Leu Ala Lys

225 230 235 240

Gly Glu Tyr Lys Met Ala Leu Lys Asn Leu Glu Met Ile Ser Asp Glu

245 250 255

Ile His Glu Arg Arg Arg Ser Ser Ala Met Gly Pro Arg Gly Cys Gly

260 265 270

Val Gly Ala Glu Gly Ser Ser Thr Ser Val Glu Asp Leu Pro Gly Ser

275 280 285

Lys Pro Glu Pro Asp Ala Ile Ser Val Ala Ser Glu Ala Phe Glu Asp

290 295 300

Asp Ser Cys Ser Asn Phe Val Ser Glu Asp Asp Ser Glu Thr Gln Ser

305 310 315 320
Val Ser Ser Phe Ser Ser Gly Pro Thr Ser Pro Ser Glu Met Pro Asp

 325 330 335
Gln Phe Pro Ala Val Val Arg Pro Gly Ser Leu Asp Leu Pro Ser Pro

 340 345 350
Val Ser Leu Ser Glu Phe Gly Met Met Phe Pro Val Leu Gly Pro Arg

 355 360 365
Ser Glu Cys Ser Gly Ala Ser Ser Pro Glu Cys Glu Val Glu Arg Gly

 370 375 380
Asp Arg Ala Glu Gly Ala Glu Asn Lys Thr Ser Asp Lys Ala Asn Asn

385 390 395 400
Asn Arg Gly Leu Ser Ser Ser Ser Gly Ser Gly Gly Ser Ser Lys Ser

 405 410 415
Gln Ser Ser Thr Ser Pro Glu Gly Gln Ala Leu Glu Asn Arg Met Lys

 420 425 430
Gln Leu Ser Leu Gln Cys Ser Lys Gly Arg Asp Gly Ile Ile Ala Asp

 435 440 445
Ile Lys Met Val Gln Ile Gly

 450 455

<210> 4583

<211> 298

<212> PRT

<213> homo sapiens

<400> 4583

Met Leu Asn His Ala Thr Gln Arg Val Met Glu Ala Glu Gln Thr Lys

1 5 10 15

Thr Arg Ser Glu Leu Val His Lys Glu Thr Ala Ala Arg Tyr Asn Ala

 20 25 30

Ala Met Gly Arg Met Arg Gln Leu Glu Lys Lys Leu Lys Arg Ala Ile

 35 40 45

Asn Lys Ser Lys Pro Tyr Phe Glu Leu Lys Ala Lys Tyr Tyr Val Gln

50 55 60
 Leu Glu Gln Leu Lys Lys Thr Val Asp Asp Leu Gln Ala Lys Leu Thr
 65 70 75 80
 Leu Ala Lys Gly Glu Tyr Lys Met Ala Leu Lys Asn Leu Glu Met Ile
 85 90 95
 Ser Asp Glu Ile His Glu Arg Arg Arg Ser Ser Ala Met Gly Pro Arg
 100 105 110
 Gly Cys Gly Val Gly Ala Glu Gly Ser Ser Thr Ser Val Glu Asp Leu

 115 120 125
 Pro Gly Ser Lys Pro Glu Pro Asp Ala Ile Ser Val Ala Ser Glu Ala
 130 135 140
 Phe Glu Asp Asp Ser Cys Ser Asn Phe Val Ser Glu Asp Asp Ser Glu
 145 150 155 160
 Thr Gln Ser Val Ser Ser Phe Ser Ser Gly Pro Thr Ser Pro Ser Glu
 165 170 175
 Met Pro Asp Gln Phe Pro Ala Val Val Arg Pro Gly Ser Leu Asp Leu

 180 185 190
 Pro Ser Pro Val Ser Leu Ser Glu Phe Gly Met Met Phe Pro Val Leu
 195 200 205
 Gly Pro Arg Ser Glu Cys Ser Gly Ala Ser Ser Pro Glu Cys Glu Val
 210 215 220
 Glu Arg Gly Asp Arg Ala Glu Gly Ala Glu Asn Lys Thr Ser Asp Lys
 225 230 235 240
 Ala Asn Asn Asn Arg Gly Leu Ser Ser Ser Ser Gly Ser Gly Gly Ser

 245 250 255
 Ser Lys Ser Gln Ser Ser Thr Ser Pro Glu Gly Gln Ala Leu Glu Asn
 260 265 270
 Arg Met Lys Gln Leu Ser Leu Gln Cys Ser Lys Gly Arg Asp Gly Ile
 275 280 285
 Ile Ala Asp Ile Lys Met Val Gln Ile Gly
 290 295
 <210> 4584

<211> 200

<212> PRT

<213> homo sapiens

<400> 4584

Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp Leu

1 5 10 15

Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp Leu Thr

20 25 30

Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn Lys Asn Ile

35 40 45

Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser Thr Asp Gln Trp

50 55 60

Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu Asn Leu Gln Ala Tyr

65 70 75 80

Arg Thr Phe His Val Leu Leu Ala Arg Leu Leu Glu Asp Gln Gln Val

85 90 95

His Phe Thr Pro Thr Glu Gly Asp Phe His Gln Ala Ile His Thr Leu

100 105 110

Leu Leu Gln Val Ala Ala Phe Ala Tyr Gln Ile Glu Glu Leu Met Ile

115 120 125

Leu Leu Glu Tyr Lys Ile Pro Arg Asn Glu Ala Asp Gly Met Pro Ile

130 135 140

Asn Val Gly Asp Gly Gly Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys

145 150 155 160

Val Leu Gln Glu Leu Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu

165 170 175

Arg Phe Ile Ser Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His

180 185 190

Tyr Ile Ala Asn Asn Lys Lys Met

195 200

<210> 4585

<211> 570

<212> PRT

<213> homo sapiens

<400> 4585

Met Pro Gly Glu Thr Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln

1 5 10 15

Glu Gly Gly Glu Ala Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg

20 25 30

Pro Pro Glu Ala Val Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg

35 40 45

Val Leu Arg Gly Gly Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala Ala

50 55 60

Ala Ala Ala Val Ser Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg

65 70 75 80

Arg Ser Ser Pro Ser Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro

85 90 95

Gln Ala Ala Lys Ser Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg

100 105 110

Leu Leu Cys Ile Glu Lys Val Thr Thr Asp Lys Asp Pro Lys Glu Glu

115 120 125

Lys Glu Glu Glu Asp Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala

130 135 140

Ala Ser Arg Pro Ser Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser

145 150 155 160

Arg His Arg Asp Thr Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly

165 170 175

Ser Leu Gln Leu Ile Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp

180 185 190

Tyr Asp Val Gly Glu Glu His Gln Ser Pro Gly Gly Ile Ser Ser Glu

195 200 205

Glu Glu Glu Glu Glu Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile

210 215 220

Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu
 225 230 235 240
 Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly Lys Val Lys Glu Glu

 245 250 255
 Lys Glu Lys Lys Glu Ile Lys Val Glu Val Glu Val Glu Val Lys Glu
 260 265 270
 Glu Glu Asn Glu Ile Arg Glu Asp Glu Glu Pro Pro Arg Lys Arg Gly
 275 280 285
 Arg Arg Arg Lys Asp Asp Lys Ser Pro Arg Leu Pro Lys Arg Arg Lys
 290 295 300
 Lys Pro Pro Ile Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr

 305 310 315 320
 Val Leu Ala His Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His
 325 330 335
 Leu Leu Lys Lys Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu
 340 345 350
 Phe Arg Leu Gln Lys Gln Leu Leu Arg His Ala Lys His His Thr Asp
 355 360 365
 Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser Ser

 370 375 380
 His Asn Leu Ala Val His Arg Met Ile His Thr Gly Glu Lys Pro Leu
 385 390 395 400
 Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu Asn
 405 410 415
 Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser Cys
 420 425 430
 Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala His

 435 440 445
 Lys Ala Lys Ser His Pro Glu Val Leu Ile Ala Glu Ala Leu Ala Ala
 450 455 460
 Asn Ala Gly Ala Leu Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro

465 470 475 480
 Glu Ser Leu Thr Gln Pro Ser Asp Gly Gln Gly Leu Pro Leu Leu Pro
 485 490 495
 Glu Pro Leu Gly Asn Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala

 500 505 510
 Glu Gly Met Ser Lys Ser Tyr Cys Ser Gly Thr Glu Arg Val Ser Leu
 515 520 525
 Met Ala Asp Gly Lys Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr
 530 535 540
 Glu Gly Leu Val Met Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val
 545 550 555 560
 Leu Ile Glu Asp Ser Asp Ser Ala Gly Pro
 565 570

<210> 4586

<211> 429

<212> PRT

<213> homo sapiens

<400> 4586

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
 1 5 10 15
 Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
 20 25 30
 Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
 35 40 45
 Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile

 50 55 60
 Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
 65 70 75 80
 Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
 85 90 95
 Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
 100 105 110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly

115 120 125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly

130 135 140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala

145 150 155 160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser

165 170 175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn

180 185 190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met

195 200 205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn

210 215 220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys

225 230 235 240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val

245 250 255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn

260 265 270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala

275 280 285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser

290 295 300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn

305 310 315 320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn

325 330 335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala

340 345 350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala

355 360 365
Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile

370 375 380
Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385 390 395 400
Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
405 410 415
Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

420 425

<210> 4587

<211> 426

<212> PRT

<213> homo sapiens

<400> 4587

Met Glu Arg Pro Ile Lys Asp Ser Met Phe Ser Leu Ala Leu Lys Cys
1 5 10 15
Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Ala Tyr
20 25 30
His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly Ala Asp Asp
35 40 45
Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile Ser Leu Glu
50 55 60

Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr Lys Phe Phe
65 70 75 80
Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg Ala Glu Ala
85 90 95
Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr Leu
100 105 110
Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala Ser
115 120 125

Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg Phe

130	135	140	
Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val			
145	150	155	160
Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Val Cys			
165	170	175	
Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala			
180	185	190	
Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met			
195	200	205	
Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile			
210	215	220	
Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys			
225	230	235	240
Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met Met Asp			
245	250	255	
Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn Val Leu Arg			
260	265	270	
Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile Asp			
275	280	285	
His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile His			
290	295	300	
Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Ser Asp Gln Ala			
305	310	315	320
Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met Tyr Asp Leu			
325	330	335	
Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys Gln Ile Gly			
340	345	350	
Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe Asn Ser Leu			
355	360	365	
Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln Gln Leu Leu			
370	375	380	

Ser Ala Ile Ile Glu Ala Arg Gly Val Ser Val Ala Val Gly Thr Thr
385 390 395 400
His Thr Pro Ile Ser Asp Ser Pro Ile Gly Val Ser Ser Thr Ser Phe
405 410 415
Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys
420 425
<210> 4588
<211> 731
<212> PRT
<213> homo sapiens
<400> 4588
Met Asp Thr Ser Gly His Phe His Asp Ser Gly Val Gly Asp Leu Asp
1 5 10 15
Glu Asp Pro Lys Cys Pro Cys Pro Ser Ser Gly Asp Glu Gln Gln Gln
20 25 30
Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Ala Pro Pro
35 40 45
Ala Ala Pro Gln Gln Pro Leu Gly Pro Ser Leu Gln Pro Gln Pro Pro
50 55 60
Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
65 70 75 80
Pro Pro His Pro Leu Ser Gln Leu Ala Gln Leu Gln Ser Gln Pro Val
85 90 95
His Pro Gly Leu Leu His Ser Ser Pro Thr Ala Phe Arg Ala Pro Pro
100 105 110
Ser Ser Asn Ser Thr Ala Ile Leu His Pro Ser Ser Arg Gln Gly Ser
115 120 125
Gln Leu Asn Leu Asn Asp His Leu Leu Gly His Ser Pro Ser Ser Thr
130 135 140
Ala Thr Ser Gly Pro Gly Gly Gly Ser Arg His Arg Gln Ala Ser Pro
145 150 155 160
Leu Val His Arg Arg Asp Ser Asn Pro Phe Thr Glu Ile Ala Met Ser

165	170	175	
Ser Cys Lys Tyr Ser Gly Gly Val Met Lys Pro Leu Ser Arg Leu Ser			
180	185	190	
Ala Ser Arg Arg Asn Leu Ile Glu Ala Glu Thr Glu Gly Gln Pro Leu			
195	200	205	
Gln Leu Phe Ser Pro Ser Asn Pro Pro Glu Ile Val Ile Ser Ser Arg			
210	215	220	
Glu Asp Asn His Ala His Gln Thr Leu Leu His His Pro Asn Ala Thr			
225	230	235	240
His Asn His Gln His Ala Gly Thr Thr Ala Ser Ser Thr Thr Phe Pro			
245	250	255	
Lys Ala Asn Lys Arg Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly His			
260	265	270	
Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala Leu			
275	280	285	
Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu Leu			
290	295	300	
Ser Trp Gly Leu Tyr Ser Lys Asp Ser Met Phe Ser Leu Ala Leu Lys			
305	310	315	320
Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile Ala			
325	330	335	
Tyr His Thr Arg Glu Val Gln Leu Phe Val Ile Asp Asn Gly Ala Asp			
340	345	350	
Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Leu Tyr Ile Ser Leu			
355	360	365	
Glu Met Leu Val Cys Ala Ile His Pro Ile Pro Gly Glu Tyr Lys Phe			
370	375	380	
Phe Trp Thr Ala Arg Leu Ala Phe Ser Tyr Thr Pro Ser Arg Ala Glu			
385	390	395	400
Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu Tyr			
405	410	415	

Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp Ala
 420 425 430
 Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr Arg
 435 440 445
 Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu
 450 455 460

 Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Val
 465 470 475 480
 Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly
 485 490 495
 Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp
 500 505 510
 Met Val Pro His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly
 515 520 525

 Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg
 530 535 540
 Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val His Asn Phe Met Met
 545 550 555 560
 Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala Ala Ala Asn Val Leu
 565 570 575
 Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile
 580 585 590

 Asp His Ala Lys Val Arg Lys His Gln Arg Lys Phe Leu Gln Ala Ile
 595 600 605
 His Gln Leu Arg Ser Val Lys Met Glu Gln Arg Lys Leu Ser Asp Gln
 610 615 620
 Ala Asn Thr Leu Val Asp Leu Ser Lys Met Gln Asn Val Met Tyr Asp
 625 630 635 640
 Leu Ile Thr Glu Leu Asn Asp Arg Ser Glu Asp Leu Glu Lys Gln Ile
 645 650 655

 Gly Ser Leu Glu Ser Lys Leu Glu His Leu Thr Ala Ser Phe Asn Ser

660 665 670
 Leu Pro Leu Leu Ile Ala Asp Thr Leu Arg Gln Gln Gln Gln Gln Leu
 675 680 685
 Leu Ser Ala Ile Ile Glu Ala Arg Gly Val Ser Val Ala Val Gly Thr
 690 695 700
 Thr His Thr Pro Ile Ser Asp Ser Pro Ile Gly Val Ser Ser Thr Ser
 705 710 715 720

Phe Pro Thr Pro Tyr Thr Ser Ser Ser Ser Cys

725 730

<210> 4589

<211> 509

<212> PRT

<213> homo sapiens

<400> 4589

Met Ser Met Gly Ala Pro Arg Ser Leu Leu Leu Ala Leu Ala Ala Gly
 1 5 10 15
 Leu Ala Val Ala Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp
 20 25 30
 Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr
 35 40 45

Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe
 50 55 60
 Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr
 65 70 75 80
 Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro
 85 90 95
 Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val
 100 105 110

Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu
 115 120 125
 Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His
 130 135 140

Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn
 145 150 155 160
 Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln
 165 170 175

 Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln
 180 185 190
 Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His
 195 200 205
 Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr
 210 215 220
 Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe
 225 230 235 240

 Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu
 245 250 255
 Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu
 260 265 270
 Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr
 275 280 285
 Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys
 290 295 300

 Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp
 305 310 315 320
 Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu
 325 330 335
 Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn
 340 345 350
 Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly
 355 360 365

 Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu
 370 375 380
 Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe

385 390 395 400
 Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys
 405 410 415
 His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp
 420 425 430

 Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala
 435 440 445
 Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu
 450 455 460
 Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala
 465 470 475 480
 Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr
 485 490 495

 Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
 500 505

 <210> 4590
 <211> 423
 <212> PRT
 <213> homo sapiens
 <400> 4590

 Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser Arg Gly Gly Leu
 1 5 10 15
 Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala Ala Arg Gly Tyr
 20 25 30
 Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val Gly Pro Glu Gly

 35 40 45
 Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe Leu Gly Ile Pro
 50 55 60
 Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr Cys Phe Pro Pro
 65 70 75 80
 Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu Val Pro Ile Pro
 85 90 95

Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro Trp Leu Pro Gly

100 105 110

Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu Met Ala Asp Ala

115 120 125

Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala Ser His His Thr

130 135 140

His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu Arg Ser Gly Arg

145 150 155 160

Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala Ala Val Gly Thr

165 170 175

Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu Glu Thr Leu Val

180 185 190

Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg Met Ser Arg Gly

195 200 205

Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr Thr Tyr Glu Gly

210 215 220

Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly His Ile Ala Pro

225 230 235 240

Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu Leu Pro Thr Leu

245 250 255

Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr Leu Asp Gly Phe

260 265 270

Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser Pro Arg Gln Ser

275 280 285

Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg Gly Val Phe Ala

290 295 300

Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr Gln Gly Ser Ala

305 310 315 320

His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala Ser Ser Ser Leu

325 330 335

Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser Lys Asp Pro Gly

340 345 350
Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala Thr Pro Glu Val

355 360 365
Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala Gln Leu Asp Ala

370 375 380
Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly Glu Asp Pro Ala

385 390 395 400
Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg Pro Ala Cys Cys

405 410 415
His Cys Pro Asp Pro His Ala

420

<210> 4591

<211> 509

<212> PRT

<213> homo sapiens

<400> 4591

Met Ser Met Gly Ala Pro Arg Ser Leu Leu Leu Ala Leu Ala Ala Gly

1 5 10 15

Leu Ala Val Ala Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp

20 25 30

Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr

35 40 45

Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe

50 55 60

Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr

65 70 75 80

Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro

85 90 95

Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val

100 105 110

Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu

115	120	125	
Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His			
130	135	140	
Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn			
145	150	155	160
Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln			
165	170	175	
Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln			
180	185	190	
Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His			
195	200	205	
Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr			
210	215	220	
Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe			
225	230	235	240
Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu			
245	250	255	
Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu			
260	265	270	
Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr			
275	280	285	
Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys			
290	295	300	
Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp			
305	310	315	320
Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu			
325	330	335	
Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn			
340	345	350	
Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly			
355	360	365	

Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu

370

375

380

Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe

385

390

395

400

Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys

405

410

415

His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp

420

425

430

Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala

435

440

445

Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu

450

455

460

Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala

465

470

475

480

Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr

485

490

495

Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala

500

505

<210> 4592

<211> 509

<212> PRT

<213> homo sapiens

<400> 4592

Met Ser Met Gly Ala Pro Arg Ser Leu Leu Leu Ala Leu Ala Ala Gly

1

5

10

15

Leu Ala Val Ala Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp

20

25

30

Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr

35

40

45

Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe

50

55

60

Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr
 65 70 75 80
 Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro
 85 90 95
 Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val
 100 105 110

 Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu
 115 120 125
 Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His
 130 135 140
 Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn
 145 150 155 160
 Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln
 165 170 175

 Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln
 180 185 190
 Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His
 195 200 205
 Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr
 210 215 220
 Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe
 225 230 235 240

 Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu
 245 250 255
 Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu
 260 265 270
 Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr
 275 280 285
 Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys
 290 295 300

 Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp

305 310 315 320
 Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu
 325 330 335
 Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn
 340 345 350
 Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly
 355 360 365

 Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu
 370 375 380
 Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe
 385 390 395 400
 Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys
 405 410 415
 His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp
 420 425 430

 Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala
 435 440 445
 Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu
 450 455 460
 Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala
 465 470 475 480
 Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr
 485 490 495

 Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
 500 505

 <210> 4593
 <211> 509
 <212> PRT
 <213> homo sapiens
 <400> 4593
 Met Ser Met Gly Ala Pro Arg Ser Leu Leu Leu Ala Leu Ala Ala Gly
 1 5 10 15

Leu Ala Val Ala Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp
 20 25 30
 Leu Gly Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr
 35 40 45
 Pro Asn Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe
 50 55 60
 Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr
 65 70 75 80
 Gly Arg Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro
 85 90 95
 Ser Ser Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val
 100 105 110
 Leu Ala Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu
 115 120 125
 Gly Val Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His
 130 135 140
 Arg Phe Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn
 145 150 155 160
 Leu Thr Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln
 165 170 175
 Gly Leu Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln
 180 185 190
 Pro Pro Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His
 195 200 205
 Asp Leu Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr
 210 215 220
 Tyr Ala Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe
 225 230 235 240
 Ala Glu Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu
 245 250 255
 Asp Ala Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu

260 265 270
 Leu Glu Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr
 275 280 285
 Met Arg Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys

290 295 300
 Gly Thr Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp
 305 310 315 320
 Pro Gly His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu
 325 330 335
 Asp Leu Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn
 340 345 350
 Val Thr Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly

355 360 365
 Lys Ser Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu
 370 375 380
 Val Arg Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe
 385 390 395 400
 Phe Thr Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys
 405 410 415
 His Ala Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp

420 425 430
 Leu Ser Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala
 435 440 445
 Gly Ala Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu
 450 455 460
 Lys Ala Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala
 465 470 475 480
 Arg Gly Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr

485 490 495
 Pro Arg Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
 500 505

<210> 4594

<211> 354

<212> PRT

<213> homo sapiens

<400> 4594

Met Ala Ala Pro Ala Leu Gly Leu Val Cys Gly Arg Cys Pro Glu Leu

1 5 10 15

Gly Leu Val Leu Leu Leu Leu Leu Ser Leu Leu Cys Gly Ala Ala

20 25 30

Gly Ser Gln Glu Ala Gly Thr Gly Ala Gly Ala Gly Ser Leu Ala Gly

35 40 45

Ser Cys Gly Cys Gly Thr Pro Gln Arg Pro Gly Ala His Gly Ser Ser

50 55 60

Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn Ala Pro Gly Pro Val

65 70 75 80

Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met Val Pro Ile Pro Ala

85 90 95

Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly

100 105 110

Glu Ala Pro Ala Arg Arg Val Thr Ile Asp Ala Phe Tyr Met Asp Ala

115 120 125

Tyr Glu Val Ser Asn Thr Glu Phe Glu Lys Phe Val Asn Ser Thr Gly

130 135 140

Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp Ser Phe Val Phe Glu Gly

145 150 155 160

Met Leu Ser Glu Gln Val Lys Thr Asn Ile Gln Gln Ala Val Ala Ala

165 170 175

Ala Pro Trp Trp Leu Pro Val Lys Gly Ala Asn Trp Arg His Pro Glu

180 185 190

Gly Pro Asp Ser Thr Ile Leu His Arg Pro Asp His Pro Val Leu His

195 200 205

Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr Trp Ala Gly Lys Arg

210 215 220

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys Arg Gly Gly Leu His

225 230 235 240

Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln Pro Lys Gly Gln His

245 250 255

Tyr Ala Asn Ile Trp Gln Gly Glu Phe Pro Val Thr Asn Thr Gly Glu

260 265 270

Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala Phe Pro Pro Asn Gly

275 280 285

Tyr	Gly	Leu	Tyr	Asn	Ile	Val	Gly	Asn	Ala	Trp	Glu	Trp	Thr	Ser	Asp	
290						295						300				
Trp	Trp	Thr	Val	His	His	Ser	Val	Glu	Glu	Thr	Leu	Asn	Pro	Ser	Tyr	
305						310						315			320	
Cys	Tyr	Arg	Tyr	Arg	Cys	Ala	Ala	Arg	Ser	Gln	Asn	Thr	Pro	Asp	Ser	
			325						330						335	
Ser	Ala	Ser	Asn	Leu	Gly	Phe	Arg	Cys	Ala	Ala	Asp	Arg	Leu	Pro	Thr	
			340						345						350	

Met Asp

<210> 4595

<211> 349

<212> PRT

<213> homo sapiens

<400> 4595

Met	Ala	Ala	Pro	Ala	Leu	Gly	Leu	Val	Cys	Gly	Arg	Cys	Pro	Glu	Leu
1			5						10					15	
Gly	Leu	Val	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Cys	Gly	Ala	Ala
			20						25					30	
Gly	Ser	Gln	Glu	Ala	Gly	Thr	Gly	Ala	Gly	Ala	Gly	Ser	Leu	Ala	Gly
			35						40					45	
Ser	Cys	Gly	Cys	Gly	Thr	Pro	Gln	Arg	Pro	Gly	Ala	His	Gly	Ser	Ser

50 55 60
 Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn Ala Pro Gly Pro Val
 65 70 75 80
 Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met Val Pro Ile Pro Ala
 85 90 95
 Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly
 100 105 110
 Glu Ala Pro Ala Arg Arg Val Thr Ile Asp Ala Phe Tyr Met Asp Ala

 115 120 125
 Tyr Glu Val Ser Asn Thr Glu Phe Glu Lys Phe Val Asn Ser Thr Gly
 130 135 140
 Tyr Leu Thr Glu Val Ala Ala Ala Pro Trp Trp Leu Pro Val Lys Gly
 145 150 155 160
 Ala Asn Trp Arg His Pro Glu Gly Pro Asp Ser Thr Ile Leu His Arg
 165 170 175
 Pro Asp His Pro Val Leu His Val Ser Trp Asn Asp Ala Val Ala Tyr

 180 185 190
 Cys Thr Trp Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Tyr
 195 200 205
 Ser Cys Arg Gly Gly Leu His Asn Arg Leu Phe Pro Trp Gly Asn Lys
 210 215 220
 Leu Gln Pro Lys Gly Gln His Tyr Ala Asn Ile Trp Gln Gly Glu Phe
 225 230 235 240
 Pro Val Thr Asn Thr Gly Glu Asp Gly Phe Gln Gly Thr Ala Pro Val

 245 250 255
 Asp Ala Phe Pro Pro Asn Gly Tyr Gly Leu Tyr Asn Ile Val Gly Asn
 260 265 270
 Ala Trp Glu Trp Thr Ser Asp Trp Trp Thr Val His His Ser Val Glu
 275 280 285
 Glu Thr Leu Asn Pro Lys Gly Pro Pro Ser Gly Lys Asp Arg Val Lys
 290 295 300

Lys Gly Gly Ser Tyr Met Cys His Arg Ser Tyr Cys Tyr Arg Tyr Arg

305 310 315 320

Cys Ala Ala Arg Ser Gln Asn Thr Pro Asp Ser Ser Ala Ser Asn Leu

325 330 335

Gly Phe Arg Cys Ala Ala Asp Arg Leu Pro Thr Met Asp

340 345

<210> 4596

<211> 374

<212> PRT

<213> homo sapiens

<400> 4596

Met Ala Ala Pro Ala Leu Gly Leu Val Cys Gly Arg Cys Pro Glu Leu

1 5 10 15

Gly Leu Val Leu Leu Leu Leu Leu Ser Leu Leu Cys Gly Ala Ala

20 25 30

Gly Ser Gln Glu Ala Gly Thr Gly Ala Gly Ala Gly Ser Leu Ala Gly

35 40 45

Ser Cys Gly Cys Gly Thr Pro Gln Arg Pro Gly Ala His Gly Ser Ser

50 55 60

Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn Ala Pro Gly Pro Val

65 70 75 80

Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met Val Pro Ile Pro Ala

85 90 95

Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly

100 105 110

Glu Ala Pro Ala Arg Arg Val Thr Ile Asp Ala Phe Tyr Met Asp Ala

115 120 125

Tyr Glu Val Ser Asn Thr Glu Phe Glu Lys Phe Val Asn Ser Thr Gly

130 135 140

Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp Ser Phe Val Phe Glu Gly

145 150 155 160

Met Leu Ser Glu Gln Val Lys Thr Asn Ile Gln Gln Ala Val Ala Ala

165 170 175

Ala Pro Trp Trp Leu Pro Val Lys Gly Ala Asn Trp Arg His Pro Glu

180 185 190

Gly Pro Asp Ser Thr Ile Leu His Arg Pro Asp His Pro Val Leu His

195 200 205

Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr Trp Ala Gly Lys Arg

210 215 220

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys Arg Gly Gly Leu His

225 230 235 240

Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln Pro Lys Gly Gln His

245 250 255

Tyr Ala Asn Ile Trp Gln Gly Glu Phe Pro Val Thr Asn Thr Gly Glu

260 265 270

Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala Phe Pro Pro Asn Gly

275 280 285

Tyr Gly Leu Tyr Asn Ile Val Gly Asn Ala Trp Glu Trp Thr Ser Asp

290 295 300

Trp Trp Thr Val His His Ser Val Glu Glu Thr Leu Asn Pro Lys Gly

305 310 315 320

Pro Pro Ser Gly Lys Asp Arg Val Lys Lys Gly Gly Ser Tyr Met Cys

325 330 335

His Arg Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn

340 345 350

Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly Phe Arg Cys Ala Ala Asp

355 360 365

Arg Leu Pro Thr Met Asp

370

<210> 4597

<211> 196

<212> PRT

<213> homo sapiens

<400> 4597

Met Arg Leu Pro Leu Leu Val Ser Ala Gly Val Leu Leu Val Ala Leu
1 5 10 15

Leu Pro Cys Pro Pro Cys Arg Ala Leu Leu Ser Arg Gly Pro Val Pro
20 25 30

Gly Ala Arg Gln Ala Pro Gln His Pro Gln Pro Leu Asp Phe Phe Gln
35 40 45

Pro Pro Pro Gln Ser Glu Gln Pro Gln Gln Pro Gln Ala Arg Pro Val
50 55 60

Leu Leu Arg Met Gly Glu Glu Tyr Phe Leu Arg Leu Gly Asn Leu Asn
65 70 75 80

Lys Ser Pro Ala Ala Pro Leu Ser Pro Ala Ser Ser Leu Leu Ala Gly
85 90 95

Gly Ser Gly Ser Arg Pro Ser Pro Glu Gln Ala Thr Ala Asn Phe Phe
100 105 110

Arg Val Leu Leu Gln Gln Leu Leu Leu Pro Arg Arg Ser Leu Asp Ser
115 120 125

Pro Ala Ala Leu Ala Glu Arg Gly Ala Arg Asn Ala Leu Gly Gly His
130 135 140

Gln Glu Ala Pro Glu Arg Glu Arg Arg Ser Glu Glu Pro Pro Ile Ser
145 150 155 160

Leu Asp Leu Thr Phe His Leu Leu Arg Glu Val Leu Glu Met Ala Arg
165 170 175

Ala Glu Gln Leu Ala Gln Gln Ala His Ser Asn Arg Lys Leu Met Glu
180 185 190

Ile Ile Gly Lys
195

<210> 4598

<211> 631

<212> PRT

<213> homo sapiens

<400> 4598

Met Pro Arg Tyr Gly Ala Ser Leu Arg Gln Ser Cys Pro Arg Ser Gly

1 5 10 15

Arg Glu Gln Gly Gln Asp Gly Thr Ala Gly Ala Pro Gly Leu Leu Trp

20 25 30

Met Gly Leu Val Leu Ala Leu Ala Leu Ala Leu Ala Leu Ala Leu Ala

35 40 45

Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu

50 55 60

Ser Pro Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu

65 70 75 80

Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly

85 90 95

Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Lys Glu Pro Asn Val Ala

100 105 110

Arg Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala

115 120 125

Pro Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met

130 135 140

Val Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly

145 150 155 160

Leu Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp

165 170 175

Asn Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser

180 185 190

Pro Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp

195 200 205

Leu His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala

210 215 220

Asp Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg

225 230 235 240

Pro Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu

245 250 255
Arg Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe

260 265 270
Asp Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp His

275 280 285
Gln Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala Leu

290 295 300
Val Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro Ala Val Gly Asn

305 310 315 320
His Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu Gly

325 330 335
Asn His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp Glu

340 345 350
Pro Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe

355 360 365
Tyr Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met

370 375 380
Asn Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp

385 390 395 400
Pro Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu

405 410 415
Asp Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly His

420 425 430
Cys Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr

435 440 445
Glu Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp Glu

450 455 460
Phe Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val

465 470 475 480
Ala Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly

485 490 495

Tyr Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val
 500 505 510
 Val Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile
 515 520 525
 Pro Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr
 530 535 540
 Tyr Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val Tyr
 545 550 555 560
 Arg Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe Leu Tyr
 565 570 575
 His Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg Leu
 580 585 590
 Ala Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser Pro Ala Leu
 595 600 605
 Cys Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala Gln Ser Leu
 610 615 620
 Trp Pro Arg Pro Leu Phe Cys
 625 630
 <210> 4599
 <211> 630
 <212> PRT
 <213> homo sapiens
 <400> 4599
 Met Pro Arg Tyr Gly Ala Ser Leu Arg Gln Ser Cys Pro Arg Ser Gly
 1 5 10 15
 Arg Glu Gln Gly Gln Asp Gly Thr Ala Gly Ala Pro Gly Leu Leu Trp
 20 25 30
 Met Gly Leu Val Leu Ala Leu Ala Leu Ala Leu Ala Leu Ala
 35 40 45
 Leu Ser Asp Ser Arg Val Leu Trp Ala Pro Ala Glu Ala His Pro Leu
 50 55 60

Ser Pro Gln Gly His Pro Ala Arg Leu His Arg Ile Val Pro Arg Leu

65 70 75 80

Arg Asp Val Phe Gly Trp Gly Asn Leu Thr Cys Pro Ile Cys Lys Gly

85 90 95

Leu Phe Thr Ala Ile Asn Leu Gly Leu Lys Glu Pro Asn Val Ala Arg

100 105 110

Val Gly Ser Val Ala Ile Lys Leu Cys Asn Leu Leu Lys Ile Ala Pro

115 120 125

Pro Ala Val Cys Gln Ser Ile Val His Leu Phe Glu Asp Asp Met Val

130 135 140

Glu Val Trp Arg Arg Ser Val Leu Ser Pro Ser Glu Ala Cys Gly Leu

145 150 155 160

Leu Leu Gly Ser Thr Cys Gly His Trp Asp Ile Phe Ser Ser Trp Asn

165 170 175

Ile Ser Leu Pro Thr Val Pro Lys Pro Pro Pro Lys Pro Pro Ser Pro

180 185 190

Pro Ala Pro Gly Ala Pro Val Ser Arg Ile Leu Phe Leu Thr Asp Leu

195 200 205

His Trp Asp His Asp Tyr Leu Glu Gly Thr Asp Pro Asp Cys Ala Asp

210 215 220

Pro Leu Cys Cys Arg Arg Gly Ser Gly Leu Pro Pro Ala Ser Arg Pro

225 230 235 240

Gly Ala Gly Tyr Trp Gly Glu Tyr Ser Lys Cys Asp Leu Pro Leu Arg

245 250 255

Thr Leu Glu Ser Leu Leu Ser Gly Leu Gly Pro Ala Gly Pro Phe Asp

260 265 270

Met Val Tyr Trp Thr Gly Asp Ile Pro Ala His Asp Val Trp His Gln

275 280 285

Thr Arg Gln Asp Gln Leu Arg Ala Leu Thr Thr Val Thr Ala Leu Val

290 295 300

Arg Lys Phe Leu Gly Pro Val Pro Val Tyr Pro Ala Val Gly Asn His

305 310 315 320
 Glu Ser Thr Pro Val Asn Ser Phe Pro Pro Pro Phe Ile Glu Gly Asn

 325 330 335
 His Ser Ser Arg Trp Leu Tyr Glu Ala Met Ala Lys Ala Trp Glu Pro
 340 345 350
 Trp Leu Pro Ala Glu Ala Leu Arg Thr Leu Arg Ile Gly Gly Phe Tyr
 355 360 365
 Ala Leu Ser Pro Tyr Pro Gly Leu Arg Leu Ile Ser Leu Asn Met Asn
 370 375 380
 Phe Cys Ser Arg Glu Asn Phe Trp Leu Leu Ile Asn Ser Thr Asp Pro

 385 390 395 400
 Ala Gly Gln Leu Gln Trp Leu Val Gly Glu Leu Gln Ala Ala Glu Asp
 405 410 415
 Arg Gly Asp Lys Val His Ile Ile Gly His Ile Pro Pro Gly His Cys
 420 425 430
 Leu Lys Ser Trp Ser Trp Asn Tyr Tyr Arg Ile Val Ala Arg Tyr Glu
 435 440 445
 Asn Thr Leu Ala Ala Gln Phe Phe Gly His Thr His Val Asp Glu Phe

 450 455 460
 Glu Val Phe Tyr Asp Glu Glu Thr Leu Ser Arg Pro Leu Ala Val Ala
 465 470 475 480
 Phe Leu Ala Pro Ser Ala Thr Thr Tyr Ile Gly Leu Asn Pro Gly Tyr
 485 490 495
 Arg Val Tyr Gln Ile Asp Gly Asn Tyr Ser Gly Ser Ser His Val Val
 500 505 510
 Leu Asp His Glu Thr Tyr Ile Leu Asn Leu Thr Gln Ala Asn Ile Pro

 515 520 525
 Gly Ala Ile Pro His Trp Gln Leu Leu Tyr Arg Ala Arg Glu Thr Tyr
 530 535 540
 Gly Leu Pro Asn Thr Leu Pro Thr Ala Trp His Asn Leu Val Tyr Arg
 545 550 555 560

Met Arg Gly Asp Met Gln Leu Phe Gln Thr Phe Trp Phe Leu Tyr His

565 570 575

Lys Gly His Pro Pro Ser Glu Pro Cys Gly Thr Pro Cys Arg Leu Ala

580 585 590

Thr Leu Cys Ala Gln Leu Ser Ala Arg Ala Asp Ser Pro Ala Leu Cys

595 600 605

Arg His Leu Met Pro Asp Gly Ser Leu Pro Glu Ala Gln Ser Leu Trp

610 615 620

Pro Arg Pro Leu Phe Cys

625 630

<210> 4600

<211> 1431

<212> DNA

<213> homo sapiens

<400> 4600

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cagcgggagc gcatgcagca acaggctgtc atgcattaca tgcagcagca gcagcagcag 120

caacagcagc agctcggagg gccgcccacc ccggccatca atacccccgt ccacttcag 180

tcgccaccac ctgtgcctgg ggaggtgttg aaggtgcagt cctacctgga gaatcccaca 240

tcctaccatc tgcagcagtc gcagcatcag aaggtgcggg agtacctgtc cgagacctat 300

gggaacaagt ttgtgccca catcagccca gcccagggt ctccgaaacc cccaccagcc 360

gcctccccag ggtgcgagc tggacacgtg ctgtcctcct ccgtggcaa cagtgtctcc 420

aatagcccca tggccatgct gcacattggc tccaacctg agaggaggtt ggatgatgtc 480

attgacaaca ttatgcgtct ggacgatgtc ctgggttaca tcaatcctga aatgcagatg 540

cccaacacgc taccctgtc cagcagccac ctgaatgtgt acagcagcga cccccaggtc 600

acagcctccc tggtagggcgt caccagcagc tcctgccctg cggacctgac ccagaagcga 660

gagctcagc atgtgagag cagggccctg gccaaaggagc ggcagaagaa agacaatcac 720

aacttaattg aaaggagacg aaggttcaac atcaatgacc gcatcaagga gttgggaatg 780

ctgatcccca aggccaatga cctggacgtg cgctggaaca agggcaccat cctcaaggcc 840

tctgtggatt acatccggag gatgcagaag gacctgcaaa agtccaggga gctggagaac 900

cactctcgcc gcctggagat gaccaacaag cagctctggc tccglatcca ggagctggag 960

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tcactgctac cgctggcctc tgatccactt ctgtccacca tgtccccga ggcctccaag 1380
gccagcagcc gccggagcag cttcagcatg gaggaggcg atgtgctgtg a 1431

<210> 4601

<211> 2058

<212> DNA

<213> homo sapiens

<400> 4601

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ggcgcgtacg tgctcgacga ctccgacggg ctgggccggg agttcgacgg catcgccgcg 180
gtcagcggcg gcggggcaac ctcccgactt ctagtaaatt acccagagcc ctatcgttct 240

cagatattgg attatctctt taagccgaat ttggtgcct ctttgcata tttaaaagtg 300
gaaataggtg gtgatgggca gacaacagac ggcaactgagc cctcccatat gcattatgca 360
ctagatgaga attatttccg aggatacgag tgggtggtga tgaaagaagc taagaagagg 420
aatccaata ttacactcat tgggttgcca tggtcattcc ctggatggct gggaaaaggt 480
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tataatgcca attatattaa gatattaaga aaaatgctga attatcaagg tctccagcga 660

gtgaaaatca tagcaagtga taatctctgg gactccatct ctgcatccat gctccttgat 720
gccgaactct tcaaggtggt tgatgttata ggggctcatt atcctggaac ccattcagca 780
aaagatgcaa agttgactgg gaagaagctt tggctctctg aagactttag cacttttaat 840
agtgacatgg gtgcaggctg ctggggtcgc attttaaatc agaattatat caatggctat 900
atgacttcca caatcgcatg gaatttagtg gctagttact atgaacagtt gccttatggg 960
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gttggccatt tagagaaagg aggaagctac gtagctctga ctgatggctt agggaacctc 1140
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tatttcaatg tgtcacaaca atttgccacc ttgtttctta agggatcttt tagtgaaata 1260
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cagctggatt ctctatggct ccttgacagc gatggcagtt tcacactgag cctgcatgaa 1380
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tttagtgaag ctccaaactt tgcgatcaa actgggtgat ttgaatat ttacaaatatt 1560
gaagacctg gcgagcatca cttcacgcta cgccaagttc tcaaccagag acccattacg 1620
tgggctgccg atgcatccaa cacaatcagt attataggag actacaactg gaccaatctg 1680
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gcaaattgat cttacagggt tacagggtat ttagctggat ggattatata tgcttttagga 1860
cgtgttgaag ttacagcaaa aaaatggat acactcacgt taactattaa gggtcatttc 1920

acctctggca tgctgaatga caagtctctg tggacagaca tccctgtgaa ttttcaaag 1980
aatggctggg ctgcaattgg aactcactcc ttgaatttg cacagtttga caactttctt 2040
gtggaagcca cacgctaa 2058

<210> 4602
<211> 942
<212> DNA
<213> Artificial sequence
<220><223> ASPA codon optimized
<400> 4602

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cacggcaacg agctcacagg agtcttcttg gtgaagcact ggctcgagaa cggagcggaa 120
atccagcgca ccggactgga agtcaagccg ttcatacta accctcgcg cgtgaagaag 180

tgcacgcgct acatcgactg cgacctcaac cgcactcttg acctcgagaa cctgggcaag 240
aagatgtctg aagacctgcc ttacgaagtg cgccgcgcgc aggagatcaa ccacctcttc 300
ggaccgaagg actctgaaga ctctgacgac atcatcttcg acctgcacaa cagcacatcg 360
aacaatgggt gcacactcat cctggaagac agccgcaaca acttcctcat ccagatgttc 420
cactacatca agacatctct cgcgcccttg ccttgctacg tctacctgat cgagcaccgc 480
agcctcaagt acgcgaccac tcgctctatc gcgaagtacc ctgtcggcat cgaagtggga 540

cctcagcctc agggagtgct gagagcggac atcctcgacc agatgcgcaa gatgatcaag 600

cacgcgctgg acttcatcca ccacttcaac gagggaaagg agttcccgcc gtgcgcatc 660

gaggtctaca agatcatcga aaaggtggac taccctcgcg acgagaacgg cgaaatcgcg 720

gcgatcatcc accccaacct gcaggaccag gactggaagc ctctccacc tggcgacccc 780

atgttctca ccttggacgg aaagactatc cccctgggcg gagactgcac tgtctacccg 840

gtcttcgtga acgaggcggc gtactacgag aagaaggaag cgttcgcgaa gacgacaaag 900

ctcacgctga acgcgaagtc gatccgctgc tgctccact ga 942

<210> 4603

<211> 420

<212> DNA

<213> Artificial sequence

<220><223> human GALC isoform 1 codon optimized

<400> 4603

atggcggagt ggctcctgag cgcgtcttgg cagcgagag ccaaggccat gacagcggcg 60

gcaggatctg ccggaagagc cgcggtcccc ctctgtctct gcgcgctgct cgcgccgggc 120

ggagcgtacg tgctcgacga ctctgacgga ctgggaagag agttcgacgg aattggcgcg 180

gtgtctggcg gcggcgcgac atcgcgctg ctctggaact acccgaacc gtaccgctcg 240

cagatcctgg actacctctt caagcctaac ttcgagcgga gcctgcacat cctcaaggtc 300

gagatcggag gcgacggaca gacgacagac ggcaactgagc ccagccacat gcactacgcg 360

ctcgacgaaa actacttccg cggctacgag tgggtggctga tgaaggaagc gaagaagcgc 420

<210> 4604

<211> 1431

<212> DNA

<213> Artificial sequence

<220><223> human TFEB (Transcription factor EB) isoform 1 codon optimized

<400> 4604

atggcgtctc gcatcggcct ccgcatgcag ctgatgagag agcaggccca gcaggaagag 60

cagcggaac gcatgcagca gcaggcggtc atgcactaca tgcaacaaca gcaacaacag 120

cagcagcagc agctcggcgg accgcctacc cctgcgatca aactcccggt gcacttcag 180

tctccccgcg ctgtgcctgg agaggtctct aaggtgcagt cgtacctgga aaacctacg 240

tcgtaccacc tccagcagag ccagcaccag aaggtgcgag agtacctgtc ggaaacatac 300

ggcaacaagt tcgcccga catctctcct gcccagggat ctctaagcc cccgcctgcc 360
gccagccctg gagtgagagc cggacacgtg ctctcttcta gcgcgggcaa ctctgcgcct 420
aactcgccca tggcgaatgct ccacatcgga tcgaaccctg agcggaact ggacgacgtc 480
atcgacaaca tcatgcgcct cgacgacgtg ctgggttaca tcaacccga gatgcagatg 540
ccgaacaccc tccctctgtc ttgagccac ctcaacgtct actcgtctga ccctcaggtg 600
acagccagcc tggtcggagt gactagctct tcttgccctg ccgacctcac acagaagaga 660

gagctgacag acgcggaatc tcgcgcgtc gcgaaggaa gccagaaga ggacaaccac 720
aacctgatcg agcgccgccc cagattcaac atcaacgacc gcatcaagga actcggcgatg 780
ctgatccga agcggaacga cctcgacgtc cgttggaaca agggaacat cctgaaggcg 840
tctgtggact acatccgagc aatgcagaag gacctccaga agagccgca gctggaaaac 900
cactctgcc gcctcgagat gactaacaag cagctctggc tgcgcatcca ggagctggaa 960
atgcaggcca gagtgacggc cctgcctaca acatctcctt ctggaatgaa catggcggag 1020
ctcgcgcagc aggtcgtgaa gcaggaactg ccgtctgagg aagggccggg agaagccctc 1080

atgtggggag cggaggtgcc tgaccggaa cctctgcctg cctcccgcc gcaggcccg 1140
ctccctctgc ccacgcagcc tccctctcct ttccaccacc tcgacttcag ccactctctg 1200
tcgttcggcg gacgcgagga cgaaggcccg cctggatacc cggaacctct cgcgccggga 1260
cacggatcgc cttccctag cctgtctaag aaggacctcg acctgatgct cctggacgac 1320
tcgtgctcc cgttgccctc tgacctctc ctgtctacaa tgtctcctga agcctctaag 1380
gccagctctc gccgctctag cttcagcatg gaggaaggcg acgtcctgtg a 1431

<210> 4605

<211> 610

<212> PRT

<213> Artificial sequence

<220><223> DHFR (version 2) amino acid sequence

<400> 4605

Met Gln Lys Pro Val Cys Leu Val Val Ala Met Thr Pro Lys Arg Gly

1 5 10 15

Ile Gly Ile Asn Asn Gly Leu Pro Trp Pro His Leu Thr Thr Asp Phe

20 25 30

Lys His Phe Ser Arg Val Thr Lys Thr Thr Pro Glu Glu Ala Ser Arg

35 40 45

Leu Asn Gly Trp Leu Pro Arg Lys Phe Ala Lys Thr Gly Asp Ser Gly

50

55

60

Leu Pro Ser Pro Ser Val Gly Lys Arg Phe Asn Ala Val Val Met Gly

65

70

75

80

Arg Lys Thr Trp Glu Ser Met Pro Arg Lys Phe Arg Pro Leu Val Asp

85

90

95

Arg Leu Asn Ile Val Val Ser Ser Ser Leu Lys Glu Glu Asp Ile Ala

100

105

110

Ala Glu Lys Pro Gln Ala Glu Gly Gln Gln Arg Val Arg Val Cys Ala

115

120

125

Ser Leu Pro Ala Ala Leu Ser Leu Leu Glu Glu Glu Tyr Lys Asp Ser

130

135

140

Val Asp Gln Ile Phe Val Val Gly Gly Ala Gly Leu Tyr Glu Ala Ala

145

150

155

160

Leu Ser Leu Gly Val Ala Ser His Leu Tyr Ile Thr Arg Val Ala Arg

165

170

175

Glu Phe Pro Cys Asp Val Phe Phe Pro Ala Phe Pro Gly Asp Asp Ile

180

185

190

Leu Ser Asn Lys Ser Thr Ala Ala Gln Ala Ala Ala Pro Ala Glu Ser

195

200

205

Val Phe Val Pro Phe Cys Pro Glu Leu Gly Arg Glu Lys Asp Asn Glu

210

215

220

Ala Thr Tyr Arg Pro Ile Phe Ile Ser Lys Thr Phe Ser Asp Asn Gly

225

230

235

240

Val Pro Tyr Asp Phe Val Val Leu Glu Lys Arg Arg Lys Thr Asp Asp

245

250

255

Ala Ala Thr Ala Glu Pro Ser Asn Ala Met Ser Ser Leu Thr Ser Thr

260

265

270

Arg Glu Thr Thr Pro Val His Gly Leu Gln Ala Pro Ser Ser Ala Ala

275

280

285

Ala Ile Ala Pro Val Leu Ala Trp Met Asp Glu Glu Asp Arg Lys Lys

290 295 300
 Arg Glu Gln Lys Glu Leu Ile Arg Ala Val Pro His Val His Phe Arg

 305 310 315 320
 Gly His Glu Glu Phe Gln Tyr Leu Asp Leu Ile Ala Asp Ile Ile Asn
 325 330 335
 Asn Gly Arg Thr Met Asp Asp Arg Thr Gly Val Gly Val Ile Ser Lys
 340 345 350
 Phe Gly Cys Thr Met Arg Tyr Ser Leu Asp Gln Ala Phe Pro Leu Leu
 355 360 365
 Thr Thr Lys Arg Val Phe Trp Lys Gly Val Leu Glu Glu Leu Leu Trp

 370 375 380
 Phe Ile Arg Gly Asp Thr Asn Ala Asn His Leu Ser Glu Lys Gly Val
 385 390 395 400
 Lys Ile Trp Asp Lys Asn Val Thr Arg Glu Phe Leu Asp Ser Arg Asn
 405 410 415
 Leu Pro His Arg Glu Val Gly Asp Ile Gly Pro Gly Tyr Gly Phe Gln
 420 425 430
 Trp Arg His Phe Gly Ala Ala Tyr Lys Asp Met His Thr Asp Tyr Thr

 435 440 445
 Gly Gln Gly Val Asp Gln Leu Lys Asn Val Ile Gln Met Leu Arg Thr
 450 455 460
 Asn Pro Thr Asp Arg Arg Met Leu Met Thr Ala Trp Asn Pro Ala Ala
 465 470 475 480
 Leu Asp Glu Met Ala Leu Pro Pro Cys His Leu Leu Cys Gln Phe Tyr
 485 490 495
 Val Asn Asp Gln Lys Glu Leu Ser Cys Ile Met Tyr Gln Arg Ser Cys

 500 505 510
 Asp Val Gly Leu Gly Val Pro Phe Asn Ile Ala Ser Tyr Ser Leu Leu
 515 520 525
 Thr Leu Met Val Ala His Val Cys Asn Leu Lys Pro Lys Glu Phe Ile
 530 535 540

His Phe Met Gly Asn Thr His Val Tyr Thr Asn His Val Glu Ala Leu
 545 550 555 560
 Lys Glu Gln Leu Arg Arg Glu Pro Arg Pro Phe Pro Ile Val Asn Ile

 565 570 575
 Leu Asn Lys Glu Arg Ile Lys Glu Ile Asp Asp Phe Thr Ala Glu Asp
 580 585 590
 Phe Glu Val Val Gly Tyr Val Pro His Gly Arg Ile Gln Met Glu Met

 595 600 605
 Ala Val

610

<210> 4606

<211> 1833

<212> DNA

<213> Artificial sequence

<220><223> DHFR (version 2) nucleic acid sequence

<400> 4606

atgcagaaac cgggtgtgtct ggctcgtcgcg atgaccccca agaggggcat cggcatcaac	60
aacggcctcc cgtggcccca cttgaccaca gatttcaaac acttttctcg tgtgacaaaa	120
acgacgcccg aagaagccag tcgcctgaac ggggtggcttc ccaggaaatt tgcaaagacg	180
ggcgactctg gacttccttc tccatcagtc ggcaagagat tcaacgccgt tgtcatggga	240
cggaaaacct gggaaagcat gcctcgaaag tttagacccc tcgtggacag attgaacatc	300
gtcgtttcct cttccctcaa agaagaagac attgcggcgg agaagcctca agctgaaggc	360
cagcagcgcg tccgagtctg tgcttcactc ccagcagctc tcagccttct ggaggaagag	420
tacaaggatt ctgtcgacca gatttttgtc gtgggaggag cgggactgta cgaggcagcg	480
ctgtctctgg gcgttgctc tcacctgtac atcacgcgtg tagcccgcga gtttcctgtc	540
gacgttttct tcctgcgtt ccccgagat gacattcttt caaacaatc aactgctgcg	600
caggctgcag ctctgccga gtctgtgttc gttccctttt gtccggagct cggaagagag	660
aaggacaatg aagcgacgta tcgacccatc ttcatttcca agaccttctc agacaacggg	720
gtaccctacg actttgttgt tctcgagaag agaaggaaga ctgacgacgc agccactgcg	780
gaaccgagca acgcaatgag ctcccttgaca tccacgaggg agacaactcc cgtgcacggg	840
ttgcaggctc ctctctcggc cgcagccatt gccccgtgt tggcgtggat ggacgaagaa	900

gaccggaaaa aacgcgagca aaaggaactg attcgggccg ttccgcatgt tcactttaga 960
 ggccatgaag aattccagta ccttgatctc attgccgaca ttattaacaa tggaaggaca 1020
 atggatgacc gaacgggcgt tgggtgcatc tccaaattcg gctgcactat gcgtactcg 1080
 ctggatcagg cttttccact tctcaccaca aagcgtgtgt tctggaaagg ggtcctcgaa 1140
 gagttgctgt ggttcattcg cggcgacacg aacgcaaacc atctttctga gaaggcgctg 1200
 aagatttggg acaagaatgt gacacgcgag ttccctcgatt cgcgcaatct cccccaccga 1260
 gaggtcggag acatcgggcc aggctacggc ttccagtga gacacttcgg cgcggcatac 1320

aaagacatgc acacagacta cacagggcag ggcgtcgacc agctgaagaa tgtgatccag 1380
 atgctgagaa cgaatccaac agatcgtcgc atgctcatga ctgcctggaa tcctgcagcg 1440
 ctggacgaaa tggcgtgcc gccttgctac ttgttggtcc agttctacgt gaacgaccag 1500
 aaggagctgt cgtgcatcat gtatcagcgg tcgtgcgatg tcggcctcgg cgtccccttc 1560
 aacatcgctt cctattcgct ttgacgctc atggttgac acgtctgcaa cctaaaacct 1620
 aaggagtcca ttcacttcac ggggaacacg catgtctaca cgaaccatgt cgaggcttta 1680
 aaagagcagc tgcggagaga accgagaccg ttccccattg tgaacatcct caacaaggaa 1740

cgcacaaagg aaatcgacga ttccaccgcc gaggattttg aggtcgtggg ctacgtcccg 1800
 cacggacgaa tccagatgga gatggctgtc tag 1833

<210> 4607

<211> 236

<212> PRT

<213> Artificial sequence

<220><223> mCherry mammalian codon optimized

<400> 4607

Met Val Ser Lys Gly Glu Glu Asp Asn Met Ala Ile Ile Lys Glu Phe

1 5 10 15

Met Arg Phe Lys Val His Met Glu Gly Ser Val Asn Gly His Glu Phe

20 25 30

Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr

35 40 45

Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp

50 55 60

Ile Leu Ser Pro Gln Phe Met Tyr Gly Ser Lys Ala Tyr Val Lys His

65 70 75 80

Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe
85 90 95

Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val Thr Val
100 105 110

Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys
115 120 125

Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys
130 135 140

Thr Met Gly Trp Glu Ala Ser Ser Glu Arg Met Tyr Pro Glu Asp Gly
145 150 155 160

Ala Leu Lys Gly Glu Ile Lys Gln Arg Leu Lys Leu Lys Asp Gly Gly
165 170 175

His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Lys Ala Lys Lys Pro Val
180 185 190

Gln Leu Pro Gly Ala Tyr Asn Val Asn Ile Lys Leu Asp Ile Thr Ser
195 200 205

His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg Ala Glu Gly
210 215 220

Arg His Ser Thr Gly Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 4608

<211> 711

<212> DNA

<213> Artificial sequence

<220><223> mCherry mammalian codon optimized

<400> 4608

atggtgagca agggcgagga ggataacatg gccatcatca aggagttcat gcgcttcaag	60
gtgcacatgg agggctccgt gaacggccac gagttcgaga tcgagggcga gggcgagggc	120
cggccctacg agggcaccca gaccgccaag ctgaaggtga ccaaggggtgg cccctgccc	180
ttgcctggg acatcctgtc cctcagttc atgtacggct ccaaggccta cgtgaagcac	240
cccgcgcaca tccccgacta cttgaagctg tccttccccg agggcttcaa gtgggagcgc	300

gtgatgaact tcgaggacgg cggcgtgggtg accgtgaccc aggactcctc cctgcaggac 360
 ggcgagtcca tctacaaggt gaagctgcgc ggcaccaact tccccccga cggccccgta 420
 atgcagaaga agaccatggg ctgggaggcc tcctccgagc ggatgtaccc cgaggacggc 480
 gccctgaagg gcgagatcaa gcagaggctg aagctgaagg acggcggcca ctacgacgt 540
 gaggtcaaga ccacctacaa ggccaagaag cccgtgcagc tgcccggcgc ctacaacgtc 600
 aacatcaagt tggacatcac ctcccacaac gaggactaca ccatcgtgga acagtacgaa 660

cgcgccgagg gccgccactc caccggcggc atggacgagc tgtacaagta a 711

<210> 4609

<211> 786

<212> DNA

<213> Artificial sequence

<220><223> 3' UTR DHFR (version 2) nucleic acid sequence

<400> 4609

aaggcgcgcc cagcccacag aagctgcccg tctctcgttt tctctcttt tcggagggat 60
 caggagaggt gcctcgggtc ggagagagct gacgaggggg tgccagagac ccctgtgtcc 120
 tttatcgaag aaaagggatg actcttcatg tggcatttca cacagtctca cctcgccttg 180
 ttttcttttt gtcaatcaga acgaaagcga gttgcgggtg acgcagatgt gcgtgtatcc 240

actcggaatg cgttatcgtt ctgtatgccg ctagagtgtc ggactgttgc tgtctgcccc 300
 cgacagcaga caactttcct tctatgcact tgcaggatgg tgcagcgcaa acgacggaga 360
 gaaaggagca ccctctcagt ttccctacga tgtgtgttca gtttcgactc ttcaccgca 420
 acgattggcg atacgtctct gttgacttgt taggctccga ccacgaagct cccttaacta 480
 gataagccgc gacacctaa ggtacacat ttgcagatcg ataactctcg accgtgaat 540
 ccgtccagat cagtaaaacc gcaccacctt agtgtaaacc ttgttttaggt cgataaaatg 600
 ctaccaaccc ccaccacaa tcgagccttg agcgtttctg cgcacgcgtt ggcctacgtg 660

acttgcgtgat gcctgcctct ggccattcat gccagtcagt gcgcataaaa atgtggacac 720
 agtcggttga caagtgttct ggcaggctac agtgacaccg cggaggagg ggatccacta 780
 gttcta 786

<210> 4610

<211> 476

<212> PRT

<213> homo sapiens

<400> 4610

Met Ala Ser Arg Ile Gly Leu Arg Met Gln Leu Met Arg Glu Gln Ala
1 5 10 15
Gln Gln Glu Glu Gln Arg Glu Arg Met Gln Gln Gln Ala Val Met His
20 25 30
Tyr Met Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gly Gly Pro
35 40 45
Pro Thr Pro Ala Ile Asn Thr Pro Val His Phe Gln Ser Pro Pro Pro
50 55 60
Val Pro Gly Glu Val Leu Lys Val Gln Ser Tyr Leu Glu Asn Pro Thr
65 70 75 80
Ser Tyr His Leu Gln Gln Ser Gln His Gln Lys Val Arg Glu Tyr Leu
85 90 95
Ser Glu Thr Tyr Gly Asn Lys Phe Ala Ala His Ile Ser Pro Ala Gln
100 105 110
Gly Ser Pro Lys Pro Pro Pro Ala Ala Ser Pro Gly Val Arg Ala Gly
115 120 125
His Val Leu Ser Ser Ser Ala Gly Asn Ser Ala Pro Asn Ser Pro Met
130 135 140
Ala Met Leu His Ile Gly Ser Asn Pro Glu Arg Glu Leu Asp Asp Val
145 150 155 160
Ile Asp Asn Ile Met Arg Leu Asp Asp Val Leu Gly Tyr Ile Asn Pro
165 170 175
Glu Met Gln Met Pro Asn Thr Leu Pro Leu Ser Ser Ser His Leu Asn
180 185 190
Val Tyr Ser Ser Asp Pro Gln Val Thr Ala Ser Leu Val Gly Val Thr
195 200 205
Ser Ser Ser Cys Pro Ala Asp Leu Thr Gln Lys Arg Glu Leu Thr Asp
210 215 220
Ala Glu Ser Arg Ala Leu Ala Lys Glu Arg Gln Lys Lys Asp Asn His
225 230 235 240
Asn Leu Ile Glu Arg Arg Arg Arg Phe Asn Ile Asn Asp Arg Ile Lys

245 250 255
 Glu Leu Gly Met Leu Ile Pro Lys Ala Asn Asp Leu Asp Val Arg Trp
 260 265 270
 Asn Lys Gly Thr Ile Leu Lys Ala Ser Val Asp Tyr Ile Arg Arg Met
 275 280 285

 Gln Lys Asp Leu Gln Lys Ser Arg Glu Leu Glu Asn His Ser Arg Arg
 290 295 300
 Leu Glu Met Thr Asn Lys Gln Leu Trp Leu Arg Ile Gln Glu Leu Glu
 305 310 315 320
 Met Gln Ala Arg Val His Gly Leu Pro Thr Thr Ser Pro Ser Gly Met
 325 330 335
 Asn Met Ala Glu Leu Ala Gln Gln Val Val Lys Gln Glu Leu Pro Ser
 340 345 350

 Glu Glu Gly Pro Gly Glu Ala Leu Met Leu Gly Ala Glu Val Pro Asp
 355 360 365
 Pro Glu Pro Leu Pro Ala Leu Pro Pro Gln Ala Pro Leu Pro Leu Pro
 370 375 380
 Thr Gln Pro Pro Ser Pro Phe His His Leu Asp Phe Ser His Ser Leu
 385 390 395 400
 Ser Phe Gly Gly Arg Glu Asp Glu Gly Pro Pro Gly Tyr Pro Glu Pro
 405 410 415

 Leu Ala Pro Gly His Gly Ser Pro Phe Pro Ser Leu Ser Lys Lys Asp
 420 425 430
 Leu Asp Leu Met Leu Leu Asp Asp Ser Leu Leu Pro Leu Ala Ser Asp
 435 440 445
 Pro Leu Leu Ser Thr Met Ser Pro Glu Ala Ser Lys Ala Ser Ser Arg
 450 455 460
 Arg Ser Ser Phe Ser Met Glu Glu Gly Asp Val Leu
 465 470 475
 <210> 4611

 <211> 685

<212> PRT

<213> homo sapiens

<400> 4611

Met Ala Glu Trp Leu Leu Ser Ala Ser Trp Gln Arg Arg Ala Lys Ala

1 5 10 15

Met Thr Ala Ala Ala Gly Ser Ala Gly Arg Ala Ala Val Pro Leu Leu

20 25 30

Leu Cys Ala Leu Leu Ala Pro Gly Gly Ala Tyr Val Leu Asp Asp Ser

35 40 45

Asp Gly Leu Gly Arg Glu Phe Asp Gly Ile Gly Ala Val Ser Gly Gly

50 55 60

Gly Ala Thr Ser Arg Leu Leu Val Asn Tyr Pro Glu Pro Tyr Arg Ser

65 70 75 80

Gln Ile Leu Asp Tyr Leu Phe Lys Pro Asn Phe Gly Ala Ser Leu His

85 90 95

Ile Leu Lys Val Glu Ile Gly Gly Asp Gly Gln Thr Thr Asp Gly Thr

100 105 110

Glu Pro Ser His Met His Tyr Ala Leu Asp Glu Asn Tyr Phe Arg Gly

115 120 125

Tyr Glu Trp Trp Leu Met Lys Glu Ala Lys Lys Arg Asn Pro Asn Ile

130 135 140

Thr Leu Ile Gly Leu Pro Trp Ser Phe Pro Gly Trp Leu Gly Lys Gly

145 150 155 160

Phe Asp Trp Pro Tyr Val Asn Leu Gln Leu Thr Ala Tyr Tyr Val Val

165 170 175

Thr Trp Ile Val Gly Ala Lys Arg Tyr His Asp Leu Asp Ile Asp Tyr

180 185 190

Ile Gly Ile Trp Asn Glu Arg Ser Tyr Asn Ala Asn Tyr Ile Lys Ile

195 200 205

Leu Arg Lys Met Leu Asn Tyr Gln Gly Leu Gln Arg Val Lys Ile Ile

210 215 220

Ala Ser Asp Asn Leu Trp Glu Ser Ile Ser Ala Ser Met Leu Leu Asp

225 230 235 240
 Ala Glu Leu Phe Lys Val Val Asp Val Ile Gly Ala His Tyr Pro Gly

 245 250 255
 Thr His Ser Ala Lys Asp Ala Lys Leu Thr Gly Lys Lys Leu Trp Ser
 260 265 270
 Ser Glu Asp Phe Ser Thr Leu Asn Ser Asp Met Gly Ala Gly Cys Trp
 275 280 285
 Gly Arg Ile Leu Asn Gln Asn Tyr Ile Asn Gly Tyr Met Thr Ser Thr
 290 295 300
 Ile Ala Trp Asn Leu Val Ala Ser Tyr Tyr Glu Gln Leu Pro Tyr Gly

 305 310 315 320
 Arg Cys Gly Leu Met Thr Ala Gln Glu Pro Trp Ser Gly His Tyr Val
 325 330 335
 Val Glu Ser Pro Val Trp Val Ser Ala His Thr Thr Gln Phe Thr Gln
 340 345 350
 Pro Gly Trp Tyr Tyr Leu Lys Thr Val Gly His Leu Glu Lys Gly Gly
 355 360 365
 Ser Tyr Val Ala Leu Thr Asp Gly Leu Gly Asn Leu Thr Ile Ile Ile

 370 375 380
 Glu Thr Met Ser His Lys His Ser Lys Cys Ile Arg Pro Phe Leu Pro
 385 390 395 400
 Tyr Phe Asn Val Ser Gln Gln Phe Ala Thr Phe Val Leu Lys Gly Ser
 405 410 415
 Phe Ser Glu Ile Pro Glu Leu Gln Val Trp Tyr Thr Lys Leu Gly Lys
 420 425 430
 Thr Ser Glu Arg Phe Leu Phe Lys Gln Leu Asp Ser Leu Trp Leu Leu

 435 440 445
 Asp Ser Asp Gly Ser Phe Thr Leu Ser Leu His Glu Asp Glu Leu Phe
 450 455 460
 Thr Leu Thr Thr Leu Thr Thr Gly Arg Lys Gly Ser Tyr Pro Leu Pro
 465 470 475 480

Pro Lys Ser Gln Pro Phe Pro Ser Thr Tyr Lys Asp Asp Phe Asn Val
485 490 495

Asp Tyr Pro Phe Phe Ser Glu Ala Pro Asn Phe Ala Asp Gln Thr Gly

500 505 510

Val Phe Glu Tyr Phe Thr Asn Ile Glu Asp Pro Gly Glu His His Phe

515 520 525

Thr Leu Arg Gln Val Leu Asn Gln Arg Pro Ile Thr Trp Ala Ala Asp

530 535 540

Ala Ser Asn Thr Ile Ser Ile Ile Gly Asp Tyr Asn Trp Thr Asn Leu

545 550 555 560

Thr Ile Lys Cys Asp Val Tyr Ile Glu Thr Pro Asp Thr Gly Gly Val

565 570 575

Phe Ile Ala Gly Arg Val Asn Lys Gly Gly Ile Leu Ile Arg Ser Ala

580 585 590

Arg Gly Ile Phe Phe Trp Ile Phe Ala Asn Gly Ser Tyr Arg Val Thr

595 600 605

Gly Asp Leu Ala Gly Trp Ile Ile Tyr Ala Leu Gly Arg Val Glu Val

610 615 620

Thr Ala Lys Lys Trp Tyr Thr Leu Thr Leu Thr Ile Lys Gly His Phe

625 630 635 640

Thr Ser Gly Met Leu Asn Asp Lys Ser Leu Trp Thr Asp Ile Pro Val

645 650 655

Asn Phe Pro Lys Asn Gly Trp Ala Ala Ile Gly Thr His Ser Phe Glu

660 665 670

Phe Ala Gln Phe Asp Asn Phe Leu Val Glu Ala Thr Arg

675 680 685

<210> 4612

<211> 1699

<212> PRT

<213> Toxoplasma gondii

<400>

4612

Met Gly Val His His Ala Leu Asp Asp Ala Gly Glu Met Pro His Ser
1 5 10 15
Gly Gly Arg Arg Ala Val Ala Pro Ile Tyr Pro Leu Asp Leu Ala Gly
20 25 30
Arg Leu Arg Pro Ala Met Leu Val Leu Ala Asp Gly Thr Glu Phe Leu
35 40 45
Gly Tyr Ser Phe Gly Tyr Pro Gly Ser Val Gly Gly Glu Val Val Phe
50 55 60

Asn Thr Gly Met Val Gly Tyr Pro Glu Ser Leu Thr Asp Pro Ser Tyr
65 70 75 80
Glu Gly Gln Ile Leu Val Leu Thr Tyr Pro Leu Ile Gly Asn Tyr Gly
85 90 95
Val Pro Ser Ser Glu Lys Asp Glu His Gly Leu Pro Lys Tyr Phe Glu
100 105 110
Gly Asp Arg Ile Tyr Val Arg Ala Leu Val Val Ala Asp Tyr Asp Asn
115 120 125

Ala Ala Val Thr Ala His Phe Arg Ala Glu Asn Ser Leu Ser Ala Trp
130 135 140
Met Asn Thr His Lys Val Pro Ala Ile Ala Gly Val Asp Thr Arg Ala
145 150 155 160
Leu Thr Lys His Leu Arg Glu Val Gly Cys Met Leu Gly Lys Ile Val
165 170 175
Val Leu Ser Glu Glu Glu Glu Arg Arg Ser Gly Leu Ser Leu Ser Ala
180 185 190

Leu Ala Ala Leu Pro Ser Ala Thr Ala Ala Glu Gln Arg Gly Glu Asn
195 200 205
Asp Ala Thr Val Thr Pro Asp Lys Ala Glu Ala Arg Leu Arg Val Glu
210 215 220
Arg Arg Gln Ala Ala Leu Thr Met Trp Glu Glu Ala Ile Arg Asn Lys
225 230 235 240
Ala Lys Asn Leu Pro Trp Glu Asp Pro Asn Lys Asp Asn Leu Val Ala

245	250	255
Leu Val Ser Arg Lys Glu Val Arg Val Tyr Lys Ser Thr Val Val Asp		
260	265	270
Pro Asn Leu Arg Asp Val Leu Ile Leu Cys Val Asp Cys Gly Met Lys		
275	280	285
Tyr Asn Ile Tyr Arg Gln Leu Leu His Ser Lys Phe Glu His Cys Asn		
290	295	300
Ile Ile Leu Lys Val Val Pro Trp Asp Phe Asp Phe Gly Asn Asp Glu		
305	310	315
		320
Phe Asp Gly Leu Phe Ile Ser Asn Gly Pro Gly Asp Pro Glu Arg Cys		
325	330	335
Glu Lys Thr Val Ala Asn Ile Arg Arg Val Met Glu Arg Lys Ile Pro		
340	345	350
Ile Phe Gly Ile Cys Leu Gly Asn Gln Leu Leu Ala Leu Ala Ala Gly		
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Ala Arg Thr Tyr Lys Met Lys Tyr Gly Asn Arg Gly Met Asn Gln Pro		
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Val Ile Asp Leu Arg Thr Ser Arg Cys Tyr Ile Thr Pro Gln Asn His		
385	390	395
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Gly Phe Ala Val Asp Glu Ser Thr Leu Pro Arg Asp Phe Leu Pro Leu		
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Phe Val Asn Ala Asn Asp Arg Ser Asn Glu Gly Ile Ile His Arg Thr		
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Leu Pro Phe Phe Ser Ala Gln Phe His Pro Glu Ala Ser Gly Gly Pro		
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Thr Asp Thr Phe Tyr Leu Phe Gly Asp Phe Ile Ala Ser Ile Met Lys		
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Ala Gln Thr Leu Lys Gln Val His Thr Thr Pro Phe Ser Phe Pro Gln		
465	470	475
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Lys Phe Gln Lys Val Leu Leu Leu Gly Ser Gly Gly Leu Ser Ile Gly		
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Gln Ala Gly Glu Phe Asp Tyr Ser Gly Ser Gln Ala Ile Lys Ala Leu
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Val Glu Tyr Glu Val Val Arg Asp Cys Lys Asn Asn Cys Ile Thr Val
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Cys Asn Met Glu Asn Leu Asp Pro Leu Gly Ile His Thr Gly Asp Ser
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Ile Val Val Ala Pro Ser Gln Thr Leu Ser Asn Glu Asp Tyr Tyr Arg
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Leu Arg Asp Thr Ala Leu Lys Val Ile Arg His Phe Gly Ile Val Gly

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Lys Ala Thr Gly Tyr Pro Leu Ala Tyr Ile Ala Ala Lys Leu Ala Leu			
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Gly Ser Thr Leu Val Glu Leu Ser Asn Ser Val Thr Lys Glu Thr Thr			
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Trp Asp Leu Arg Lys Phe Glu Ser Cys Asp Pro Leu Met Gly Ser Ala			
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Pro Leu Ala Ala Thr Pro Ser Val Ser Ala Val Phe Ala Gly Ala		
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Arg Ala Glu Lys Arg Glu Glu Glu Asn Ala Glu Thr Cys Arg Asp		
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Asp Glu Asp Glu Ser Leu Leu Arg Arg Leu Ser Lys Ser Ser Ser		
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1430	1435	1440
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<211> 1699

<212> PRT

<213> *Toxoplasma gondii*

<400> 4615

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20 25 30

Arg Leu Arg Pro Ala Met Leu Val Leu Ala Asp Gly Thr Glu Phe Leu

35 40 45

Gly Tyr Ser Phe Gly Tyr Pro Gly Ser Val Gly Gly Glu Val Val Phe

50 55 60

Asn Thr Gly Met Val Gly Tyr Pro Glu Ser Leu Thr Asp Pro Ser Tyr

65 70 75 80

Glu Gly Gln Ile Leu Val Leu Thr Tyr Pro Leu Ile Gly Asn Tyr Gly

85 90 95

Val Pro Ser Ser Glu Lys Asp Glu His Gly Leu Pro Lys Tyr Phe Glu

100 105 110
Gly Asp Arg Ile Tyr Val Arg Ala Leu Val Val Ala Asp Tyr Asp Asn

115 120 125
Ala Ala Val Thr Ala His Phe Arg Ala Glu Asn Ser Leu Ser Ala Trp

130 135 140
Met Asn Thr His Lys Val Pro Ala Ile Ala Gly Val Asp Thr Arg Ala

145 150 155 160
Leu Thr Lys His Leu Arg Glu Val Gly Cys Met Leu Gly Lys Ile Val

165 170 175
Val Leu Ser Glu Glu Glu Glu Arg Arg Ser Gly Leu Ser Leu Ser Ala

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Leu Ala Ala Leu Pro Ser Ala Thr Ala Ala Glu Gln Arg Gly Glu Asn

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Asp Ala Thr Val Thr Pro Asp Lys Ala Glu Ala Arg Leu Arg Val Glu

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Arg Arg Gln Ala Ala Leu Thr Met Trp Glu Glu Ala Ile Arg Asn Lys

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Ala Lys Asn Leu Pro Trp Glu Asp Pro Asn Lys Asp Asn Leu Val Ala

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Pro Asn Leu Arg Asp Val Leu Ile Leu Cys Val Asp Cys Gly Met Lys

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Tyr Asn Ile Tyr Arg Gln Leu Leu His Ser Lys Phe Glu His Cys Asn

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Ile Ile Leu Lys Val Val Pro Trp Asp Phe Asp Phe Gly Asn Asp Glu

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Phe Asp Gly Leu Phe Ile Ser Asn Gly Pro Gly Asp Pro Glu Arg Cys

325 330 335
Glu Lys Thr Val Ala Asn Ile Arg Arg Val Met Glu Arg Lys Ile Pro

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Ile Phe Gly Ile Cys Leu Gly Asn Gln Leu Leu Ala Leu Ala Ala Gly
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Ala Arg Thr Tyr Lys Met Lys Tyr Gly Asn Arg Gly Met Asn Gln Pro
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Leu Pro Phe Phe Ser Ala Gln Phe His Pro Glu Ala Ser Gly Gly Pro
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Lys Phe Gln Lys Val Leu Leu Leu Gly Ser Gly Gly Leu Ser Ile Gly
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Gln Ala Gly Glu Phe Asp Tyr Ser Gly Ser Gln Ala Ile Lys Ala Leu
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Leu His Glu Gln Gly Val Leu Ala Lys Phe Gly Cys Lys Ile Leu Gly
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Ser Pro Ile Glu Ala Ile Ile Ala Thr Glu Asp Arg Lys Val Phe Ala

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 Trp Asp Leu Arg Lys Phe Glu Ser Cys Asp Pro Leu Met Gly Ser Ala
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850 855 860

Ser Leu Gln Lys Ala Leu Arg Met Val Asp Glu Lys Ala Gly Gly Phe
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Asp Glu Ser Val Cys His Phe Phe Ser Thr Asp Glu Asp Cys Ala Pro
885 890 895

Ser Leu Pro Gly Ser Asp Phe Lys Thr Ser Ser Ser Gly Glu Cys Met
900 905 910

Arg Gly Gly Cys Gly Arg Thr Asp Ser Gly Ala Glu Arg Gln Ala Ala
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Leu Leu Glu Ala Glu Leu Arg Arg Pro Ser Pro Asn Arg Ile Trp Ala
930 935 940

Leu Ala Leu Ala Phe Gln Leu Gly Trp Thr Val Asp Ala Leu His Glu
945 950 955 960

Lys Thr Lys Ile Asp Lys Trp Phe Leu Ser Lys Leu Gln Asn Ile Asn
965 970 975

Asp Ile Lys Arg Gln Leu Thr Gln Leu Thr Leu Asp Asp Leu Thr Arg
980 985 990

Ala Asp Phe Phe Tyr Ile Lys Lys Tyr Gly Phe Ser Asp Arg Gln Ile
995 1000 1005

Ala Gln Tyr Leu Met Asn Ser Pro Ser Ala Ala Ala Leu Ser Gln
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Phe Asp Val Arg Arg Arg Arg Leu His Leu Gly Val Arg Pro Ser
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Val Lys Gln Ile Asp Thr Leu Ala Ala Glu Phe Pro Ala His Thr
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Asn Tyr Leu Tyr Leu Thr Tyr Gln Gly Ile Asp Asp Asp Val Ser
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Pro Leu Ala Ala Thr Ser Ser Val Ser Ala Val Phe Ala Gly Ala
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<211> 490

<212> PRT

<213> homo sapiens

<400> 4618

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35

40

45

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gly Gly Pro Pro Thr
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 Pro Ala Ile Asn Thr Pro Val His Phe Gln Ser Pro Pro Pro Val Pro
 65 70 75 80
 Gly Glu Val Leu Lys Val Gln Ser Tyr Leu Glu Asn Pro Thr Ser Tyr
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 His Leu Gln Gln Ser Gln His Gln Lys Val Arg Glu Tyr Leu Ser Glu
 100 105 110
 Thr Tyr Gly Asn Lys Phe Ala Ala His Ile Ser Pro Ala Gln Gly Ser
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 Pro Lys Pro Pro Pro Ala Ala Ser Pro Gly Val Arg Ala Gly His Val
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 Gln Met Pro Asn Thr Leu Pro Leu Ser Ser Ser His Leu Asn Val Tyr
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 Ser Ser Asp Pro Gln Val Thr Ala Ser Leu Val Gly Val Thr Ser Ser
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 Ser Cys Pro Ala Asp Leu Thr Gln Lys Arg Glu Leu Thr Asp Ala Glu
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 Ala Arg Val His Gly Leu Pro Thr Thr Ser Pro Ser Gly Met Asn Met
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 Ala Glu Leu Ala Gln Gln Val Val Lys Gln Glu Leu Pro Ser Glu Glu

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 Pro Leu Pro Ala Leu Pro Pro Gln Ala Pro Leu Pro Leu Pro Thr Gln
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<211> 2280

<212> DNA

<213> homo sapiens

<400> 4619

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<211> 476

<212> PRT

<213> homo sapiens

<400> 4620

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35 40 45

Pro Thr Pro Ala Ile Asn Thr Pro Val His Phe Gln Ser Pro Pro Pro

50 55 60

Val Pro Gly Glu Val Leu Lys Val Gln Ser Tyr Leu Glu Asn Pro Thr

65 70 75 80

Ser Tyr His Leu Gln Gln Ser Gln His Gln Lys Val Arg Glu Tyr Leu

85 90 95

Ser Glu Thr Tyr Gly Asn Lys Phe Ala Ala His Ile Ser Pro Ala Gln

100 105 110

Gly Ser Pro Lys Pro Pro Pro Ala Ala Ser Pro Gly Val Arg Ala Gly

115 120 125

His Val Leu Ser Ser Ser Ala Gly Asn Ser Ala Pro Asn Ser Pro Met

130 135 140

Ala Met Leu His Ile Gly Ser Asn Pro Glu Arg Glu Leu Asp Asp Val

145 150 155 160

Ile Asp Asn Ile Met Arg Leu Asp Asp Val Leu Gly Tyr Ile Asn Pro

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Glu Leu Gly Met Leu Ile Pro Lys Ala Asn Asp Leu Asp Val Arg Trp						
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Leu Glu Met Thr Asn Lys Gln Leu Trp Leu Arg Ile Gln Glu Leu Glu						
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	325		330		335	
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Glu Glu Gly Pro Gly Glu Ala Leu Met Leu Gly Ala Glu Val Pro Asp						
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Pro Glu Pro Leu Pro Ala Leu Pro Pro Gln Ala Pro Leu Pro Leu Pro						
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Thr Gln Pro Pro Ser Pro Phe His His Leu Asp Phe Ser His Ser Leu						
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Ser Phe Gly Gly Arg Glu Asp Glu Gly Pro Pro Gly Tyr Pro Glu Pro						
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Leu Asp Leu Met Leu Leu Asp Asp Ser Leu Leu Pro Leu Ala Ser Asp
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<211> 4618

<212> DNA

<213> homo sapiens

<400> 4621

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<211> 476

<212> PRT

<213> homo sapiens

<400> 4622

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Tyr Met Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gly Gly Pro

35 40 45

Pro Thr Pro Ala Ile Asn Thr Pro Val His Phe Gln Ser Pro Pro Pro

50 55 60

Val Pro Gly Glu Val Leu Lys Val Gln Ser Tyr Leu Glu Asn Pro Thr

65 70 75 80

Ser Tyr His Leu Gln Gln Ser Gln His Gln Lys Val Arg Glu Tyr Leu

85 90 95

Ser Glu Thr Tyr Gly Asn Lys Phe Ala Ala His Ile Ser Pro Ala Gln

100 105 110

Gly Ser Pro Lys Pro Pro Pro Ala Ala Ser Pro Gly Val Arg Ala Gly

115 120 125

His Val Leu Ser Ser Ser Ala Gly Asn Ser Ala Pro Asn Ser Pro Met

130 135 140

Ala Met Leu His Ile Gly Ser Asn Pro Glu Arg Glu Leu Asp Asp Val

145 150 155 160

Ile Asp Asn Ile Met Arg Leu Asp Asp Val Leu Gly Tyr Ile Asn Pro

165 170 175

Glu Met Gln Met Pro Asn Thr Leu Pro Leu Ser Ser Ser His Leu Asn

180 185 190

Val Tyr Ser Ser Asp Pro Gln Val Thr Ala Ser Leu Val Gly Val Thr

195 200 205

Ser Ser Ser Cys Pro Ala Asp Leu Thr Gln Lys Arg Glu Leu Thr Asp

210 215 220

Ala Glu Ser Arg Ala Leu Ala Lys Glu Arg Gln Lys Lys Asp Asn His

225 230 235 240

Asn Leu Ile Glu Arg Arg Arg Arg Phe Asn Ile Asn Asp Arg Ile Lys

245 250 255

Glu Leu Gly Met Leu Ile Pro Lys Ala Asn Asp Leu Asp Val Arg Trp

260 265 270

Asn Lys Gly Thr Ile Leu Lys Ala Ser Val Asp Tyr Ile Arg Arg Met

275 280 285

Gln Lys Asp Leu Gln Lys Ser Arg Glu Leu Glu Asn His Ser Arg Arg

290 295 300

Leu Glu Met Thr Asn Lys Gln Leu Trp Leu Arg Ile Gln Glu Leu Glu

305 310 315 320

Met Gln Ala Arg Val His Gly Leu Pro Thr Thr Ser Pro Ser Gly Met

325 330 335

Asn Met Ala Glu Leu Ala Gln Gln Val Val Lys Gln Glu Leu Pro Ser

340 345 350

Glu Glu Gly Pro Gly Glu Ala Leu Met Leu Gly Ala Glu Val Pro Asp

355 360 365

Pro Glu Pro Leu Pro Ala Leu Pro Pro Gln Ala Pro Leu Pro Leu Pro

370 375 380

Thr Gln Pro Pro Ser Pro Phe His His Leu Asp Phe Ser His Ser Leu

385 390 395 400

Ser Phe Gly Gly Arg Glu Asp Glu Gly Pro Pro Gly Tyr Pro Glu Pro

405 410 415

Leu Ala Pro Gly His Gly Ser Pro Phe Pro Ser Leu Ser Lys Lys Asp

420 425 430

Leu Asp Leu Met Leu Leu Asp Asp Ser Leu Leu Pro Leu Ala Ser Asp

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Pro Leu Leu Ser Thr Met Ser Pro Glu Ala Ser Lys Ala Ser Ser Arg

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Arg Ser Ser Phe Ser Met Glu Glu Gly Asp Val Leu

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<212> PRT

<213> homo sapiens

<400> 4624

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Tyr Met Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gly Gly Pro

35 40 45

Pro Thr Pro Ala Ile Asn Thr Pro Val His Phe Gln Ser Pro Pro Pro

50 55 60

Val Pro Gly Glu Val Leu Lys Leu Asp Asp Val Ile Asp Asn Ile Met

65 70 75 80

Arg Leu Asp Asp Val Leu Gly Tyr Ile Asn Pro Glu Met Gln Met Pro

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Pro Gln Val Thr Ala Ser Leu Val Gly Val Thr Ser Ser Ser Cys Pro		
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Ala Asp Leu Thr Gln Lys Arg Glu Leu Thr Asp Ala Glu Ser Arg Ala		
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Leu Ala Lys Glu Arg Gln Lys Lys Asp Asn His Asn Leu Ile Glu Arg		
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Arg Arg Arg Phe Asn Ile Asn Asp Arg Ile Lys Glu Leu Gly Met Leu		
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Ile Pro Lys Ala Asn Asp Leu Asp Val Arg Trp Asn Lys Gly Thr Ile		
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Leu Lys Ala Ser Val Asp Tyr Ile Arg Arg Met Gln Lys Asp Leu Gln		
195	200	205
Lys Ser Arg Glu Leu Glu Asn His Ser Arg Arg Leu Glu Met Thr Asn		
210	215	220
Lys Gln Leu Trp Leu Arg Ile Gln Glu Leu Glu Met Gln Ala Arg Val		
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His Gly Leu Pro Thr Thr Ser Pro Ser Gly Met Asn Met Ala Glu Leu		
245	250	255
Ala Gln Gln Val Val Lys Gln Glu Leu Pro Ser Glu Glu Gly Pro Gly		
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Glu Ala Leu Met Leu Gly Ala Glu Val Pro Asp Pro Glu Pro Leu Pro		
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Ala Leu Pro Pro Gln Ala Pro Leu Pro Leu Pro Thr Gln Pro Pro Ser		
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Pro Phe His His Leu Asp Phe Ser His Ser Leu Ser Phe Gly Gly Arg		
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Glu Asp Glu Gly Pro Pro Gly Tyr Pro Glu Pro Leu Ala Pro Gly His		
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