



(19) 대한민국특허청(KR)
(12) 등록특허공보(B1)

(45) 공고일자 2024년09월26일
(11) 등록번호 10-2709778
(24) 등록일자 2024년09월20일

(51) 국제특허분류(Int. Cl.)
G16B 20/00 (2019.01) C07K 14/47 (2006.01)
G16B 30/10 (2019.01)
(52) CPC특허분류
G16B 20/00 (2019.02)
C07K 14/4748 (2013.01)
(21) 출원번호 10-2020-7000642
(22) 출원일자(국제) 2018년07월12일
심사청구일자 2021년01월21일
(85) 번역문제출일자 2020년01월08일
(65) 공개번호 10-2020-0029443
(43) 공개일자 2020년03월18일
(86) 국제출원번호 PCT/EP2018/069032
(87) 국제공개번호 WO 2019/012082
국제공개일자 2019년01월17일
(30) 우선권주장
17181026.0 2017년07월12일
유럽특허청(EPO)(EP)

(56) 선행기술조사문헌
Yvette Schwitalle 외, Immunogenic peptides generated by frameshift mutations in DNA mismatch repair-deficient cancer cells, Cancer Immun., 2004.11.25., Vol.4.
S M Woerner 외, Systematic identification of genes with coding microsatellites mutated in DNA mismatch repair-deficient cancer cells, Inter J Cancer, 2001.07.01., Vol.93, No.1.
Shen Luhui 외, Abstract 469: Progress towards developing a universal, prophylactic cancer vaccine, Cancer Res, 2013.04.15., Vol.73.
WO2016187508 A2

(73) 특허권자
노우스콤 아게
스위스, 바젤 4051, 보임라인가체 18
(72) 발명자
니코시아 알프레도
이탈리아, 80123 나폴리, 비아 파르코 카렐리 70
스카르셀리 엘리사
이탈리아, 00147 로마, 비아 메로피아 78
(뒷면에 계속)
(74) 대리인
특허법인한얼

전체 청구항 수 : 총 22 항

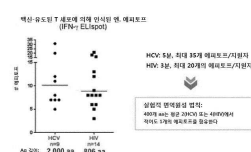
심사관 : 정태수

(54) 발명의 명칭 미세부수체 불안정성(MSI) 암의 예방 및 치료를 위한 공유된 종양 신생항원을 기반으로 한 범용 백신

(57) 요약

본 발명은 프레임-쉬프트 펩타이드의 수집물(CFSP)을 선택하여 유전성 및 산발성 미세부수체 불안정성(MSI) 종양을 갖는 환자의 예방 및 치료를 위한 범용 암 백신 펩타이드 수집물(CVP)을 생산하는 방법에 관한 것이다. 본 발명은 또한 CFSP로부터 프레임-쉬프트 펩타이드(FSP)의 서브세트를 선택하고 FSP의 아미노산(aa) 서열을 임의로 변형시켜 변형된 FSP(mFSP)를 생성함으로써 CVP를 생산하는 방법에 관한 것이다. 본 발명은 또한 동시에 사용될 수도 있는 하나 이상의 백신 벡터 속에서 FSP의 CVP를 암호화하는 핵산 수집물에 관한 것이다. 이러한 CVP, 핵산 및 벡터는 MSI 암의 예방 또는 치료에 사용된다.

대표도



(52) CPC특허분류

G16B 30/10 (2019.02)

(72) 발명자

레오니 귀도

이탈리아, 00134 로마, 비아 피아 날리 100

람 아르민

이탈리아, 00153 롬, 18, 피아자 산타 마리아 리베
라트리체

명세서

청구범위

청구항 1

다음의 단계 (i) 및 (ii)를 포함하는, 유전성 및 산발성 미세-부수체 불안정성(micro-satellite instability: MSI) 암을 포함하는 암을 지니거나, 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료를 위한 범용 MSI 암 백신 펩타이드 수집물(CVP)을 생산하기 위한 프레임-쉬프트 펩타이드의 수집물(CFSP)을 선택하는 방법:

(i) 각각이 프레임-쉬프트 돌연변이(FSM)를 포함하는 핵산의 수집물 (CFSM)을 선택하는 단계로서, 각각의 FSM은 각각의 상이한 환자의 적어도 M개의 암 샘플(CS) 중 하나 이상에 존재하며, 여기서 환자의 암은 MSI 표현형을 지닌 암 세포를 포함하고;

여기서 선택된 FSM의 적어도 50%는 기준 (a), (b), (c) 및 (d)를 충족하는 단계:

(a) FSM은 6개 이상의 뉴클레오타이드의 길이를 지닌 암호화 유전자(coding gene)의 모노뉴클레오타이드 반복체(MNR) 속에 존재함;

(b) FSM은 1개의 뉴클레오타이드의 결실에 해당함;

(c) FSM을 포함한 DNA 서열분석 관독물(DNA sequencing read)의 수는, 매치된 정상 샘플(matched normal sample)과 비교하여 중앙 샘플 속에서 유의적으로 더 높음(0.05 이하의 FDR-교정된 피셔 시험(Fisher test) p-값);

(d) FSM은, 매치된 정상 샘플 속에 25% 미만의 대립유전자 빈도로 존재함,

(ii) X개의 상이한 프레임-쉬프트 펩타이드(FSP)를 선택하는 단계로서, 여기서 각각의 선택된 FSP가, FSM이 없는 상응하는 야생형(wt) 핵산의 번역 생성물과 비교하여 상이한 첫 번째 아미노산을 암호화하는 코돈(codon)으로부터 시작되는, 적어도 4개의 아미노산 길이의 CFSM의 FSM을 포함하는 핵산의 단백질-암호화 분절의 완전한 번역 생성물인 단계,

여기서 X는 적어도 20개 또는 적어도 35개이고 M은 적어도 5개이다.

청구항 2

제1항에 있어서, 선택된 FSP의 적어도 50%가 다음의 기준 (a) 내지 (c) 중 하나 이상을 충족하는 방법:

(a) FSP는 FSM에 의해 암호화되고, 여기서 FSM은 M개의 상이한 CS의 수집물의 부분인 특정 암 유형의 CS 서브세트(subset)에 대해 관찰된 암 유형-특이적인 빈도(CF)로 관찰되고, 상기 CF는 CS 내에 존재하는 암 유형 중 적어도 하나에 대해 적어도 5%임;

(b) FSP를 암호화하는 FSM을 지닌 유전자의 평균 mRNA 발현 수준은, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 80번째 백분위수 이내임; 및

(c) FSP를 생성하는 FSM은 암이 없는 대상체의 집단(cohort) 내의 정상 조직 내에서 2% 미만으로 관찰됨.

청구항 3

제1항에 있어서, 하기 특징 중 적어도 하나를 갖는, 방법:

(i) CS가 MSI 종양; 결장직장 암, 위암, 및 자궁내막 암 중 하나 이상; 또는 결장직장 암, 위암 및 자궁내막 암을 가진 환자로부터 유래됨;

(ii) M이 적어도 10, 적어도 30, 적어도 50, 적어도 100, 적어도 200, 또는 적어도 300임; 및

(iii) X가 적어도 35, 적어도 50, 적어도 100, 또는 적어도 200임.

청구항 4

다음의 단계를 포함하는, CVP에 포함된 펩타이드의 아미노산 서열 또는 CVP에 포함된 펩타이드를 암호화하는 핵

산 서열을 결정하는 방법:

(a) 제1항 내지 제3항 중 어느 한 항에 따라 선택된 CFSP로부터 적어도 Y개의 FSP 또는 이의 적어도 8개의 아미노산 길이의 단편을 선택하는 단계;

(b) 다음의 기준:

(i) FSP는 길이가 4 내지 9개 아미노산임,

(ii) FSP가, 동일한 FSM에 의해 암호화되는 둘 이상의 FSP 내에 존재하는 8개 이상의 아미노산 길이의 하나 이상의 동일한 연속된 스트레치(stretch)를 함유함, 및

(iii) FSP가 야생형(wt) 사람 단백질 내에 또한 존재하는 8개 이상의 아미노산 길이의 하나 이상의 연속된 스트레치를 함유함

중 하나 이상을 충족하는 FSP 중 하나 이상 또는 모두의 아미노산 서열을 변형시키는 단계로서,

여기서 (i)에 따른 FSP의 아미노산 서열은 FSP의 바로 상부(immediately upstream)에 존재하는 야생형(wt) 아미노산 서열의 1 내지 4개의 아미노산을 FSP의 N-말단에 첨가함으로써 변형되고 여기서 변형된 FSP(mFSP)는 길이가 적어도 8개 아미노산이고; (ii)에 따른 FSP의 아미노산 서열은, 가장 긴 FSP를 제외한 모두에서 이러한 연속된 스트레치를 제거함으로써 변형되며, 단 연속된 스트레치의 제거 후 4개 미만의 아미노산 길이를 지닌 FSP는 CVP로부터 배제되고; (iii)에 따른 FSP의 아미노산 서열은 이러한 스트레치를 제거함으로써 변형되고; 연속된 스트레치의 제거 후 4개 미만의 아미노산의 길이를 지닌 변형된 FSP는 CVP로부터 배제되는, 단계;

여기서 CVP의 아미노산 서열은, 단계 (a)에서 선택되거나 단계 (b)에서 변형된 FSP 또는 이의 단편의 아미노산 서열을 포함하고;

여기서 Y는 적어도 20, 또는 적어도 35이다.

청구항 5

제4항에 있어서, 단계 (a)에서 CVP의 FSP는 CFSP로부터 연이어 선택되고, 각각의 선택 단계에서, 역치 값(threshold value; TV) 미만인 최대 수의 압 샘플에서 역치 값에 이르도록 총 FSP 아미노산 길이의 누적량(CAFSPL)을 증가시키는 새로운 FSP가 CFSP로부터 선택되고, 임의로, CAFSPL이 여전히 역치 값 미만인 최대 수의 압 샘플에 대한 CAFSPL이 둘 이상의 FSP에 의해 증가할 경우, 최고 점수를 지닌 FSP가 선택되는 방법.

청구항 6

제4항에 있어서, 하기 특징 중 적어도 하나를 갖는, 방법:

(i) 각각의 압 샘플에 대한 CAFSPL이, CVP의 이미 일부분인 FSP의 아미노산 길이 및 상응하는 FSM이 상기 압 샘플 속에 존재하는 CFSP로부터의 새로운 FSP의 아미노산 길이를 합함으로써 결정됨;

(ii) 역치 값(threshold value; TV)이 특정 압 유형에 속하는 CS로부터의 샘플의 각각의 서브세트에 대해 별도로 정의됨;

(iii) 점수는, 임의로 CF가 5% 미만인 압 유형으로부터의 CS 내 FSM을 계수함이 없이, FSP의 아미노산 길이와, FSP를 생성하는 FSM이 CS 내에서 관찰되는 전체적인 빈도 사이의 곱(product)으로서 정의됨;

(iv) 압 샘플의 서브세트는 종양 유형으로부터의 모든 압 샘플을 포함하고 여기서 FSM은 5% 이상의 CF로 존재함;

(v) 5% 미만의 전체적인 빈도로 FSM에 의해 생성된 FSP는 선택으로부터 배제됨;

(vi) CVP로의 혼입이 CAFSPL이 여전히 TV 미만인 임의의 압 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지 또는 CVP 내에 존재하는 모든 FSP의 누적 길이가 V개 아미노산의 최대 값에 도달할 때까지 새로운 FSP 또는 변형된 FSP의 첨가가 진행됨; 및

(vii) 동일한 FSM으로부터 유래된 FSP는 개개의 FSP의 점수의 합으로서 계산된 합해진(combined) 점수를 지닌 하나의 FSP로서 취급됨.

청구항 7

제5항에 있어서, CVP 내 혼입이 CAFSPL이 여전히 TV 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지, 새로운 FSP의 첨가가 진행되거나; 또는

동일한 FSM으로부터 유래된 FSP가 개개의 FSP의 점수의 합으로서 계산된 합해진 점수를 지닌 하나의 FSP로서 취급되는 방법.

청구항 8

제6항에 있어서,

(a) TV가 적어도 400개 아미노산, 적어도 600개 아미노산, 또는 적어도 800개 아미노산이거나;

(b) TV가:

(i) 결장직장 암 및 위암의 경우 적어도 400개 아미노산, 적어도 600개 아미노산, 또는 적어도 800개 아미노산이고;

(ii) 자궁내막 암의 경우 적어도 200개 아미노산, 적어도 300개 아미노산, 또는 적어도 400개 아미노산인 방법.

청구항 9

제4항에 있어서, 하기 특징 중 적어도 하나를 갖는, 방법:

(i) CVP가 CFSP로부터 선택된 각각의 FSP의 적어도 4개의 아미노산을 포함함;

(ii) CVP의 일부인 모든 펩타이드의 누적 아미노산 길이 V가 적어도 280개 아미노산, 또는 적어도 6000개 아미노산이 되도록 Y가 선택됨;

(iii) Y가 적어도 35, 적어도 50, 적어도 100, 또는 적어도 200임; 및

(iv) CVP가, 서열 번호 1 내지 1087의 그룹으로부터 선택되거나 또는 서열 번호 1 내지 209의 그룹으로부터 선택되는 FSP 또는 mFSP를 포함함.

청구항 10

(i) 제4항에 따른 방법에서 결정된 아미노산 또는 핵산 서열 정보를 수득하는 단계; 및

(ii) 하나 이상의 폴리펩타이드 중의 CVP의 아미노산 서열 또는 이러한 서열을 지닌 핵산의 수집물을 합성하고 임의로 핵산의 수집물을 하나 이상의 발현 카세트 또는 발현 벡터의 수집물 내로 삽입시키는 단계를 포함하는, CVP 또는 CVP를 암호화하는 핵산의 수집물을 생산하는 방법.

청구항 11

서열 번호 1 내지 209에 따른 209개의 프레임-쉬프트 펩타이드(FSP) 및 변형된 FSP(mFSP)를 포함하는, 암 백신 펩타이드 수집물(CVP).

청구항 12

제11항에 있어서, CVP가 서열 번호 1088 내지 1091(레이아웃 A), 서열 번호 1092 내지 1095(레이아웃 B), 서열 번호 1155 내지 1158(레이아웃 C) 또는 서열 번호 1159 내지 1162(레이아웃 D)에 따른 아미노산 서열을 가지는 4개의 폴리펩타이드로 이루어지거나 이를 포함하는 CVP.

청구항 13

제11항에 있어서, CVP의 하나 이상의 펩타이드가 CVP의 면역원성을 향상시키는 다음의 성분 중 하나 이상에 연결되거나, 또는 펩타이드 결합에 의해 연결되는, CVP: 불변 쇠 서열 또는 이의 단편; 조직형 플라스미노겐 활성화 인자; PEST 서열; 사이클린 파괴 박스; 유비퀴틴화 신호; 수모일화 신호(SUMOylation signal); 인터루킨, 인터루킨 2, 인터루킨 12, 또는 인터루킨 15; 체크포인트 단백질(checkpoint protein) 특이적인 리간드, 항-PD1 항체 또는 이의 PD1-결합 단편, 항-CTLA4 항체 또는 이의 항-CTLA4-결합 단편, 항-LAG3 항체 또는 항-LAG3-결합 단편, 항-TIM3 항체 또는 이의 항-TIM3-결합 단편.

청구항 14

제11항 내지 제13항 중 어느 한 항에 따른 CVP를 암호화하는 핵산의 수집물.

청구항 15

제14항의 핵산의 수집물의 모두 또는 부분을 각각 포함하는 하나 이상의 발현 벡터의 수집물로서, 여기서 발현 벡터의 수집물의 전체가 제14항의 핵산의 수집물 모두를 포함하는 수집물.

청구항 16

제15항에 있어서, 발현 벡터 중 적어도 하나가 발현 벡터의 면역원성을 향상시키는 하나 이상의 성분을 포함하는 발현 벡터의 수집물.

청구항 17

제15항에 있어서, 발현 벡터 중 적어도 하나가 CVP의 면역원성을 향상시키는 성분을 암호화하는 하나 이상의 핵산을 포함하는 발현 벡터의 수집물: 불변 세 서열 또는 이의 단편; 조직형 플라스미노겐 활성화인자; PEST 서열; 사이클린 파괴 박스; 유비퀴틴화 신호; 수모일화 신호(SUMOylation signal); 인터루킨, 인터루킨 2, 인터루킨 12, 또는 인터루킨 15; 체크포인트 단백질 특이적인 리간드, 항-PD1 항체 또는 이의 PD1-결합 단편, 항-CTLA4 항체 또는 이의 항-CTLA4-결합 단편, 항-LAG3 항체 또는 항-LAG3-결합 단편, 항-TIM3 항체 또는 이의 항-TIM3-결합 단편.

청구항 18

제15항에 있어서, 각각의 발현 벡터가 플라스미드; 코스미드; RNA; 보조제(adjuvant)와 함께 제형화된 RNA; 리포좀 입자 중에 제형화된 RNA; 자가-증폭하는 RNA(SAM); 보조제와 함께 제형화된 SAM; 리포좀 입자 중에 제형화된 SAM; 바이러스 벡터; 알파바이러스 벡터, 베네주엘라 말 뇌염(VEE) 바이러스 벡터, 신드비스(SIN) 바이러스 벡터, 쉼리키 포레스트 바이러스(semliki forest virus: SFV) 바이러스 벡터, 복제가능하거나 불가능한 아데노바이러스 벡터, 침팬지 또는 난쟁이 침팬지 또는 고릴라로부터 유래된 복제가능하거나 불가능한 아데노바이러스 벡터, 포크바이러스 벡터, 박시니아 바이러스 벡터 또는 변형된 박시니아 안카라(modified vaccinia ankara: MVA) 벡터, 시미안 또는 사람 사이토메갈로바이러스(CMV) 벡터, 림프구 맥락수막염 바이러스(Lymphocyte choriomeningitis virus: LCMV) 벡터, 레트로바이러스 또는 렌티바이러스 벡터로 이루어진 그룹으로부터 선택되는 발현 벡터의 수집물.

청구항 19

제11항 내지 제13항 중 어느 한 항에 따른 CVP를 포함하거나, 상기 CVP를 암호화하는 핵산의 수집물을 포함하거나, 또는 상기 핵산의 수집물의 모두 또는 부분을 포함하는 발현 벡터의 수집물로서, 발현 벡터의 수집물의 전체가 상기 핵산의 수집물 모두를 포함하는 발현 벡터의 수집물을 포함하는,

MSI 표현형을 지닌 암 세포를 포함하는 암을 지니거나 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료에 사용하기 위한 약제학적 조성물.

청구항 20

제19항에 있어서, 상기 예방이 미스매치 복구 시스템(MMR), 예를 들면, MLH-1, MSH-2, MSH-6, PMS2 및 TACSTD1/EPCAM에 관여하는 유전자에 배선 돌연변이(germline mutation)를 지닌 환자를 포함하는, 임상 가이드라인에 따른 MSI 암으로 진행될 위험이 있는 것으로 알려진 환자를 위한 것이며, 여기서 치료가 가장 최근의 임상 가이드라인에 따른 MSI 상태의 진단 후 임의의 조직 내에서 발생하는, 모든 단계(I 내지 IV)에서의 암을 지닌 환자를 위한 것이며 여기서 이러한 조성물의 용도는 자발적으로 또는 약리학적으로 유도될 수 있는 MSI 상태를 지닌 암의 치료를 위해 의도되고 여기서 암이 결장직장암, 위암, 자궁내막암, 소장암, 간담즙성 관 암, 간암, 신경내분비암, 자궁경부암, 난소암, 자궁육종, 뇌암 및 피부 암으로 이루어진 그룹으로부터 선택되는, 약제학적 조성물.

청구항 21

(i) 제14항의 핵산의 수집물, (ii) 상기 핵산의 수집물의 모두 또는 부분을 포함하는 발현 벡터의 수집물로서, 발현 벡터의 수집물의 전체가 상기 핵산의 수집물 모두를 포함하는 발현 벡터의 수집물, 또는 (i) 및 (ii) 둘

모두를 포함하는, MSI 표현형을 지닌 암 세포를 포함하는 암을 지니거나 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료에 사용하기 위한, 억제학적 조성물로서, 여기서 핵산의 수집물 또는 발현 벡터의 수집물이 이중 프라임-부스트 백신접종 계획(heterologous prime-boost vaccination scheme)으로 투여되는, 억제학적 조성물.

청구항 22

제21항에 있어서, 프라임은 아데노바이러스 벡터, 그리고 하나 이상의 부스트는 폭스바이러스 벡터 또는 MVA 벡터를 사용하는 것이며, 여기서 예방이 미스매치 복구 시스템(MMR), 예를 들면, MLH-1, MSH-2, MSH-6, PMS2 및 TACSTD1/EPCAM에 관여하는 유전자에 배선 돌연변이를 지닌 환자를 포함하는, 임상 가이드라인에 따른 MSI 암으로 진행될 위험이 있는 것으로 알려진 환자를 위한 것이며 여기서 치료가 가장 최근의 임상 가이드라인에 따른 MSI 상태의 진단 후 임의의 조직 내에서 발생하는, 모든 단계(I 내지 IV)에서의 암을 지닌 환자를 위한 것이며 여기서 이러한 조성물의 용도는 자발적으로 또는 약리학적으로 유도될 수 있는 MSI 상태를 지닌 암의 치료를 위해 의도되고 여기서 암이 결장직장암, 위암, 자궁내막암, 소장암, 간담즙성 관 암, 간암, 신경내분비암, 자궁경부암, 난소암, 자궁육종, 뇌암 및 피부 암으로 이루어진 그룹으로부터 선택되는, 억제학적 조성물.

청구항 23

삭제

청구항 24

삭제

청구항 25

삭제

청구항 26

삭제

청구항 27

삭제

발명의 설명

기술 분야

[0001] 본 발명은 프레임-쉬프트 펩타이드의 수집물(collection of frame-shift peptide: CFSP)을 선택하여 유전성 및 산발성 미세부수체 불안정성(micro-satellite instability: MSI) 종양을 지닌 환자의 예방 및 치료용의 범용 암 백신 펩타이드 수집물(CVP)을 생산하는 방법에 관한 것이다. 본 발명은 또한 CFSP로부터 프레임-쉬프트 펩타이드(FSP)의 서브세트(subset)를 선택하고 임의로 FSP의 아미노산(aa) 서열을 변형시킴으로써 변형된 FSP(mFSP)를 생성하는 CVP의 생산 방법에 관한 것이다. 본 발명은 또한 동시에 사용될 수도 있는 하나 이상의 백신 벡터 내에서 FSP 및/또는 mFSP의 CVP를 암호화하는 핵산 수집물에 관한 것이다. 이러한 CVP, 핵산 및 벡터는 MSI 암의 예방 또는 치료를 위해 사용된다.

배경 기술

[0002] 발명의 배경

[0003] 암 백신의 분야는 종양-관련된 및, 보다 최근에는 종양-특이적인 항원을 표적화하는데 장기간 집중되어 왔다. 후자는 정상 세포에는 존재하지 않으므로 자체로 정의된, 종양 신생 항원의 생산을 야기하는 암호화 유전자내 종양원성 바이러스 단백질 또는 체세포 돌연변이로부터 암 세포내에서 발생할 수 있다. 자가-내성 및 자가면역성의 보다 낮은 위험성에 있어서 보다 매력적이지만, 종양 신생항원은 정해진 환자의 암 세포 중에서 및 사람 집단에 걸쳐 유의적으로 변하므로, 공유된 종양 신생항원을 기반으로 한 효과적인 범용 암 백신의 발달을 방해한다.

그러나 이의 근본적인 생물학으로 인하여 이러한 일반적인 역할을 따르지 않는 암의 그룹이 존재한다: DNA mismatch 복구 유전자(mismatch repair 유전자: MMR)내 돌연변이에 의해 흔히 유발된 미세부수체 불안정성(MSI) 종양. 결함이 있는 MMR 시스템은 미세부수체로 불리는 반복된 뉴클레오타이드 서열의 영역내에 돌연변이의 축적을 야기한다. 암호화 유전자의 미세부수체내 돌연변이는 이의 C-말단이 신규의 비-자가 펩타이드, 소위 프레임 쉬프트 펩타이드(frame shift peptide: FSP)로 구성된 키메라 단백질을 생성하는 번역 관독 프레임의 쉬프트를 초래할 수 있다. 대부분의 암과는 달리, MSI 종양내 돌연변이는 모노뉴클레오타이드 반복체(MNR)로 이루어진 미세부수체에서 우선적으로 발생한다. 암호화 영역내에서, 이러한 돌연변이는 대부분 1개의 뉴클레오타이드 결실로 이루어지며 제한된 수의 유전자에 영향을 미치므로, 환자 중에서 공유되어 있다(Kim, T.M., *et al.* (2013) Cell 155(4): 858-868).

[0004] 삭제

[0005] 따라서, MSI-관련된 암은 공유된 종양 신생항원을 기반으로 한 범용 백신을 설계하는 유일한 기회를 제공한다. MSI-종양은 MMR 유전자내에서 체세포 및 배선 돌연변이 각각에 의해 유발된 산발성 암 및 유전된 암 둘 다를 포함한다. 린치 증후군(Lynch syndrome: LS)은 제2 그룹 속에 속하는 희귀 질환(ORPHA144)이다. 특히, MMR 경로(유전성 LS 단체의 ~90%)의 MSH2 또는 MLH1 유전자내 이형접합성 배선 돌연변이를 지닌 개인은 암 발달에 대해 보다 높은 위험에 처해 있다. 구체적으로, 이들은 이들의 수명 동안 >50%의 경우에 결장 또는 자궁내막 암으로 발달하는 성향이 있다(Boland, C.R. and A. Goel (2010) Gastroenterology 138(6): p. 2073-2087 e3).

발명의 내용

해결하려는 과제

[0006] 삭제

[0007] 요약하면, 본원에 기술된 발명은 MSI 종양에 걸쳐 공유된 FSP 신생항원(shared FSP neoantigen)의 확인 및 특히 LS 보인자에서, MSI 암의 치료 및 이들의 예방을 위해 CFSP로부터 유래된 FSP 및 변형된 FSP(CVP로 정의됨)의 서브세트를 기반으로 한 범용 백신의 개발에 관한 것이다. 이러한 CVP는 특히 다음의 장점을 제공할 수 있다: (i) 다양한 MSI 암에 대한 우수한 치료학적 및/또는 예방학적 면역 반응; (ii) 이것이 공유된 FSP의 큰 세트를 암호화하므로 사용하기 용이하고 환자의 큰 집단(cohort)에서 효과적인 기성 백신(off-the-shelf vaccine); (iii) 예방학적 세팅에서 특히 유용한, 임의의 MSI 암의 치료 및 예방에 적합한 방식으로 선택될 수 있는 특정 CVP; (iv) 잠재적인 자가-에피토프의 배제로 인한 자가면역 반응의 위험의 부재.

본 발명자들이 아는 한, 본 발명의 방법은 다음을 포함하는, 기존에 알려지지 않은 다양한 특징에 의해 특성화된다:

[0008] (i) 보호 수단의 다양성, 예를 들면,

[0009] a) 평균적으로, 선택된 종양형에서 역치(threshold) 초과로 표시되는, 유전자로부터의 프레임쉬프트 펩타이드의 선택,

[0010] b) 건강한 대상체의 조직 내에 부재하거나 매우 드문 프레임쉬프트 펩타이드의 선택,

[0011] c) 정상인 사람 단백질에서 8개 아미노산 이상의 길이를 지닌 분절(segment)과 동일한 프레임쉬프트 펩타이드로부터의 분절의 배제, 및

[0012] c) 다수의 암 샘플의 사용.

[0013] (ii) 최소의 추정된 CD8+ T 세포 에피토프(8mer)의 것보다 더 짧은 길이를 지닌 프레임쉬프트 펩타이드의 혼입. 이는 4개 이하의 야생형 아미노산을 첨가하여 적어도 8개의 아미노산의 펩타이드를 생성함으로써 달성된다.

(iii) 각각의 개개 암 샘플(암 샘플은 백신에 의해 표적화된 집단을 나타낸다)이 백신에 의해 암호화된 프레임쉬프트 펩타이드의 일부를 함유하고 이러한 부분에 나타난 프레임쉬프트 펩타이드의 총 길이가 적어도 400개 아미노산이 되도록 백신 내에 포함될 프레임쉬프트 펩타이드의 최적의 수집물의 선택. 바이러스 항원을 표적화하는 백신에서의 임상 시험은 평균적으로, 400개 아미노산의 바이러스 항원, 즉, 프레임쉬프트 펩타이드와 같은

비-자가 항원이 각각의 환자에서 적어도 하나의 면역원성 T 세포 반응을 생성하는데 필요함을 나타내었다. 각각의 암 샘플의 경우 커버되는 프레임쉬프트 펩타이드의 부분이 상이할 것이지만(즉, 각각의 암 샘플은 프레임쉬프트 돌연변이의 상이한 서브세트를 함유하며, 그 결과, 최적의 수집물로부터의 프레임쉬프트 펩타이드의 상이한 서브세트가 존재할 것이다), 최적의 수집물은 각각의 종양 샘플에 커버되는 프레임쉬프트 펩타이드의 분획이 총 길이가 적어도 400개의 아미노산을 갖도록 선택된다. 이러한 400개 아미노산의 규칙(400 amino acid rule)을 제시된 선택 방법에 포함함으로써 백신 표적 집단의 종양 속에 존재하는 FSP에 대한 T 세포의 유도를 보증한다.

삭제

과제의 해결 수단

발명의 요약

제1 양태에서, 본 발명은 다음의 단계 (i) 및 (ii)를 포함하는, 유전성 및 산발성 미세-부수체 불안정성(micro-satellite instability: MSI) 암을 포함하는 암을 지니거나, 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료를 위한 범용 MSI 암 백신 펩타이드 수집물(CVP)을 생산하기 위한 프레임-쉬프트 펩타이드의 수집물(CFSP)을 선택하는 방법 에 관한 것이다:

(i) 각각이 프레임-쉬프트 돌연변이(FSM)를 포함하는 핵산의 수집물 (CFSM)을 선택하는 단계로서, 각각의 FSM은 각각의 상이한 환자의 적어도 M개의 암 샘플(CS) 중 하나 이상에 존재하며, 여기서 환자의 암은 MSI 표현형을 지닌 암 세포를 포함하고;

여기서 선택된 FSM의 적어도 50%는 기준 (a), (b), (c) 및/또는 (d)를 충족하는 단계:

(a) FSM은 6개 이상의 뉴클레오타이드의 길이를 지닌 암호화 유전자(coding gene)의 모노뉴클레오타이드 반복체(MNR) 속에 존재함;

(b) FSM은 1개의 뉴클레오타이드의 결실에 해당함;

(c) FSM을 포함한 DNA 서열분석 판독물(DNA sequencing read)의 수는, 매치된 정상 샘플(matched normal sample)과 비교하여 종양 샘플 속에서 유의적으로 더 높음(0.05 이하의 FDR-교정된 피셔 시험(Fisher test) p-값);

(d) FSM은, 매치된 정상 샘플 속에 25% 미만의 대립유전자 빈도(allele frequency)로 존재함,

(ii) X개의 상이한 프레임-쉬프트 펩타이드(FSP)를 선택하는 단계로서, 여기서 각각의 선택된 FSP가, FSM이 없는 상응하는 야생형(wt) 핵산의 번역 생성물과 비교하여 상이한 첫 번째 아미노산을 암호화하는 코돈(codon)으로부터 시작되는, 적어도 4개의 아미노산 길이의 CFSM의 FSM을 포함하는 핵산의 단백질-암호화 분절의 완전한 번역 생성물인 단계,

여기서 X는 적어도 20개, 보다 바람직하게는 적어도 35개이고 M은 적어도 5개이다.

제2 양태에서, 본 발명은 다음의 단계를 포함하는, CVP에 포함된 펩타이드의 아미노산 서열 또는 CVP에 포함된 펩타이드를 암호화하는 핵산 서열을 결정하는 방법에 관한 것이다:

(a) 제1 양태에 따라 선택된 CFSP로부터 적어도 Y개의 FSP 또는 이의 적어도 8개의 아미노산 길이의 단편을 선택하는 단계;

(b) 다음의 기준:

(i) FSP는 길이가 4 내지 9개 아미노산임, 및/또는

(ii) FSP가, 동일한 FSM에 의해 암호화되는 둘 이상의 FSP 내에 존재하는 8개 이상의 아미노산 길이의 하나 이상의 동일한 연속된 스트레치(stretch)를 함유함, 및/또는

(iii) FSP가 야생형(wt) 사람 단백질 내에 또한 존재하는 8개 이상의 아미노산 길이의 하나 이상의 연속된 스트레치를 함유함

을 충족하는 FSP 중 하나 이상 또는 모두의 아미노산 서열을 변형시키는 단계로서,

여기서 (i)에 따른 FSP의 아미노산 서열은 FSP의 바로 상부(immediately upstream)에 존재하는 야생형(wt) 아

미노산 서열의 1 내지 4개의 아미노산을 FSP의 N-말단에 첨가함으로써 변형되고 여기서 변형된 FSP(mFSP)는 길이가 적어도 8개 아미노산이고/이거나; (ii)에 따른 FSP의 아미노산 서열은, 가장 긴 FSP를 제외한 모두에서 이러한 연속된 스트레치를 제거함으로써 변형되며, 단 연속된 스트레치의 제거 후 4개 미만의 아미노산 길이를 지닌 FSP는 CVP로부터 배제되고/되거나; (iii)에 따른 FSP의 아미노산 서열은 이러한 스트레치를 제거함으로써 변형되고; 연속된 스트레치의 제거 후 4개 미만의 아미노산의 길이를 지닌 변형된 FSP는 CVP로부터 배제되는, 단계;

여기서 CVP의 아미노산 서열은, 단계 a)에서 선택되고/되거나 단계 (b)에서 변형된 FSP 또는 이의 단편의 아미노산 서열을 포함하고;

여기서 Y는 적어도 20, 보다 바람직하게는 적어도 35이다.

제3 양태에서, 본 발명은

(i) 본 발명의 제2 양태의 방법에서 결정된 아미노산 또는 핵산 서열 정보를 수득하는 단계; 및

(ii) 하나 이상의 폴리펩타이드 중의 CVP의 아미노산 서열 또는 이러한 서열을 지닌 핵산의 수집물을 합성하고 임의로 핵산의 수집물을 하나 이상의 발현 카세트 및/또는 발현 벡터의 수집물 내로 삽입하는 단계를 포함하는, CVP 또는 CVP를 암호화하는 핵산의 수집물을 생산하는 방법에 관한 것이다.

제4 양태에서, 본 발명은 CVP 또는 본 발명의 제3 양태의 방법에 의해 생산가능한 상기 CVP의 펩타이드를 암호화하는 핵산의 수집물에 관한 것이다.

제5 양태에서, Y개의 상이한 FSP 및/또는 mFSP를 포함하거나 이로 이루어진 CVP로서,

여기서 각각의 FSP 또는 mFSP로 변형되는 FSP는, 길이가 적어도 4개 아미노산인 경우에서의 FSM이 없는 상응하는 wt 핵산의 번역물과 비교하여 상이한 첫 번째 아미노산을 암호화하는 코돈으로부터 시작되는 핵산을 함유하는 FSM의 단백질-암호화 분절의 단편 또는 완전한 번역 생성물이고,

여기서 FSP 또는 mFSP로 변형되는 FSP의 적어도 50%는 다음의 기준:

(a) FSP는 FSM에 의해 암호화되고, 여기서 FSM은 M개의 상이한 CS의 수집물의 부분인 특정 암 유형의 CS 서브세트(subset)에 대해 관찰된 암 유형-특이적인 빈도(CF)로 관찰되고, 상기 CF는 CS 내에 존재하는 암 유형 중 적어도 하나에 대해 적어도 5%임; 및/또는

(b) FSP를 암호화하는 FSM을 지닌 유전자의 평균 mRNA 발현 수준은, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 80번째 백분위수 이내임; 및/또는

(c) FSP를 생성하는 FSM은 암이 없는 대상체의 집단(cohort)내의 정상 조직내에서 2% 미만으로 관찰됨

중 하나 이상을 충족하고,

여기서 다음의 기준:

(i) FSP는 길이가 4 내지 9개의 아미노산임, 및/또는

(ii) FSP가, 동일한 FSM에 의해 암호화되는 둘 이상의 FSP 내에 존재하는 8개 이상의 아미노산 길이의 하나 이상의 동일한 연속적인 스트레치를 함유함, 및/또는

(iii) FSP가 wt 사람 단백질 내에 또한 존재하는 8개 이상의 아미노산 길이의 하나 이상의 연속된 스트레치를 함유함

을 충족하는 FSP 중 하나 이상 또는 모두의 아미노산 서열은, (i)에 따른 FSP의 경우에는, FSP의 바로 상부에 존재하는 야생형(wt) 아미노산 서열의 1 내지 4개 아미노산을 FSP의 N-말단에 첨가함으로써 변형되며 여기서 변형된 FSP(mFSP)는 길이가 적어도 8개 아미노산이고/이거나; (ii)에 따른 FSP의 경우에는, 가장 긴 FSP를 제외한 모두에서 이러한 연속된 스트레치를 제거함으로써 변형되며, 단 연속된 스트레치의 제거 후 길이가 4개 미만의 아미노산인 FSP가 CVP로부터 배제되고/되거나; (iii)에 따른 FSP의 경우에는, 이러한 스트레치를 제거함으로써 변형되며; 연속된 스트레치의 제거 후 길이가 4개 미만의 아미노산인 변형된 FSP는 CVP로부터 배제되며;

여기서 Y는 적어도 20이고 보다 바람직하게는 적어도 35이며 M은 적어도 5인, CVP.

제6 양태에서, 본 발명은 본 발명의 제5 양태의 CVP를 암호화하는 핵산 수집물에 관한 것이다.

제7 양태에서, 본 발명은 본 발명의 제4 또는 제6 양태의 핵산 수집물의 모두 또는 일부분을 각각 포함하는, 하나 이상의 발현 벡터의 수집물에 관한 것이며, 여기서 발현 벡터의 수집물의 전체는 본 발명의 제4 또는 제6 양태의 핵산 수집물 모두를 포함한다.

제8 양태에서, 본 발명은 MSI 표현형을 지닌 암 세포를 포함하는 암을 갖거나 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료에 사용하기 위한, 본 발명의 제4 또는 제5 양태의 CVP, 본 발명의 제4 또는 제6 양태의 핵산 수집물, 본 발명의 제7 양태의 발현 벡터 수집물에 관한 것이며, 여기서 암은 결장직장암(colorectal cancer), 위암(gastric cancer), 자궁내막암(endometrial cancer), 소장암(small intestine cancer), 간담즙성관 암(hepatobiliary tract cancer), 간암(liver cancer), 신경내분비암(neuroendocrine cancers), 자궁경부암(cervical cancer), 난소암(ovarian cancer), 자궁육종(uterine sarcomas), 뇌암(brain cancer) 및 피부 암(skin cancer)으로 이루어진 그룹으로부터 바람직하게 선택된다.

제8 양태에서, 본 발명은 MSI 표현형을 지닌 암 세포를 포함하는 암을 갖거나 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료에 사용하기 위한, 본 발명의 제4 또는 제6 양태의 핵산 수집물 및/또는 본 발명의 제7 양태의 발현 벡터 수집물에 관한 것이며, 여기서 핵산 수집물 및/또는 발현 벡터 수집물은 이중 프라임-부스트 백신접종 계획(heterologous prime-boost vaccination scheme)으로 투여되며, 바람직하게는 프라임은 아데노바이러스 벡터와 함께 존재하고 하나 이상의 부스트는 MVA 벡터와 함께 존재한다.

[0016] 삭제

[0017] 삭제

[0018] 삭제

[0019] 삭제

[0020] 삭제

[0021] 삭제

[0022] 삭제

[0023] 삭제

[0024] 삭제

[0025] 삭제

[0026] 삭제

[0027] 삭제

- [0028] 삭제
- [0029] 삭제
- [0030] 삭제
- [0031] 삭제
- [0032] 삭제
- [0033] 삭제
- [0034] 삭제
- [0035] 삭제
- [0036] 삭제
- [0037] 삭제
- [0038] 삭제
- [0039] 삭제
- [0040] 삭제
- [0041] 삭제
- [0042] 삭제
- [0043] 삭제
- [0044] 삭제

도면의 간단한 설명

[0045]

도면 범례

도 1: 항원 길이는 백신-유도된 면역원성 에피토프의 수를 결정한다.

도 2: MSI 세포주내에서 Nous-209의 면역원성 적용범위(coverage).

도 3: MSI CRC 생검에서 Nous-209의 면역원성 적용범위.

도 4: MSI 환자의 생검에서 Nous-209로부터 발생하는 예측된 MHC-I 결합 에피토프의 수.

도 5: Nous-209에 포함된 서열 번호 123에 상응하는 FSP는 HLA.A02 유전자도입 마우스내에서 생체내(*in vivo*)에서 면역원성이다. 인터페론 γ (IFN- γ)에 대한 세포내 염색(ICS)에 의해 측정된 바와 같은, FSP 서열 번호 123에 나타난 HLA-A02 9량체(nonamer)에 대한 5마리의 동물에서의 대표적인 CD8 T 세포 반응(패널 A). FSP-반응성 T 세포의 유의적인 백분율(percentage)(5.6%)을 나타내는 이들 마우스 중 하나로부터 IFN- γ + CD8 T 세포에 대한 게이팅 전략(gating strategy)의 FACS 플롯(패널 B).

도 6: 레이아웃 A 및 B에서 Nous-209 FSP를 함유하는 8개의 인공 폴리펩타이드에 대해 IUPRED로 예측한 무질서 프로파일(disorder profile).

도 7: 발현 카세트의 개략도.

도 8: 마우스에서 Gad20-209-FSPs/MVA-209-FSPs 프라임/부스트 요법의 면역원성. IFN γ ELISpot 반응을 Gad20-209-FSPs 프라임(GAd) 후 2주째 및 MVA-209-FSPs 부스트(GAd/MVA) 후 1주째에 측정한다. 백신에 의해 암호화된 209개의 FSP의 폴리펩타이드 서열을 포함하는 합성 펩타이드(P1-P16)의 16개의 혼주물에 대한 반응(수백만개의 비장세포당 IFN γ 를 생산하는 T 세포의 수)이 나타나 있다.

도 9: 209 FSP 서열을 포함하는 16개의 혼주물(pool) 각각에 대한 면역 반응의 측정. Gad20-209-FSPs/MVA-209-FSPs로 백신접종된 마우스의 비장세포에서 부스트 후 측정된 IFN γ ELISpot 반응. 백신에 의해 암호화된 209 FSP의 폴리펩타이드 서열을 포함하는 합성 펩타이드(P1 내지 P16)의 16개의 혼주물 각각에 대한 반응(수백만개의 비장세포당 IFN γ 를 생산하는 T 세포의 수)이 나타나 있다.

도 10: 단일 백신에 의해 암호화된 FSP에 대한 백신-유도된 면역 반응은 백신 공동-투여에 의해 영향받지 않는다. IFN γ ELISpot 반응은 백신 혼합물 또는 단일 백신으로 면역화시킨 마우스내에서 프라임 후(2주째, 회색 바아(gray bar)) 및 부스트 후(3주째, 검정색 바아) 측정한다. 백신 FSPA1에 의해 암호화된 FSP의 서열을 포함하는 합성 펩타이드의 4개의 혼주물(P1-P4) (A)에 대한 및 백신 FSPA2에 의해 암호화된 FSP의 서열을 포함하는 합성 펩타이드의 4개의 혼주물(P5-P8)(B)에 대한 반응(수백만개의 비장세포당 IFN γ 를 생산하는 T 세포의 수)이 나타나 있다. 통계자료(통계학)는 비-매개변수 만-휘트니 U 시험(Mann-Whitney U test)($ns = p > 0.05$)으로 계산한다.

도 11: Nous-209에 포함된 서열 번호 123(FSP-펩타이드)에 상응하는 FSP는 HLA.A02 유전자도입 마우스에서 생체내에서 면역원성이다. A) IFN γ + CD8+ FSP-특이적인 T 세포 반응의 백분율 및 DMSP 대조군에 대해 관찰된 반응. B) DMSO 대조군(상부) 및 FSP 펩타이드(하부)에 대한 하나의 대표적인 마우스 샘플로부터의 IFN- γ + CD8 T 세포에 대한 게이팅 전략의 FACS 플롯.

발명을 실시하기 위한 구체적인 내용

[0046]

본 발명을 하기에 상세히 기술하기 전에, 본 발명은 본원에 기술된 특수한 방법론, 프로토콜 및 시약에 한정되지 않는데, 이는 이들이 변할 수 있기 때문임을 이해하여야 한다. 또한 본원에 사용된 전문용어는 특수한 구현에 만들 기술할 목적을 위한 것이며 첨부된 청구범위에 의해서만 제한될 본 발명의 영역을 제한하는 것으로 의도되지 않음이 이해되어야 한다. 달리 정의하지 않는 한, 본원에 사용된 모든 기술 및 과학 용어는 당해 분야의 통상의 기술자에 의해 일반적으로 이해되는 바와 동일한 의미를 갖는다.

[0047]

바람직하게는, 본원에 사용된 용어는 "A multilingual glossary of biotechnological terms: (IUPAC Recommendations)", Leuenberger, H.G.W, Nagel, B. and Kibbl, H. eds. (1995), Helvetica Chimica Acta, CH-4010 Basel, Switzerland)에 기술된 바와 같이 및 악셀 클리만(Axel Kleemann) 및 위르겐 엔젤(Jurgen Engel)에 의한 "Pharmaceutical Substances: Syntheses, Patents, Applications", Thieme Medical Publishing, 1999; 수잔 부다바리(Susan Budavari) 등에 의해 편집된 "Merck Index: An Encyclopedia of Chemicals, Drugs, and Biologicals", CRC Press, 1996, 및 2001년에 메릴랜드주 록빌(Rockville) 소재의 United States

Pharmcopeial Convention, Inc.에 의해 발표된, 미국 약전-25/국가 의약품집-20에 기술된 바와 같이 정의된다.

[0048] 내용이 달리 필요로 하지 않는 한, 다음의 본 명세서 및 청구범위 전체에서, 용어 "포함하다(comprise)", 및 "포함하다(comprises)" 및 "포함하는(comprising)"과 같은 변형은 기술된 특징, 정수 또는 단계 또는 특징들, 정수들 또는 단계들의 그룹의 혼입을 내포하나 임의의 다른 특징, 정수 또는 단계 또는 정수들 또는 단계들의 그룹의 배제하지 않는 것으로 이해될 것이다. 다음의 구절에서 본 발명의 상이한 양태가 보다 상세히 정의된다. 이렇게 정의된 각각의 양태는 달리 명확하게 나타내지 않는 한 임의의 다른 양태 또는 양태들과 조합될 수 있다. 특히, 바람직하거나 유리한 것으로 나타낸 임의의 특징은 바람직하거나 유리한 것으로 나타낸 임의의 다른 특징 또는 특징들과 조합될 수 있다.

[0049] 몇가지 문서가 본 명세서 내용 전체에서 인용된다. 본원에 인용된 문서 각각(모든 특허, 특허원, 과학 공보, 제조업자의 명세서, 설명서 등을 포함)은 상기 또는 하기에 상관없이 이의 전문이 본원에 참고로 포함된다. 본원의 어느 것도 본 발명이 선행 발명으로 인하여 이러한 개시내용을 선행하는 자격이 없는 것으로 인정하는 것으로 해석되지 않아야 한다.

[0050] 정의

[0051] 다음에, 본 명세서에서 흔히 사용된 용어의 일부 정의가 제공된다. 이러한 용어는 명세서의 나머지 부분에서, 이의 용도의 각각의 예에서, 각각의 정의된 의미 및 바람직한 의미를 가질 것이다.

[0052] 본원에 사용된 바와 같이, 용어 "단리된"은 이와 천연적으로 결합된 다른 분자가 실질적으로 없는 분자를 지칭한다. 특히, '단리된'은 분자가 동물 신체 또는 동물 신체 샘플 속에 존재하지 않음을 의미한다. 따라서, 단리된 분자는 동물내에서 직면하거나 접촉할 수 있는 다른 분자가 없음을 의미한다. 단리된 본원에 기술된 바와 같이 결합된 다른 성분으로부터 단리됨을, 예컨대, 분자가 포함된 조성물의 다른 성분으로부터 단리됨을, 또는 이것이 포함된 벡터 또는 세포로부터 단리됨을 의미하지 않는다.

[0053] 용어 "폴리뉴클레오타이드" 및 "핵산"은 본원에서 상호교환적으로 사용되며 뉴클레오타이드 단량체로 제조된 중합체성 또는 올리고머성 거대분자로서 이해된다. 뉴클레오타이드 단량체는 핵염기, 5탄당(예를 들면, 이에 한정되지 않는 리보스 또는 2'-데옥시리보스), 및 1 내지 3개의 포스페이트 그룹으로 구성된다. 전형적으로, 핵산은 개개의 뉴클레오타이드 단량체 사이의 포스포디에스테르 결합을 통해 형성된다. 본 발명의 맥락에서 바람직한 핵산 분자는 리보핵산(RNA), 변형된 RNA, 데옥시리보핵산(DNA), 및 예컨대, RNA-DNA 하이브리드와 같은 이의 혼합물을 포함하나, 이에 한정되지 않는다. 핵산은 예컨대, 포스포디에스테르 방법(참고: 예를 들면, Uhlmann, E. & Peyman, A. (1990) Chemical Reviews, 90, 543-584)에 따라서, 예컨대, 화학적으로 합성될 수 있다.

용어 "ORF"로 약칭된 "개방 판독 프레임"은 본 발명의 맥락에서 아미노산의 연속된 스트링(string)으로 번역될 수 있는 뉴클레오타이드의 서열을 지칭하기 위해 사용된다. 전형적으로, ORF는 출발 코돈, 일반적으로 다수의 3개 뉴클레오타이드이지만, 제공된 판독 프레임내에 정지 코돈(TAG, TAA, TGA, UAG, UAA, 또는 UGA)을 함유하지 않는 길이를 갖는 후속된 영역을 함유한다. ORF는 단백질을 암호화하며 여기서 이것이 번역될 수 있는 아미노산은 펩타이드-연결된쇄를 형성한다.

[0054] 삭제

[0055] 본원에 사용된 바와 같은, 용어 "단백질", "펩타이드", "폴리펩타이드", "펩타이드" 및 "폴리펩타이드"는 전반에 걸쳐서 상호교환적으로 사용된다. 이러한 용어는 본 발명의 맥락에서 천연적으로 존재하는 펩타이드, 예컨대, 천연적으로 존재하는 단백질 및 천연적으로 또는 비-천연적으로 존재하는 아미노산을 포함할 수 있는 합성된 펩타이드를 지칭하기 위해 사용된다. 펩타이드는 또한 천연적으로 또는 비-천연적으로 존재하는 아미노산의 측쇄 또는 유리 아미노 또는 카복시-말단을 변형시킴으로써 화학적으로 변형시킬 수 있다. 이러한 화학적 변형은 추가의 화학적 모이어티 뿐만 아니라 글리코실화와 같은, 아미노산의 측쇄내 작용 그룹의 변형을 포함한다. 펩타이드는 바람직하게는 적어도 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 또는 적어도 100개의 아미노산, 가장 바람직하게는 적어도 8개 또는 적어도 30개의 아미노산을 갖는 중합체이다.

[0056] "FSM"으로 약칭된 용어 "프레임-쉬프트 돌연변이(frame-shift mutation)"는 본 발명의 맥락에서 단백질을 암호화하는 OFR내 핵산 서열의 변경을 지칭하기 위해 사용되며, 이는 돌연변이의 하부의 개방 프레임의 변경을 야기하므로, 야생형 단백질과 비교하여 변경된 서열을 지닌 단백질을 야기한다. 프레임-쉬프트 돌연변이는, 다수의

뉴클레오타이드가 삽입되거나 결실되는 경우, 3으로 나누어질 수 없는 ORF를 생산한다. 전형적으로, 1 또는 2개의 뉴클레오타이드가 결실되거나 삽입되는 경우 FSM이 생성된다. 결실은 삽입보다 더 흔하다. 1개 또는 2개의 뉴클레오타이드가 ORF의 코돈내에서 결실되는 경우, 변경된 코돈은 영향받은 코돈의 3'의 1개 또는 2개의 뉴클레오타이드로 형성될 것이다. 이러한 변경된 코돈이 정지 코돈이 아닌 경우 ORF의 번역 생성물은 변경된 코돈 및 다음 정지 코돈까지 변경된 코돈의 대안적 ORF 3'에 의해 결정될 것이다. 1개 또는 2개의 뉴클레오타이드가 코돈내로 삽입된 경우 앞서의 뉴클레오타이드의 2개 또는 1개의 뉴클레오타이드 및 1개 또는 2개의 삽입된 뉴클레오타이드를 포함할 새로운 코돈이 생성된다. 이러한 신규한 코돈이 정지 코돈이 아닌 경우, ORF의 번역 생성물은 다음의 정지 코돈까지 신규한 코돈 및 신규한 코돈의 대안적 ORF 3'에 의해 결정될 것이다.

[0057] "FC"로 약칭된 용어 "프레임-쉬프트 코돈"은 본 발명의 맥락에서 야생형 서열과 비교하여 상이한 아미노산을 암호화하는 FSM의 3'에서 첫번째 코돈을 지칭하기 위해 사용된다.

[0058] "CFSM"으로 약칭된 용어 "FSM을 포함하는 핵산의 수집물"은 본 발명의 맥락에서 특정 MSI 압 유형, 예컨대, 결장직장, 자궁내막 또는 위암 또는 2개 이상의 MSI 압 또는 하기에 상세히 요약된 하나 이상의 기준에 따라 선택된 FSM의 소그룹에서 관찰된 모든 FSM을 나타낼 수 있는 FSM을 각각 포함하는 별개의 뉴클레오타이드 서열의 목록을 지칭하기 위해 사용된다.

[0059] "FSP"로 약칭된 용어 "프레임-쉬프트 펩타이드"는 본 발명의 맥락에서 FC로부터 출발하여 CFSM의 FSM을 포함하는 핵산의 단백질-암호화 분절의 완전한 번역 생성물을 지칭하기 위해 사용된다.

[0060] "CFSP"로 약칭된 용어 "프레임-쉬프트 펩타이드의 수집물"은 본 발명의 맥락에서 특히 MSI 압 유형, 예컨대, 결장직장, 자궁내막 또는 위암 또는 2개 이상의 MSI 압 또는 하기에 상세히 요약된 하나 이상의 기준에 따라 선택된 FSP의 소그룹에서 관찰된 모든 FSP를 나타낼 수 있는 FSP의 아미노산 서열의 목록을 지칭하기 위해 사용된다.

[0061] "mFSP"로서 약칭된 용어 "변형된 FSP"는 본 발명의 맥락에서 FSP를 기반으로 하지만 특정 FSP가 암 백신 펩타이드 수집물을 형성하는 펩타이드의 수집물내로 포함시키기에 보다 적합하도록 하는 아미노산의 첨가 또는 결실에 의해 FSP와 비교하여 변형된 아미노산 서열을 갖는 펩타이드를 지칭하기 위해 사용된다. 변형 및 특정 변형으로부터 유리할 수 있는 FSP를 선택하기 위한 기준은 하기에 상세히 요약되어 있다.

[0062] "CVP"로 약칭된 용어 "암 백신 펩타이드 수집물"은 본 발명의 맥락에서 개개 펩타이드의 형태로 또는 서로 연결된 것으로서, FSP 및/또는 mFSP를 지칭하기 위해 사용된다. 바람직하게는 2개 이상의 상이한 FSP 및/또는 mFSP는 폴리펩타이드를 형성하는 펩타이드 결합에 의해 서로 연결된다. 연결은 직접적으로 또는 하나 이상의 링커 아미노산, 예컨대, Gly, Ser, 또는 Ala와 같은 작은 골격성 아미노산을 통할 수 있다. 추가의 항원의 생성을 피하기 위해, 폴리펩타이드가 서로 직접 연결되는 것이 바람직하다. FSP 및/또는 mFSP를 함께 연결시켜 폴리펩타이드를 형성하는 것이 바람직하다. 매우 긴 mRNA의 번역 효율이 감소되는 공지되어 있으므로, 전체 길이가 1,000개 아미노산 이상, 보다 바람직하게는 1,500개 아미노산 이상인 FSP 및 mFSP를 포함하는 CVP가 별도의 폴리펩타이드로 분할되는 것이 바람직하다. 예컨대, CVP가 약 6,000개 아미노산의 FSP 및/또는 mFSP를 포함하는 경우, FSP 및/또는 mFSP가 연결되어 총 길이가 약 1,500개 아미노산인 FSP 및/또는 mFSP를 각각 포함하는 4개의 별도의 폴리펩타이드를 형성하는 것이 바람직하다.

[0063] "MSI"로 약칭된 용어 "미세부수체 불안정성"은 미세부수체 영역 내 하나 이상의 반복 단위의 결실 또는 삽입으로 인하여 미세부수체의 길이 내 변경으로서 정의된다. 이는 동일한 개인으로부터의 정상/배선(germline) 세포 내 게놈 DNA와 비교하는 경우 종양 세포의 게놈 DNA 내 변경된 전체 길이와 신규의 미세부수체 대립유전자를 생성한다. 유전적 초돌연변이성(genetic hypermutability)의 이러한 조건은 손상된 DNA 미스매치 복구(mismatch repair: MMR)로부터 생성된다. MMR은 DNA 복제 동안 게놈성 DNA 내에서 발생하는 자발적 돌연변이를 수정하는 메커니즘이다. 전형적으로, 돌연변이는 짧은 뉴클레오타이드 삽입 또는 결실의 단일 염기 미스매치이다. 후자의 2개는 ORF내에 발생하는 경우 및 삽입되거나 결실된 뉴클레오타이드 서열의 길이가 3으로 나누어지지 않는 경우 프레임쉬프트 돌연변이를 생성할 수 있다(참고: FSM의 상기 정의).

[0064] 용어 "MSI 표현형"은 가장 흔히 GT/CA 반복체인, 반복된 뉴클레오타이드의 길이 내 변화의 진단을 지칭한다. 이러한 반복체는 건강한 대상체의 게놈 DNA 전체에서 발생하며 사람 게놈의 약 3%를 구성한다. 기술자는 샘플내에서 MSI 표현형을 결정하는 방법을 알고 있다. 바람직한 방법은 Promega(위스콘신주 매디슨 소재) MSI 분석 시스템(v 1.2), 미세부수체 불안정성에 있어서 국립 암 협회(National Cancer Institute(NCI)) 워크숍 동안 확립된 가이드라인에 따른, 7개 마커의 중합 시험의 사용이다.

[0065] 용어 "신생-에피토프"는 본 발명의 맥락에서 정상/배선 세포내에서 존재하지 않지만 특히 MSI 표현형을 갖는

전암성 및/또는, 암성 세포내에서 존재하는 종양에 의해 암호화된 에피토프(epitope)를 지칭한다.

[0066] 용어 "발현 카세트"는 본 발명의 맥락에서 발현될 적어도 하나의 핵산 서열, 예컨대, 전사 및 번역 조절 서열에 작동적으로 연결된, 본 발명의 CVP를 암호화하는 핵산 또는 이의 부분을 암호화하는 핵산 분자를 지칭하기 위해 사용된다. 바람직하게는, 발현 카세트는 제공된 유전자의 효율적인 발현을 위한 시스-조절되는 성분, 예를 들면, 프로모터, 개시-부위 및/또는 폴리아데닐화-부위를 포함한다. 바람직하게는, 발현 카세트는 환자의 세포 내에서 핵산의 발현에 요구되는 추가의 성분 모두를 함유한다. 따라서, 대표적인 발현 카세트는 발현될 핵산 서열에 작동적으로 연결된 프로모터 및 전사체, 리보솜 결합 부위, 및 번역 종결의 효율적인 폴리아데닐화에 요구되는 신호를 함유한다. 카세트의 추가의 성분은 예를 들면, 인핸서(enhancer)를 포함할 수 있다. 발현 카세트는 바람직하게는 또한 구조 유전자의 하부의 전사 말단 영역을 함유함으로써 효율적인 종결을 제공한다. 종결 영역은 프로모터 서열과 동일한 유전자로부터 수득될 수 있거나 상이한 유전자로부터 수득될 수 있다.

[0067] 본 발명의 맥락에서 사용된 바와 같이 용어 "작동적으로 연결된"은 성분들의 정렬을 지칭하며, 여기서 이렇게 기술된 구성성분은 이들의 일반적인 기능을 수행하도록 구성된다. 핵산은 다른 핵산 서열과 기능적 관계로 위치하는 경우 "작동적으로 연결된"다. 예를 들면, 프로모터는 이것이 하나 이상의 이식유전자(transgene)의 전사에 영향을 미치는 경우, 하나 이상의 이식유전자에 작동적으로 연결된다. 또한, 암호화 서열에 작동적으로 연결된 조절 성분은 암호화 서열의 발현에 영향을 미칠 수 있다. 대조군 성분은 이의 발현을 지시하도록 기능하지 않는 한, 이들은 암호화 서열과 연속적일 필요가 없다. 따라서, 예를 들어, 개재하는 아직 번역되지 않고 전사된 서열은 프로모터 서열과 암호화 서열 사이에 존재할 수 있으며 프로모터 서열은 여전히 암호화 서열에 "작동적으로 연결된" 것으로 고려될 수 있다.

[0068] 용어 "발현 벡터"는 본 발명의 핵산 또는 본 발명의 핵산의 수집물의 부분인 하나의 핵산을 세포, 바람직하게는 포유동물 세포내로 도입될 수 있거나 도입할 수 있는 폴리뉴클레오타이드 또는 폴리뉴클레오타이드와 단백질의 혼합물을 지칭한다. 벡터의 예는 플라스미드, 코스미드, 파아지, 바이러스 또는 인공 염색체를 포함하나, 이에 한정되지 않는다. 특히, 벡터는 프로모터 및 핵산 또는 본 발명의 핵산의 수집물의 부분인 하나의 핵산의 수집물을 적합한 숙주 세포내로 수송하는데 사용된다. 발현 벡터는 숙주 세포내에서 발현 벡터의 자가 복제를 촉진하는 "레플리콘(replicon)" 폴리뉴클레오타이드 서열을 함유할 수 있다. 일단 숙주 세포내에 있는 경우, 발현 벡터는 숙주 염색체 DNA와는 별도로 또는 이와 동시에 복제할 수 있으며, 수개 카피의 벡터 및 이의 삽입된 DNA가 생성될 수 있다. 복제가 불가능한 발현 벡터가 사용되는 경우에 - 이는 흔히 안전성 이유를 위한 경우이다 - 벡터는 복제할 수 없지만 핵산의 단지 직접적인 발현을 지시할 수 있다. 발현 벡터의 유형에 따라서 발현 벡터는 세포로부터 손실될 수 있거나, 즉, 핵산에 의해 암호화된 CVP를 단지 일시적으로 발현하거나 또는, 세포내에서 안정해질 수 있다. 발현 벡터는 전형적으로 발현 카세트, 즉, mRNA 분자내로 핵산의 전사를 허용하는 필수 성분을 함유한다.

[0069] 용어 "항원"은 본 발명의 맥락에서 면역 반응의 분자에 의해 인식된 임의의 구조, 예컨대, 항체, T 세포 수용체(TCR) 등을 지칭하기 위해 사용된다. 바람직한 항원은 특정 질환과 관련된 세포 단백질이다. 항원은 조정된 면역계의 고 가변성 항원 수용체(B-세포 수용체 또는 T-세포 수용체)에 의해 인식되며 체액 또는 세포 면역 반응을 유발할 수 있다. 이러한 반응을 유발하는 항원은 또한 면역원으로 지칭된다. 이들이 외부의 또는 세포성인 것에 상관없이, 세포내 단백질의 분획은 보다 작은 펩타이드로 가공되며 주요 조직 적합성 복합체(MHC)에 의해 나타난다. 작은 펩타이드 단편이 T-세포 수용체에 의해 결합되는 경우, 세포 면역 반응이 유발된다.

[0070] 항원 결정인자로서 또한 공지된 용어 "에피토프"는 본 발명의 맥락에서 항원의 분절, 바람직하게는 면역계의 분자에 의해 결합된 펩타이드, 예컨대, B-세포 수용체, T-세포 수용체 또는 항체를 지칭하는데 사용된다. 항체 또는 B 세포에 의해 결합된 에피토프는 "B-세포 에피토프"로 지칭되며, T 세포에 의해 결합된 에피토프는 "T 세포 에피토프"로 지칭된다. 이러한 맥락에서, 용어 "결합"은 바람직하게는 특이적인 결합에 관한 것이며, 이는 항체 또는 T 세포 수용체(TCR)와 1×10^5 M⁻¹ 이상, 바람직하게는 1×10^6 M⁻¹, 1×10^7 M⁻¹, 1×10^8 M⁻¹ 이상의 각각의 에피토프사이에 결합 상수를 지닌 결합으로서 정의된다. 기술자는 결합 상수를 결정하는 방법을 잘 인식하고 있다(참고: 예컨대, Caoili, S.E. (2012) Advances in Bioinformatics Vol. 2012). 바람직하게는, 에피토프에 대한 항체의 특이적인 결합은 항체의 Fab(단편, 항원 결합) 영역에 의해 매개되며, B-세포의 특이적인 결합은 B-세포 수용체에 의해 포함된 항체의 Fab 영역에 의해 매개되고 T-세포의 특이적인 결합은 T-세포 수용체의 가변(V) 영역에 의해 매개된다. T 세포 에피토프는 항원 제시 세포(antigen presenting cell)의 표면에 나타나며, 여기서 이들은 주요 조직적합성(Major Histocompatibility: MHC) 분자에 결합된다. MHC 부류 I, II 및 III 분자로 각각 명명된 MHC 분자의 적어도 3개의 상이한 부류가 존재한다. MHC-I 경로를 통해 나타난 에피토프는

세포독성 T 림프구(CD8+ 세포)에 의한 반응을 유발하는 반면, MHC-II 경로를 통해 나타난 에피토프는 T-헬퍼 세포(CD4+ 세포)에 의한 반응을 유발한다. MHC 제I 부류 분자에 의해 나타난 T 세포 에피토프는 전형적으로 길이가 8 내지 11개 아미노산인 펩타이드이며, MHC 제II 부류 분자에 의해 나타난 T 세포 에피토프는 전형적으로 길이가 13 내지 17개 아미노산인 펩타이드이다. MHC 제III 부류 분자는 또한 당지질과 같은 비-펩타이드 에피토프를 나타낸다. 따라서, 용어 "T 세포 에피토프"는 바람직하게는 MHC 제I 부류 또는 MHC 제II 부류 분자에 의해 나타날 수 있는 길이가 8 내지 11개 또는 13 내지 17개 아미노산인 펩타이드를 지칭한다. 에피토프는 일반적으로 아미노산의 화학적으로 활성인 표면 그룹핑(grouping)으로 이루어지며, 이는 당 측쇄를 수반하거나 수반하지 않을 수 있고 일반적으로 특이적인 3-차원 구조 특성 뿐만 아니라 특이적인 전하 특성도 갖는다. 구조적 및 비-구조적 에피토프는 후자에 대한 결합이 아닌 전자에 대한 결합이 변성 용매의 존재하에서 손실된다는 점에서 구분된다.

[0071] 본 발명의 맥락에서 사용된 바와 같은 용어 "연결 에피토프"는 주어진 CVP의 단리된 FSP, mFSP 및/또는 이의 항원성 단편 내에 존재하지 않지만 펩타이드 결합에 의한 2개의 펩타이드, 예컨대, 2개의 FSP인 에피토프의 연결 시 형성된 아미노산 서열을 포함하는 에피토프를 지칭한다. 예를 들면, 8개의 연속된 아미노산을 지닌 조립된 펩타이드의 모든 잠재적인 연결 에피토프의 목록이 생성될 수 있으며, 여기서 연결 펩타이드 결합을 포함하는 첫번째 펩타이드의 1 내지 7개의 아미노산 및 두번째 펩타이드로부터의 7 내지 1개의 아미노산이 포함된다. 이러한 목록은 이후에 CVP의 모든 FSP 및 mFSP의 아미노산 서열과 비교하여 모든 잠재적인 연결 에피토프를 확인한다.

[0072] 용어 "비-MSI 암 에피토프"는 암 세포내에서 특이적으로 발현되지만 FSM에 기인하지 않는 단백질의 에피토프를 지칭한다. 이러한 에피토프는 건강한 세포에서보다 암 세포내에서 적어도 10배 이상 풍부한 경우 특이적인 것으로 고려된다. 이러한 에피토프의 예는 이의 발현이 암 세포내에서 상향조절된 단백질, 예컨대, 흑색종내에서 타 이로시나제 또는 유방암에서 Her-2 수용체, 또는 특정 암에서 돌연변이된 단백질, 예컨대, p53이다.

[0073] 용어 "면역원성 적용범위(coverage)"는 백신이 환자에서 유발시키는 경향이 있는 예측된 수의 면역원성 에피토프를 지칭한다. 400개 아미노산의 누적된 길이에 대한 환자의 종양 속에 존재하는 FSP의 세트를 암호화하는 백신은 평균 3개의 면역원성 에피토프를 유발하는 것으로 예측되며 양호한 면역원성 적용범위를 제공한다.

[0074] 본 발명의 맥락에서 사용된 바와 같은 용어 "이의 항원성 단편"은 항원, 바람직하게는 FSP 또는 mFSP의 단편을 지칭하며, 여기서 단편은 또한 항원성인데, 즉, 포유동물내에서 B 및/또는 T 세포 면역 반응을 유발할 수 있다. 바람직하게는 항원성의 "FSP 및/또는 mFSP의 단편"은 상기 및 하기에 보다 상세히 정의된 바와 같은 FSP 및 mFSP의 적어도 8개의 아미노산 길이의 연속된 스트레치이다. mFSP의 단편은 mFSP를 기반으로 하는 FSP의 적어도 4개의 아미노산을 포함한다.

[0075] 용어 "CVP를 암호화하는 핵산의 수집물"은 본 발명의 맥락에서 CVP의 모든 FSP 및/또는 mFSP 또는 이의 항원성 단편을 포함하는 폴리펩타이드를 암호화하고, CVP의 모든 FSP 및/또는 mFSP를 포함하는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상, 바람직하게는 4개의 폴리펩타이드를 암호화하는, 하나 이상의 연속된(consecutive) 핵산 서열을 지칭하기 위해 사용된다. 따라서, 용어는 일 구현예에서 CVP를 암호화하는 단일 핵산을 포함하며 다른 대부분의 극도의 구현예에서 핵산의 수집물은 각각의 FSP 및/또는 mFSP에 대한 별개의 핵산 또는 이의 항원성 단편을 포함한다.

[0076] 본 발명의 맥락에 사용된 바와 같은 용어 "제조" 및 "조성물"은 활성 성분, 예컨대, 본 발명의 VLP와 담체 및/또는 부형제의 제형을 포함하는 것으로 의도된다.

[0077] 본 발명의 맥락에서 사용된 바와 같은 용어 "약제학적으로 허용되는"은 동물, 및 보다 특히 사람에서 사용하기 위해 연방 또는 주 정부의 규제기관에 의해 승인되거나 미국 약전 또는 다른 일반적으로 인식된 약전에 나열됨을 의미한다.

[0078] 본원에 사용된 바와 같은, 용어 "담체"는 이와 함께 치료학적으로 활성인 성분이 투여되는 희석제, 부형제, 계면활성제, 안정화제, 생리학적 완충 용액 또는 비히클과 같은 그러나 이에 한정되지 않는 약리학적으로 불활성인 물질을 지칭한다. 이러한 약제학적 담체는 액체 또는 고체일 수 있다. 액체 담체는 멸균 액체, 예를 들면, 물 및 오일 속의 염수 용액, 예를 들면, 석유, 동물성, 식물성 또는 합성 기원, 예를 들면, 땅콩 오일, 대두 오일, 광 오일, 참깨 오일 등의 것을 포함하나, 이에 한정되지 않는다. 염수 용액 및 수성 텍스트로즈 및 글리세롤 용액은 또한 특히 주사가능한 용액에 대한 액체 담체로서 사용될 수 있다. 염수 용액은 약제학적 조성물이 정맥내 투여되는 경우 바람직한 담체이다. 적합한 약제학적 담체의 예는 이. 엠. 마틴(E. W. Martin)에 의한

"Remington's Pharmaceutical Sciences"에 기술되어 있다.

- [0079] 적합한 약제학적 "부형제"는 전분, 글루코즈, 락토즈, 슈크로즈, 젤라틴, 맥아, 쌀, 밀가루, 백악, 실리카 겔, 스테아르산나트륨, 글리세롤 모노스테아레이트, 활석, 염화나트륨, 탈지 분유, 글리세롤, 프로필렌, 글리콜, 물, 에탄올 등을 포함한다.
- [0080] "계면활성제"는 음이온성, 양이온성, 및 비-이온성 표면활성제, 예를 들면, 그러나 이에 한정되지 않는 나트륨 데옥시콜레이트, 나트륨 도데실설페이트, 트리톤 X-100, 및 폴리소르베이트, 예를 들면, 폴리소르베이트 20, 폴리소르베이트 40, 폴리소르베이트 60, 폴리소르베이트 65 및 폴리소르베이트 80을 포함한다.
- [0081] "안정화제"는 만니톨, 슈크로즈, 트레할로즈, 알부민뿐만 아니라, 프로테아제 및/또는 뉴클레아제 길항제를 포함하나, 이에 한정되지 않는다.
- [0082] 본 발명의 내용에서 사용될 수 있는 "생리학적 완충제 용액"은 염화나트륨 용액, 탈염수 뿐만 아니라 적합한 유기 또는 무기 완충제 용액, 예를 들면, 그러나 이에 한정되지 않는 포스페이트 완충제, 시트레이트 완충제, 트리스 완충제 (트리스(하이드록시메틸)아미노메탄), HEPES 완충제 ([4 (2 하이드록시에틸)피페라지노]에탄설폰산) 또는 MOPS 완충제 (3 모르폴리노-1 프로판설폰산)을 포함하나, 이에 한정되지 않는다. 일반적으로 각각의 완충제의 선택은 바람직한 완충제 몰 농도에 의존한다. 포스페이트 완충제는 예를 들면, 주사 및 주입 용액용으로 적합하다.
- [0083] 용어 "보조제(adjuvant)"는 세포성 또는 체액성 수준에서 조성물의 활성 성분에 대한 면역 반응을 증강시키거나, 자극하거나, 활성화시키거나, 강화시키거나, 조절하는 제제를 지칭하는데, 예컨대, 면역원성 보조제는 실제 항원에 대한 면역계의 반응을 자극하지만 면역학적 효과 자체를 가지지 않는다. 이러한 보조제의 예는 무기 보조제(예컨대, 인산알루미늄 또는 수산화알루미늄과 같은 무기 금속염), 유기 보조제(예컨대, 사포닌 또는 스쿠알렌), 오일-기반 보조제(예컨대, 프루언트 완전 보조제(Freund's complete adjuvant) 및 프루언트 불완전 보조제), 사이토킨(예컨대, IL-1 β , IL-2, IL-7, IL-12, IL-18, GM-CSF, 및 INF- γ), 입자화된 보조제(예컨대, 면역-자극성 복합체(ISCOMS), 리포솜, 또는 생분해가능한 미세구), 비로솜(virosome), 세균 보조제(예컨대, 모노포스포릴 지질 A, 또는 무라밀 펩타이드), 합성 보조제(예컨대, 비-이온성 공중합체, 무라밀 펩타이드 유사체, 또는 합성 지질 A), 또는 합성 폴리뉴클레오타이드 보조제(예컨대, 폴리아르기닌 또는 폴리라이신)을 포함하나, 이에 한정되지 않는다.
- [0084] "유효량" 또는 "치료학적 유효량"은 의도된 목적을 달성하기에 충분한 치료제의 양이다. 제공된 치료제의 유효량은 제제의 특성, 투여 경로, 치료제를 제공받는 동물의 크기 및 종, 및 투여 목적과 같은 인자에 따라 변할 수 있다. 각각의 개개 경우에서 유효량은 당해 분야에 확립된 방법에 따라 기술자에 의해 실험적으로 결정될 수 있다.
- [0085] 본원에 사용된 바와 같은, 질병 또는 장애의 "치료하다", "치료하는", "치료" 또는 "요법(therapy)"은 다음 중 하나 이상을 달성함을 의미한다: (a) 장애의 중증도의 감소; (b) 치료되는 장애(들)의 증상적 특성의 발달의 제한 또는 방지; (c) 치료되는 장애(들)의 증상적 특징의 악화 억제; (d) 이미 장애(들)가 있는 개인에서 장애(들)의 재발의 제한 또는 방지; 및 (e) 이미 장애(들)에 대한 증상이 있던 개인에서 증상의 재발의 제한 또는 방지.
- [0086] 발명의 양태 및 바람직한 구현예
- 제1 양태에서, 본 발명은 다음의 단계 (i) 및 (ii)를 포함하는, 유전성 및 산발성 미세-부수체 불안정성(MSI) 암을 포함하는 암을 지니거나, 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료를 위한 범용 MSI 암 백신 펩타이드 수집물(CVP)을 생산하기 위한 프레임-쉬프트 펩타이드의 수집물(CFSP)을 선택하는 방법에 관한 것이다:
- (i) 각각이 프레임-쉬프트 돌연변이(FSM)를 포함하는 핵산의 수집물 (CFSM)을 선택하는 단계로서, 각각의 FSM은 각각의 상이한 환자의 적어도 M개의 암 샘플(CS) 중 하나 이상에 존재하며, 여기서 환자의 암은 MSI 표현형을 지닌 암 세포를 포함하고;
- 여기서 선택된 FSM의 적어도 50%는 기준 (a), (b), (c) 및/또는 (d)를 충족하는 단계:
- (a) FSM은 6개 이상의 뉴클레오타이드의 길이를 지닌 암호화 유전자(coding gene)의 모노뉴클레오타이드 반복체(MNR) 속에 존재함;

(b) FSM은 1개의 뉴클레오타이드의 결실에 해당함;

(c) FSM을 포함한 DNA 서열분석 관독물(DNA sequencing read)의 수는, 매치된 정상 샘플(matched normal sample)과 비교하여 종양 샘플 속에서 유의적으로 더 높음(0.05 이하의 FDR-교정된 피셔 시험(Fisher test) p-값);

(d) FSM은, 매치된 정상 샘플 속에 25% 미만의 대립유전자 빈도로 존재함,

(ii) X개의 상이한 프레임-쉬프트 펩타이드(FSP)를 선택하는 단계로서, 여기서 각각의 선택된 FSP가, FSM이 없는 상응하는 야생형(wt) 핵산의 번역 생성물과 비교하여 상이한 첫 번째 아미노산을 암호화하는 코돈(codon)으로부터 시작되는, 적어도 4개의 아미노산 길이의 CFSM의 FSM을 포함하는 핵산의 단백질-암호화 분절의 완전한 번역 생성물인 단계,

여기서 X는 적어도 20개, 보다 바람직하게는 적어도 35개이고 M은 적어도 5개이다.

제1 양태의 방법에 따른 FSP의 특정 수 및 유형을 선택함으로써, 다수의 FSP에 대한 T 세포의 유도는 백신접종(vaccination)에 의해 보증된다. 400개 aa 규칙에 기반하여 예측되는 T 세포 면역원성 에피토프 수는 400aa마다 적어도 하나의 면역원성 에피토프이며, 따라서 6021aa의 총 길이를 암호화하는 백신의 경우 적어도 16개이다. 본 발명자들은 실제로 마우스 모델에서 6021aa의 총 길이에 대한 209개 FSP를 사용한 백신접종이 376aa 마다 적어도 1개에 상응하는, 적어도 16개의 상이한 FSP에 대해 T 세포 반응을 유도할 수 있었음을 입증하였으며(도 9), 이는 면역원성 규칙을 확인한다. 펩타이드 백신접종과는 상이한, 유전 벡터를 기반으로 하는 선택된 백신접종 플랫폼은 개개 FSP의 면역원성이 백신 내에 존재하는 다른 FSP에 의해 억제되지 않음을 보증하였다. 본 발명자들은 마우스 모델에서 4개의 백신 벡터의 혼합물의 투여와 비교하여 4개의 백신 벡터 중 하나만의 투여가 실질적으로 동일한 반응을 생성함을 나타냄으로써, 경쟁이 일어나지 않음을 입증하였다.

[0087] 삭제

[0088] 삭제

[0089] 삭제

[0090] 삭제

[0091] 삭제

[0092] 삭제

[0093] 삭제

[0094] 삭제

[0095] 삭제

[0096] 삭제

[0097] 일 구현예에서, 단계 (ii)에서 선택된 FSP는 유전성 및 산발성 MSI 암을 포함하거나 이러한 암으로 진행될 위험

이 있는 암을 지닌 환자의 예방 또는 치료를 위한 범용의 MSI CVP를 생산하기 위한 후보물 FSP로서 기술될 수 있다. "후보물"은 FSP가 잠재적으로 예방 또는 치료 효과를 가짐을 의미한다. 이는 선택 공정 및 이들의 구조를 기반으로 예측할 수 있다.

선택 기준 (c)는 주어진 FSM의 출현율(prevalence)이 건강한 대상체 또는 건강한 대상체들의 매치된 정상 샘플(matched normal sample)에서보다 하나 이상의 종양 샘플의 게놈 DNA에서 유의적으로 더 높음을, 즉, 더 우세함을 필요로 한다. 이러한 맥락에서 용어 "유의적으로 더 높음"은 야생형의 돌연변이되지 않은 MNR의 출현율과 비교하여 주어진 FSM의 출현율이, 0.1 이하, 보다 바람직하게는 0.05 이하, 보다 바람직하게는 0.01 이하 및 심지어 보다 바람직하게는 0.005 이하의 거짓-발견-율(false-discovery-rate: FDR) 교정된 피셔-시험 p-값에 따라, 정상 샘플과 비교하여 종양 샘플에서 유의적으로 더 높음을 의미한다. 건강한 조직에 대한 원치 않는 면역 반응의 자극의 경향성은 감소하므로 이러한 값이 낮을 수록 FSM이 CFSM 내에 포함시키기에 보다 적합하게 된다. 이러한 기준은 샘플로부터의 게놈 DNA 또는 cDNA를 서열분석함으로써 평가한다. CFSM에 대해 선택된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (c)를 충족하는 것이 바람직하다.

기준 (c)는 주어진 FSM의 상대적인 출현율에 관한 것이지만, 기준 (d)는 정상 샘플의 대립유전자(allele)에서 주어진 FSM의 절대 출현율에 관한 것이다. CFSM에 대해 선택된 FSM이 정상 샘플의 대립유전자에서 낮은 전체 출현율을 갖는 것이 바람직하다. 바람직하게는, 정상 샘플에서의 대립유전자 빈도는 40% 미만, 보다 바람직하게는 35% 미만, 보다 바람직하게는 30% 미만, 보다 바람직하게는 25% 미만, 보다 바람직하게는 20% 미만 및 심지어 보다 바람직하게는 10% 미만이다. CFSM에 대해 선택된 FSM의 50%, 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (d)를 충족하는 것이 바람직하다.

[0098] 삭제

[0099] 삭제

[0100] CFSM에 대해 선택된 FSM이 기준 (c) 및 (d) 둘 다를 충족하는 것이 바람직하다. CFSM에 대해 선택된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (c) 및 (d)를 충족하는 것이 바람직하다. 바람직하게는, 적어도 50%가 또한 기준 (a) 및/또는 (b)를 충족하는 것이 바람직하다.

[0101] 다른 바람직한 구현예에서, CFSM에 대해 선택된 FSM은 기준 (a)를 충족한다. CFSM에 대해 선택된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (a)를 충족하는 것이 바람직하다.

[0102] 다른 바람직한 구현예에서, CFSM에 대해 선택된 FSM은 기준 (b)를 충족한다. CFSM에 대해 선택된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (b)를 충족하는 것이 바람직하다.

[0103] 다른 바람직한 구현예에서, CFSM에 대해 선택된 FSM은 기준 (a), (c) 및 (d)를 충족한다. CFSM에 대해 선택된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (a), (c) 및 (d)를 충족하는 것이 바람직하다.

[0104] 다른 바람직한 구현예에서 CFSM에 대해 선택된 FSM은 기준 (b), (c) 및 (d)를 충족한다. CFSM에 대해 선택된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (b), (c) 및 (d)를 충족하는 것이 바람직하다.

[0105] 다른 바람직한 구현예에서 CFSM에 대해 선택된 FSM은 기준 (a), (b), (c) 및 (d)를 충족한다. CFSM에 대해 선택

된 FSM의 50%, 보다 바람직하게는 적어도 60%, 보다 바람직하게는 적어도 70%, 보다 바람직하게는 적어도 80%, 보다 바람직하게는 적어도 90%, 보다 바람직하게는 적어도 95% 및 가장 바람직하게는 적어도 100%가 기준 (a), (b), (c) 및 (d)를 충족하는 것이 바람직하다.

[0106] 본 발명의 방법은 특정 환자 뿐만 아니라 MSI 암을 지닌 많은 상이한 환자의 MSI 암을 치료하기에 적합한, 즉, MSI 암의 치료를 위한 범용 CVP인 CVP를 제공한다. 동일한 이유로, MSI 암의 발달에 대해 예방 효과를 갖는 것이 또한 적합할 것이다. 따라서, 본 발명의 방법에서 FSM의 선택은 단지 1명의 환자로부터의 암 샘플의 분석을 기반으로 하는 것이 아니라 상이한 환자로부터의 수개의 암 샘플의 정보를 사용한다. 적절한 다양성을 획득하기 위하여 상이한 환자의 적어도 5개의 암 샘플(CS)을 분석하여 FSM을 결정한다. 상기 요약한 바와 같이, 이는 바람직하게는 전체 게놈 서열분석에 의해, 진유전체(exome) 서열분석에 의해 또는 샘플로부터 단리된 mRNA로부터 생성된 cDNA의 서열분석에 의해 수행된다. 암 샘플은 MSI 암을 가진 환자로부터의 것이 사용된다. 이는 암 샘플 속에 포함된 세포 내 MSI 표현형을 검출함으로써 확인할 수 있다. CS는 동일한 MSI 암일 수 있는데, 즉, 동일한 조직으로부터 기원할 수 있거나 2개 이상의 상이한 MSI 암으로부터 기원할 수 있다. 이는 2개 이상의 상이한 MSI 암의 MIS 암의 CS를 선택 공정에서 사용하는 경우 특히 바람직하고 특히 광범위하게 이용가능한 CVP를 제공한다. 이로부터 샘플이 유래되는 바람직한 MSI 암은 결장직장암 및 위암, 결장직장암 및 자궁내막암, 위암 및 자궁내막암 및 위암, 결장직장암 및 자궁내막암이다.

[0107] FSM을 기반으로 요약된 선택 공정은 또한 FSM을 포함하는 특정 핵산에 의해 암호화된 FSP를 기반으로 수행할 수 있는데, 즉, 기준 (c) 및 (d)는 또한 핵산 서열보다는 각각의 암호화된 아미노산 서열을 비교함으로써 평가할 수 있다. 암 또는 정상 샘플내에서 FSM의 존재를 또한 야생형 단백질 서열의 C-말단보다는 C-말단에서 FSP를 포함하는 암호화된 단백질 아미노산 서열의 수를 결정함으로써 평가할 수 있음이 통상의 기술자에게 바로 명백하다.

[0108] 본 발명자들은 또한 다음의 기준 중 하나 이상을 사용함으로써 CFSP 내에 포함되는 FSP를 선택하는 것을 고려한다:

(a) FSP는 FSM에 의해 암호화되고, 여기서 FSM은 M개의 상이한 CS의 수집물의 부분인 특정 암 유형의 CS 서브세트(subset)에 대해 관찰된 암 유형-특이적인 빈도(CF)로 관찰되고, 상기 CF는 CS 내에 존재하는 암 유형 중 적어도 하나에 대해 적어도 5%임; 및/또는

(b) FSP를 암호화하는 FSM을 지닌 유전자의 평균 mRNA 발현 수준은, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 80번째 백분위수 이내임; 및/또는

(c) FSP를 생성하는 FSM은 암이 없는 대상체의 집단(cohort) 내의 정상 조직내에서 2% 미만으로 관찰됨.

[0109] 삭제

[0110] 삭제

[0111] 삭제

[0112] 바람직하게는, CFSP내에 포함된 FSP의 적어도 50%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족한다. CFSP에 대해 선택된 FSP의 60%가 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하고, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 70%가 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하며, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 80%가 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하며, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 90%가 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하며, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 95%가 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하고 가장 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 100%가 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족한다.

기준 (a)와 관련하여, FSP는 FSM에 의해 암호화되고, FSM은 M개의 상이한 CS의 수집물 중 일부인 특정 암 유형의 CS의 서브세트에 대해 관찰되는 CF로 관찰되고, 상기 CF는 CS 내에 존재하는 암 유형 중 적어도 하나 또는

모두에 대해 적어도 5%, CS 내에 존재하는 암 유형 중 적어도 하나 또는 모두에 대해 바람직하게는 적어도 10%, 바람직하게는 적어도 15%, 바람직하게는 적어도 20%, 바람직하게는 적어도 25%, 바람직하게는 적어도 30%, 보다 바람직하게는 적어도 35%, 보다 바람직하게는 적어도 40%인 것이 바람직하다.

기준 (b)와 관련하여, FSP를 암호화하는 FSM을 지닌 유전자의 평균 mRNA 발현 수준이, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수(percentile), 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내인 것이 바람직하다. FSP의 상대적인 풍부성이 더 높을 수록 면역 반응의 유도가 MSI 암의 치료 또는 예방에 있어서 더 효과적일 경향이 있다. 단지 명확성을 위하여 어구 "상위 80번째 백분위수"는 최대 발현된 mRNA를 포함하는 수준 이내의 발현 수준을 갖는 모든 FSM을 지칭하며 mRNA의 최저로 발현된 19% 만을 배제한다. 따라서, "상위 30번째 백분위"는 최대 발현된 mRNA를 포함하는 발현 수준을 갖는 모든 FSM을 지칭하며 mRNA의 최저로 발현된 69%는 배제한다.

기준 (a) 및 (b)의 바람직한 조합은 적어도 5%의 CF이며, FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75 번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다. 기준 (a) 및 (b)의 다른 바람직한 조합은 적어도 10%의 CF이고 FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다. 기준 (a) 및 (b)의 다른 바람직한 조합은 적어도 15%의 CF이고 FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55 번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다. 기준 (a) 및 (b)의 다른 바람직한 조합은 적어도 20%의 CF이고 FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다.

기준 (c)와 관련하여, FSP를 생성하는 FSM가 암이 없는 대상체의 집단에서의 정상 조직 내에서 2% 미만, 보다 바람직하게는 1.9% 미만, 1.8% 미만, 1.7% 미만, 1.6% 미만, 1.5% 미만, 1.4% 미만, 1.3% 미만, 1.2% 미만, 1.1% 미만, 1.0% 미만으로 관찰된다.

[0113] 삭제

[0114] 삭제

[0115] 삭제

[0116] 삭제

[0117] 본 발명의 제1 양태의 방법의 바람직한 구현예에서:

[0118] (i) CS는 MSI 종양, 바람직하게는 결장직장 암 및/또는 위암 및/또는 자궁내막 암, 보다 바람직하게는 결장직장

암, 위암 및 자궁내막 암을 가진 환자로부터 유래되고/되거나;

[0119] (ii) M은 적어도 30, 바람직하게는 적어도 50, 보다 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 가장 바람직하게는 적어도 300이고/이거나;

[0120] (iii) X는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이다.

[0121] 바람직하게는, M은 적어도 30이고 X는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 보다 바람직하게는 적어도 300이고, 바람직하게는, M은 적어도 50이며 X는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이고, M은 적어도 100이며 X는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이고, M은 적어도 200이며 X는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이고, 심지어 보다 바람직하게는 M은 적어도 300이며 X는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이다.

샘플 수 M의 증가는 CVP의 보다 광범위한, 즉, 보다 범용인 적용능을 확인한다. 그러나, FSM의 통계적 분포로 인하여, 특정 MSI 암 유형에서 발생하는 모든 FSM의 결정의 완성도는 주어진 수의 샘플에 대해 점근적으로 최대에 이를 것이다. 따라서, 특정 MSI 암 유형의 400개 초과 샘플을 포함해도, 어떠한 유의적인 개선도 수득되지 않는다. MSI 암 유형에 존재하는 FSM의 광범위한 적용범위를 개선시키기 위하여, 2개 이상의 MSI 암의 CS를 사용하는 것이 바람직하다. 치료 및 예방에 대해 동시에 처리할 수 있는 바람직한 MSI 암은 결장직장 암, 및 위암, 결장직장 암 및 자궁내막 암, 위암 및 자궁내막 암, 및 결장직장 암, 위암 및 자궁내막 암이다.

제2 양태에서, 본 발명은 다음의 단계를 포함하는, CVP에 포함된 펩타이드의 아미노산 서열 또는 CVP에 포함된 펩타이드를 암호화하는 핵산 서열을 결정하는 방법에 관한 것이다:

(a) 본 발명의 제1 양태에 따라 선택된 CFSP로부터 적어도 Y개의 FSP 또는 이의 항원성 단편을 선택하는 단계;

(b) 다음의 기준:

(i) FSP는 길이가 4 내지 9개 아미노산임, 및/또는

(ii) FSP가, 동일한 FSM에 의해 암호화되는 둘 이상의 FSP 내에 존재하는 8개 이상의 아미노산 길이의 하나 이상의 동일한 연속된 스트레치(stretch)를 함유함, 및/또는

(iii) FSP가 야생형(wt) 사람 단백질 내에 또한 존재하는 8개 이상의 아미노산 길이의 하나 이상의 연속된 스트레치를 함유함

을 충족하는 FSP 중 하나 이상 또는 모두의 아미노산 서열을 변형시키는 단계로서,

여기서 (i)에 따른 FSP의 아미노산 서열은 FSP의 바로 상부(immediately upstream)에 존재하는 야생형(wt) 아미노산 서열의 1, 2, 3, 또는 4개, 바람직하게는 4개의 아미노산을 FSP의 N-말단에 첨가함으로써 변형되고 여기서 변형된 FSP(mFSP)는 길이가 적어도 8개 아미노산이고/이거나; (ii)에 따른 FSP의 아미노산 서열은, 가장 긴 FSP를 제외한 모두에서 이러한 연속된 스트레치를 제거함으로써 변형되며, 단 연속된 스트레치의 제거 후 4개 미만의 아미노산 길이를 지닌 FSP는 CVP로부터 배제되고/되거나; (iii)에 따른 FSP의 아미노산 서열은 이러한 스트레치를 제거함으로써 변형되고; 연속된 스트레치의 제거 후 4개 미만의 아미노산의 길이를 지닌 변형된 FSP는 CVP로부터 배제되는, 단계;

여기서 CVP의 아미노산 서열은, 단계 a)에서 선택되고/되거나 단계 (b)에서 변형된 FSP 또는 이의 단편의 아미노산 서열을 포함하고;

여기서 Y는 적어도 20, 보다 바람직하게는 적어도 35이다.

제2 양태의 맥락에서, 용어 "결정하는"은 단계 (b)로부터 즉시 명확하므로, 펩타이드의 서열을 (예컨대, 서열분석에 의해) "확인하는(identifying)"의 의미로서가 아니라 "정의하는(defining)", 고정시키는(fixing)", "체계화하는(codifying)" 또는 "변형시키는(modifying)"의 의미로서 사용됨을 주목한다.

[0122] 삭제

[0123] 삭제

[0124] 삭제

[0125] 삭제

[0126] 삭제

[0127] 삭제

[0128] 삭제

[0129] 삭제

[0130] 일 구현예에서, 단계 (b)에서 변형된 FSP의 적어도 하나는 i) 면역원성이거나 면역원성인 것으로 예측되고 ii) 환자 종양에 존재하거나 존재하는 것으로 예측된다. 바람직하게는, 이러한 FSP의 면역원성은 선택되거나 변형된 다른 FSP에 의해 억제되지 않는다.

[0131] 추가의 구현예에서, 단계 (b)에서 변형된 FSP는 유전성 및 산발성 MSI 암을 포함하는 암을 갖거나 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료를 위한 범용 MSI CVP를 생산하기 위한 후보물 FSP이다.

[0132] 단계 (b)에 따른 FSP의 변형은 FSP의 항원성을 개선시키기 위한 목적으로 제공된다. 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 50%가 변형되고, 보다 바람직하게는 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 60%가 변형되며, 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 70%가 변형되고, 보다 바람직하게는 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 80%가 변형되며, 보다 바람직하게는 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 90%가 변형되고, 보다 바람직하게는 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 95%가 변형되며, 가장 바람직하게는 기준 (i), (ii), (iii), (i)+(ii), (i)+(iii), (ii)+(iii), 또는 (i)+(ii)+(iii)을 충족하는 FSP의 적어도 100%가 변형되는 것이 바람직하다.

본 발명의 제2 양태의 바람직한 구현예에서, FSP 및 mFSP의 선택은 단계 (a)에서 수행되며, 여기서 FSP는 CFSP로부터 연이어 선택되고 각각의 선택 단계에서, 역치 값 미만인 최대 수의 암 샘플에서 역치 값에 이르도록 총 FSP 아미노산 길이의 누적량(CAFSPL)을 증가시키는 새로운 FSP가 CFSP로부터 선택되고, 임의로, CAFSPL이 여전히 역치 값 미만인 최대 수의 암 샘플에 대한 CAFSPL이 둘 이상의 FSP에 의해 증가할 경우, 최고 점수를 지닌 FSP가 선택된다.

본 발명의 제2 양태의 바람직한 구현예에서:

(i) 각각의 암 샘플에 대한 CAFSPL이, CVP의 이미 일부분인 FSP의 아미노산 길이 및 상응하는 FSM이 상기 암 샘플 속에 존재하는 CFSP로부터의 새로운 FSP의 아미노산 길이를 합함으로써 결정되고/되거나;

(ii) 여기서 역치 값이 특정 암 유형에 속하는 CS로부터의 샘플의 각각의 서브세트에 대해 별도로 정의되고/되거나;

(iii) 여기서 점수는, 임의로 CF가 5% 미만, 보다 바람직하게는 4% 미만, 보다 바람직하게는 3% 미만인 암 유형으로부터의 CS 내 FSM을 계수함이 없이, FSP의 아미노산 길이와, FSP를 생성하는 FSM이 CS 내에서 관찰되는 전체적인 빈도 사이의 곱(product)으로서 정의되고/되거나;

(iv) 여기서 암 샘플의 서브세트는 종양 유형으로부터의 모든 암 샘플을 포함하고 여기서 FSM는 5% 이상, 보다 바람직하게는 10% 이상 또는 15% 이상의 CF로 존재하고/하거나;

(v) 여기서 5% 미만의 전체적인 빈도로 FSM에 의해 생성된 FSP는 선택으로부터 배제되고/되거나;

(vi) 여기서 CVP로의 혼입이 CAFSPL이 여전히 역치 값(TV) 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지 또는 CVP 내에 존재하는 모든 FSP의 누적 길이가 V개 아미노산의 최대 값에 도달할 때까지 새로운 FSP 및/또는 변형된 FSP의 첨가가 진행되고/되거나;

(vii) 여기서 동일한 FSM으로부터 유래된 FSP는 개개의 FSP의 점수의 합으로서 계산된 합해진(combined) 점수를 지닌 하나의 FSP로서 취급된다.

[0133] 삭제

[0134] 삭제

[0135] 삭제

[0136] 삭제

[0137] 삭제

[0138] 삭제

[0139] 삭제

[0140] 삭제

[0141] 삭제

[0142] 기준 (i) 내지 (vii)은 하나 이상의 유형의 MSI 암을 지닌 환자의 집단에게 고 면역원성 적용범위를 제공함으로써 CVP에 대해 선택된 FSP의 범용성을 개선시킬 목적을 제공한다. 또한, 기준 (vi)은 또한 백신 속에 암호화될 수 있는 항원의 총량을 제한함으로써 실질적으로 실현가능한 CVP를 선택하도록 한다. 점수매김 시스템의 사용은 보다 높은 관찰된 빈도(따라서 다수의 환자 내에 존재하는 것으로 예측됨) 및 보다 긴 총 아미노산 길이(즉, 보다 높은 총 면역원성 잠재능을 지닌 FSP)를 지닌 FSP가 바람직하게는 CVP 내에 포함되는 것을 보증한다.

[0143] 바람직한 구현예에서, 기준 (i)+(iii)+(vi)는 FSP의 적어도 50%, 보다 바람직하게는 적어도 60%, 적어도 70%, 적어도 80%, 적어도 90%, 적어도 95%를 충족한다.

[0144] 따라서, 적어도 50%의 FSP가 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되며, 보다 바람직하게는 적어도 60%의 FSP는 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi),

(i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되며, 보다 바람직하게는 적어도 70%의 FSP는 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되며, 보다 바람직하게는 적어도 80%의 FSP는 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되며, 보다 바람직하게는 적어도 90%의 FSP는 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되고, 가장 바람직하게는 100%의 FSP는 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택된다.

점수가 또한 예를 들면, FSP를 생성하는 FSM의 전체적인 빈도, FSP의 길이 또는 상호간의 길이(reciprocal length)만을 기반으로, 또는 암-특이적인 점수의 합으로, 또는 점수의 계산으로부터 하나 이상의 암 유형을 배제한 후, 대안적 방식으로 정의될 수 있음이 기술자에게 즉시 명백하다. 대안적 점수는 또한 각각의 FSP 내에 예측된 MHC 제I 및/또는 제II 에피토프의 수를 추가로 포함하거나 전적으로 기반으로 한다. 기준 (vii)은 FSM을 포함하는 특정 mRNA 동형(isoform)의 발현 수준이 공지되어 있는 경우 변형될 수 있음이 기술자에게 또한 즉시 명백하다. 이러한 경우에, 동일한 FSM에 의해 생성된 하나 이상의 FSP는 선택으로부터 배제될 수 있거나 FSM을 포함하는 개개 mRNA 동형으로부터 발생된 FSP의 점수는 동형의 관찰된 상대적인 발현 수준에 따라 가중(weight)될 수 있다.

본 발명의 제2 양태의 바람직한 구현예에서:

- (i) CVP 내 혼입이 CAFSPL이 여전히 TV 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용 가능하지 않을 때까지, 새로운 FSP의 첨가가 진행되고/되거나;
- (ii) 동일한 FSM으로부터 유래된 FSP가 개개의 FSP의 점수의 합으로서 계산된 합해진 점수를 지닌 하나의 FSP로서 취급된다.

[0145]

삭제

- [0146] 삭제
- [0147] 삭제
- [0148] 삭제
- [0149] 본 발명의 제2 양태의 바람직한 구현예에서
- [0150] (a) TV는 적어도 400개 아미노산, 바람직하게는 적어도 600개 아미노산, 보다 바람직하게는 적어도 800개 아미노산이거나;
- [0151] (b) TV는:
- [0152] (i) 결장직장 암 및 위암의 경우 적어도 400개 아미노산, 바람직하게는 적어도 600개 아미노산, 보다 바람직하게는 적어도 800개 아미노산이고;
- [0153] (ii) 자궁내막 암의 경우 적어도 200개 아미노산, 바람직하게는 적어도 300개 아미노산, 보다 바람직하게는 적어도 400개 아미노산이다.
- [0154] TV의 값은 선택이 상이한 유형의 암, 예컨대, 결장직장 암, 위암, 자궁내막 암, 소장 암, 간담즙성 관 암, 간암, 신경내분비 암, 자궁경부 암, 난소 암, 자궁 육종, 뇌 암 및/또는 피부 암으로부터의 샘플의 조합을 포함하는 CS에서 수행되는 임의의 상황으로 연장시킬 수 있음이 당해 분야의 기술자에게 즉시 명확하다.
- [0155] 본 발명의 제2 양태의 바람직한 구현예에서:
- [0156] (i) CVP는 CFSP로부터 선택된 각각의 FSP의 적어도 4개의 아미노산을 포함하고/하거나;
- [0157] (ii) Y는 CVP의 일부인 모든 펩타이드의 누적 아미노산 길이 V가 적어도 280개 아미노산, 바람직하게는 적어도 6000개 아미노산이도록 선택되며;
- [0158] (iii) Y는 적어도 35, 바람직하게는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200이고/이거나
- (iv) CVP가, 서열 번호 1 내지 1087에 따른 FSP 및/또는 mFSP의 그룹으로부터 선택되는 FSP 및/또는 mFSP, 바람직하게는 서열 번호 1 내지 209에 따른 FSP 및/또는 mFSP의 그룹으로부터 선택되는 FSP 및/또는 mFSP를 포함한다.
- 제3 양태에서, 본 발명은
- (i) 본 발명의 제2 양태의 방법에서 결정된 아미노산 또는 핵산 서열 정보를 수득하는 단계; 및
- (ii) 하나 이상의 폴리펩타이드 중의 CVP의 아미노산 서열 또는 이러한 서열을 지닌 핵산의 수집물을 합성하고 임의로 핵산의 수집물을 하나 이상의 발현 카세트 및/또는 발현 벡터의 수집물내로 삽입시키는 단계를 포함하는, CVP 또는 CVP를 암호화하는 핵산의 수집물을 생산하는 방법에 관한 것이다.
- [0159] 삭제
- [0160] 삭제
- [0161] 삭제
- [0162] 삭제

[0163] FSP 및, 변형된 경우 mFSP, 또는 CVP의 이의 항원성 단편은 FSP 및, 변형된 경우 mFSP 또는 이의 항원성 단편을 암호화하는 핵산의 수집물의 재조합 발현에 의해 또는 화학적 합성에 의해 수행될 수 있다. 유사하게, CVP의 펩타이드를 암호화하는 핵산의 수집물의 합성은 고체 상에서 화학적 합성을 포함하는 공지된 방법에 의해 수행될 수 있다.

제4 양태에서, 본 발명은 본 발명의 제2 양태의 방법에 의해 생산가능한 CVP 또는 상기 CVP의 펩타이드를 암호화하는 핵산의 수집물에 관한 것이다.

제5 양태에서, CVP는 Y개의 상이한 FSP 및/또는 mFSP 또는 길이가 적어도 8개의 아미노산인 FSP 및/또는 mFSP의 항원성 단편을 포함하거나 이로 이루어지며,

여기서 각각의 FSP 또는 mFSP로 변형되는 FSP는, 길이가 적어도 4개 아미노산인 경우에서의 FSM이 없는 상응하는 wt 핵산의 번역물과 비교하여 상이한 첫 번째 아미노산을 암호화하는 코돈으로부터 시작되는 핵산을 함유하는 FSM의 단백질-암호화 분절의 단편 또는 완전한 번역 생성물이고,

여기서 FSP 또는 mFSP로 변형되는 FSP의 적어도 50%는 다음의 기준:

(a) FSP는 FSM에 의해 암호화되고, 여기서 FSM은 M개의 상이한 CS의 수집물의 부분인 특정 암 유형의 CS 서브세트(subset)에 대해 관찰된 암 유형-특이적인 빈도(CF)로 관찰되고, 상기 CF는 CS 내에 존재하는 암 유형 중 적어도 하나에 대해 적어도 5%임; 및/또는

(b) FSP를 암호화하는 FSM을 지닌 유전자의 평균 mRNA 발현 수준은, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 80번째 백분위수 이내임; 및/또는

(c) FSP를 생성하는 FSM은 암이 없는 대상체의 집단(cohort)내의 정상 조직 내에서 2% 미만으로 관찰됨

중 하나 이상을 충족하고,

여기서 다음의 기준:

(i) FC에 의해 암호화된 아미노산으로부터 시작되는 FSM을 포함하는 핵산에 의해 암호화된 FSP는 길이가 4 내지 9개의 아미노산임, 및/또는

(ii) FSP가, 동일한 FSM에 의해 암호화되는 둘 이상의 FSP 내에 존재하는 8개 이상의 아미노산 길이의 하나 이상의 동일한 연속적인 스트레치를 함유함, 및/또는

(iii) FSP가 wt 사람 단백질 내에 또한 존재하는 8개 이상의 아미노산 길이의 하나 이상의 연속된 스트레치를 함유함

을 충족하는 FSP 중 하나 이상 또는 모두의 아미노산 서열은, (i)에 따른 FSP의 경우에는, FSP의 바로 상부에 존재하는 야생형(wt) 아미노산 서열의 1 내지 4개 아미노산을 FSP의 N-말단에 첨가함으로써 변형되며 여기서 변형된 FSP(mFSP)는 길이가 적어도 8개 아미노산이고/이거나; (ii)에 따른 FSP의 경우에는, 가장 긴 FSP를 제외한 모두에서 이러한 연속된 스트레치를 제거함으로써 변형되며, 단 연속된 스트레치의 제거 후 길이가 4개 미만의 아미노산인 FSP가 CVP로부터 배제되고/되거나; (iii)에 따른 FSP의 경우에는, 이러한 스트레치를 제거함으로써 변형되며; 연속된 스트레치의 제거 후 길이가 4개 미만의 아미노산인 변형된 FSP는 CVP로부터 배제되며;

여기서 Y는 적어도 20이고 보다 바람직하게는 적어도 35이며 M은 적어도 5이다.

[0164] 삭제

[0165] 삭제

[0166] 삭제

[0167] 삭제

[0168] 삭제

[0169] 삭제

[0170] 삭제

[0171] 삭제

[0172] 바람직하게는, CVP에 포함된 FSP의 적어도 50%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족한다. CFSP에 대해 선택된 FSP의 60%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하고, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 70%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하며, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 80%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하고, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 90%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하며, 보다 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 95%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족하고 가장 바람직하게는 CFSP에 대해 선택된 FSP의 적어도 100%는 기준 (a), (b), (c), (a)+(b), (a)+(c), (b)+(c) 또는 (a)+(b)+(c)를 충족한다.

기준 (a)와 관련하여 FSP는 FSM에 의해 암호화되고, 여기서 FSM은 M개의 상이한 CS의 수집물의 부분인 특정 암 유형의 CS 서브세트에 대해 관찰되는 CF로 관찰되고, 상기 CF는 CS 내에 존재하는 암 유형 중 적어도 하나 또는 모두에 대해 적어도 10%, CS내에 존재하는 암 유형 중 적어도 하나 또는 모두에 대해 바람직하게는 적어도 15%, 바람직하게는 적어도 20%, 바람직하게는 적어도 25%, 바람직하게는 적어도 30%, 보다 바람직하게는 적어도 35%, 보다 바람직하게는 적어도 40%인 것이 바람직하다.

기준 (b)와 관련하여, FSP를 암호화하는 FSM을 지닌 유전자의 평균 mRNA 발현 수준이, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내인 것이 바람직하다. FSP의 상대적인 풍부성이 더 높을 수록, 면역 반응의 유도가 MSI 암의 치료 또는 예방에 있어서 더 효과적일 경향이 있다. 단지 명확성을 위하여, 어구 "상위 80번째 백분위수"는 최대 발현된 mRNA를 포함하는 수준 이내의 발현 수준을 갖는 모든 FSM을 지칭하며 mRNA의 최저로 발현된 19% 만을 배제한다. 따라서, "상위 30번째 백분위수"는 최대 발현된 mRNA를 포함하는 발현 수준을 갖는 모든 FSM을 지칭하며 mRNA의 최저로 발현된 69%는 배제한다.

기준 (a) 및 (b)의 바람직한 조합은 적어도 5%의 CF이며, FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다. 기준 (a) 및 (b)의 다른 바람직한 조합은 적어도 10%의 CF이고, FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다. 기준 (a) 및 (b)의 다른 바람직한 조합은 적어도 15%의 CF이고, FSM을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 값을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다. 기준 (a) 및 (b)의 다른 바람직한 조합은 적어도 20%의 CF이고, FSM

을 지닌 유전자의 mRNA 발현 수준은, 바람직하게는 특정 유형의 암의, CS 전체에 걸쳐 각각의 단백질-암호화 유전자의 평균 mRNA 발현 수준을 설명하는 분포의 상위 75번째 백분위수, 바람직하게는 상위 70번째 백분위수, 바람직하게는 상위 65번째 백분위수, 바람직하게는 상위 60번째 백분위수, 바람직하게는 상위 55번째 백분위수, 보다 바람직하게는 상위 50번째 백분위수, 보다 바람직하게는 상위 40번째 백분위수, 보다 바람직하게는 상위 30번째 백분위수 이내이다.

- [0173] 삭제
- [0174] 삭제
- [0175] 삭제
- [0176] 기준 (c)와 관련하여, FSP를 생성하는 FSM가 암이 없는 대상체의 집단에서의 정상 조직내에서 2% 미만, 보다 바람직하게는 1.9% 미만, 1.8% 미만, 1.7% 미만, 1.6% 미만, 1.5% 미만, 1.4% 미만, 1.3% 미만, 1.2% 미만, 1.1% 미만, 1.0% 미만으로 관찰된다.
- [0177] 본 발명의 제5 양태의 CVP의 바람직한 구현예에서:
- [0178] (i) CS는 MSI 종양, 바람직하게는 결장직장 암 및/또는 위암 및/또는 자궁내막 암, 보다 바람직하게는 결장직장 암, 위암 및 자궁내막 암을 가진 환자로부터 유래되고/되거나;
- [0179] (ii) M은 적어도 10, 바람직하게는 적어도 20, 바람직하게는 적어도 30, 바람직하게는 적어도 50, 보다 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 가장 바람직하게는 적어도 300이고/이거나;
- [0180] (iii) Y는 적어도 35, 바람직하게는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200이고/이거나;
- [0181] (iv) CVP는 각각의 FSP의 적어도 4개, 바람직하게는 적어도 6개, 보다 바람직하게는 적어도 8개의 아미노산을 포함하고/하거나;
- [0182] (v) Y는 모든 FSP 및/또는 mFSP 또는 CVP의 일부인 이의 항원성 단편의 누적 아미노산 길이 V가 적어도 280개 아미노산, 바람직하게는 적어도 500개 아미노산, 바람직하게는 적어도 1,000개 아미노산, 바람직하게는 적어도 1,500개 아미노산, 바람직하게는 적어도 2,000개 아미노산, 바람직하게는 적어도 2,500개 아미노산, 바람직하게는 적어도 3,000개 아미노산, 바람직하게는 적어도 3,500개 아미노산, 바람직하게는 적어도 4,000개 아미노산, 바람직하게는 적어도 4,500개 아미노산, 바람직하게는 적어도 5,000개 아미노산, 바람직하게는 적어도 5,500개 아미노산, 바람직하게는 적어도 6,000개 아미노산이도록 선택되고/되거나;
- [0183] (vi) CVP의 FSP 및/또는 mFSP는, 서열 번호 1 내지 1087에 따른 FSP 및/또는 mFSP의 그룹으로부터 선택되고, 바람직하게는 서열 번호 1 내지 209에 따른 FSP 및/또는 mFSP의 그룹으로부터 선택된다.
- [0184] 바람직하게는, M은 적어도 30이고 Y는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 보다 바람직하게는 적어도 300이고, 바람직하게는, M은 적어도 50이며 Y는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이고, M은 적어도 100이며 Y는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이고, M은 적어도 200이며 Y는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이고, 심지어 보다 바람직하게는 M은 적어도 300이며 Y는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 및 보다 바람직하게는 적어도 300이다.
- [0185] 본 발명의 일 구현예에서, 본 발명의 제5 양태의 CVP는 하나 이상의 비-MSI 암 특이적인 항원을 추가로 포함한다. 바람직하게는, 이러한 항원은 치료될 하나 이상의 암 유형에 대해 또한 특이적이다.
- [0186] 바람직한 구현예에서, CVP의 FSP 및/또는 mFSP 또는 이의 항원성 단편의 적어도 35, 바람직하게는 적어도 50, 바람직하게는 적어도 100, 보다 바람직하게는 적어도 200, 보다 바람직하게는 적어도 209개는 서열 번호 1 내지 1087에 따른 FSP 및/또는 mFSP의 그룹으로부터 선택되고, 바람직하게는 서열 번호 1 내지 209에 따른 FSP 및/또

는 mFSP의 그룹으로부터 선택된다.

[0187]

서열 번호 1 내지 1087에 따른 FSP 및 mFSP는 MSI 종양, 특히 결장직장 암중, 위암 및 자궁내막 암의 예방 또는 치료를 위한 관련성의 감소되는 순서로 1 내지 1087로 배열되어 있다. 특히 적합한 서브세트는 서열 번호 1 내지 50, 1 내지 75, 1 내지 100, 1 내지 125, 1 내지 150, 1 내지 175, 1 내지 200, 특히 바람직하게는 1 내지 209, 1 내지 225, 1 내지 250, 1 내지 275, 1 내지 300, 1 내지 325, 1 내지 350 1 내지 375, 1 내지 400, 1 내지 450, 1 내지 500, 1 내지 550, 1 내지 600, 1 내지 650, 1 내지 700, 1 내지 750, 1 내지 800, 1 내지 850, 1 내지 900, 1 내지 950, 1 내지 1000, 1 내지 1050 또는 1 내지 1087의 아미노산 서열을 지닌 FSP 및 mFSP를 포함하거나 이로 이루어진다. 서브세트가 정확하게 각각 나타낸 FSP 및/또는 mFSP를 포함하거나 이로 이루어진 것이 바람직하지만, 이러한 FSP 및/또는 mFSP의 1 내지 10%는 이의 활성에 있어서 임의의 실질적인 손실 없이 세트로부터 빠질 수 있음이 기술자에 의해 이해된다. 유사하게, 및 "포함하는" 언어가 내포하는 바와 같이, 예컨대, 서열 번호 1 내지 200의 아미노산 서열을 포함하는 서브세트는 또한 1 내지 100개 이상의 서열 번호 201 내지 1087의 FSP 또는 mFSP 및/또는 하나 이상의 다른 FSP 또는 mFSP 또는 비-MSI 암 특이적인 항원을 추가로 포함할 수 있다.

본 발명의 제5 양태의 CVP의 바람직한 구현예에서, CVP의 FSP는 CFSP로부터 연이어 선택되었고 여기서 각각의 선택 단계에서, 역치 값 미만인 최대 수의 암 샘플에서 역치 값에 이르도록 CAFSPL을 증가시키는 새로운 FSP 또는 이의 항원성 단편이 CFSP로부터 선택되고, 임의로, CAFSPL이 여전히 역치 값 미만인 최대 수의 암 샘플에 대한 CAFSPL이 둘 이상의 FSP에 의해 증가할 경우, 최고 점수를 지닌 FSP가 선택된다.

본 발명의 제5 양태의 CVP의 바람직한 구현예에서:

- (i) 각각의 암 샘플에 대한 CAFSPL은, CVP의 이미 부분인 FSP의 아미노산 길이 및 상응하는 FSM이 상기 암 샘플 속에 존재하는 CFSP로부터의 새로운 FSP의 아미노산 길이를 합함으로써 결정되고/되거나;
- (ii) 역치 값은 특정 암 유형에 속하는 CS로부터의 샘플의 각각의 서브세트에 대해 별도로 정의되고/되거나;
- (iii) 점수는 FSP의 아미노산 길이와 FSP를 생성하는 FSM이 CS내에서 관찰된 전체 빈도 사이의 곱으로서 정의되고/되거나;
- (iv) CFP로의 혼입이 CAFSPL이 여전히 역치 값(TV) 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지 새로운 FSP의 첨가가 진행되고/진행되거나;
- (v) 여기서 동일한 FSM으로부터 기원하는 FSP는 개개 FSP의 점수의 합으로 계산된 합해진 점수를 지닌 하나의 FSP로서 취급된다.

본 발명의 제5 양태의 CVP의 바람직한 구현예에서,

- (i) 각각의 암 샘플에 대한 CAFSPL은 CVP의 이미 일부인 FSP의 아미노산 길이 및 암 샘플 속에 존재하는 상응하는 FSM에 대한 CFSP로부터의 새로운 FSP의 아미노산 길이를 합함으로써 결정되고/되거나;
- (ii) 여기서 역치 값은 특정 암 유형에 속하는 CS로부터의 샘플의 각각의 서브세트에 대해 별도로 정의되고/되거나;
- (iii) 여기서 점수는 CF가 5% 미만, 보다 바람직하게는 4% 미만 및 보다 바람직하게는 3% 미만인 암 유형으로부터의 암 샘플 내 FSM을 계수함이 없이, FSP의 아미노산 길이와 FSP를 생성하는 FSM의 전체 빈도 사이의 곱으로서 정의되고/되거나;
- (iv) 여기서 암 샘플의 서브세트는 종양 유형으로부터의 모든 암 샘플을 포함하고 여기서 FSM은 5% 이상, 보다 바람직하게는 10% 이상 또는 15% 이상의 CF로 존재하고/하거나;
- (v) 여기서 5% 미만, 보다 바람직하게는 4% 미만 및 보다 바람직하게는 3% 미만의 전체적인 빈도로 FSM에 의해 생성된 FSP가 선택으로부터 배제되고/되거나;
- (vi) 여기서 CVP로의 혼입이 CAFSPL이 여전히 TV 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지 또는 CVP 내에 존재하는 모든 FSP의 누적 길이가 V개 아미노산의 최대 값에 도달할 때까지 새로운 FSP의 첨가가 진행되고/되거나;
- (vii) 여기서 동일한 FSM으로부터 유래되는 FSP는 개개의 FSP의 점수의 합으로서 계산된 합해진 점수를 지닌 하나의 FSP로서 취급된다.

[0188]	삭제
[0189]	삭제
[0190]	삭제
[0191]	삭제
[0192]	삭제
[0193]	삭제
[0194]	삭제
[0195]	삭제
[0196]	삭제
[0197]	삭제
[0198]	삭제
[0199]	삭제
[0200]	삭제
[0201]	삭제
[0202]	삭제
[0203]	제5 양태에 따른 CVP는 제1 및 제2의 양태의 방법에 의해 설계될 수 있으며 따라서 선택 단계 및 제1 및 제2 양태에 관해 요약된 기준은 동일하게 사용되어 제5 양태의 CVP를 특징화시킬 수 있다. 따라서, 바람직한 구현예에서 기준 (i)+(iii)+(vi)은 FSP의 적어도 50%, 보다 바람직하게는 적어도 60%, 적어도 70%, 적어도 80%, 적어도 90%, 적어도 95%를 충족한다.
[0204]	따라서, FSP의 적어도 50%는 바람직하게는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하게는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람

직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택됨이 바람직하며, 보다 바람직하계는 FSP의 적어도 60%는 바람직하계는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되며, 보다 바람직하계는 FSP의 적어도 70%는 바람직하계는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되며, 보다 바람직하계는 FSP의 적어도 80%는 바람직하계는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택되고, 보다 바람직하계는 FSP의 적어도 90%는 바람직하계는 기준 (i)+(iii)+(vi)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(vi), (i)+(iii)+(iv)+(vi), (i)+(iii)+(v)+(vi) 또는 (i)+(iii)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(vi), (i)+(ii)+(iii)+(v)+(vi), (i)+(ii)+(iii)+(vi)+(vii), (i)+(iii)+(iv)+(v)+(vi), (i)+(iii)+(iv)+(vi)+(vii) 또는 (i)+(iii)+(v)+(vi)+(vii)을 기반으로, 보다 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi), (i)+(ii)+(iii)+(iv)+(vi)+(vii), (i)+(ii)+(iii)+(v)+(vi)+(vii) 또는 (i)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로, 가장 바람직하계는 기준 (i)+(ii)+(iii)+(iv)+(v)+(vi)+(vii)을 기반으로 선택된다.

- [0205] 본 발명의 제5 양태의 CVP의 바람직한 구현예에서, TV는:
- [0206] (a) TV는 적어도 400개 아미노산, 바람직하계는 적어도 600개 아미노산, 보다 바람직하계는 적어도 800개 아미노산이거나;
- [0207] (b) TV는:
- [0208] (i) 결장직장 암 및 위암의 경우 적어도 400개 아미노산, 바람직하계는 적어도 600개 아미노산, 보다 바람직하계는 적어도 800개 아미노산이고;
- [0209] (ii) 자궁내막 암의 경우 적어도 200개 아미노산, 바람직하계는 적어도 300개 아미노산, 보다 바람직하계는 적어도 400개 아미노산이다.
- [0210] 본 발명의 제5 양태의 CVP의 바람직한 구현예에서, CVP의 펩타이드는 별개이거나 적어도 2개의 FSP 및/또는 mFSP는 하나 이상의 폴리펩타이드 내에 포함된다. 2개 이상의 FSP 및/또는 mFSP가 폴리펩타이드에 연결되는 경우 펩타이드 결합과 직접, 즉 아미노산 링커의 부재 하에 이루어지는 것이 바람직하다.
- [0211] 또한, 수득되는 집합 서열(junction sequence)이 wt 사람 단백질 속에 또한 존재하는 8개 이상의 아미노산의 하

나 이상의 연속된 스트레치를 함유하는 지를, 폴리펩타이드내에 2개의 FSP 및/또는 mFSP를 연결시키기 전에 평가하는 것이 바람직하다. 그렇다면 이러한 2개의 펩타이드는 이러한 방식으로 연결되지 않는다. 따라서, 연결된 FSP 및/또는 mFSP의 수득되는 폴리펩타이드는 wt 사람 단백질 속에 또한 존재하는 8개 이상의 아미노산의 하나 이상의 연속된 스트레치를 함유하지 않을 것이다. CVP 속에 포함된 FSP 및/또는 mFSP의 총 길이에 따라서, FSP 및/또는 mFSP는 2, 3, 4, 5, 또는 6개 이상의 폴리펩타이드 속에 포함될 수 있다.

본 발명자들은 서열 번호 1 내지 209의 209개 FSP 및 mFSP, 또는 이의 항원성 단편을 4개의 폴리펩타이드에 조립하였고 이것이 이러한 항원을 제공하는 특히 적합한 방식임을 발견하였다. 4개의 폴리펩타이드 내 서열 번호 1 내지 209의 FSP 및 mFSP의 바람직한 정렬은 서열 번호 1088 내지 1091(레이아웃 A), 서열 번호 1092 내지 1095(레이아웃 B), 서열 번호 1155 내지 1158(레이아웃 C) 또는 서열 번호 1159 내지 1162(레이아웃 D)에 따른 아미노산 서열을 가지는 이하의 4개의 폴리펩타이드로 이루어지거나 이를 포함한다.

동일한 CVP, 즉 동일한 FSP 및 mFSP를 포함하는 CVP의 투여의 후속 라운드에서, 예컨대, 서열 번호 1 내지 209에 따른 FSP 및 mFSP를 포함하는 폴리펩타이드는 상이한 순서로 정렬되는 것이 바람직하다. 이는 접합 에피토프(junctional epitope)에 대한 원치 않은 면역 반응을 최소화시킨다. 예를 들면, 폴리펩타이드 레이아웃 A와 폴리펩타이드 레이아웃 B, 레이아웃 A와 레이아웃 C, 레이아웃 A와 레이아웃 D, 레이아웃 B와 레이아웃 C, 레이아웃 B와 레이아웃 D, 레이아웃 C와 레이아웃 D, 레이아웃 A와 레이아웃 B 및 레이아웃 C, 레이아웃 A와 레이아웃 B 및 레이아웃 D, 레이아웃 B와 레이아웃 C 및 레이아웃 D, 레이아웃 A와 레이아웃 B, 레이아웃 C 및 레이아웃 D에서 CVP의 투여를 조합하는 것이 바람직하다.

따라서, 본 발명은 또한 폴리펩타이드의 2, 3, 4, 5, 6개 이상의 상이한 레이아웃을 포함하며, 여기서 각각의 세트는 하나 이상, 바람직하게는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의, 동일한 FSP 및 mFSP 또는 이의 항원성 단편으로 이루어지거나 이를 포함하는, 즉 동일한 CVP인 폴리펩타이드를 포함한다. 따라서, 각각의 세트 사이의 차이는 FSP, mFSP 또는 이의 항원성 단편의 아미노산 서열이 아니라, 각각의 수의 폴리펩타이드 내 FSP, mFSP 또는 이의 항원성 단편의 정렬(arrangement)이다. 이는 특히 주어진 CVP가, 2개의 상이한 레이아웃으로 제공되고, 동일한 FSP 및 mFSP 또는 이의 항원성 단편을 포함하거나 이로 이루어진 하나 이상, 바람직하게는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 폴리펩타이드, 가장 바람직하게는 4개의 폴리펩타이드를 포함하고; 3개의 상이한 레이아웃으로 제공되고, 동일한 FSP 및 mFSP 또는 이의 항원성 단편을 포함하거나 이로 이루어진 하나 이상, 바람직하게는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 폴리펩타이드, 가장 바람직하게는 4개의 폴리펩타이드를 포함하고; 4개의 상이한 레이아웃으로 제공되고, 동일한 FSP 및 mFSP 또는 이의 항원성 단편을 포함하거나 이로 이루어진 하나 이상, 바람직하게는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 폴리펩타이드, 가장 바람직하게는 4개의 폴리펩타이드를 포함하고; 5개의 상이한 레이아웃으로 제공되고, 동일한 FSP 및 mFSP 또는 이의 항원성 단편을 포함하거나 이로 이루어진 하나 이상, 바람직하게는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 폴리펩타이드, 가장 바람직하게는 4개의 폴리펩타이드를 포함하는 것이 바람직하다. 바람직하게는, 각각의 상이한 레이아웃은 다른 레이아웃으로부터 상이한 접합 서열에 의해 구별되는데, 즉, 2개의 레이아웃은 다음 FSP 또는 mFSP까지 하나의 FSP 또는 mFSP의 동일한 N- 내지 C-말단 연결 사이에 연결을 포함하지 않는다.

[0212] 삭제

[0213] 삭제

[0214] 삭제

[0215] 각각의 레이아웃은 전형적으로 환자에게 별도로 투여될 것이므로, 상이한 레이아웃은 또한 동일한 CVP의 별도의 조성물로서 간주될 수 있다.

[0216] 본 발명의 제5 양태의 CVP의 바람직한 구현예에서 CVP의 하나 이상 FSP 및/또는 mFSP 또는 2개 이상의 FSP 및/또는 mFSP를 포함하는 폴리펩타이드는 바람직하게는 펩타이드 결합에 의해 CVP의 면역원성을 향상시키는 다음의 성분 중 하나 이상에 연결된다: 불변 쇠 서열 또는 이의 단편; 조직형 플라스미노겐 활성인자; PEST 서열; 사이클린 파괴 박스; 유비퀴틴화 신호; 수모일화 신호(SUMOylation signal); 인터루킨, 바람직하게는 인터루킨 2, 인터루킨 12, 또는 인터루킨 15; 체크포인트 단백질(checkpoint 단백질) 특이적인 리간드, 바람직하게는 항-PD1

항체 또는 이의 PD1-결합 단편, 항-CTLA4 항체 또는 이의 항-CTLA4-결합 단편, 항-LAG3 항체 또는 항-LAG3-결합 단편, 항-TIM3 항체 또는 이의 항-TIM3-결합 단편.

- [0217] 바람직한 구현예에서, 분류 신호(사람 조직 플라스미노겐 활성화인자 신호 펩타이드(hTPA; 서열 번호 1104 또는 hTPA로서 분류된 이의 작용성 단편) 또는 사람 불변 쇠(hINV; 서열 번호 1105 또는 hINV로서 분류된 이의 작용성 단편)는 서열 번호 1088 내지 1091(레이아웃 A), 서열 번호 1092 내지 1095(레이아웃 B), 서열 번호 1155 내지 1158(레이아웃 C) 또는 서열 번호 1159 내지 1162(레이아웃 D)의 폴리펩타이드의 N-말단에 가해지며, 임의로 인플루엔자 HA-tag 서열(서열 번호 1106)은 상기 폴리펩타이드의 C-말단에서 가해진다.
- [0218] 이렇게 작제된 폴리펩타이드의 바람직한 아미노산 서열은 hTPA의 경우 서열 번호 1107 내지 1110(레이아웃 A), 서열 번호 1111 내지 1114(레이아웃 B), 서열 번호 1171 내지 1174(레이아웃 C) 및 서열 번호 1179 내지 1182(레이아웃 D)에 의해 및 hINV의 경우 서열 번호 1115 내지 1118(레이아웃 A), 서열 번호 1119 내지 1122(레이아웃 B), 서열 번호 1175 내지 1178(레이아웃 C) 및 서열 번호 1183 내지 1186(레이아웃 D)로서 제공된다.
- [0219] 제6 양태에서, 본 발명은 본 발명의 제5 양태의 CVP를 암호화하는 핵산의 수집물에 관한 것이다. 핵산은 바람직하게는 DNA, RNA 또는 이의 혈청 반감기를 증가시키도록 변형된 RNA일 수 있다.
- [0220] CVP에 관한 상기 나타난 이유로, FSP, mFSP 또는 이의 항원성 단편을 포함하는 1, 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 폴리펩타이드의 2, 3, 4, 5, 6, 7, 8, 9, 10개 또는 그 이상, 바람직하게는 4개의 상이한 레이아웃을 사용하는 것이 바람직하다. 지속적으로 각각의 수의 폴리펩타이드를 암호화하는 핵산의 수집물은 상이한 레이아웃을 갖는다. 바람직한 구현예에서 FSB 및/또는 mFSB를 암호화하는 핵산의 수집물은 서열 번호 1088 내지 1091(레이아웃 A), 서열 번호 1092 내지 1095(레이아웃 B), 서열 번호 1155 내지 1158(레이아웃 C) 또는 서열 번호 1159 내지 1162(레이아웃 D)에 따른 4개의 폴리펩타이드를 암호화하며 사람 코돈 용도를 기반으로 코돈-최적화된다.
- [0221] CVP를 주어진 CVP를 암호화하는 핵산의 수집물의 형태로 투여하는 경우 핵산의 2, 3, 4, 5, 6개 또는 그 이상의 상이한 레이아웃을 사용하는 것이 바람직하며, 여기서 각각의 레이아웃은 동일한 FSP 및 mFSP 또는 이의 항원성 단편을 포함하거나 이로 이루어진 폴리펩타이드를 암호화하는 하나 이상, 바람직하게는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 핵산을 포함하는데, 즉, 동일한 CVP를 암호화한다. 이는 특히, 본 발명의 제4 또는 제5 양태의 CVP를 암호화하는 핵산의 주어진 수집물이 2개의 상이한 레이아웃으로 제공되고 하나 이상, 바람직하게는 폴리펩타이드를 암호화하는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 핵산, 가장 바람직하게는 동일한 FSP 및 mFSP를 포함하거나 이로 이루어진 폴리펩타이드를 암호화하는 4개의 핵산 또는 이의 항원성 단편을 포함하고, 3개의 상이한 레이아웃으로 제공되고 하나 이상, 바람직하게는 폴리펩타이드를 암호화하는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 핵산, 가장 바람직하게는 동일한 FSP 및 mFSP를 포함하거나 이로 이루어진 폴리펩타이드를 암호화하는 4개의 핵산 또는 이의 항원성 단편을 포함하고, 4개의 상이한 레이아웃으로 제공되고 하나 이상, 바람직하게는 폴리펩타이드를 암호화하는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 핵산, 가장 바람직하게는 동일한 FSP 및 mFSP를 포함하거나 이로 이루어진 폴리펩타이드를 암호화하는 4개의 핵산 또는 이의 항원성 단편을 포함하고, 5개의 상이한 레이아웃으로 제공되고 하나 이상, 바람직하게는 폴리펩타이드를 암호화하는 2, 3, 4, 5, 6, 7, 8, 9, 또는 10개 이상의 핵산, 가장 바람직하게는 동일한 FSP 및 mFSP를 포함하거나 이로 이루어진 폴리펩타이드를 암호화하는 4개의 핵산 또는 이의 항원성 단편을 포함하는 것이 바람직하다.
- [0222] 동일한 CVP를 암호화하는 서열 번호 1 내지 209의 FSP 및 mFSP를 암호화하지만, 상이한 레이아웃을 지닌 이러한 핵산 수집물의 추가의 예가 레이아웃 A의 경우 서열 번호 1123 내지 1126에 및 hTPA를 지닌 레이아웃 C의 경우에 서열 번호 1187 내지 1190; 레이아웃 B의 경우에 서열 번호 1127 내지 1130 및 hTPA를 지닌 레이아웃 D의 경우에 서열 번호 1191 내지 1194; 레이아웃 A의 경우에 서열 번호 1131 내지 1134 및 hINV를 지닌 레이아웃 C의 경우에 서열 번호 1195 내지 1198 및 레이아웃 B의 경우에 서열 번호 1135 내지 1138 및 hINV를 지닌 레이아웃 D의 경우에 서열 번호 1199 내지 1202에 제공된다.
- [0223] 바람직한 구현예에서, 코작 서열(Kozak sequence)(CGCGACTTCGCCGCC)을 본 발명의 제4 또는 제6 양태에 따라 핵산 수집물의 출발 코돈의 바로 상부에 위치시킴으로써 번역의 효율적인 개시를 허용할 수 있으며 TAA 출발 코돈은 HA tag의 하부에 위치시켰다. 최종적으로, 핵산의 수집물이 유일한 제한 부위를 포함하는 2개의 플랜킹 분절을 포함함으로써 뉴클레오타이드 서열의 5'- 및 3'-말단 각각에 첨가된 카세트의 아-클로닝(sub-cloning)을 촉진시키는 것이 바람직하다(도 7).
- [0224] 본 발명의 제4 및 제6 양태의 핵산의 수집물은 또한 발현 카세트 내에 포함될 수 있다.

- [0225] 제7 양태에서 본 발명은 본 발명의 제4 또는 제6 양태의 핵산의 수집물의 모두 또는 일부를 각각 포함하는 하나 이상의 발현 벡터의 수집물에 관한 것이며, 여기서 발현 벡터의 수집물의 전체는 본 발명의 제4 또는 제6 양태의 핵산의 수집물 모두를 포함하는데, 즉, 여기서 발현의 수집물은 주어진 CVP의 모든 FSP, mFSP 또는 이의 항원성 단편을 암호화하는 핵산을 포함한다.
- [0226] 발현 벡터의 수집물이 발현 벡터의 면역원성을 향상시키는 하나 이상의 성분을 포함하는 것이 바람직하다. 바람직하게는 이러한 성분은 FSP, mFSP 또는 이의 항원성 단편에 대한 융합물로서 발현되거나 벡터, 바람직하게는 발현 카세트 내에 포함된 다른 핵산에 의해 암호화된다.
- [0227] 바람직한 구현예에서 CVP의 면역원성을 향상시키는 성분은 불변 쇄 서열 또는 이의 면역 자극성 단편; 조직-유형 플라즈미노겐 활성인자; PEST 서열; 사이클린 파괴 박스; 유비퀴틴화 신호(ubiquitination signal); 수모일화 신호; 인터루킨, 바람직하게는 인터루킨 2, 인터루킨 12, 또는 인터루킨 15; 체크포인트 단백질 특이적인 리간드, 바람직하게는 항-PD1 항체 또는 이의 PD1-결합 단편, 항-CTLA4 항체 또는 이의 항-CTLA4-결합 단편, 항-LAG3 항체 또는 항-LAG3-결합 단편, 항-TIM3 항체 또는 이의 항-TIM3-결합 단편으로 이루어진 그룹으로부터 선택된다.
- 제7 양태의 발현 벡터의 수집물의 바람직한 구현예에서, 수집물의 각각의 발현 벡터는 플라스미드; 코스미드; RNA; 보조제(adjuvant)와 함께 제형화된 RNA; 리포좀 입자 중에 제형화된 RNA; 자가-증폭하는 RNA(SAM); 보조제와 함께 제형화된 SAM; 리포좀 입자 중에 제형화된 SAM; 바이러스 벡터; 바람직하게는 알파바이러스 벡터, 베네주엘라 말 너염(VEE) 바이러스 벡터, 신드비스(SIN) 바이러스 벡터, 쉼리키 포레스트 바이러스(semliki forest virus: SFV) 바이러스 벡터, 또한 바람직하게는 침팬지 또는 난쟁이 침팬지 또는 고릴라로부터 유래된 복제가능하거나 불가능한 아데노바이러스 벡터, 폭스바이러스 벡터, 박시니아 바이러스 벡터 또는 변형된 박시니아 안카라(modified vaccinia ankara: MVA) 벡터, 시미안 또는 사람 사이토메갈로바이러스(CMV) 벡터, 림프구 맥락수막염 바이러스(Lymphocyte choriomeningitis virus: LCMV) 벡터, 레트로바이러스 또는 렌티바이러스 벡터로 이루어진 그룹으로부터 독립적으로 선택된다. 하나의 수집물에 사용된 모든 발현 벡터는 동일한 유형, 예컨대, 복제 불가능한 아데노바이러스 벡터의 것이 바람직하다.
- [0228] 삭제
- [0229] 가장 바람직한 발현 벡터는 아데노바이러스 벡터, 특히 사람 또는 비-사람 영장류로부터 유래된 아데노바이러스 벡터이다. 아데노바이러스가 유래되는 바람직한 유인원은 침팬지(Pan), 고릴라(Gorilla) 및 오랑우탄(Pongo), 바람직하게는 난쟁이 침팬지(판 파니스쿠스(Pan paniscus)) 및 일반적인 침팬지(판 트로글로디테스(Pan troglodytes))이다. 전형적으로, 천연적으로 존재하는 비-사람 유인원 아데노바이러스는 각각의 유인원의 대변 샘플로부터 분리된다. 가장 바람직한 벡터는 hAd5, hAd11, hAd26, hAd35, hAd49, ChAd3, ChAd4, ChAd5, ChAd6, ChAd7, ChAd8, ChAd9, ChAd10, ChAd11, ChAd16, ChAd17, ChAd19, ChAd20, ChAd22, ChAd24, ChAd26, ChAd30, ChAd31, ChAd37, ChAd38, ChAd44, ChAd55, ChAd63, ChAd73, ChAd82, ChAd83, ChAd146, ChAd147, PanAd1, PanAd2, 및 PanAd3 벡터를 기반으로 한 복제하지 않는 아데노바이러스 벡터 또는 복제-가능한 Ad4 및 Ad7 벡터이다. 사람 아데노바이러스 hAd4, hAd5, hAd7, hAd11, hAd26, hAd35 및 hAd49는 당해 분야에 잘 공지되어 있다. 천연적으로 존재하는 ChAd3, ChAd4, ChAd5, ChAd6, ChAd7, ChAd8, ChAd9, ChAd10, ChAd11, ChAd16, ChAd17, ChAd19, ChAd20, ChAd22, ChAd24, ChAd26, ChAd30, ChAd31, ChAd37, ChAd38, ChAd44, ChAd63 및 ChAd82를 기반으로 하는 벡터는 제WO 2005/071093호에 상세히 기술되어 있다. 천연적으로 존재하는 PanAd1, PanAd2, PanAd3, ChAd55, ChAd73, ChAd83, ChAd146, 및 ChAd147를 기반으로 하는 벡터는 제WO 2010/086189호에 상세히 기술되어 있다.
- [0230] 특수한 구현예에서, 아데노벡터는 Gad20(또한 GADNOU20로 명명됨, 서열 번호 1219)이거나 이로부터 유래된다. 일 구현예에서, '이로부터 유래된'은 아데노벡터가 서열 번호 1219에 대해 적어도 85%, 및 바람직하게는 적어도 90%, 95%, 96%, 97%, 98% 또는 99% 서열 동일성을 가짐을 의미한다. 그러나, 바람직한 구현예에서, 이는 다음을 의미한다:
- [0231] 아데노벡터는 다음을 포함하는 아데노바이러스 핵손(hexon) 단백질을 암호화한다:
- [0232] (i) 서열 번호 1219의 뉴클레오타이드 19386 내지 19472에 의해 암호화된 아미노산(aa) 서열을 포함하는 제1의 추가변 영역 HVR1, 또는 적어도 85% aa 서열 동일성을 가지고 27번 aa 위치에서 A가 없고 바람직하게는 V를 지닌 이의 변이체,

- [0233] (ii) 서열 번호 1219의 뉴클레오타이드 19527 내지 19571에 의해 암호화된 aa 서열을 포함하는 제2의 추가변 영역 HVR2, 또는 적어도 85% aa 서열 동일성을 가지고 1번 aa 위치에서 L이 없고 바람직하게는 I를 지닌 이의 변이체,
- [0234] (iii) 서열 번호 1219의 뉴클레오타이드 19623 내지 19643에 의해 암호화된 aa 서열을 포함하는 제3의 추가변 영역 HVR3, 또는 적어도 85% aa 서열 동일성을 가지고 7번 aa 위치에서 V가 없고 바람직하게는 A를 지닌 이의 변이체,
- [0235] (iv) 서열 번호 1219의 뉴클레오타이드 19737 내지 19772에 의해 암호화된 aa 서열을 포함하는 제4의 추가변 영역 HVR4, 또는 적어도 85% aa 서열 동일성을 갖는 이의 변이체,
- [0236] (v) 서열 번호 1219의 뉴클레오타이드 19794 내지 19838에 의해 암호화된 aa 서열을 포함하는 제5의 추가변 영역 HVR5, 또는 적어도 85% aa 서열 동일성을 갖는 이의 변이체,
- [0237] (vi) 서열 번호 1219의 뉴클레오타이드 19908 내지 19934에 의해 암호화된 aa 서열을 포함하는 제6의 추가변 영역 HVR6, 또는 적어도 85% aa 서열 동일성을 갖는 이의 변이체, 및
- [0238] (vii) 서열 번호 1219의 뉴클레오타이드 20259 내지 20336에 의해 암호화된 aa 서열을 포함하는 제7의 추가변 영역 HVR7, 또는 1번 aa 위치에서 I가 없고 바람직하게는 V를 지닌 적어도 85% aa 서열 동일성을 갖는 이의 변이체.
- [0239] 바람직한 구현예에서, HVR 변이체는 적어도 90%, 및 보다 바람직하게는 적어도 95% 서열 동일성을 갖는다. 서열 동일성의 백분율 수준에 의한 정의의 대안으로서, HVR 변이체는 암호화된 서열과 비교하여 특정 수의 아미노산 변형을 갖는 것으로 정의된다. 이후에 돌연변이의 수는 다음과 같다: 적어도 85%의 서열 동일성 대신에, HVR1 내에서 4개 이하의 돌연변이, HVR2 내에서 2개 이하의 돌연변이, HVR3 내에서 1개 이하의 돌연변이, HVR4 내에서 1개 이하의 돌연변이, HVR5 내에서 2개 이하의 돌연변이, HVR6 내에서 1개 이하의 돌연변이, 및 HVR7 내에서 3개 이하의 돌연변이; 적어도 90% 서열 동일성 대신에, HVR1 내에서 2개 이하의 돌연변이, HVR2 내에서 1개 이하의 돌연변이, HVR3 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, HVR4 내에서 1개 이하의 돌연변이, HVR5 내에서 1개 이하의 돌연변이, HVR6 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, 및 HVR7내에서 2개 이하의 돌연변이; 적어도 95% 서열 동일성 대신에, HVR1 내에서 1개 이하의 돌연변이, HVR2 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, HVR3 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, HVR4 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, HVR5 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, HVR6 내에서 1개 이하의 돌연변이 및 바람직하게는 돌연변이 없음, 및 HVR7 내에서 1개 이하의 돌연변이.
- [0240] 당해 분야에 공지된 바와 같이, 예컨대, 브래들리(Bradley) 등(J Virol., 2012 Jan;86(2):1267-72)으로부터, 아데노바이러스 중화 항체는 핵소 추가변 영역을 표적화하며, 아데노바이러스의 HVR 영역을 혈청중현율 (serumprevalence)로 대체함으로써, 이러한 아데노바이러스는 면역 숙주내에서 면역계를 회피할 수 있다. 따라서, 상기 HVR은 하기 정의된 각각의 핵소 단백질과 함께 사용될 수 있지만, 이들은 즉, 다른 핵소, 펜톤 및/또는 섬유 단백질을 가진 상이한 아데노바이러스내에서 핵소 HVR을 대체함으로써, 이러한 핵소 단백질로부터 및 또한 하기 펜톤 및 섬유 단백질과 독립적인 유용성을 가진다.
- [0241] 바람직한 구현예에서, 핵소 단백질은 서열 번호 1219의 뉴클레오타이드 18981 내지 21845에 의해 암호화된 아미노산 서열, 또는 적어도 85% 서열 동일성을 갖는 이의 변이체를 포함한다.
- [0242] 바람직한 구현예에서, 핵소 변이체는 적어도 90%, 및 바람직하게는 적어도 95%, 96%, 97%, 98% 또는 99% 서열 동일성을 갖는다. 서열 동일성의 퍼센트 수준에 의한 정의의 대안으로서, 핵소 변이체는 암호화된 서열과 비교하여 특정한 수의 아미노산 돌연변이를 갖는 것으로 정의될 수 있다. 이후에, 돌연변이의 수는 다음과 같다: 적어도 85% 서열 동일성 대신에, 143개 이하의 돌연변이; 적어도 90% 서열 동일성 대신에, 95개 이하의 돌연변이; 적어도 95% 서열 동일성 대신에, 47개 이하의 돌연변이; 적어도 96% 서열 동일성 대신에, 38개 이하의 돌연변이; 적어도 97% 서열 동일성 대신에, 28개 이하의 돌연변이; 적어도 98% 서열 동일성 대신에, 19개 이하의 돌연변이; 적어도 99% 서열 동일성 대신에, 9개 이하의 돌연변이. 핵소 변이체는 상기 각각의 HVR에 대해 정의된 것보다 이들의 HVR에서 서열 동일성을 더 적게 가지지 않거나 더 많은 돌연변이를 가지지 않는다.
- [0243] 일 구현예에서, 아데노백터는 또한 서열 번호 1219의 뉴클레오타이드 14021 내지 15973에 의해 암호화된 아미노산 서열, 또는 적어도 85% 서열 동일성을 갖는 이의 변이체를 포함하는 아데노바이러스 펜톤 단백질을 추가로

암호화한다. 바람직한 구현예에서, 펜톤 변이체는 암호화된 서열과 비교하여 적어도 90%, 및 바람직하게는 적어도 95%, 96%, 97%, 98% 또는 99% 서열 동일성을 갖는다. 서열 동일성의 백분율 수준에 의한 정의의 대안으로서, 펜톤 변이체는 특정한 수의 아미노산 돌연변이를 갖는 것으로 정의될 수 있다. 이후에 돌연변이의 수는 다음과 같다: 적어도 85% 서열 동일성 대신에, 97개 이하의 돌연변이; 적어도 90% 서열 동일성 대신에, 65개 이하의 돌연변이; 적어도 95% 서열 동일성 대신에, 32개 이하의 돌연변이; 적어도 96% 서열 동일성 대신에, 26개 이하의 돌연변이; 적어도 97% 서열 동일성 대신에, 19개 이하의 돌연변이; 적어도 98% 서열 동일성 대신에, 13개 이하의 돌연변이; 적어도 99% 서열 동일성 대신에, 6개 이하의 돌연변이.

[0244] 바람직하게는, 펜톤 변이체는 289번 아미노산 위치에서 D를 가지지 않고 바람직하게는 G를 가지며 341번 아미노산 위치에서 D를 가지지 않고 바람직하게는 N을 가진다.

[0245] 다른 구현예에서, 아데노백터는 또한(즉, 핵손 및 가능하게는 펜톤 단백질 다음에) 서열 번호 1219의 뉴클레오타이드 32163 내지 33956에 의해 암호화된 아미노산 서열, 또는 적어도 85% 서열 동일성을 가진 이의 변이체를 포함하는 아데노바이러스 섬유 단백질을 암호화한다. 바람직한 구현예에서, 섬유 변이체는 적어도 90%, 및 바람직하게는 적어도 95%, 96%, 97%, 98% 또는 99%의 서열 동일성을 갖는다. 서열 동일성의 백분율 수준에 의한 정의의 대안으로서, 섬유 변이체는 암호화된 서열과 비교하여 특정 수의 아미노산 돌연변이를 갖는 것으로 정의될 수 있다. 이후에 돌연변이의 수는 다음과 같다: 적어도 85% 서열 동일성 대신에, 89개 이하의 돌연변이; 적어도 90% 서열 동일성 대신에, 59개 이하의 돌연변이; 적어도 95%의 서열 동일성 대신에, 29개 이하의 돌연변이; 적어도 96% 서열 동일성 대신에, 23개 이하의 돌연변이; 적어도 97% 서열 동일성 대신에, 17개 이하의 돌연변이; 적어도 98% 서열 동일성 대신에, 11개 이하의 돌연변이; 적어도 99% 서열 동일성 대신에, 5개 이하의 돌연변이.

[0246] 바람직하게는, 섬유 변이체는 181번 아미노산 위치에서 A를 가지지 않고 바람직하게는 P를 가지고/가지거나, 474번 아미노산 위치에서 V를 가지지 않고 바람직하게는 I를 가지고/가지거나 4 및 5번 아미노산 위치 사이에 S가 삽입되지 않고 바람직하게는 아미노산 삽입을 가지지 않는다.

[0247] 다른 구현예에서, 아데노백터는 또한(즉, 핵손 및 가능하게는 펜톤 및/또는 섬유 단백질 다음에) 서열 번호 1219의 뉴클레오타이드 10724 내지 10897에 따른 뉴클레오타이드 서열을 포함하는 VA RNA II 비-암호화 RNA, 또는 적어도 85% 서열 동일성을 갖는 뉴클레오타이드 서열의 변이체를 암호화한다. 대안적으로 또는 추가로, 이는 서열 번호 1219의 뉴클레오타이드 10492 내지 10659에 따른 뉴클레오타이드 서열, 또는 적어도 85% 서열 동일성을 갖는 뉴클레오타이드 서열의 변이체를 포함하는 VA RNA I 비-암호화 RNA를 암호화할 수 있다. 바람직한 구현예에서, VA RNA 변이체는 적어도 90%, 및 바람직하게는 적어도 95%, 96%, 97%, 98% 또는 99% 서열 동일성을 갖는다. 서열 동일성의 백분율 수준에 의한 정의의 대안으로서, VA RNA 변이체는 특정 수의 뉴클레오타이드 돌연변이를 갖는 것으로 정의될 수 있다. 이후 돌연변이의 수는 다음과 같다: 적어도 85% 서열 동일성 대신에, VA RNA I내 25개 이하의 돌연변이 및 VA RNA II내 26개 이하의 돌연변이; 적어도 90% 서열 동일성 대신에, VA RNA I내 16개 이하의 돌연변이 및 VA RNA II내 17개 이하의 돌연변이; 적어도 95% 서열 동일성 대신에, 임의의 VA RNA내 8개 이하의 돌연변이; 적어도 96% 서열 동일성 대신에, 임의의 VA RNA내 6개 이하의 돌연변이; 적어도 97% 서열 동일성 대신에, 임의의 VA RNA내 5개 이하의 돌연변이; 적어도 98% 서열 동일성 대신에, 임의의 VA RNA내 3개 이하의 돌연변이; 적어도 99% 서열 동일성 대신에, 임의의 VA RNA내 1개 이하의 돌연변이.

[0248] 바람직하게는, VA RNA II 변이체는 (a) 79번 위치에서 C를 가지지 않고/않거나 80번 위치에서 A를 가지지 않고, 바람직하게는 79번 위치에서 T를 가지고/가지거나 80번 위치에서 G를 가지며, (b) 81번 위치에서 A를 가지지 않고, 바람직하게는 81번 위치에서 G를 가진다. VA RNA I 변이체는 바람직하게는 80번 위치에서 G를 가지지 않고 바람직하게는 80번 위치에서 A를 갖는다.

[0249] 본 발명에 따른 VA RNA는 개선된 아데노바이러스 생산을 야기한다.

[0250] 아데노백터가 다른 아데노바이러스 유전자 및 뉴클레오타이드 분절을 추가로 포함하는 것이 바람직하며, 이는 참고로서 서열 번호 1219를 사용한 아데노바이러스 게놈내 핵손, 펜톤 및/또는 섬유 유전자와 인접한다. 아데노백터는 또한 폴리뉴클레오타이드를 아데노바이러스 입자내로 패키징(packaging)하는데 필요한 서열을 포함하는 것이 특히 바람직하다.

[0251] 일반적으로, 아데노백터는 다음 중 적어도 하나를 포함한다:

[0252] (a) 아데노바이러스 5'-말단, 바람직하게는 아데노바이러스 5' 역위된 말단 반복체;

[0253] (b) 아데노바이러스 EIa 영역, 또는 13S, 12S 및 9S 영역 중에서 선택된 이의 단편;

- [0254] (c) 아데노바이러스 E1b 영역, 또는 작은(small) T, 큰(large) T 및 IX 영역으로 이루어진 그룹 중에서 선택된 이의 단편;
- [0255] (d) 아데노바이러스 VA RNA 영역; 또는 VA RNA I 및 VA RNA II 영역으로 이루어진 그룹 중에서 선택된 이의 단편;
- [0256] (e) 아데노바이러스 E2b 영역; 또는 작은 pTP, 폴리머라제 및 IVa2 영역으로 이루어진 그룹 중에서 선택된 이의 단편;
- [0257] (f) 아데노바이러스 L1 영역, 또는 이의 단편으로서, 상기 단편은 28.1 kD 단백질, 폴리머라제, 아그노단백질(agnoprotein), 52/55 kDa 단백질, 및 IIIa 단백질로 이루어진 그룹으로부터 선택된 아데노바이러스 단백질을 암호화하는 단편;
- [0258] (g) 아데노바이러스 L2 영역, 또는 이의 단편으로서, 상기 단편은 상기 정의한 바와 같은 펜톤 단백질, VII, V, 및 X 단백질로 이루어진 그룹으로부터 선택된 아데노바이러스 단백질을 암호화하는 단편;
- [0259] (h) 아데노바이러스 L3 영역, 또는 이의 단편으로서, 상기 단편은 VI 단백질, 상기 정의한 바와 같은 핵소 단백질, 및 엔도프로테아제로 이루어진 그룹으로부터 선택된 아데노바이러스 단백질을 암호화하는 단편;
- [0260] (i) 아데노바이러스 E2a 영역, 또는 이의 단편으로서, 상기 단편은 DBP 단백질로 이루어진 아데노바이러스 단백질을 암호화하는 단편;
- [0261] (j) 아데노바이러스 L4 영역, 또는 이의 단편으로서, 상기 단편은 100 kD 단백질, 22 kD 동족체, 33 kD 동족체, 및 단백질 VIII로 이루어진 그룹으로부터 선택된 아데노바이러스 단백질을 암호화하는 단편;
- [0262] (k) 아데노바이러스 E3 영역, 또는 E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8 및 E3 ORF9로 이루어진 그룹으로부터 선택된 이의 단편;
- [0263] (l) 아데노바이러스 L5 영역, 또는 이의 단편으로서, 상기 단편은 상기 정의된 바와 같은 섬유 단백질을 암호화하는 단편;
- [0264] (m) 아데노바이러스 E4 영역, 또는 E4 ORF6/7, E4 ORF6, E4 ORF5, E4 ORF4, E4 ORF3, E4 ORF2, 및 E4 ORF1로 이루어진 그룹으로부터 선택된 이의 단편;
- [0265] (n) 아데노바이러스 3'-말단, 바람직하게는 아데노바이러스 3' 역위된 말단 반복체; 및/또는
- [0266] (o) 아데노바이러스 E1 영역.
- [0267] 이러한 성분은 서열 번호 1219에 따른 동일한 아데노바이러스로부터, 또는 상이한 아데노바이러스로부터, 특히 상이한 종 중 하나, 예컨대, 사람 아데노바이러스로부터 유래되어 키메라 아데노바이러스를 형성할 수 있다.
- [0268] 아데노백터의 일부 구현예에서, 이것이 상기 요약한 바와 같이((a) 내지 (m)에서와 같이) 하나 이상의 게놈성 영역을 포함하지 않는 것이 바람직할 수 있다. 특히, 이는 E1, E3 및/또는 E4 영역을 포함하지 않을 수 있고/있거나 적어도 하나의 유전자가 비-작용성이 되도록 하는 결실 및/또는 돌연변이를 포함하는 아데노바이러스 유전자를 포함한다. 이러한 바람직한 구현예에서, 적합한 아데노바이러스 영역은 변형되어 전술한 영역(들)/유전자(들)을 포함하지 않거나 선택된 영역(들)/유전자(들)이 비-작용성이도록 한다. 이들을 비-작용성이 되도록 하는 한가지 가능성은 하나 이상의 인공 정지-코돈(예컨대, TAA)을 이러한 유전자의 개방 판독 프레임 내로 도입시키는 것이다. 바이러스가 복제-결합성이 되도록 하는 방법은 당해 분야에 잘 알려져 있다(참고: 예컨대, Brody et al, 1994 Ann NY Acad Sci., 716: 90-101). 결실은 바람직하게는 발현 카세트 내에, 예를 들면, 미니유전자 카세트(minigene cassette)내에 전이유전자를 삽입시킬 공간을 만들 수 있다. 또한, 결실을 사용하여 당해 분야에 잘 공지된 바와 같은 패키징 세포주 또는 헬퍼 바이러스를 사용하지 않고 복제할 수 없는 아데노바이러스 백터를 생성할 수 있다. 하나 이상의 규정된 유전자/영역 결실 또는 기능의 손실(loss-of-function) 돌연변이를 포함하는 이러한 재조합체 아데노바이러스는 예컨대, 유전자 치료요법 또는 백신접종을 위한 보다 안전한 재조합 아데노바이러스를 제공할 수 있다.
- [0269] 아데노백터는 본원에 요약된 바와 같은 적어도 하나의 게놈성 영역/유전자(예를 들면, 영역 E1, E3 및/또는 E4 과 같은), 구체적으로 E1A, E1B, E2A, E2B, E3 ORF1, E3 ORF2, E3 ORF3, E3 ORF4, E3 ORF5, E3 ORF6, E3 ORF7, E3 ORF8, E3 ORF9, E4 ORF6/7, E4 ORF6, E4 ORF5, E4 ORF4, E4 ORF3, E4 ORF2 및/또는 E4 ORF1, 바람직하게는 E1A, E1B, E2A, E2B, E3 및/또는 E4를 포함하지 않을 수 있고/있거나 적어도 하나의 유전자가 비-작용성

이도록 하는 결실 및/또는 돌연변이를 포함하는 아데노바이러스 유전자를 포함하지만, 완전한 E1a 및/또는 E1b 영역을 보유하는 것이 바람직하다. 이러한 완전한 E1 영역은 아데노바이러스 게놈내에서 이의 천연 위치에 위치할 수 있거나 천연의 아데노바이러스 게놈내(예컨대, E3 영역내)에서 결실 부위에 위치할 수 있다.

[0270] 바람직한 구현예에서, 아데노백터는 다음의 아데노바이러스 단백질 중 하나 이상, 바람직하게는 모두를 추가로 암호화한다: 단백질 VI, 단백질 VIII, 단백질 IX, 단백질 IIIa 및 단백질 IVa2.

[0271] 아데노바이러스의 분야에서 평균 기술자는 상술한 아데노바이러스 단백질을 암호화하는 개방 판독 프레임을 결정하기 위한 방법을 잘 알고 있다. 기술자는 또한 아데노바이러스 게놈의 구조를 알고 있으며 과도한 부담없이 본원에 요약된 개개의 아데노바이러스 영역 및 ORF를 임의의 아데노바이러스 게놈으로 맵핑할 수 있다.

[0272] 용어 "핵소 단백질"은 아데노바이러스내에 포함된 핵소(II) 단백질을 지칭한다. 본 발명에 따른 핵소 단백질 또는 이의 변이체는 감염성 아데노바이러스 비리온내에서 핵소 단백질 또는 이의 단편과 동일한 작용을 갖는다. 따라서, 바람직하게는 캡시드 단백질로서 상기 핵소 또는 이의 변이체를 포함하는 아데노바이러스는 숙주 세포로 도입될 수 있다. 핵소 단백질의 변이체를 생성하기에 적합한 방법은 미국 특허 제5,922,315호에 기술되어 있다. 이러한 방법에서, 아데노바이러스의 적어도 하나의 루프 영역은 다른 아데노바이러스 혈청형의 적어도 하나의 루프 영역으로 변화된다. 이는 재조합 아데노바이러스가 숙주 세포내로 도입되는 경우 용이하게 결정될 수 있다. 예를 들면, 숙주 세포를 아데노바이러스와 접촉시킨 후, 재조합체 숙주 세포를 세척하고 분해하며 아데노바이러스 RNA 및/또는 DNA가 예컨대, 아데노바이러스 RNA 및/또는 DNA에 대해 특이적인 적절한 하이브리드화 프로브를 사용함에 의해 숙주 세포내에서 발견되는지의 여부를 결정할 수 있다. 대안적으로 또는 추가로, 재조합체 아데노바이러스와 접촉된 후 세포를 세척하고, 분해하며 아데노바이러스 특이적인 항체, 예컨대 웨스턴 블롯(Western blot)을 사용하여 프로브(probing)할 수 있다. 여전히 또 다른 대안에서, 예컨대, 생체내에서 숙주 세포가 숙주 세포내에서 유전자 생성물을 발현하는데 적합한 발현 카세트를 포함하는 재조합체 아데노바이러스를 사용한 감염시 유전자 생성물, 예를 들면, 형광성 단백질을 발현하는지의 여부가 관찰된다.

[0273] 용어 "초가변 영역"(HVR)은 바이러스 캡시드 밖에 노출되므로, 핵소 단백질의 용매-노출된 표면에 위치한, 고서열 변이를 지닌 도메인을 지칭한다. 이들은 중화 항체의 주요 결정인자이다. HVR은 예를 들면, 다른 핵소 단백질과의 서열 정렬에 의해 확인될 수 있다.

[0274] "아데노바이러스 펜톤 단백질"은 아데노바이러스내에 포함된 펜톤 염기(III) 단백질을 지칭한다. 아데노바이러스 펜톤 단백질은 이것이 캡시드의 정20면체 대칭의 모서리에 위치함을 특징으로 한다. 본 발명에 따른 펜톤 단백질 또는 이의 변이체는 감염성 아데노바이러스 비리온내에서 펜톤 단백질과 동일한 작용을 갖는다. 따라서, 바람직하게는 캡시드 단백질로서 상기 펜톤 또는 이의 변이체를 포함하는 아데노바이러스는 숙주 세포를 도입시킬 수 있으며, 이는 상술한 바와 같이 시험할 수 있다. 또한, 작용성 펜톤은 아데노바이러스 섬유 단백질에 대한 친화성을 갖는다. 평균적인 기술자는 단백질-단백질 친화성을 시험하는 방법을 잘 알고 있다. 제1의 단백질이 제2 단백질을 결합시킬 수 있는지를 결정하기 위하여, 기술자는 예를 들면, 유전적 효소 2개의 하이브리드 검정 또는 생화학적 검정, 예를 들면, 풀-다운(pull-down), 효소-연결된 면역흡수성 검정(ELISA), 형광성-활성화된 세포 분류(FACS)-기반한 검정 또는 플라스몬 공명 검정을 사용할 수 있다. 풀-다운 또는 플라스몬 공명 검정을 사용하는 경우, 적어도 하나의 단백질을 생화학 분야에 잘 알려져 있는 바와 같이, 친화성 tag, 예를 들면, HIS-tag, GST-tag 또는 기타에 융합시키는데 유용하다.

[0275] 용어 "섬유 단백질"은 아데노바이러스에 포함된 노베드 섬유(knobbed fiber) (IV) 단백질을 지칭한다. 본 발명에 따른 섬유 단백질 또는 이의 변이체는 감염성 아데노바이러스 비리온내에서 섬유 단백질 또는 이의 단편과 동일한 작용을 갖는다. 따라서, 바람직하게는 캡시드 단백질로서 상기 섬유 또는 섬유 변이체를 포함하는 아데노바이러스는 숙주 세포로 도입할 수 있으며, 이는 상술한 바와 같이 시험할 수 있다. 또한, 작용성 섬유 단백질은 아데노바이러스 펜톤 단백질에 대한 친화성을 갖는다. 또한, 이의 글리코실화된 형태에서 작용성 아데노바이러스 섬유 단백질은 삼량체화(trimerizing)될 수 있다. 따라서, 변이체는 글리코실화되고/되거나 삼량체를 형성할 수 있음이 바람직하다. 친화성, 예를 들면, 삼량체화는 상술한 바와 같이 시험할 수 있으며, 글리코실화 검정은 또한 당해 분야에 잘 공지되어 있다.

[0276] "VA(바이러스 관련된) RNA"는 아데노바이러스에서 발견된 비-암호화 유형이다. 이는 번역을 조절하는 데 있어 역할을 담당한다. VAI 또는 VA RNA I 및 VAII 또는 VA RNA II로 불리는 이러한 RNA의 2개의 카피가 존재한다. 2개의 VA RNA 유전자는 아데노바이러스 게놈내에 명백한 유전자이다. VA RNA I은 보다 낮은 수준으로 발현된 VA RNA II를 지닌 주요 종이다. 전사체는 폴리아데닐화되지 않으며 둘 다 Po1III에 의해 전사된다.

- [0277] 폴리뉴클레오타이드, 폴리펩타이드 또는 단백질 서열의 맥락에서 용어 "동일성" 또는 "동일한"은 최대의 상응성으로 정렬되는 경우 동일한 2개의 서열내에 다수의 잔기를 지칭한다. 구체적으로, 2개의 서열의 서열 동일성 퍼센트는 핵산 또는 아미노산 서열에 상관없이, 보다 짧은 서열의 길이로 나누고 100을 곱한 2개이 정렬된 서열 사이의 정확한 매치의 수이다. 2개의 서열을 정렬하는데 사용될 수 있는 정렬 도구는 당해 분야의 기술자에게 잘 공지되어 있으며 예를 들면, World Wide Web, 예컨대, 폴리펩타이드 정렬의 경우 Clustal Omega(<http://www.ebi.ac.uk/Tools/msa/clustalo/>) 또는 폴리뉴클레오타이드 정렬의 경우 MUSCLE(<http://www.ebi.ac.uk/Tools/msa/muscle/>) 또는 MAFFT(<http://www.ebi.ac.uk/Tools/msa/mafft/>) 또는 폴리뉴클레오타이드 및 폴리펩타이드 정렬의 경우 WATER(http://www.ebi.ac.uk/Tools/psa/emboss_water/)에서 취득할 수 있다. 2개의 서열 사이의 정렬은 디폴트 매개변수 설정(default parameters setting)을 사용하여 수행할 수 있는데, 예컨대, 예컨대, MAFFT의 경우 바람직하게는: Matrix: Blossum62, Gap Open 1.53, Gap Extend 0.123, WATER 폴리뉴클레오타이드의 경우 바람직하게는: MATRIX: DNAFULL, Gap Open: 10.0, Gap Extend 0.5 및 WATER 폴리펩타이드의 경우 바람직하게는 MATRIX: BLOSUM62, Gap Open: 10.0, Gap Extend: 0.5을 사용하여 수행할 수 있다. 당해 분야의 기술자는 만족스러운 정렬을 생산하기 위해 서열내에 갭을 도입하는데 필수적일 수 있음을 이해한다. "가장 우수한 서열 정렬"은 최소의 수의 갭을 가지지만 최대 수의 정렬된 동일한 잔기를 생산하는 정렬로서 정의된다. 바람직하게는, 이는 포괄적인 정렬이며, 이는 정렬내에 모든 서열내에 모든 잔기를 포함한다.
- [0278] 용어 "변이체"는 폴리펩타이드와 관련하여, 일반적으로 폴리펩타이드의 변형된 버전, 예컨대, 돌연변이를 지칭하므로, 폴리펩타이드의 하나 이상 아미노산은 결실되고/되거나, 삽입되고/되거나, 변형되고/되거나 치환된다. 일반적으로, 변이체는 작용성이며, 이는 작용성 변이체를 포함하는 아데노바이러스가 숙주 세포를 감염시킬 수 있음을 의미한다. 보다 구체적인 작용이 본원에 정의되어 있으며 일반적인 정의에 우선한다. "돌연변이" 또는 "아미노산 돌연변이"는 아미노산 치환, 결실 및/또는 삽입일 수 있다("및" 하나 이상의 돌연변이가 존재할 경우 적용할 수 있다). 바람직하게는, 이는 치환(즉, 보존적 또는 비-보존적 아미노산 치환), 보다 바람직하게는 보존적 아미노산 치환이다. 일부 구현예에서, 치환은 또한 천연적으로 존재하는 아미노산의 천연적으로 존재하지 않는 아미노산으로의 교환을 포함한다. 보존적인 치환은 아미노산의 치환된 아미노산과 유사한 화학적 특성을 갖는 다른 아미노산으로의 치환을 포함한다. 바람직하게는, 보존적 치환은 다음으로 이루어진 그룹으로부터 선택된 치환이다:
- [0279] (i) 염기성 아미노산의 다른, 상이한 염기성 아미노산으로의 치환;
- [0280] (ii) 산성 아미노산의 다른, 상이한 산성 아미노산으로의 치환;
- [0281] (iii) 방향족 아미노산의 다른, 상이한 방향족 아미노산으로의 치환;
- [0282] (iv) 비-극성의, 지방족 아미노산의 다른, 상이한 비-극성의, 지방족 아미노산으로의 치환; 및
- [0283] (v) 극성의 하전되지 않은 아미노산의 다른, 상이한 극성의, 하전되지 않은 아미노산으로의 치환.
- [0284] 염기성 아미노산은 바람직하게는 아르기닌, 히스티딘, 및 라이신으로 이루어진 그룹으로부터 선택된다. 산성 아미노산은 바람직하게는 아스파르테이트 또는 글루타메이트이다. 방향족 아미노산은 바람직하게는 페닐알라닌, 타이로신 및 트립토판으로 이루어진 그룹으로부터 선택된다. 비-극성의, 지방족 아미노산은 바람직하게는 글리신, 알라닌, 발린, 루이신, 메티오닌 및 이소루이신으로 이루어진 그룹으로부터 선택된다. 극성의 하전되지 않은 아미노산은 바람직하게는 세린, 트레오닌, 시스테인, 프롤린, 아스파라긴 및 글루타민으로 이루어진 그룹으로부터 선택된다. 보존적 아미노산 치환과는 대조적으로, 비-보존적 아미노산 치환은 하나의 아미노산의 위에 요약한 보존적 아미노산 (i) 내지 (v)에 속하지 않는 임의의 아미노산으로의 치환이다.
- [0285] 서열 동일성을 결정하기 위한 수단은 상기에 기술되어 있다.
- [0286] 단백질의 아미노산은 또한 변형될 수 있는데, 예컨대, 화학적으로 변형될 수 있다. 예를 들면, 단백질 또는 폴리펩타이드의 아미노산의 측쇄 또는 유리 아미노 또는 카복시-말단은 예컨대, 글리코실화, 아미드화, 포스포릴화, 유비퀴틴화(ubiquitination) 등에 의해 변형될 수 있다. 화학적 변형은 또한 당해 분야에 잘 공지된 바와 같이, 생체내, 예컨대, 숙주-세포내에서 일어날 수 있다. 예를 들면, 적합한 화학적 변형 모티프, 예컨대, 단백질의 아미노산 서열내에 존재하는 글리코실화 서열 모티프는 단백질을 글리코실화시킬 수 있을 것이다. 변형이 변형된 아미노산의 동일성내에서 변화(예컨대, 치환 또는 결실)를 유발하지 않는 한, 변형된 폴리펩타이드는 언급된 폴리펩타이드의 영역내에 있는데, 즉, 이는 본원에 정의된 바와 같은 변이체가 아니다.

- [0287] 용어 "변이체"는 폴리뉴클레오타이드와 관련하여, 일반적으로 폴리뉴클레오타이드의 변형된 버전, 예컨대, 돌연변이를 지칭하므로, 폴리뉴클레오타이드의 하나 이상의 뉴클레오타이드는 결실되고/되거나, 삽입되고/되거나, 변형되고/되거나 치환된다. 일반적으로, 변이체는 작용성이며, 이는 작용성 변이체를 포함하는 아데노바이러스가 숙주 세포를 감염시킬 수 있음을 의미한다. 보다 구체적인 작용이 본원에 정의되어 있으며 일반적인 정의에 걸쳐 우선한다. "돌연변이"는 뉴클레오타이드 치환, 결실 및/또는 삽입("땀" 하나 이상의 돌연변이가 존재하는 경우 적용할 수 있다)일 수 있다. 바람직하게는, 이는 치환이며, 보다 바람직하게는 이는 아미노산 치환, 가장 바람직하게는 보존적 아미노산 치환을 유발한다.
- [0288] 일반적으로, 발현 벡터의 수집의 모든 발현 벡터, 즉, 각각의 CVP의 모든 FSP, mFSP 및 이의 항원성 단편을 암호화하는 핵산을 포함하는 발현 벡터의 수집물은 하나의 유형, 예컨대, 복제 가능한 아데노바이러스인 것이 바람직하다. 동일한 CVP 또는 이를 암호화하는 핵산의 상이한 레이아웃이 사용되는 본 발명의 구현예에서, 각각의 레이아웃은 발현 벡터의 별도의 수집물 속에 포함될 것이다. 따라서, 각각의 레이아웃은 동일한 발현 벡터 또는 상이한 발현 벡터 내에 포함될 수 있다. 후자는 발현 벡터 자체가 환자에서 항원성인 예에서 바람직하다. 따라서, 바람직하게는 상이한 레이아웃에서, 동일한 CVP의 2회 이상의 반복된 투여 사이에 발현 벡터의 유형의 변화는 환자내에서 CVP가 발현되는 기회를 증가시킨다.
- [0289] 본 발명은 또한 의약으로 사용하기 위한 본 발명의 제4 또는 제5 양태의 CVP, 본 발명의 제4 또는 제6 양태의 핵산의 수집물, 또는 본 발명의 제7 양태의 발현 벡터 수집물에 관한 것이다.
- [0290] 본 발명은 또한 본 발명의 제4 또는 제5 양태의 CVP, 본 발명의 제4 또는 제6 양태의 핵산의 수집물, 또는 본 발명의 제7 양태의 발현 벡터 수집물을 포함하는 약제학적 조성물에 관한 것이다.
- [0291] 동일한 CVP의 상이한 레이아웃, 동일한 CVP의 이러한 상이한 레이아웃을 암호화하는 핵산 또는 상이한 레이아웃을 지닌 이러한 핵산을 포함하는 발현 벡터를 동종 또는 이종 프라임-부스트 투여 요법에서 사용하는 경우에(하기 참고) 용어 "약제학적 조성물"은 또한 동일한 CVP, 동일한 CVP의 이러한 상이한 레이아웃을 암호화하는 핵산 또는 상이한 레이아웃을 지닌 이러한 핵산을 포함하는 발현 벡터의 별도의 투여를 허용하는 2개의 물리적으로 분리된 조성물을 포함한다.
- [0292] 바람직한 구현예에서 약제학적 조성물은 약제학적으로 허용되는 담체 및/또는 부형제 및 임의로 하나 이상의 추가의 활성 물질을 추가로 포함한다. 바람직하게는, 제5 양태의 조성물은 바람직하게는 정제된 형태의 치료학적 유효량의 화합물과 함께, 적합한 양의 담체 및/또는 부형제를 함유함으로써 환자에게 적절한 투여를 제공한다. 제형은 투여 방식에 적합하여야 한다.
- [0293] 약제학적 조성물은 액체, 현탁제, 유제, 정제, 환제, 캡셀제, 산제, 지속-방출 제형 등의 형태를 취할 수 있다. 약제학적 조성물은 전통적인 결합제 및 담체, 예를 들면 트리글리세라이드와 함께, 좌제로서 제형화될 수 있다.
- [0294] 본 발명의 약제학적 조성물을 제조하기 위하여, 약제학적으로 허용되는 담체는 고체 또는 액체일 수 있다. 고체형 조성물은 산제, 정제, 환제, 캡셀제, 로젠지제, 좌제, 및 분산성 과립제를 포함한다. 고체 부형제는 하나 이상의 물질일 수 있으며, 이는 또한 희석제, 충전재, 결합제, 방부제, 정제 붕해제, 또는 캡셀화 물질로서 작용할 수 있다. 산제에서, 부형제는 바람직하게는 미분 고체이며, 이는 본 발명의 미분된 억제제와의 혼합물로 존재한다. 정제에서, 활성 성분은 필수 결합 특성을 갖는 담체와 적합한 비율로 혼합되어 목적인 형태 및 크기로 압축될 수 있다. 적합한 부형제는 탄산마그네슘, 스테아르산마그네슘, 활석, 당, 락토즈, 펙틴, 덱스트린, 전분, 젤라틴, 트라가칸트, 메틸셀룰로즈, 나트륨 카복시메틸셀룰로즈, 저 융점 왁스, 코코아 버터 등이다. 좌제를 제조하기 위하여, 저 융점 왁스, 예를 들면, 지방산 글리세라이드 또는 코코아 버터의 혼합물을 우선 용융시키고 활성 성분을 이에 교반에 의해서 균질하게 분산시킨다. 용융된 균질 혼합물을 이후 편리한 크기의 주형에 부어서, 냉각되도록 함으로써, 고화시킨다. 정제, 산제, 캡셀제, 환제, 카세트(cachet), 및 로젠지제(lozenge)를 경구 투여에 적합한 고체 용량형으로 사용할 수 있다.
- [0295] 액체형 조성물은 액체, 현탁제 및 유제, 예를 들면, 물, 염수 용액, 수성 텍스트로즈, 글리세롤 용액 또는 물/프로필렌 글리콜 용액을 포함한다. 비경구 주사(예컨대, 피내, 동맥내, 골내 주입, 근육내, 피하, 경피내, 피내, 및 척추강내 주사)의 경우, 액체 제제는 예컨대, 수성 프로필렌 글리콜 용액 속에 용액으로 제형화될 수 있다. 염수 용액은 약제학적 조성물이 정맥내 투여되는 경우 바람직한 담체이다.
- [0296] 바람직하게는, 약제학적 조성물은 단위 투여량 형태이다. 이러한 형태에서 조성물은 활성 구성성분의 적절한 양을 함유하는 단위 투여량으로 소분될 수 있다. 단위 투여량 형태는 포장된 조성물일 수 있으며, 포장은 별개의 양의 조성물, 예를 들면, 포장된 정제, 캡셀제, 및 산제를 바이알 또는 앰플 속에 함유한다. 또한, 단위 투여형

은 캡셀제, 주사 바이알, 정제, 카세트, 또는 로젠지제 자체일 수 있거나, 이는 포장된 형태의 이들 중 임의의 적절한 수일 수 있다.

[0297] 조성물은, 경우에 따라, 또한 소량의 습윤제 또는 유화제, 또는 pH 완충제를 함유할 수 있다.

[0298] 또한, 이러한 약제학적 조성물은 또한 부형제 및/또는 추가의 활성 성분과 같은 그러나 이에 한정되지 않는 다른 약리학적으로 활성인 물질을 포함할 수 있다. 본 발명의 문맥에서 보조제는 무기 보조제, 유기 보조제, 오일 계 보조제, 사이토킨, 입자화된 보조제, 비로솜, 세균 보조제, 합성 보조제, 또는 합성 폴리뉴클레오타이드 보조제를 포함하나, 이에 한정되지 않는다.

[0299] 제8 국면에서, 본 발명은 MSI 표현형을 지닌 암 세포를 포함하거나 이러한 암으로 진행될 위험이 있는 환자의 치료 또는 예방에 사용하기 위한 제4 또는 제5 양태의 CVP, 본 발명의 제4 또는 제6 양태의 핵산의 수집물, 또는 본 발명의 제7 양태의 발현 백터 수집물에 관한 것이며, 여기서 암은 바람직하게는 결장직장 암, 위암, 자궁 내막 암, 소장 암, 간담즙성 관 암, 간 암, 신경내분비 암, 자궁경부 암, 난소 암, 자궁 육종, 뇌 암 및 피부 암으로 이루어진 그룹으로부터 바람직하게 선택된다.

[0300] 상기 요약한 바와 같이 본 발명의 범용 백신의 하나의 특수한 장점은 이것이 단지 하나 이상의 암 유형의 예방 또는 치료요법을 제공한다는 사실이다. 따라서, 제8 양태에 따라서 2개 유형의 MSI 암, 보다 바람직하게는 적어도 3개 유형의 MSI 암에 대한 예방 또는 치료요법을 제공하는 것이 바람직하다. 바람직하게는, 결장직장 암, 위암, 자궁내막 암, 소장 암, 간담즙성 관 암, 간 암, 신경내분비 암, 자궁경부 암, 난소 암, 자궁 육종, 뇌 암 및 피부 암.

[0301] 예방은 본 발명의 문맥에서 바람직하게는 미스매치 복구 시스템(MMR), 예를 들면, MLH-1, MSH-2, MSH-6, PMS2 및 TACSTD1/EPCAM에 관여하는 유전자에 배선 돌연변이를 지닌 환자를 포함하는, 임상 가이드라인에 따른 MSI 암 발생 위험이 있는 것으로 알려진 환자를 위한 것이다. 치료는 가장 최근의 임상 가이드라인에 따른 MSI 상태의 진단 후 임의의 조직내에서 발생하는, 모든 단계(I 내지 IV)에서의 암을 지닌 환자를 위한 것이다. 이러한 백신의 용도는 자발적으로 또는 약리학적으로 유도될 수 있는 MSI 상태를 지닌 암의 치료를 위해 의도된다.

[0302] 많은 경우에, CVP의 단일 투여는 종양 질환의 효과적인 보호 또는 종양 질환을 치료학적으로 치료하는 데 필요한 다수의 장기-지속하는 면역 세포를 생성하는 데 충분하지 않다. 결과적으로, 특수한 질환에 특이적인 생물학적 체제를 사용한 반복된 챌린지(challenge)는 상기 질환에 대한 지속된 및 보호 면역성을 확립하거나 주어진 질환을 치유하기 위해 요구된다. CVP, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물의 반복된 투여를 포함하는 투여 요법은 "프라임-부스트 백신접종 요법"으로서 현재 지칭된다. 바람직하게는, 프라임-부스트 백신접종 요법은 CVP의 적어도 2회 투여, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물을 포함한다. CVP, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물의 제1 투여는 "프라이밍(priming)"으로 지칭되며 동일한 CVP, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물의 투여는 "부스팅(boosting)"으로 지칭된다. 상기 설명으로부터 동일한 CVP가 그럼에도 불구하고 CVP, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물의 각각의 후속적인 투여시 상이한 레이아웃으로 투여될 수 있음이 이해된다.

[0303] 따라서, 본 발명의 바람직한 구현예에서, 프라임-부스팅 백신접종 요법은 면역 반응을 프라이밍하기 이러한 CVP, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물의 1회 투여 및 면역 반응을 부스팅하기 위한 적어도 하나의 후속적인 투여를 포함한다. 면역 반응을 부스팅하기 위한 2, 3, 4 또는 심지어 5회 투여가 본 발명에 의해 고려됨이 이해되어야 한다.

[0304] 프라임과 부스트 사이의 기간은 바람직하게는, 1주, 2주, 4주, 6주 또는 8주이다. 보다 바람직하게는, 이는 4주 또는 8주이다. 1회 이상의 부스트를 수행하는 경우, 후속적인 부스트는 바람직하게는, 이전 부스트 후 1주, 2주, 4주, 6주 또는 8주째에 투여된다. 보다 바람직하게는, 임의의 2개의 부스트 사이의 간격은 4주 또는 8주이다.

[0305] 본 발명의 프라임-부스트 백신접종 요법은 동종 또는 이종일 수 있다. 동종 프라임-부스트 요법에서 프라이밍 및 적어도 하나의 부스팅 둘 다는 CVP, 이러한 CVP를 암호화하는 핵산의 수집물 또는 이러한 핵산을 포함하는 발현 백터의 수집물의 투여의 동일한 수단을 사용하여 수행된다. 이종 프라임-부스팅 요법에서 이종 프라임-부스팅 요법은 예를 들면, 면역 반응의 프라이밍을 위한 폭스바이러스 백터 및 면역 반응의 부스팅을 위한 상이한 발현 백터 또는 CPV를 포함한다.

[0306] 본 발명의 하나의 바람직한 구현예에서, 프라임-부스팅 백신접종 요법은 동종이며 본 발명의 다른 바람직한 구현예에서 프라임-부스팅 백신접종 요법은 이종이다.

[0307] 따라서, 일 양태에서, 본 발명은 MSI 표현형을 지닌 암 세포를 포함하는 암을 지니거나 이러한 암으로 진행될 위험이 있는 환자의 예방 또는 치료에 사용하기 위한 본 발명의 제4 또는 제6 양태의 핵산의 수집물 및/또는 본 발명의 제7 양태의 발현 벡터 수집물에 관한 것이며, 여기서 핵산의 수집물 및/또는 발현 벡터 수집물은 이종 프라임-부스트 백신접종 계획에서 투여되며, 바람직하게는 프라임은 아데노바이러스 벡터를 사용하고 하나 이상의 부스트는 포크바이러스 벡터, 바람직하게는 MVA 벡터를 사용한다.

[0308] 실시예

[0309] 실시예 1: MSI 종양 샘플의 단백질-암호화 유전자내 모노뉴클레오타이드 반복체(MNR) 돌연변이의 선택

전체 진유전체 서열 데이터(발표일: 2016년 10월 4일)를 기반으로 하며 TCGA 데이터 포털(<https://gdc-portal.nci.nih.gov/>)로부터 이용가능한 돌연변이 주석 양식(Mutation Annotation Format: MAF) 파일을, 단백질-암호화 유전자의 진유전체(exome)의 단백질-암호화 분절 내에 위치한 6개 이상의 뉴클레오타이드의 MNR 내의 프레임쉬프트 돌연변이(FSM)의 존재에 대해 분석하였다. TCGA 샘플 주석 데이터에 정의된 바와 같은 MSI 표현형을 지닌 종양만을 분석 시 고려했다. 이러한 그룹은 69개의 MSI-높은(MSI-H) 결장직장암(CRC), 85개의 MSI 위암 및 166개의 MSI 자궁내막암(EC)에 해당하는, 총 320개의 종양 샘플 및 정상 대조군 샘플을 포함하였다. 제2의 필터링(filtering) 단계에서, 1개의 뉴클레오타이드 결실로부터 유래된 FSM 만을 허용하였는데, 이는 이러한 유형의 FSM이 CRC 및 EC 종양에서 가장 흔히 관찰되기 때문이다(1). 수득되는 목록은 다음의 기준을 충족하는 FSM 만을 허용함으로써 추가로 개선하였다: (i) 돌연변이를 지닌 판독물(read)의 수는 매치된 정상 샘플과 비교하여 종양에서 유의적으로 더 높았다(FDR-교정된 피셔-시험 $p\text{-값} \leq 0.05$); (ii) 매치된 정상 샘플에서 FSM의 대립유전자 빈도는 $\leq 25\%$ 이었다. 3개의 분석된 종양 유형(CRC, 위암, EC) 중 하나에서 종양 샘플 중 적어도 5%에서 존재하는 FSM 만을 보유함으로써 나머지 FSM를 추가로 필터링했다. 최종 선택 단계에서, 다음의 범주에 속하는 FSM는 백신에 부적절한 것으로 고려되어 배제시켰다: (i) 정상 샘플의 수집물로부터의 샘플 중 $\geq 2\%$ 내에서의 FSM의 존재(EXAC 데이터베이스 <http://exac.broadinstitute.org/>) 및/또는 (ii) FSM-운반 유전자의 mRNA 발현(RSEM $\log_2$ 발현 값)이, 모든 3개의 종양 형(CRC, EC 및 위암)을 고려하여, 모든 발현된 단백질-암호화 유전자(TCGA 유전자-수준 mRNA 발현 데이터)의 20 백분위수(percentile) 미만 값 내에 있었음. 이렇게 수득된 목록은 1283개의 FSM을 포함하였으며 이들 종양에 대한 CFMS를 나타낸다.

[0310] 삭제

[0311] 실시예 2: 허용되는 특성을 지닌 프레임쉬프트 펩타이드의 목록의 선택

이어서 실시예 1에서 선택된 CFMS의 FSM 각각을, NCBI REFSEQ 데이터베이스로부터의 상응하는 mRNA 서열(또는 서열들) 위에 ANNOVAR(Wang K, et al. (2010) NAR, 38:e164)을 사용하여 맵핑하고, 야생형(wt) 및 수득되는 돌연변이된 mRNA 둘 다를 단백질로 번역시켰다. wt 및 돌연변이된 단백질의 비교에 의해 상응하는 프레임 쉬프트 펩타이드(FSP)의 아미노산(aa) 서열을 결정하였다. FSM이 다수의 mRNA 동형의 존재로 인하여, 상이한 길이 및/또는 aa 서열을 지닌 다수의 FSP를 생성한 경우, 모든 수득되는 FSP가 보유되었다. 수득되는 목록을 필터링하여 잠재적인 CD8 T 신생-에피토프를 수득할 수 없다는 점에서 4개의 aa보다 더 짧은 모든 FSP를 배제시켰다.

또한, CVP에 포함될 FSP의 아미노산 서열은 이들이 특정의 기준을 충족하는 경우 아미노산의 첨가 또는 결실에 의해 변형시켰다(또는 특정 기준을 충족하지 않는 FSP는 변형 후 배제시켰다): (i) FSP가 10개의 aa보다 더 짧은 경우, FC에 의해 암호화된 아미노산의 바로(immediately) N-말단 측에 자연 발생하는 4개의 wt aa를 FSP의 N-말단에 가하여 추정된 CD8 T 세포 신생-에피토프(8 내지 10mer)의 최소 길이에 이르는 펩타이드(이는, FSM이 없는 상응하는 야생형(wt) 핵산의 번역 생성물과 비교하여 상이한 첫 번째 아미노산을 암호화하는 코돈으로부터 시작되는, FSM을 포함하는 핵산의 단백질-암호화 분절의 완전한 번역 생성물이라고 본 발명의 문맥에서 정의되는 FSP와는 상이하므로 mFSP로서 지칭된다)를 보증한다. 동일한 FSM으로부터 유래되는 다수의 FSP 사이에 공유된 아미노산 스트레치(amino acid stretch)는 가장 긴 FSP에서만 보유되었는데, 즉, 보다 짧은 FSP에서 이러한 아미노산 스트레치가 결실되었다. 최종 단계에서, wt 사람 프로테오믹(proteome)(NCBI REFSEQ 데이터베이스)내에 또한 존재하는 8개 이상의 연속된 아미노산(continuous amino acid)의 임의의 분절을 FSP로부터 제거하여 자가면역성을 유도할 위험성을 최소화하였다. wt 분절의 배제 후, 수득되는 FSP가 4개의 aa보다 짧은 경우, 이는 목록에서 제거하였다. 이렇게 수득된 FSP의 최종 그룹은 1059개의 FSM에 의해 암호화된 1087개의 아미노산 서열

(서열 번호 1 내지 1087)을 포함하며(표 1) CVP로 지칭된다.

[0312] 삭제

[0313] 삭제

표 1

각각의 1087 FSP 의 경우, 서열 번호는 FSP 를 생성하는 FSM 의 계층성 조직화(hg19 조립체)와 함께 보고된다.

서열 번호	계층성 조직화 FSM	서열 번호	계층성 조직화 FSM	서열 번호	계층성 조직화 FSM	서열 번호	계층성 조직화 FSM
1	chr18:34205516	273	chr1:85331665	545	chr8:144621235	817	chr12:117615412
2	chr18:34205516	274	chr2:170665008	546	chr7:42005573	818	chr17:73814802
3	chr1:6257785	275	chr6:33178990	547	chr16:72991758	819	chr1:12052736
4	chr2:148683686	276	chr12:51392999	548	chr12:54645832	820	chr11:65653077
5	chr17:56435161	277	chr4:56765965	549	chr6:4031881	821	chrX:131762582
6	chr3:51417604	278	chr16:58589340	550	chr1:1961598	822	chr12:57921002
7	chr5:79970915	279	chr11:6662142	551	chr13:114523858	823	chr20:36627613
8	chr18:57013194	280	chr15:28200305	552	chr10:52005194	824	chr11:970195
9	chr5:145647320	281	chrX:10188763	553	chr11:45948373	825	chr6:30157254
10	chr11:77784147	282	chr4:118005517	554	chr19:58084579	826	chr1:230798959
11	chr13:115057211	283	chr2:24086326	555	chr1:52305912	827	chr12:12814274
12	chr11:126137087	284	chr19:19906351	556	chr1:52305912	828	chr10:129913974
13	chr2:165551296	285	chr2:152112048	557	chr2:204305619	829	chr9:124536637
14	chr6:80751897	286	chr5:131944382	558	chr7:107395909	830	chr11:104874011
15	chr7:151874148	287	chr11:119213688	559	chr13:46543661	831	chr5:1074698
16	chr12:122242658	288	chr19:38028415	560	chr1:110300580	832	chr15:72190580
17	chr6:108214755	289	chr5:57753012	561	chr12:8281937	833	chr17:38552642
18	chr19:49850473	290	chr12:49443667	562	chr16:4944500	834	chr1:35370731
19	chr7:77423460	291	chr16:15131990	563	chr15:86287017	835	chr9:135277388
20	chr8:103289349	292	chr8:22472975	564	chr4:142143532	836	chr15:75499804
21	chr3:100039736	293	chrX:56591874	565	chr12:56559113	837	chr3:54596940
22	chr1:27621108	294	chr20:18287008	566	chr12:110344435	838	chr9:125861042
23	chr3:136573486	295	chr20:18287008	567	chr5:127610311	839	chr8:92352747
24	chr1:14108749	296	chr20:18287008	568	chr10:127697969	840	chr11:111896977
25	chr14:24040436	297	chr1:1116223	569	chr12:88512305	841	chr2:160604680
26	chr16:10867203	298	chr22:46931227	570	chr3:142030643	842	chr11:111904183
27	chr12:64812755	299	chr12:95650969	571	chr7:94174999	843	chr18:265348
28	chr17:48433967	300	chr2:240002823	572	chr19:33167776	844	chr18:45566519
29	chr1:231131567	301	chr2:175213713	573	chr9:33385690	845	chr2:225738848
30	chr6:71508370	302	chr3:195595229	574	chr14:94088050	846	chr4:129869675
31	chr19:49458971	303	chr12:57572242	575	chr2:211018375	847	chr9:139945517
32	chr10:78729786	304	chr4:3432431	576	chr14:27066542	848	chr3:121573659
33	chr11:62649529	305	chr12:27950769	577	chr10:89717770	849	chr9:35091693
34	chr1:160589601	306	chr6:107391602	578	chr2:203168133	850	chr4:122723894
35	chr3:114058003	307	chr1:16462199	579	chr12:123351892	851	chr15:57489984
36	chr3:20216050	308	chr3:169700664	580	chr1:36636626	852	chr19:50333113
37	chr10:70182521	309	chr14:93761193	581	chr4:140291445	853	chr11:6292451
38	chr9:96422612	310	chr19:6477251	582	chr13:100925452	854	chr15:49309051
39	chr5:140049102	311	chr14:52481919	583	chr13:79918807	855	chr7:140482927

[0314]

40	chr3:183665257	312	chr6:109850222	584	chr16:28909714	856	chr7:126173278
41	chr5:145886723	313	chr9:138379043	585	chr4:113570754	857	chr3:182987674
42	chr15:79750586	314	chr6:13206135	586	chr5:98206409	858	chr2:190626331
43	chr1:45407182	315	chr2:196866535	587	chr12:63541343	859	chr8:145150876
44	chr4:3430399	316	chr1:27876869	588	chr2:113060881	860	chr2:16082314
45	chr1:28785730	317	chr1:247319909	589	chr1:200822549	861	chr8:113241029
46	chr11:118220583	318	chr3:50099450	590	chr12:970297	862	chr12:7310658
47	chr2:203922058	319	chr18:29453418	591	chr20:23065992	863	chr9:98209617
48	chrX:37312611	320	chr22:43213780	592	chr3:142142409	864	chr17:46135788
49	chr10:111893350	321	chr11:58962827	593	chr11:134048586	865	chr14:74967607
50	chr10:93601946	322	chr4:153864507	594	chr3:126735391	866	chr17:7496122
51	chr1:155308000	323	chr2:86831015	595	chr6:161469776	867	chr16:1270496
52	chr6:131481276	324	chr12:57883053	596	chr1:52991780	868	chr3:169802469
53	chr1:23240246	325	chr17:73498973	597	chr20:56735727	869	chr7:47955186
54	chr6:139097330	326	chr4:164428219	598	chr2:220504282	870	chr6:34839369
55	chr2:207174428	327	chr2:197649614	599	chr2:58373509	871	chr12:72038781
56	chr15:56736723	328	chr19:38899416	600	chr2:242179467	872	chr7:86978480
57	chr21:38524243	329	chr2:1652960	601	chr9:35547974	873	chr7:86978480
58	chr2:203420130	330	chr17:16285785	602	chr14:35331423	874	chr13:60582734
59	chr10:890939	331	chr16:77356311	603	chr2:219529514	875	chr6:90415853
60	chr5:131931452	332	chr14:102718303	604	chr3:176769342	876	chr6:111498763
61	chr14:45693722	333	chr4:170428203	605	chr4:156273869	877	chr5:125939712
62	chr20:49508204	334	chr12:58025103	606	chr2:20200211	878	chr22:32794006
63	chr1:65306997	335	chr14:31074772	607	chr4:76891521	879	chr19:38102620
64	chr2:165365288	336	chr21:33949091	608	chr4:68530907	880	chr20:47989891
65	chr11:77920856	337	chr16:66599895	609	chr20:5924808	881	chr7:100028068
66	chr17:57247171	338	chr4:170613460	610	chr2:103334978	882	chr1:53543377
67	chr6:158508009	339	chr4:170613460	611	chr13:95735432	883	chr3:150289746
68	chr3:142274740	340	chr1:36935323	612	chr19:5590343	884	chr17:54921519
69	chr1:91967357	341	chr3:15084406	613	chr1:155448996	885	chr5:137803132
70	chr16:19725706	342	chr7:158704353	614	chr6:36181729	886	chr11:69063724
71	chr1:74575213	343	chr17:28505167	615	chr2:88327536	887	chr2:42488302
72	chr2:178988920	344	chr7:115594657	616	chr5:37226878	888	chr12:122018740
73	chr8:124384893	345	chr18:10741064	617	chr8:27364393	889	chr14:104642560
74	chr1:27105931	346	chr2:99778781	618	chr16:50825519	890	chr15:23890894
75	chr12:57422573	347	chr13:114542718	619	chr4:83827648	891	chr17:56448298
76	chr3:157081227	348	chr12:31448178	620	chr10:18834895	892	chr16:15131931
77	chr17:49077041	349	chr7:91603085	621	chrX:41089035	893	chr2:43452512
78	chr17:49077041	350	chr5:35874637	622	chr3:113380090	894	chr12:7173239
79	chr17:42756253	351	chr6:80720630	623	chr1:207642044	895	chr2:149447829
80	chr21:16338330	352	chr17:7751137	624	chr17:17119709	896	chr12:80201042
81	chr17:20108263	353	chr20:45875072	625	chr6:84896233	897	chr12:80201042
82	chr9:35059647	354	chr8:67488453	626	chr18:67697249	898	chr12:104476535
83	chr1:93667516	355	chr15:62244050	627	chr7:100285170	899	chr17:4837373
84	chr15:64967247	356	chr3:48465485	628	chr18:21745097	900	chr7:107763584
85	chr1:204228411	357	chr4:2242634	629	chr6:30572795	901	chr7:139833448
86	chr17:7798765	358	chr4:107156505	630	chr9:109689491	902	chr12:77449827
87	chr6:163899920	359	chr11:61539013	631	chr4:95173910	903	chr6:112389434
88	chr13:50235209	360	chr2:152320541	632	chr19:13882968	904	chr8:90967512
89	chrX:129190011	361	chr2:201683505	633	chr10:124758127	905	chr10:27322259

[0315]

90	chr5:64023941	362	chr2:201683505	634	chr13:103381996	906	chr2:55138130
91	chr2:74687410	363	chr1:65339111	635	chr16:709106	907	chr16:74976691
92	chr7:100802405	364	chr7:92760738	636	chr22:41257115	908	chr15:49036443
93	chr7:8198251	365	chr13:95696016	637	chr12:40713870	909	chr21:34799292
94	chr15:42742957	366	chr10:13151192	638	chr13:23914687	910	chrX:63412648
95	chr10:98336475	367	chr11:125505378	639	chr15:44843099	911	chr12:19514518
96	chr9:115806416	368	chr10:115662308	640	chr7:29070262	912	chr3:160143940
97	chr1:89473442	369	chr1:68171151	641	chr8:124707762	913	chr12:131283100
98	chr17:55028016	370	chr1:155152179	642	chr13:114514859	914	chr12:131283100
99	chr1:240072444	371	chr16:88504203	643	chr1:35365852	915	chr2:220502413
100	chr7:108205526	372	chr1:19467923	644	chr9:35043650	916	chr15:55759242
101	chr5:35705894	373	chr9:37357250	645	chr17:46629737	917	chr10:91359120
102	chr1:109560141	374	chr16:88691141	646	chr2:227661664	918	chr2:236649677
103	chr17:4875738	375	chr11:32637520	647	chr14:89878534	919	chr16:31151942
104	chr1:35846960	376	chr17:63532585	648	chr3:168833257	920	chr10:135111566
105	chr19:1430254	377	chr2:210887680	649	chr8:6289099	921	chr10:96352051
106	chr19:48197891	378	chr3:57276921	650	chr8:105509429	922	chr4:87769943
107	chr1:237969494	379	chr13:32954023	651	chr7:120971879	923	chr1:215793922
108	chr3:122433232	380	chr16:9857380	652	chr7:2641075	924	chr15:53908071
109	chr10:90682146	381	chr16:30007665	653	chr5:140857742	925	chr15:34444996
110	chr1:24078404	382	chr5:72264329	654	chr11:34910341	926	chr7:104746985
111	chr16:48622229	383	chr9:131019390	655	chr12:4719362	927	chr16:11141159
112	chr21:34882122	384	chr5:43173517	656	chr2:132021078	928	chr19:5667115
113	chr10:64159513	385	chr12:102108338	657	chr8:70514026	929	chrX:53112052
114	chrX:13764946	386	chr17:67218780	658	chr17:25975972	930	chr17:28296061
115	chr5:147499875	387	chr2:201437004	659	chr12:124848228	931	chr1:35578941
116	chr5:147499875	388	chr16:3817721	660	chr12:124848228	932	chr9:114695180
117	chr5:147499875	389	chr4:40144449	661	chr1:228559450	933	chr1:214830653
118	chr11:71948748	390	chr15:59186310	662	chr12:110019240	934	chr7:25200833
119	chr2:172549339	391	chr7:150656679	663	chr9:90321802	935	chr8:86114461
120	chr2:37454908	392	chr6:74351590	664	chr19:42838298	936	chr1:231487256
121	chr5:36985083	393	chr19:18887993	665	chr10:64952699	937	chr12:99071207
122	chrX:154157686	394	chr12:56347514	666	chr15:59376343	938	chrX:99854070
123	chr10:29760116	395	chr5:60822215	667	chr8:144941378	939	chr14:54896992
124	chr3:41860985	396	chr5:140502487	668	chr4:38774956	940	chr11:65314283
125	chr12:416953	397	chr8:133150233	669	chr7:22197474	941	chr11:75905667
126	chr1:156642804	398	chr5:137627690	670	chr2:71650549	942	chrX:21675046
127	chr4:15067858	399	chr1:10177642	671	chr1:91406040	943	chr19:16314384
128	chr15:52901069	400	chr2:71337212	672	chr17:44248731	944	chr19:16314384
129	chr6:90432675	401	chr9:17135271	673	chr7:44120414	945	chr15:101438350
130	chr4:114823494	402	chr11:17352468	674	chr3:141326548	946	chr11:400077
131	chr1:204924033	403	chr16:53263000	675	chr6:116967058	947	chr19:42383610
132	chr2:196788374	404	chr20:37146233	676	chr2:220081103	948	chr19:39663913
133	chr6:36867371	405	chrX:153042691	677	chr20:17581680	949	chr1:149895562
134	chr16:19722724	406	chr3:142775212	678	chr2:128238676	950	chr5:108290522
135	chr7:2968323	407	chr9:115941002	679	chr16:28913640	951	chrX:19560215
136	chr4:15995680	408	chr5:96315249	680	chr19:17039884	952	chr18:31319986
137	chr2:27248517	409	chr14:92472698	681	chr1:153751860	953	chr16:30041821
138	chr11:32635951	410	chr5:109940905	682	chr19:50158042	954	chr5:140953309
139	chr9:5968044	411	chr1:158058203	683	chr6:99849343	955	chr2:169997025

[0316]

140	chr12:6924043	412	chr19:58264857	684	chr3:42679036	956	chr22:41195058
141	chr5:162917426	413	chr8:124140521	685	chr4:39462464	957	chr22:41195058
142	chr2:71191573	414	chr3:133670083	686	chr18:54358513	958	chr19:36357214
143	chr19:55815036	415	chr9:69421905	687	chr5:61847115	959	chr12:130184705
144	chr13:35733663	416	chr17:7193637	688	chr5:76358967	960	chr8:37728933
145	chr15:81271633	417	chr1:62253580	689	chr9:35108148	961	chr2:26534413
146	chr15:55631503	418	chr17:33749493	690	chr12:20522723	962	chr1:156884483
147	chr1:147091501	419	chr8:70488249	691	chr16:71668442	963	chr11:64032517
148	chr17:26653807	420	chr14:65035126	692	chr11:88068108	964	chr19:52888438
149	chr18:45567076	421	chr1:113471890	693	chr11:88068108	965	chr14:75230947
150	chr11:107325228	422	chr15:91019925	694	chr9:84208132	966	chr2:203848308
151	chr9:136918529	423	chr19:7987519	695	chr1:100588802	967	chr8:32453511
152	chr2:97749725	424	chr6:52334208	696	chr5:38923329	968	chr7:97933623
153	chr1:151318741	425	chr6:90576391	697	chr4:38690460	969	chr2:169948389
154	chr19:50434211	426	chr10:131666125	698	chr5:131007941	970	chr1:206821441
155	chr9:131591120	427	chr3:167507159	699	chr14:75265533	971	chr16:84213651
156	chr12:88524079	428	chr20:40739003	700	chr10:62149221	972	chr7:154782740
157	chr18:46474795	429	chr5:137505021	701	chr3:169557805	973	chr4:153244156
158	chr18:46474795	430	chr16:29818054	702	chr11:35513670	974	chr3:126142183
159	chr3:180666228	431	chr10:116730192	703	chr12:113442830	975	chrX:54497148
160	chr11:16822525	432	chr4:160253755	704	chr14:95662949	976	chr11:118770652
161	chr16:89951020	433	chrX:70327614	705	chr2:219508084	977	chr18:30349862
162	chr20:50400983	434	chr10:116887435	706	chr12:117624320	978	chr12:42706971
163	chr2:103149137	435	chr8:67716612	707	chr8:72958792	979	chr2:196801374
164	chr1:150530506	436	chr15:76958036	708	chr17:38546381	980	chr8:124368685
165	chr11:118969143	437	chr1:226352491	709	chr12:75893593	981	chr13:31480852
166	chr6:160485488	438	chr13:77581683	710	chr1:170004605	982	chr6:18122226
167	chr1:25775375	439	chr14:23745310	711	chr12:122748169	983	chr3:71821968
168	chr11:4703475	440	chr22:38895455	712	chr16:88694459	984	chr4:71844995
169	chr11:75694431	441	chr6:71546674	713	chr6:4052975	985	chr2:159077217
170	chr12:123794283	442	chr11:63313709	714	chr4:128564917	986	chr19:47969003
171	chr6:15496722	443	chr19:5587282	715	chr15:69331226	987	chr22:50277679
172	chr18:21750331	444	chr13:20638677	716	chr4:76539580	988	chr12:88566417
173	chr11:31812317	445	chr15:55912892	717	chr5:13701426	989	chr8:53062482
174	chr3:57509313	446	chr9:138715800	718	chr3:89499363	990	chr10:93247481
175	chr1:40756543	447	chr12:50025258	719	chr2:170493804	991	chr5:13766239
176	chr5:179149920	448	chr10:13696452	720	chr4:170359358	992	chr9:32633025
177	chr13:33344580	449	chr6:87969484	721	chr19:12155504	993	chr11:73021527
178	chr9:18680350	450	chr12:88449444	722	chr22:31485922	994	chr1:178412041
179	chr2:54093345	451	chr10:100186987	723	chr9:140356679	995	chr16:27509009
180	chr13:34398063	452	chr19:4816465	724	chr11:380921	996	chr15:85634360
181	chr5:176675269	453	chr13:103524612	725	chr17:61781804	997	chr16:31373986
182	chr13:27255387	454	chr4:38691476	726	chr17:61781804	998	chr19:35435665
183	chr1:49201967	455	chr2:173368931	727	chr17:61781804	999	chr6:126176317
184	chr11:111953289	456	chr11:124845049	728	chr18:45567085	1000	chr10:32311826
185	chr2:234394237	457	chr16:14346300	729	chr15:28525215	1001	chr6:71235776
186	chr1:100534122	458	chr11:6629392	730	chr19:7976149	1002	chr4:37447379
187	chr2:44145165	459	chr12:57921401	731	chr19:7976149	1003	chr6:45390355
188	chr8:74507471	460	chr15:41029894	732	chr3:33602361	1004	chr2:157185029
189	chr11:71948209	461	chr16:77775744	733	chr11:45955607	1005	chr14:50930796

[0317]

190	chr20:23066469	462	chr20:31041556	734	chr4:186515044	1006	chr7:91732039
191	chr17:40939870	463	chr14:88940113	735	chr2:176995417	1007	chr4:47939172
192	chr17:76046980	464	chr4:25849258	736	chr7:128852004	1008	chr10:27329038
193	chr9:34257623	465	chr8:95531563	737	chr16:30409310	1009	chr1:229422305
194	chr3:182602674	466	chr20:39990829	738	chr14:75514604	1010	chr6:76423416
195	chr13:53049034	467	chr2:74763924	739	chr10:17363321	1011	chr1:154932028
196	chr5:143853531	468	chr8:24257686	740	chr9:21007046	1012	chr13:108518338
197	chr1:203786225	469	chr19:49218106	741	chr5:154173390	1013	chr9:20912931
198	chr7:91936914	470	chr7:100479332	742	chr8:24167473	1014	chr8:125080031
199	chr13:109661386	471	chr17:80615786	743	chr11:64572093	1015	chr5:14487781
200	chr1:169366580	472	chr17:17046886	744	chr3:194147850	1016	chr1:154942911
201	chr6:101296336	473	chr3:42679486	745	chr4:1980559	1017	chr3:63981832
202	chr7:102584993	474	chr11:94230059	746	chr8:6302639	1018	chr17:4575894
203	chr1:1290110	475	chr19:49982166	747	chr13:73337684	1019	chr12:39734129
204	chr3:77657038	476	chr4:169317264	748	chr14:100594927	1020	chr12:29450110
205	chr7:1037311	477	chr1:149884981	749	chr18:40857246	1021	chr11:66055105
206	chr21:33073336	478	chr17:55028118	750	chr10:103826900	1022	chr11:66055105
207	chr18:12699829	479	chr1:169790867	751	chr14:20846338	1023	chr11:108044069
208	chr19:12430217	480	chr4:39515753	752	chr5:72199545	1024	chr12:6657974
209	chrX:48887952	481	chr17:26449740	753	chr12:49374348	1025	chr5:41181560
210	chr5:130815369	482	chr2:219449364	754	chr16:24942180	1026	chr19:11577605
211	chr11:47196853	483	chr1:237024474	755	chr14:105174185	1027	chr7:44684936
212	chr11:47196853	484	chr19:36223002	756	chr2:203831759	1028	chr1:8716109
213	chr2:148657041	485	chr1:156694023	757	chr1:7998254	1029	chr13:50065970
214	chrX:302052	486	chr11:64004663	758	chr12:57860075	1030	chr5:180432665
215	chr6:80751910	487	chr19:20228702	759	chr19:12384448	1031	chr14:100728644
216	chr8:31001132	488	chr8:68992721	760	chr11:9735070	1032	chr8:145727027
217	chr9:88937823	489	chr18:13746253	761	chr2:10059788	1033	chr7:105655642
218	chr9:88937823	490	chr1:151774033	762	chr17:73491063	1034	chr4:8616156
219	chr1:108700183	491	chr9:103111633	763	chr9:33464082	1035	chr2:110926098
220	chr16:67645339	492	chr9:106885501	764	chr16:71483562	1036	chr11:82877219
221	chr10:70156583	493	chr2:39074185	765	chr17:61497894	1037	chr8:145065718
222	chr11:62381084	494	chr7:99817848	766	chr18:13681751	1038	chr1:55081757
223	chr6:96999786	495	chr12:6711546	767	chr4:2698177	1039	chr19:14593640
224	chr6:31323363	496	chr12:6711546	768	chr12:53452903	1040	chr17:2579802
225	chr3:108229398	497	chr1:156715104	769	chr3:25647591	1041	chr2:230661315
226	chr17:79803764	498	chr19:39330959	770	chr8:39068767	1042	chr3:40529660
227	chr22:42564716	499	chr10:81072446	771	chr22:33255324	1043	chr9:123954450
228	chr20:31022442	500	chr7:6196443	772	chr7:151845524	1044	chr9:125141077
229	chr2:207174869	501	chr7:100855927	773	chr9:135277541	1045	chr10:115481532
230	chr3:154032978	502	chr12:107937778	774	chr7:33014804	1046	chr10:91514406
231	chr1:67390426	503	chr2:172546762	775	chr2:99976805	1047	chr8:92406218
232	chr20:25422397	504	chr11:121475905	776	chr12:54971060	1048	chr21:37605286
233	chr16:29825016	505	chr12:117977605	777	chr4:26417146	1049	chr20:44050026
234	chr21:33074655	506	chr17:44109601	778	chr19:36210764	1050	chr8:68128856
235	chr6:76599858	507	chr7:21939669	779	chr10:91203598	1051	chr5:132534817
236	chr6:31504446	508	chr8:133826909	780	chr7:102760123	1052	chr15:65994675
237	chr7:94185017	509	chrX:70472854	781	chr5:68492902	1053	chr22:42610948
238	chr2:206166298	510	chr1:26671971	782	chr14:55818555	1054	chr19:17836781
239	chr2:95815035	511	chr11:33117910	783	chr1:46494559	1055	chr8:55538813

240	chr17:67125767	512	chr7:92146721	784	chr14:96761299	1056	chr1:233388513
241	chr10:61823946	513	chr13:45008838	785	chr3:26751758	1057	chr1:38274674
242	chr2:169699563	514	chr3:53889347	786	chr9:6012690	1058	chr4:678571
243	chr7:50531075	515	chr2:163134716	787	chr8:100990178	1059	chr4:678571
244	chr1:27106804	516	chr13:23912864	788	chr11:27362973	1060	chr7:23775341
245	chr20:56227349	517	chr20:30789952	789	chr6:17788023	1061	chr20:62193251
246	chr20:58452519	518	chr6:114292040	790	chr3:37367468	1062	chr11:1902786
247	chr12:122720397	519	chr1:168054869	791	chr17:18181545	1063	chr1:179337955
248	chr7:150698398	520	chr2:55176077	792	chr6:42832627	1064	chr1:192779369
249	chr16:28883208	521	chr15:49776644	793	chr2:99977965	1065	chr4:74313372
250	chr11:65836146	522	chr18:19154750	794	chr11:102713563	1066	chr4:110756541
251	chr15:91304139	523	chr7:19738024	795	chr4:3133117	1067	chr8:27634577
252	chr3:58089788	524	chr1:93599280	796	chr1:153362605	1068	chr14:24032654
253	chr9:134007993	525	chr5:131676327	797	chrX:133378875	1069	chr6:144086414
254	chr20:57769140	526	chr2:109086477	798	chr14:105614481	1070	chr19:50098808
255	chr10:94243045	527	chr8:99168468	799	chr17:19641649	1071	chr10:105363391
256	chr13:51530587	528	chr3:185212518	800	chr17:40134398	1072	chr16:88504852
257	chr10:75560464	529	chr6:102503432	801	chr9:19063047	1073	chr2:97637864
258	chr11:108216477	530	chr6:102503432	802	chr19:45996513	1074	chr15:63986203
259	chr22:50898756	531	chr6:102503432	803	chr2:231931680	1075	chr11:118402960
260	chr17:25910016	532	chr16:50745399	804	chr8:30703516	1076	chr2:241808308
261	chr11:95555113	533	chr16:30736371	805	chr10:91163033	1077	chr6:29641359
262	chr11:95555113	534	chr10:63958149	806	chr1:89732166	1078	chr8:145773375
263	chr18:43459143	535	chr1:100889837	807	chr20:2816204	1079	chr11:17794004
264	chr11:74336609	536	chr1:46752129	808	chr1:89206848	1080	chr12:57704152
265	chr12:57921732	537	chr22:18300932	809	chr16:53348351	1081	chr5:56219767
266	chr2:201436992	538	chr19:10433828	810	chr9:90582463	1082	chr19:33703794
267	chr9:39073899	539	chr6:33263965	811	chr3:38949441	1083	chr8:26221272
268	chr19:21992087	540	chr19:45556129	812	chr19:48789818	1084	chr16:25232875
269	chr6:84634231	541	chr18:12370885	813	chr7:89929188	1085	chr7:4830445
270	chr20:36361416	542	chr1:28920547	814	chr3:195487898	1086	chr6:86275080
271	chr12:98921672	543	chr1:197145703	815	chr15:42738788	1087	chr19:46025663
272	chr14:35585935	544	chr12:121432118	816	chr9:95221949		

[0319]

[0320]

실시예 3: 높은 "면역원성 적용범위"를 지닌 MSI 백신에 대한 FSP의 최적의 서브세트의 선택

서열 번호 1 내지 1087은 본 발명의 CVP에 포함될 수 있는 FSP 및 mFSP의 아미노산 서열을 나타낸다. 이러한 예시적인 CFSP는 1087개의 FSP 및 mFSP를 포함한다. 실시예 1 및 2에 요약된 기준이 변경되는 경우, CFSP는 추가의 또는 보다 적은 FSP를 포함할 것이며, 따라서 CVP는 추가의 또는 보다 적은 FSP 및 mFSP를 포함할 것이다. CVP, 예컨대, 바이러스 벡터, 네이크드 DNA/RNA의 투여 방법에 따라서, 이러한 다수의 FSP 및 mFSP의 CVP를 생성하는 것은 실제적이거나 경제적이지 않을 수 있다. 따라서, 본 발명자들은, 특정 MSI 암으로 고통 받는 환자의 대부분의 최적의 면역화 또는 MSI 암의 발병 가능성이 있는 환자에서 최적의 예방을 달성하기 위해, 실시예 1 및 2에 요약된 바와 같이 생성된 CFSP로부터, CVP에 포함되는 CFSP의 FSP로부터 유래된 FSP 또는 mFSP의 적합한 수를 선택하는 추가의 선택 기준을 개발하였다. 다음에서 본 발명자들이 바람직한 CVP에 포함되는 FSP 및 mFSP의 서브세트를 결정하는 데 사용된, 이러한 추가의 선택 기준을 기술한다.

상이한 바이러스 항원으로 백신접종된 사람 대상체에서의 앞서의 연구는 약 400 aa의 항원성 서열이 평균 3개의 면역원성 에피토프(최소 1, 최대 12)를 함유함을 나타냈다(도 1)(Borthwick, N., *et al.* (2017) PLoS One 12(4), Swadling, L., *et al.* (2014) Sci Transl Med 6(261)). 따라서, 본원에서 3개의 면역원성 에피토프의 예측된 평균으로서 의도되는, 양호한 "면역원성 적용범위(immunogenic coverage)"를 수득하기 위해서는, 백신에 대해 선택된 FSP가, 각각의 환자의 종양에 있어서 적어도 400 aa의 총 길이를 나타내는 것이 바람직할 수 있다. 따라서, 본 발명자들은 400 aa의 실험적으로 확립된 최소의 면역원성 적용범위 역치가 실험한 MSI 종양의 최대 수에 이르도록 하는 방식으로 CFSP로부터 FSP를 선택하기 위한 알고리즘을 개발하였다. 실현가능한 경우, 본 발명자들은, FSP의 일부가 종양 세포에서 번역되지 않거나 제시되지 않을 가능성을 상쇄하고자, 800 aa의 표적 면역원성 적용범위에 도달하는 것을 목표로 하였다. 이러한 기준은 다음을 보증한다: (i) 환자의 큰 집단(large cohort)에서 효과적인 면역 반응을 유도할 높은 가능성; 및 (ii) 주어진 환자 내에서 다수의 암 세포는 백신-유도된 면역성에 의해 표적화될 것임.

추가적 제한을 알고리즘에 도입하여 최종의 백신 세트에서 모든 FSP에 대해 최대 6000 aa의 총 길이를 달성하였다. 이러한 길이 컷오프(cutoff)는, 연속적으로 결합된(continuous joined) FSP 및/또는 mFSP의 약 ~1500 aa를 암호화하는 벡터당 약 4,500개 뉴클레오타이드의 최대 삽입 크기를 고려하여 백신 벡터(n = 4)의 바람직한 총 수를 반영하였다.

CVSP 수집물에서 FSP를 생성하는 각각의 1059개의 FSM의 경우, 320개의 TCGA MSI 종양 (69개 MSI-H 결장직장암, 85개 MSI 위암 및 166개 MSI 자궁내막암) 각각에서, 1 또는 0의 값을 각각 FSM의 존재 또는 부재를 기반으로 부여하였다. 각각의 종양 유형의 경우, 빈도가 < 5%인 FSM에 0의 값을 지정하여, 각각의 종양 그룹 내에서 보다 공유된 이러한 FSM의 백신 목록으로의 포함이 유리하도록 했다.

제1 단계로서, 알고리즘은 각각의 FSM에 의해 생성된 모든 FSP의 총 길이와 320개의 MSI 종양에 걸쳐 FSM의 관찰된 빈도 사이의 곱인 점수에 따라 1059개의 FSM을 순위를 매겼다(aa 길이 $\times$ FSM을 함유하는 샘플의 수/총 샘플).

백신 목록에 포함된 제1의 FSM은 최고 점수를 지닌 것이었다. 후속적으로, 각각의 라운드에서 종양의 최대 수를 가능하게 하는 FSM을 선택하여 이들의 면역원성 적용범위를 증가시킴으로써, 주기적인 방식으로 알고리즘을 진행시켰다. 하나 초과인 FSM이 이러한 조건을 충족하는 경우, 최고 점수를 가진 FSM을 선택하였다. FSM이 선택되면, FSM에 의해 암호화된 모든 FSP를 백신 목록에 추가하고, 상응하는 FSP의 총 aa 길이를 가함으로써, 선택된 FSM을 수반하는 샘플의 면역원성 적용범위를 그에 따라 업데이트하였다. 일단 샘플이 표적 면역원성 적용범위 역치(본 경우에서 결장직장암 및 위암의 경우 800 aa , 자궁내막암의 경우 400 aa 이 되도록 선택함)에 도달하면, 알고리즘은 표적 적용범위에 아직 도달하지 않은 이러한 샘플 만을 고려하면서, 후속적인 FSM의 선택을 위해 이를 중지한다.

[0321] 삭제

[0322] 삭제

[0323] 삭제

[0324] 삭제

[0325] 삭제

[0326] 삭제

[0327] 알고리즘을 지속함으로써 FSP 또는 mFSP를 백신 목록, 즉, CVP를 형성하는 아미노산 서열에, 다음 3개의 조건 중 하나가 충족될 때까지 추가하였다: (i) 선택된 FSM에 의해 암호화되는 모든 선택된 FSP의 총 aa 길이를 6000 aa 로 대체함; (ii) 모든 암 샘플은 면역원성 적용범위 $\geq$ 표적 역치를 가짐; 또는 (iii) 역치 이하의 샘플의 면역원성 적용범위를 증가시키는 더 이상의 FSM이 존재하지 않았음.

[0328] 기술된 알고리즘을 사용하여 선택된 FSP의 최종 서브세트는 6021 aa 의 총 길이에 대한 204개의 FSM으로부터 발생한 209개의 FSP(서열 번호 1 내지 209)를 포함하고 Nous-209로 지칭된다. FSP의 이러한 서브세트는 TCGA 결장직장암 샘플의 98%에 대해 면역원성 적용범위 ≥ 400 aa 를 제공하며 중앙값(median number)이 샘플당 50개 FSP이고 면역원성 적용범위의 중앙값(median immunogenic coverage)이 1322 aa 이다. 유사하게, Nous-209 내 FSP는 위암 샘플의 95%에서 면역원성 적용범위 ≥ 400 aa 를 제공하며 중앙값이 샘플당 46개 FSP, 적용범위 중앙값이 1178 aa 이다. 최종적으로, 면역원성 적용범위 ≥ 400 aa 는, 샘플당 21개의 FSP의 중앙값 및 512 aa 의 적용범위 중앙값과 함께, 70%의 TCGA 자궁내막암에 의해 도달된다. 면역원성 적용범위는 800 aa 의 표적 값에 대해 계산한 경우 결장직장암 및 위암에 대해 매우 높게 남는다(각각 93% 및 83%).

[0329] **실시예 4: 높은 면역원성 적용범위를 지닌 후보물 MSI 암 백신으로서 Nous-209의 확인(validation)**

[0330] Nous-209에 포함된 FSP 및 mFSP의 목록에 대한 제1의 확인 단계로서, 본 발명자들은 MSI 세포주(7개의 CRC 및 1개의 EC)의 패널에서 차세대 서열분석(NGS)을 수행하였다. 게놈 수준(진유전체-서열분석)에서, Nous-209에 또한 포함된 각각의 세포주에서 검출된 FSM의 수는, 모든 세포주가 2037 aa 의 평균 적용범위(FSP 누적 길이)와 함께,

400 aa의 최소의 면역원성 적용범위 역치를 크게 극복할 정도였다(도 2의 A).

- [0331] 둘째로, 본 발명자들은 RNA-seq에 의한 동일한 세포주를 분석함으로써 진유전체 서열분석에 의해 검출된 Nous-209 내 FSM이 전사 수준에서도 얼마나 많이 발현되는지를 확인했다. 특히, 400aa 초과 면역원성 적용범위를 모든 세포주에 대해 RNA-seq 수준에서 또한 유지시켰다(도 2의 B).
- [0332] MSI 세포주에 대해 수득된 것에 대한 유사한 결과를 6개의 신선한 동결된 MSI 결장직장 암 매치된 생검(종양 및 정상 조직)의 진유전체 서열분석에 의해 수득하였다. 분석된 모든 환자의 경우, 면역원성 적용범위는 400 aa의 최소의 역치보다 더 높았으며, 평균 적용범위는 926 aa이었다. 6개 샘플 중 4개는 800 aa의 표적 역치를 초과하였다(도 3).
- [0333] 더욱이, Nous-209의 면역원성 잠재능을 평가하기 위하여, 본 발명자들은 MSI CRC 생검에서 백신-암호화된 FSP 중 얼마나 많은 것이 MHC-I 분자에 대해 양호한 결합 프로파일($IC_{50} \leq 500$ nM)을 지닌 에피토프를 생성할 것으로 예측되었는지를 계산하였다. 이러한 목표를 위해, 본 발명자는 우선 6명의 환자의 생검의 서열분석 데이터로부터 이들의 HLA 일배체형(haplotype)을 유도시켰다. 후속적으로, 본 발명자는 IEDB 소프트웨어(<http://www.iedb.org/>)를 사용하여 각각의 환자에 존재하는 백신-암호화된 FSP의 서브세트에 있어서 HLA-I-매치된 환자-특이적인 결합 예측을 수행하였다. 각각의 MSI 환자는 이들 자체의 HLA-I 일배체형을 결합시키는 것으로 예측된 평균 67개의 에피토프(최소 29, 최대 141)를 가졌다(도 4).
- [0334] 이와 함께, 이러한 결과는 높은 면역원성 적용범위가 MSI 세포주 및 원발성 종양 생검 둘 다에서, Nous-209에 포함된 서브세트와 같이, FSP의 서브세트를 통해 달성될 수 있음을 입증한다.
- [0335] 이후에, 본 발명자들은 Nous-209 내 FSP에 대한 면역원성 반응이 생체 내에서 측정될 수 있는지의 여부를 입증하였다. 이러한 목표를 위해, 본 발명자들은 HLA-A02⁺ 형질도입 마우스를 Nous-209 FSP의 서브세트로 면역화시켰다. 백신-유도된 면역 반응을, HLA-A02에 대한 결합 예측을 기반으로 이러한 FSP로부터 선택된 9량체를 사용하여 세포형광측정기(cytofluorimetry: FACS)로 평가하였다. 인터페론 γ (IFN- γ)에 대한 세포내 염색(ICS)에 의해 측정된 바와 같이, 도 5는 5마리의 동물에서 서열 번호 123에 상응하는 FSP로부터 유래된 HLA-A02 9량체에 대한 대표적인 CD8 T 세포 반응을 나타낸다(패널 A). 이러한 마우스 중 하나로부터 IFN- γ ⁺ CD8 T 세포에 대한 게이팅 전략의 FACS 플롯을 패널 B에 나타내며, 이는 FSP-반응성 T 세포의 유의적인 퍼센트(5.6%)를 나타낸다.
- [0336] **실시예 5: Nous-209에 대한 핵산 카세트의 작제**
- [0337] Nous-209에서 FSP를 4개의 서브세트로 분할하여 약 4500개 뉴클레오타이드의 길이의 인공 유전자를 생성하였으며, 각각은 다음의 바이러스 골격으로 클로닝하기에 적합한 약 1500 aa을 암호화한다: 유인원 아데노바이러스(GAd) 및 변형된 박시니아 안카라(Modified Vaccinia Ankara: MVA). 각각의 유전자를 임의의 링커의 부재하에 하나 그 뒤에 또 다른 것에 FSP 서열을 결합시킴으로써 조립하였다. 각각의 유전자가 실시예 3에 기술된 알고리즘에 따라 유사한 순위를 지닌 대략 동일한 수의 FSP를 함유할 수 있고 FSP를 함유할 수 있도록 보증하는 방식으로, 209개의 FSP를 4개의 유전자에 걸쳐 분포시켰으며 여기서 상응하는 FSM은 3개의 암 유형에 걸쳐 관찰된 빈도의 유사한 전체 분포를 갖는다. 이러한 과정은 다음을 생성하였다:
- [0338] 유전자 1 = 1507aa (46 FSPs)
- [0339] 유전자 2 = 1501aa (54 FSPs)
- [0340] 유전자 3 = 1506aa (59 FSPs)
- [0341] 유전자 4 = 1507aa (51 FSPs).
- [0342] 각각의 인공 유전자를 FSP의 상이한 순서에 상응하는 4개의 상이한 레이아웃(A, B, C 및 D)에서 조립하였다(표 2). 이중 프라임-부스트 백신접종 전략을 기반으로 하여, 레이아웃 A 및 C 내 유전자를 사용하여 GAd 벡터를 작제하였으며, 레이아웃 B 및 D 내 유전자는 MVA 골격에서 클로닝하였다. 레이아웃 A와 B 사이 및 레이아웃 C와 D 사이의 FSP의 스크램블링(scrambling)을 설계하여 인접한 FSP 사이에 동일한 접합 aa 서열을 암호화하는 GAd 및 MVA 둘다를 갖지 않도록 하였으며, 이는 접합 에피토프에 대해 면역 반응을 부스트할 수 있었다. 2개의 레이아웃 내 각각의 유전자에 대한 FSP의 순서를 선택하기 위하여, 본 발명자는 50,000개의 상이한 폴리펩타이드를 생성하는 과정을 사용하였으며 여기서 FSP는 무작위 순서로 결합된다. 이들 중에서, 본 발명자는 상이한 접합(junction)을 가지며, IUPRED 소프트웨어(Dosztanyi Z., *et al.* (2005) *Bioinformatics* 21, 3433)에 의해 평가된 바와 같이, 처음 50 aa 내에 무질서 서열(disordered sequence) (평균 무질서 경향성 >0.50) 을 지닌 2개

를 선택하였다(도 6). 후자의 선택은, 무질서한 N-말단이 프로테아좀에 의한 가공을 선호하므로, 따라서 MHC-I 분자에서 FSP-유래된 에피토프의 제시의 기회를 증가시켜야 한다는 개념을 기반으로 하였다. 후속적으로, 인공 폴리펩타이드를 사람 참고 단백질에 대한 유사성에 대해 가상환경(*in silico*)에서 스크리닝하여 사람 프로테오솜과 교차-반응성인 영역이 생성을 피하였다. 레이아웃 A, B, C 및 D에서 4개의 폴리-FSP 스트링의 aa 서열을, FSP의 상이한 순서에 상응하는 서열 번호 1088 내지 1091(레이아웃 A), 서열 번호 1092 내지 1095(레이아웃 B), 서열 번호 1155 내지 1158(레이아웃 C) 및 서열 번호 1159 내지 1162(레이아웃 D)로서 나열하였다(표 2). 이중 프라임-부스트 백신접종 전략을 기반으로, 레이아웃 A 및 C 내 유전자를 사용하여 GAd 벡터를 작제하였고, 레이아웃 B 및 D 내 유전자는 MVA 골격내에서 클로닝하였다. 레이아웃 A와 B 사이 및 레이아웃 C와 D 사이의 FSP의 스크램블링을 각각 설계하였다. 이들의 상응하는 nt 서열은 서열 번호 1096 내지 1099(레이아웃 A), 서열 번호 1100 내지 1103(레이아웃 B), 서열 번호 1163 내지 1166(레이아웃 C) 및 서열 번호 1167 내지 1170(레이아웃 D)이다.

[0343] 발현 카세트를 작제하기 위하여, 분류 신호(사람 조직 플라스미노겐 활성화인자 신호 펩타이드(hTPA; 서열 번호 1104) 또는 사람 불변 쇄(hINV; 서열 번호 1105)를 N-말단에 가하고, 각각의 폴리펩타이드 서열의 C-말단에 인플루엔자 HA-tag 서열(서열 번호 1106)을 가하였다(도 7). 이렇게 작제된 폴리펩타이드의 연장된 서열을 hTPA의 경우 서열 번호 1107 내지 1110(레이아웃 A), 서열 번호 1111 내지 1114(레이아웃 B), 서열 번호 1171 내지 1174(레이아웃 C) 및 서열 번호 1179 내지 1182(레이아웃 D)로, 및 hINV의 경우 서열 번호 1115 내지 1118(레이아웃 A), 서열 번호 1119 내지 1122(레이아웃 B), 서열 번호 1175 내지 1178(레이아웃 C) 및 서열 번호 1183 내지 1186(레이아웃 D)로 제공한다. 나타난 폴리-FSP 스트링을 생성하기 위한 상응하는 nt 서열을 사람 코돈 용도를 기반으로 코돈-최적화하였다(레이아웃 A의 경우 서열 번호 1123 내지 1126, 레이아웃 B의 경우 서열 번호 1127 내지 1130, 레이아웃 C의 경우 서열 번호 1187 내지 1190 및 hTPA를 지닌 레이아웃 D의 경우 서열 번호 1191 내지 1194; 레이아웃 A의 경우 서열 번호 1131 내지 1134, 레이아웃 B의 경우 서열 번호 1135 내지 1138, 레이아웃 C의 경우 서열 번호 1195 내지 1198 및 hINV를 지닌 레이아웃 D의 경우 서열 번호 1199 내지 1202). 또한, 코작 서열(CGCGACTTCGCCGCC)을 출발 코돈의 바로 상부에 위치시켜 효과적인 번역 개시를 허용하고 TAA 정지 코돈을 HA tag의 하부에 위치시켰다. 최종적으로, 카세트의 아-클로닝을 촉진시키는 고유의 제한 부위(unique restriction site)를 포함하는 2개의 플랭킹 분절을 뉴클레오타이드 서열의 5'- 및 3'-말단에 각각 가하였다(도 7). 인공 유전자를 나타내는 nt 서열(hTPA를 지닌, 레이아웃 A의 경우 서열 번호 1139 내지 1142, 레이아웃 B의 경우 서열 번호 1143 내지 1146, 레이아웃 C의 경우 서열 번호 1203 내지 1206 및 레이아웃 D의 경우 서열 번호 1207 내지 1210; hINV를 지닌, 레이아웃 A의 경우 서열 번호 1147 내지 1150, 레이아웃 B의 경우 서열 번호 1151 내지 1154, 레이아웃 C의 경우 서열 번호 1211 내지 1214 및 레이아웃 D의 경우 서열 번호 1215 내지 1218)을 표준 올리고뉴클레오타이드 합성 방법에 의해 생성시키고 TetO-CMV 프로모터(Tet 리프레서에 대한 결합 부위를 지닌 hCMV 프로모터)와 BGH(소 성장 호르몬) 폴리A 사이에 아-클로닝하였다.

표 2

레이아웃 A, B, C 및 D에서 유전자 1, 유전자 2, 유전자 3 및 유전자 4에 대한 조립된 폴리펩타이드의 FSP 조성물. 각각의 경우에 FSP의 서열 번호는 조립된 폴리펩타이드내 이들의 위치를 기반으로 한 목록이다(N-말단으로부터 C-말단까지).

1A	2A	3A	4A	1B	2B	3B	4B	1C	2C	3C	4C	1D	2D	3D	4D
58	183	135	57	58	183	135	57	70	11	126	128	55	183	139	161
93	103	172	113	18	92	49	177	58	39	49	161	42	100	184	73
178	92	40	9	51	100	172	113	42	150	184	177	149	11	125	54
18	106	139	25	174	71	8	78	118	100	8	148	87	199	206	67
180	100	168	54	127	79	147	148	110	90	135	83	74	150	209	177
129	3	8	155	141	194	44	33	1	35	125	50	1	187	208	33
63	199	126	121	55	187	197	21	102	162	152	169	14	47	176	5
102	86	192	128	14	52	107	161	145	59	36	54	170	159	160	89
87	195	91	82	118	23	156	17	149	43	197	13	63	117	107	140
42	47	143	189	102	3	204	165	182	203	160	57	101	167	16	157
166	154	49	193	1	19	139	181	101	31	32	37	70	116	99	108
101	7	131	140	10	195	137	45	166	71	95	140	102	35	32	181
22	15	95	205	62	117	176	193	186	75	68	113	22	124	147	155
30	123	202	61	22	94	28	54	2	7	53	205	26	109	156	169
2	194	60	5	170	154	208	157	18	195	192	17	18	75	188	121
51	115	80	153	74	179	80	136	55	123	12	108	182	142	91	50
151	138	107	148	166	7	202	37	190	207	107	77	118	207	4	77
145	117	99	97	145	106	188	155	141	167	209	89	30	115	168	144
127	159	24	161	66	199	184	89	93	199	28	136	114	162	48	104
62	116	197	33	93	146	88	29	34	116	84	132	133	203	172	82
186	150	20	13	186	86	76	25	10	47	98	165	66	195	68	148
74	167	81	21	114	15	200	50	129	94	139	29	38	71	36	132
70	79	28	29	110	159	32	173	66	86	176	67	145	130	40	113
14	179	152	177	42	167	40	205	127	142	196	155	51	7	49	153
133	109	160	37	46	35	60	69	30	194	44	5	129	31	76	65
46	27	164	41	87	116	4	67	85	52	131	158	166	59	95	165
38	43	206	67	34	142	131	153	105	79	201	73	34	123	200	189
174	35	204	50	178	124	20	120	14	154	204	185	190	92	204	61
141	52	188	69	30	198	201	108	151	163	206	153	174	79	53	9
66	142	53	108	38	123	119	158	180	117	156	61	85	86	60	120
149	162	208	73	2	43	160	97	114	106	16	189	110	163	131	41
190	163	209	77	129	130	24	128	87	138	168	82	105	90	119	45
1	94	12	78	105	150	168	41	174	130	164	25	58	52	175	17
110	203	44	83	133	162	125	73	63	179	64	181	127	103	112	193
55	75	137	89	182	191	196	144	38	146	208	121	46	179	143	69
10	11	36	96	85	115	91	82	46	187	72	69	2	198	192	37
118	59	196	104	180	39	95	83	51	27	99	78	178	111	24	25
85	23	48	45	70	207	81	132	170	124	188	157	10	43	126	83
114	124	64	120	26	56	12	189	22	15	20	144	151	27	20	57
170	56	72	65	149	109	164	104	62	92	147	9	62	194	28	185
182	198	156	132	63	111	175	13	133	103	112	96	93	19	98	96
26	191	98	136	151	103	98	77	178	3	60	41	6	146	202	205
105	19	76	144	101	75	206	9	6	111	137	65	180	15	152	29
6	130	119	157	190	47	143	185	26	171	4	45	141	134	197	21
34	187	147	158	6	138	209	121	74	23	48	33	186	23	88	128
	146	125	165		90	99	169		115	80	193		154	201	78
	71	176	17		27	72	65		109	172	21		39	72	173
	90	84	169		134	16	96		183	202	120		56	12	158
	207	200	173		203	36	5		191	76	104		106	81	136
	171	88	181		171	122	61		56	122	173		171	137	97
	111	112	185		163	126	140		134	40	97		138	164	13
	134	184			59	112			19	200			191	135	
	39	4			11	192			198	175			94	84	
	31	68			31	84			159	88			3	122	
		122				152				91				8	
		32				53				119				44	
		201				64				143				196	
		16				68				24				64	
		175				48				81				80	

[0344]

[0345] 실시예 6: 면역원성의 확인

[0346] 레이아웃 A(폴리펩타이드 서열 서열 번호 1107 내지 1110, 뉴클레오타이드 서열 서열 번호 1139 내지 1142) 내에 4개의 유전자를 함유하는 4개의 Gad 벡터(Gad20-209-FSP) 및 레이아웃 B (폴리펩타이드 서열 서열 번호 1111 내지 1114, 뉴클레오타이드 서열 서열 번호 1143 내지 1146) 내 4개의 유전자를 함유하는 4개의 MVA 벡터(MVA-209-FSPs)의 면역원성을 마우스(CB6F1 마우스 균주)에서 평가하였다. Gad20-209-FSP를, 영역 E3가 결실되고 영역 E1이 유전자에 의해 치환된 Gad20(서열 번호 1219)으로부터 작제하였다. 마우스를 Gad20-209-FSP의 단일 근육내 면역화에 의해 각각의 벡터에 대해 10⁸ 개의 바이러스 입자(vp)의 용량에서 면역화하고 2주 후 MVA-209-FSP에 의해 10⁷ 플라크 형성 단위(pfu)의 용량에서 부스트하였다. 백신 암호화된 FSP에 대한 T-세포 반응의 유도를, ELIspot 검정에 의해 209개의 FSP 서열을 커버하는 합성 펩타이드를 사용하여 측정하였다. 합성 펩타이드를 DMSO 속에 희석시키고 혼합하여 16개의 혼주물(pool)을 형성시켰다. 면역 반응(백만개의 비장세포당 인터

페론-감마(IFN- γ)를 생산하는 T 세포의 수)을 프라임 2주 후 및 부스트 1주 후 분석하였다. 데이터는, GAd20-209-FSP를 사용한 프라이밍 후 T-세포 매개된 면역 반응의 유도 및 MVA-209-FSP의 투여 후 수득된 면역 반응의 강력한 부스트를 나타낸다(도 8). 이들이 16개의 펩타이드 혼주물 각각에 대해 검출되므로, 반응은 백신 작제물에 걸쳐 분포된 다수의 FSP에 대한 것이었다(도 9). 중요하게도, 벡터 공-투여는 단일 벡터에 의해 암호화된 FSP에 대해 면역 반응에 영향을 미치지 않았고, 따라서 FSP의 백신 혼합물의 존재 하에서의 면역 간섭을 배제시켰다(도 10). 최종적으로, T 세포 반응의 품질을 2개의 펩타이드 혼주물(혼주물 1 및 혼주물3)를 사용하고 FSP-특이적인 CD4 및 CD8 IFN 감마+ T 세포의 유도를 나타냄으로써 세포내 염색(ICS)으로 평가하였다(도 11).

[0347] 실시예 4에 나타난 바와 같이, Nous-209 내에서 FSP에 대한 면역원성 반응이 또한 생체 내에서 측정될 수 있는지를 입증하였다. HLA-A02+ 형질도입 마우스를 Nous-209 FSP의 서브세트(30개의 FSP) 또는 DMSO 음성 대조군으로 면역화하였다. 백신-유도된 면역 반응을, HLA-A02에 대한 결합 예측을 기반으로 30개의 FSP로부터 선택된 9량체를 사용하여 세포플루오로측정법(FACS)으로 평가하였다. 도 11은 인터페론 γ (IFN- γ)에 대한 세포내 염색(ICS)에 의해 측정된 바와 같이(패널 A), FSP 서열 번호 123에 존재하는 HLA-A02 9량체에 대한 5마리의 동물에서 대표적인 CD8 T 세포 반응을 나타낸다. 이러한 마우스 중 하나로부터의 IFN- γ + CD8 T 세포에 대한 게이팅 전략의 FACS 플롯을 패널 B에 묘사하며, 이는 FSP-반응성 T 세포의 유의적인 퍼센트(5.6%)를 나타낸다.

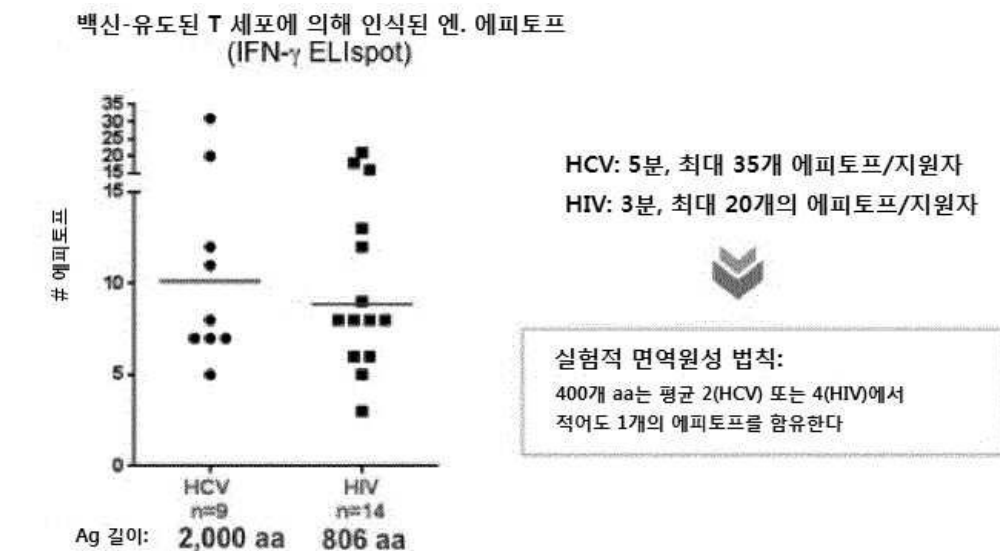
[0348] 이와 함께, 이러한 결과는 다음을 입증한다:

[0349] i) 작제물이 고도로 면역원성이며 CD4 및 CD8 면역 반응을 유도한다. ii) 면역 반응은 16개의 상이한 펩타이드 혼주물에 대해 지시되므로 적어도 16개의 상이한 에피토프(각각의 혼주물에 대해 1개)를 인식한다. 근친교배된 마우스(실제로 유전적으로 동일한 마우스)에서조차, 400개 aa에서의 적어도 하나의 에피토프의 규칙이 확인됨을 나타내는데, 이는 백신의 6000개 aa에 걸쳐 16개의 에피토프를 가지는 것이 평균적으로 375개 aa내에서 적어도 하나의 면역원성 에피토프에 상응하기 때문이다.

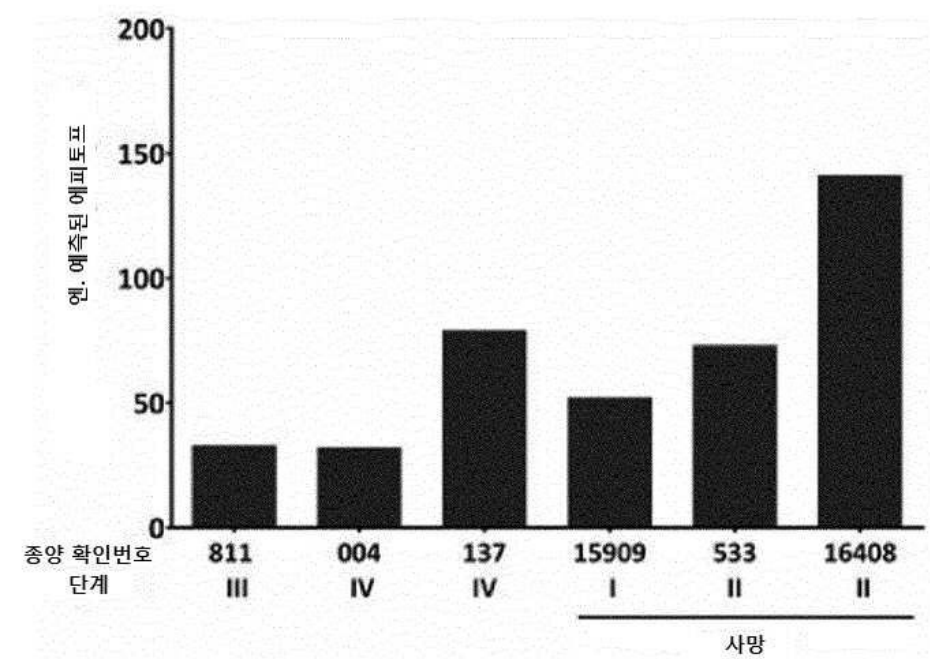
[0350] iii) 벡터 1이 단독으로 사용되거나 다른 3개의 벡터와 조합된 것에 상관없이, 벡터 1 암호화된 항원에 대한 비교할만한 면역 반응이 측정되므로 명백한 간섭 효과, 특히 개개 벡터 사이에 억제 존재하지 않는다. 유사하게, 벡터 2가 단독으로 사용되거나 다른 3개와 조합되는 것에 상관없이, 벡터 2 암호화된 항원에 대한 비교할만한 면역 반응이 측정되었다.

도면

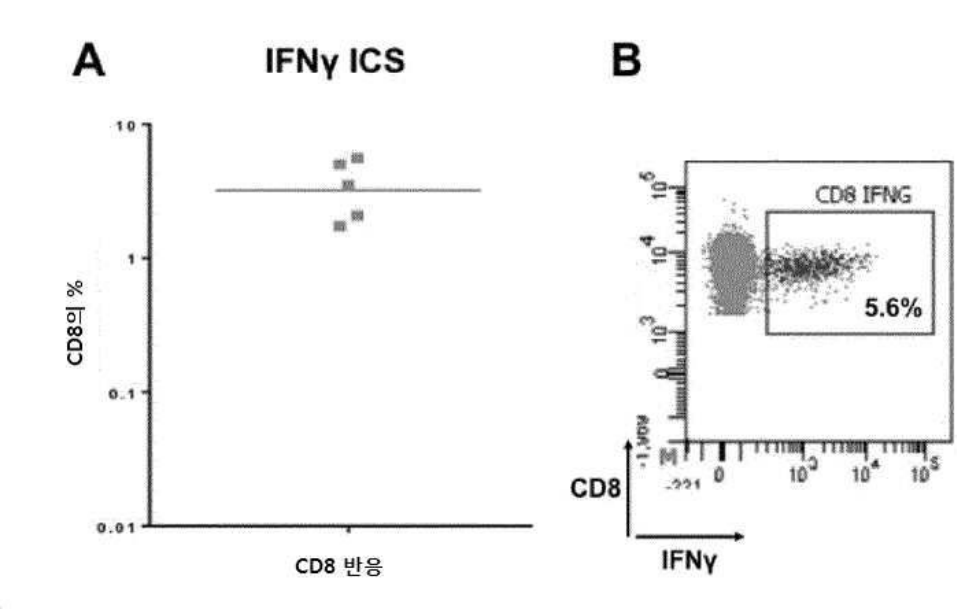
도면1



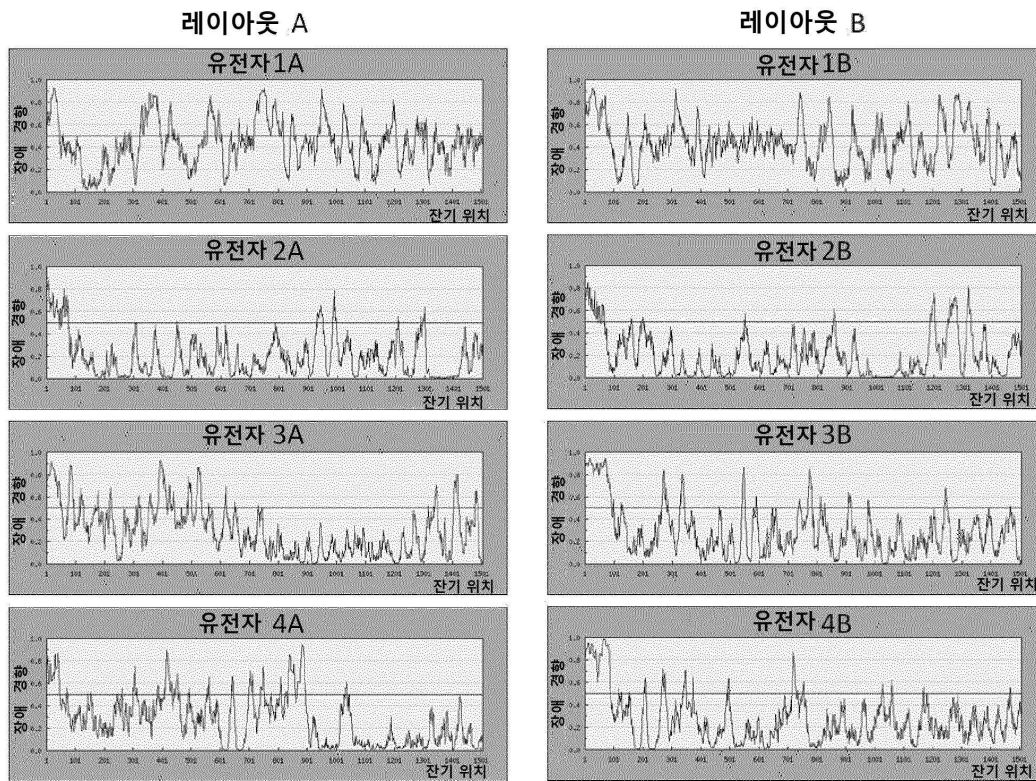
도면4



도면5



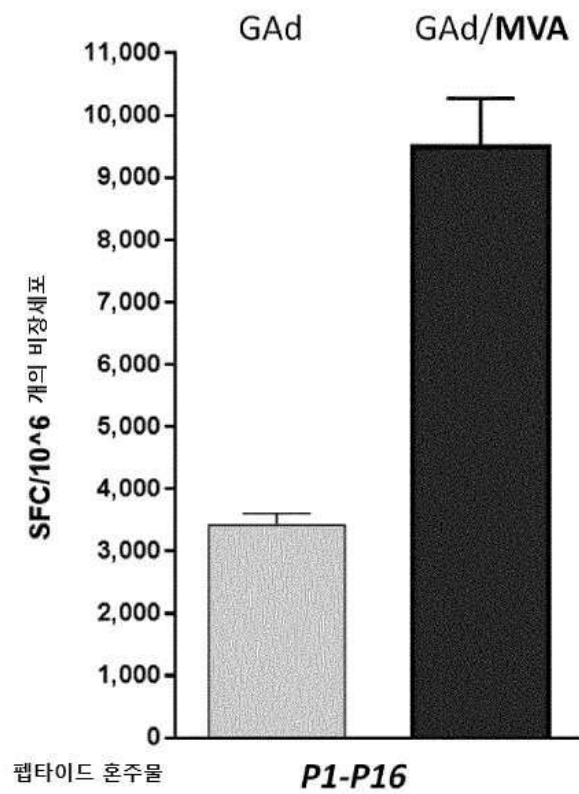
도면6



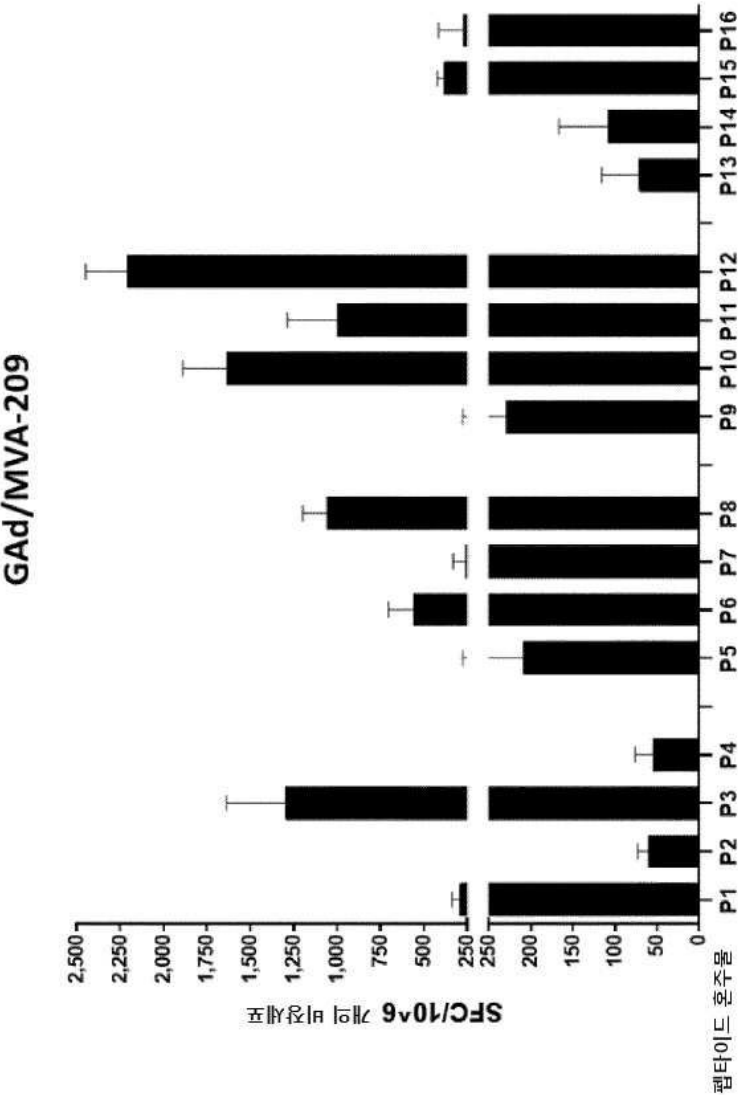
도면7



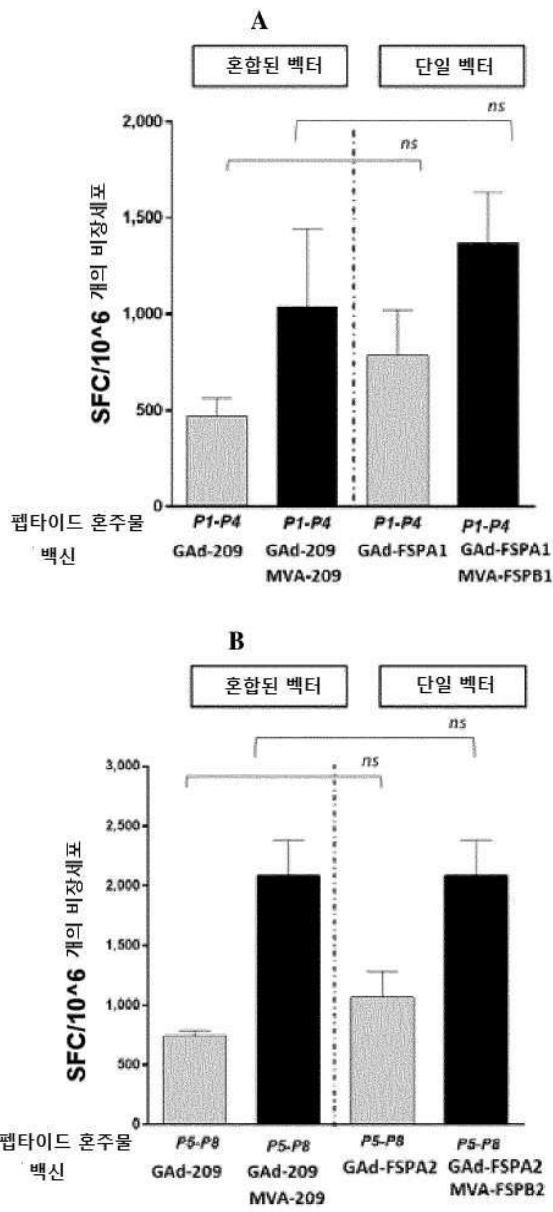
도면8



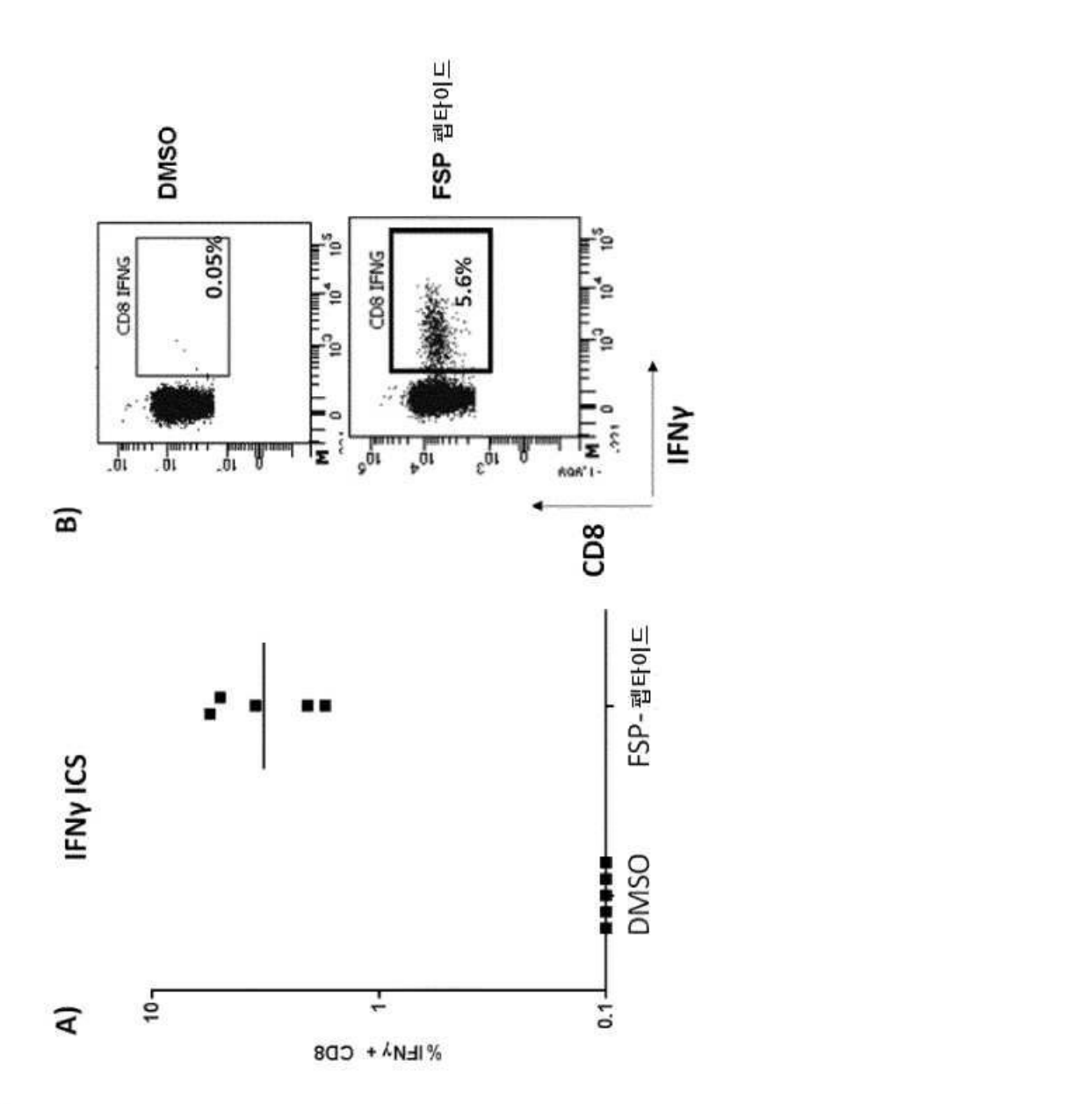
도면9



도면10



도면11



서열 목록

SEQUENCE LISTING

<110> NOUSCOM AG

<120> A UNIVERSAL VACCINE BASED ON SHARED TUMOR NEOANTIGENS FOR
PREVENTION AND TREATMENT OF MICRO SATELLITE INSTABLE (MSI) CANCERS

<130> IPA191630-DE

<150> EP 17181026.0

<151> 2017-07-12

<160> 1219

<170> PatentIn version 3.5

<210> 1

<211> 154

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1

Val Gly Ala Gly Thr Gly Gly Gly Pro Ala Cys Val Pro Val Ala Glu

1 5 10 15

Ala Ser Thr Gly Ala Trp Thr Ala Glu Gly Ala Ala Gly Thr Arg Cys

20 25 30

Arg Ala Ser Arg Ala Pro Cys Arg Gln Leu Pro Ala Ser Ser Pro Thr

35 40 45

Lys Cys Glu Ile Cys Val Lys Arg Arg Arg Arg Arg Lys Arg Ser Ser

50 55 60

Gln Ser Arg Ser Pro Val Pro Lys Lys Arg Glu Arg Met Met Leu Pro

65 70 75 80

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

85 90 95

Leu Glu Gly Met Leu Leu Pro Arg Ala Leu Pro Ser Leu Leu Ser Arg

100 105 110

Met Pro Ala Arg Arg Glu Ser Arg Phe Trp Leu Ala Leu Gln Ala Leu

115 120 125

Gly Leu Arg Pro Pro His Leu Pro Ser Cys His Pro Leu Pro Gln Leu

130 135 140

Leu Gly Pro Pro Pro Pro His Gln Ala Pro

145 150

<210> 2

<211> 74

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 2

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

1 5 10 15

Leu Ile Thr Pro Gln Asp Pro His Leu Asp Pro Val Cys His Pro His

20 25 30

Arg Arg Pro Gly Trp Lys Gly His His Arg Val Val Phe Ser His His

35 40 45

Pro Ser Gly Ser Thr Lys Ser His Trp Gln Gln Arg Glu Arg Gly Gly

50 55 60

Gly Arg Arg Glu Lys Lys Gly Cys Arg Glu

65 70

<210> 3

<211> 8

<212> PRT

<213> Homo sapiens

<400> 3

Gly Gly Lys Lys Arg Ser Lys Phe

1 5

<210> 4

<211> 8

<212> PRT

<213> Homo sapiens

<400> 4

Val His Lys Lys Arg Gly Leu Phe

1 5

<210> 5

<211> 40

<212> PRT

<213> Homo sapiens

<400> 5

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

1 5 10 15

Thr Gln Leu Ala Arg Phe Phe Pro Ile Thr Pro Pro Val Trp His Ile

20 25 30
 Leu Gly Pro Gln Arg His Thr Pro
 35 40
 <210> 6
 <211> 44
 <212> PRT
 <213> Homo sapiens
 <400> 6
 Gln Pro Ser Leu Pro Gly Pro Cys Ala Ser Leu Leu Ser Thr Leu Ser

1 5 10 15
 Gln Pro Pro Pro Gln Ala Pro Ser Gln Val Trp Thr Ala Ala Thr Leu
 20 25 30
 Arg Cys Pro Ala Val Pro Ala Ala Ala Cys Pro Pro
 35 40
 <210> 7
 <211> 31
 <212> PRT
 <213> Homo sapiens
 <400> 7
 Arg Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro Gln Ala

1 5 10 15
 Arg Leu Cys Leu Ile Val Ser Arg Thr Leu Leu Leu Val Gln Ser

20 25 30
 <210> 8
 <211> 21
 <212> PRT
 <213> Homo sapiens
 <400> 8
 Arg Asn Ser Arg Arg Ala Thr Pro Thr Ser Lys Gly Ser Leu Arg Arg
 1 5 10 15
 Lys Tyr Leu Arg Val

20
 <210> 9

<211> 8

<212> PRT

<213> Homo sapiens

<400> 9

Val Leu Lys Lys Asn Arg Lys Gln

1 5

<210> 10

<211> 10

<212> PRT

<213> Homo sapiens

<400> 10

Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu

1 5 10

<210> 11

<211> 12

<212> PRT

<213> Homo sapiens

<400> 11

Arg Gln Ile Asn Arg Arg Lys Leu Gln Arg Lys Lys

1 5 10

<210> 12

<211> 32

<212> PRT

<213> Homo sapiens

<400> 12

Arg Gly Pro Arg Arg Lys Val Leu Met Val Leu Trp Leu Pro Ala Asn

1 5 10 15

Gln Ser Leu Gln Lys Ser Gln Val Phe Gln Trp Val Leu Arg Thr Glu

20 25 30

<210> 13

<211> 11

<212> PRT

<213> Homo sapiens

<400> 13

Cys Arg Cys Arg Arg Glu Tyr Arg Val Thr Met

1 5 10

<210> 14

<211> 38

<212> PRT

<213> Homo sapiens

<400> 14

Gly Glu Lys Asn Asp Leu Gln Leu Phe Val Met Ser Asp Thr Thr Tyr

1 5 10 15

Lys Ile Tyr Trp Thr Val Ile Leu Leu Asn Pro Cys Gly Asn Leu His

20 25 30

Leu Lys Thr Thr Ser Leu

35

<210> 15

<211> 25

<212> PRT

<213> Homo sapiens

<400> 15

Arg Asn Lys Lys Thr Lys Leu Trp Phe Ser Leu Ile Asn Ile His His

1 5 10 15

Arg Lys Asn Pro Leu Leu Pro Met Arg

20 25

<210> 16

<211> 26

<212> PRT

<213> Homo sapiens

<400> 16

Thr Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg Ala Arg

1 5 10 15

Gly Gly Thr Thr Ile Gly Glu Val Thr Ser

20 25

<210> 17

<211> 27
 <212> PRT
 <213> Homo sapiens
 <400> 17
 Asn Leu His Leu Cys Tyr Tyr His Ser Gln Ser Asn Arg Asn Lys Ser
 1 5 10 15
 Arg Gln Met Glu Ser Leu Gly Met Lys Leu Gln
 20 25

<210> 18
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 18
 Met Pro Ser Ser Trp Ser Ser Ser Gly Arg Thr
 1 5 10

<210> 19
 <211> 10
 <212> PRT
 <213> Homo sapiens
 <400> 19
 Pro Gly Thr Ser Leu Gln Cys Tyr Leu Asn
 1 5 10

<210> 20
 <211> 27
 <212> PRT
 <213> Homo sapiens
 <400> 20
 Lys Gly Lys Asn Ser Pro Cys Cys Gln Lys Lys Leu Arg Val Gln Asn
 1 5 10 15

Gln Gly His Leu Leu Met Ile Leu Leu His Asn
 20 25
 <210> 21
 <211> 17
 <212> PRT

<213> Homo sapiens

<

<400> 21

Asn Ile Leu Asn Ser Leu Pro Ser Ser Met Glu Ile Ala Val Leu Gln

1 5 10 15

Glu

<210> 22

<211> 11

<212> PRT

<213> Homo sapiens

<400> 22

Asn Met Gly Gly Asn Arg Ser Ile Cys Leu Thr

1 5 10

<210> 23

<211> 17

<212> PRT

<213> Homo sapiens

<400> 23

Glu Leu Ser Leu Glu Pro Trp Ile Pro Tyr Leu His Gln Gln Lys Thr

1 5 10 15

Gln

<210> 24

<211> 73

<212> PRT

<213> Homo sapiens

<400> 24

Phe Leu Ile His Leu Arg Lys Val Asp Thr His His Leu Gln Val Val

1 5 10 15

Thr Lys Thr Val Thr Ala Thr Thr Ala Asp Gly Gln Arg Met Arg Arg

20 25 30

Leu Lys Cys Lys Ala Cys Arg Leu Arg Trp Ala Arg Pro Glu Pro Ala

35 40 45

Ala Gln Ala Pro Pro Lys Ser His Phe Pro Pro His Pro Ser Gly Pro

50 55 60

Ser Arg Thr Ser Ser Leu Gln Leu Arg

65 70

<210> 25

<211> 11

<212> PRT

<213> Homo sapiens

<400> 25

Glu Trp Gly Gly Gln Ala His Arg Gln Arg Asn

1 5 10

<210> 26

<211> 10

<212> PRT

<213> Homo sapiens

<400> 26

Ile Val Phe Phe Leu Ala Pro Tyr Phe Pro

1 5 10

<210> 27

<211> 9

<212> PRT

<213> Homo sapiens

<400> 27

Pro Lys Phe Phe Leu Thr Phe Ser Gln

1 5

<210> 28

<211> 77

<212> PRT

<213> Homo sapiens

<400> 28

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

1 5 10 15

Met Ala Pro Val Gly Ser Val Met Ser Cys Ser Leu Leu Thr Gln Pro

20 25 30
Ser Pro Ala Ser Ala Cys Thr Met Pro Pro Leu Leu His Pro Gln Trp
35 40 45

Ala Pro His Ser Ala Gly Leu Ser Pro Gly Ala Cys Arg Pro Ala Cys
50 55 60

Thr Cys Ile Ser Met Thr Thr Ile Ser Arg Ala Thr Trp

65 70 75

<210> 29

<211> 11

<212> PRT

<213> Homo sapiens

<400> 29

Thr Ala Lys Lys Ser Pro Thr Ser Phe Cys Cys

1 5 10

<210> 30

<211> 38

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<

400> 30

Arg Lys Arg Lys Arg Glu Lys Arg Ser Gln Lys Ser Arg Gln Asn His

1 5 10 15

Leu Gln Leu Lys Ser Cys Arg Arg Lys Ile Ser Asn Trp Ser Lys Leu

20 25 30

Arg Ser Pro Trp Ile Phe

35

<210> 31

<211> 18

<212> PRT

<213> Homo sapiens

<400> 31

Arg His Pro Ser Trp Pro Trp Thr Arg Cys Leu Arg Met Arg Pro Pro

1 5 10 15

Arg Ser

<210> 32

<211> 16

<212> PRT

<213> Homo sapiens

<400> 32

Ser Asn Gly Met Glu Ala Cys Gly Thr His Pro Thr Pro Arg Leu Ser

1 5 10 15

<210> 33

<211> 30

<212> PRT

<213> Homo sapiens

<400> 33

Arg Ala Ser Val Ser Phe Trp Thr Leu Leu Pro Thr Thr Gly Val Arg

1 5 10 15

Thr Arg Gly Ser Pro Leu Arg Leu Thr Leu Trp Pro Pro Arg

20 25 30

<210> 34

<211> 53

<212> PRT

<213> Homo sapiens

<400> 34

Ala Leu Arg Ser Met Pro Lys Ser Arg Asn Gln Val Leu Phe Arg Arg

1 5 10 15

Asn Leu Thr Pro Ser Gln Leu Arg Thr Leu Ala Pro Pro Tyr Met Leu

20 25 30

Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser Arg Lys Gln Ile Pro Ser

35 40 45

Gln Ser Met Leu Val

50

<210> 35

<211> 34

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 35

Leu Gln Ala His Pro Gln Val Pro Ala Leu Ala Pro Gln Ala Trp Trp

1 5 10 15

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

20 25 30

Leu Thr

<210> 36

<211> 27

<212> PRT

<213> Homo sapiens

<400> 36

Cys Thr Asn Leu Ser Val Pro Met Met Leu Thr Ile Leu Ile Trp Lys

1 5 10 15

Arg Val Phe Ile Leu Leu Leu Ser Asp Lys Lys

20 25

<210> 37

<211> 9

<212> PRT

<213> Homo sapiens

<400> 37

Pro Leu Phe Phe His Gly Asp Leu Cys

1 5

<210> 38

<211> 9

<212> PRT

<213> Homo sapiens

<400> 38

Val Ser Lys Lys Arg Leu Pro Lys Leu

1 5
 <210> 39
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 39
 Arg Arg Lys Lys Arg Glu Asp His Cys Gly Leu

1 5 10

<210> 40
 <211> 17
 <212> PRT
 <213> Artificial Sequence
 <220><223> modified Homo sapiens FSP

<400> 40
 Cys Leu Arg Val Arg Cys Gly Gly Trp Leu Cys Gly Trp Thr Pro Arg

1 5 10 15

Gly

<210> 41
 <211> 16
 <212> PRT
 <213> Homo sapiens
 <400> 41

Arg Glu Ser Thr Leu Gly Asn Phe Trp Met Lys Leu Leu Gln Leu Pro

1 5 10 15

<210> 42
 <211> 10
 <212> PRT
 <213> Homo sapiens
 <400> 42

Ala Ser Ser Pro Gly His Pro Leu Gly Pro

1 5 10

<210> 43

<211> 56

<212> PRT

<213> Homo sapiens

<400> 43

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

1 5 10 15

Cys Ser Ser Trp Leu Met Lys Gln Thr Trp Met Lys Ser Trp Ser Leu

20 25 30

Arg Asp Pro Ser Tyr Arg Ser Ile Leu Glu Tyr Val Ser Thr Arg Val

35 40 45

Leu Trp Met Pro Thr Ser Thr Val

50 55

<210> 44

<211> 31

<212> PRT

<213> Homo sapiens

<400> 44

Asn Ile Arg Lys Leu Ile Trp Thr Lys Gln Arg Ser Phe Leu Ser Leu

1 5 10 15

Phe Pro Lys Leu Arg Ala Thr Glu Gln Met Thr Asn Val Gly Cys

20 25 30

<210> 45

<211> 11

<212> PRT

<213> Homo sapiens

<400> 45

Val Val Ile Asn Leu Lys Arg Leu Gln Lys Phe

1 5 10

<210> 46

<211> 39

<212> PRT

<213> Homo sapiens

<400> 46

Asn Gly Ile Trp Glu Val Met Pro Arg Thr Leu Glu Gly Cys Ile Ser

1 5 10 15

Val Lys Asp His Arg Thr Ser Gln Asn His Ser Lys Cys Ile Thr Glu

20 25 30

Cys Val Arg Thr Ala Leu Asn

35

<210> 47

<211> 13

<212> PRT

<213> Homo sapiens

<400> 47

Arg Arg Lys Trp Gln Ile Arg His Val Leu Lys Asn Leu

1 5 10

<210> 48

<211> 18

<212> PRT

<213> Homo sapiens

<400> 48

His Gln Met Lys Cys Leu Thr Ala Val Asp Cys Leu Gln Ala Phe Trp

1 5 10 15

Asp Met

<210> 49

<211> 11

<212> PRT

<213> Homo sapiens

<400> 49

Lys Asn Lys Lys Arg Arg Lys Leu Arg Pro Lys

1 5 10

<210> 50

<211> 28

<212> PRT

<213> Homo sapiens

<400> 50

Thr Gly Met Glu Ile Leu Leu Trp Ile Leu Leu Lys Met Glu Ile Gln

1 5 10 15

Ile Phe Lys Ile Cys Leu Gly Glu Met Gln Leu Cys

20 25

<210> 51

<211> 43

<212> PRT

<213> Homo sapiens

<400> 51

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

1 5 10 15

Asp Gly Ile Thr Asn Gly Asn Asp Ser Thr Arg Ser Cys Ser Ile Ser

20 25 30

Leu Lys Lys Ser Leu Glu Lys Met Pro Leu Met

35 40

<210> 52

<211> 20

<212> PRT

<213> Homo sapiens

<400> 52

Arg Glu Lys Ile Ile Asn Pro Thr Ile Ser Cys Pro Phe Gln Ser Pro

1 5 10 15

Thr Lys Arg Leu

20

<210> 53

<211> 62

<212> PRT

<213> Homo sapiens

<400> 53

Arg Glu Trp Glu Lys Arg Lys Gln Ile Leu Gly Gly Gly Lys Tyr

1 5 10 15

Lys Glu Tyr Phe Leu Lys Arg Ile Leu Ile Arg Lys Ala Met Thr Val

20 25 30
Leu Ala Gly Asp Lys Lys Gly Leu Gly Arg Phe Met Arg Cys Val Gln

35 40 45
Ser Glu Thr Lys Ala Val Ser Leu Gln Leu Pro Leu Gly Arg

50 55 60

<210> 54

<211> 8

<212> PRT

<213> Homo sapiens

<400>

54

Asn Ala Lys Lys Met Pro Phe Gln

1 5

<210> 55

<211> 8

<212> PRT

<213> Homo sapiens

<400> 55

Ala Asp Lys Lys Asn Val Arg Ser

1 5

<210> 56

<211> 12

<212> PRT

<213> Homo sapiens

<400> 56

Gln Glu Lys Lys Ser Arg Lys Leu Met Ser Ser Cys

1 5 10

<210> 57

<211> 8

<212> PRT

<213> Homo sapiens

<400> 57

Ile Gln Lys Lys Lys Gln Lys Ser

1 5

<210> 58

<211> 43

<212> PRT

<213> Homo sapiens

<400> 58

Thr Glu Ile Gln Leu Thr Met Asn Asp Ser Lys His Lys Leu Glu Ser

1 5 10 15

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

20 25 30

Gln Thr Pro Gln Asp Ser Arg Gln Val Leu Ala

35 40

<210> 59

<211> 46

<212> PRT

<213> Homo sapiens

<400> 59

His Trp Asn Ser Ala Tyr Leu Gly Arg Thr Leu Leu Val Thr Cys Ile

1 5 10 15

Leu Tyr His Arg Trp Ile Val Thr Ser Met Cys Gln Ser Gln Arg Trp

20 25 30

Leu Thr Ser Thr Thr Ser Arg Ser Ser Ala Leu Met Trp Thr

35 40 45

<210> 60

<211> 13

<212> PRT

<213> Homo sapiens

<400> 60

Arg Lys Ser Gly Val Met Lys Cys Trp Asp Leu Cys Pro

1 5 10

<210> 61

<211>

> 13

<212> PRT

<213> Homo sapiens

<400> 61

Cys Gln Lys Lys Val Pro Ser Ala Ser Pro Trp Gly Leu

1 5 10

<210> 62

<211> 10

<212> PRT

<213> Homo sapiens

<400> 62

Arg Leu Pro Cys Lys Val Thr Glu Ser Ser

1 5 10

<210> 63

<211> 15

<212> PRT

<213> Homo sapiens

<400> 63

Asn Gln Gln Leu Lys Trp Thr Pro His Ile Leu Lys Ser Ala Ser

1 5 10 15

<210> 64

<211> 22

<212> PRT

<213> Homo sapiens

<400> 64

Asn Met Glu His Arg Leu Thr Met Asp Ser Ala Leu Ser Leu Thr Lys

1 5 10 15

Arg Glu Gly Pro Glu Thr

20

<210> 65

<211> 22

<212> PRT

<213> Homo sapiens

<400> 65

Pro Ala Cys Thr Ser Lys Ala Trp Thr Pro Arg Lys Leu Val Gly Arg

1 5 10 15

Ala Val Arg Arg Lys Gly

20

<210> 66

<211> 12

<212> PRT

<213> Homo sapiens

<400> 66

Phe Lys Lys Lys Lys Pro Leu Thr Phe Ser Pro Ser

1 5 10

<210> 67

<211> 8

<212> PRT

<213> Homo sapiens

<400> 67

Gln Arg Pro Pro Leu Gln Pro Val

1 5

<210> 68

<211> 8

<212> PRT

<213> Homo sapiens

<400> 68

Leu Lys Lys Lys Tyr Leu Val Gln

1 5

<210> 69

<211> 50

<212> PRT

<213> Homo sapiens

<400>

> 69

Thr Ser Arg Ile Leu Asn Leu Gln Val Leu Lys Lys Ile Leu Arg Ser

1 5 10 15

Phe Met Lys Leu Tyr His Ser Leu Val Met Cys Leu Arg Leu Arg Thr

20 25 30

Lys Leu Glu Lys Ala Leu Ser Ala Leu Phe Ile Trp Pro Gln His Ser

35 40 45

Tyr Lys

50

<210> 70

<211> 40

<212> PRT

<213> Homo sapiens

<400> 70

Ser Thr Arg Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro Gly

1 5 10 15

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

20 25 30

Leu Arg Leu Arg Asn Thr Ser Pro

35 40

<210> 71

<211> 16

<212> PRT

<213> Homo sapiens

<400> 71

Asn Ser Arg Lys Lys Leu Leu Glu Asp Met Lys Gln Asn Gly Phe Thr

1 5 10 15

<210> 72

<211> 10

<212> PRT

<213>

> Homo sapiens

<400> 72

Cys Lys Lys Lys Leu Leu Leu Lys Leu Leu

1 5 10

<210> 73

<211> 11

<212> PRT

<213> Homo sapiens

<400> 73

Asp Lys Lys Lys Lys Ser Thr Glu Lys Thr Lys

1 5 10

<210> 74

<211> 32

<212> PRT

<213> Homo sapiens

<400> 74

Thr Pro Leu Ser Ile Ser Arg Pro Thr Ser Arg Ala Arg Gln Ser Cys

1 5 10 15

Cys Leu Pro Gly Leu Thr His Pro Ala His Gln Pro Leu Gly Ser Met

20 25 30

<210> 75

<211> 11

<212> PRT

<213> Homo sapiens

<400> 75

Arg Tyr Lys Lys Arg Gly Val Ile Ala Trp Arg

1 5 10

<210> 76

<211> 8

<212> PRT

<213> Homo sapiens

<400> 76

His Leu Lys Lys Thr Ser Ala Lys

1 5

<210> 77

<211> 15

<212> PRT

<213> Homo sapiens

<400> 77

Gly Gln Ala Phe Gly Ser Phe Ser Ala Asp Phe Ser Ala Pro Gln

1 5 10 15

<210> 78

<211> 31

<212> PRT

<213> Homo sapiens

<400> 78

Gly Gln Ala Phe Gly Ser Leu Cys Gln Leu Val Ser Ala Asp Phe Ser

1 5 10 15

Ala Pro Gln Val Thr Arg Leu Arg Ser Leu Asn His Leu Leu Ile

20 25 30

<210> 79

<211> 19

<212> PRT

<213> Homo sapiens

<400> 79

Gly His Arg Glu Gly Ser Glu Ser Asp Asn Leu Gly Leu Leu Tyr Ser

1 5 10 15

Phe Pro Pro

<210> 80

<211> 8

<212> PRT

<213> Homo sapiens

<400> 80

Ser Glu Lys Lys Arg Lys Leu Pro

1 5

<210> 81

<211> 62

<212> PRT

<213> Homo sapiens

<400> 81

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

1 5 10 15

Leu Pro Lys Leu Leu Cys Arg Gln Met Leu Pro Thr Leu Ser Thr Leu

20 25 30

Gln Gln Arg His Pro Gln Gly Pro Cys Pro Pro Pro Val Thr Pro Leu

35 40 45
 Arg Val Gln Ser Val Leu Leu Leu Gly Val Pro Gln Thr Ala
 50 55 60
 <210> 82
 <211> 62
 <212> PRT
 <213> Homo sapiens
 <400> 82
 Met Cys Ser Ser Leu Ala Leu Pro Thr Gly Leu Thr Ser Leu Ile Leu
 1 5 10 15
 Pro Ser Ser Asp Leu Ala Val Leu Ile Ser Ser Ser Thr Ser His Phe
 20 25 30
 Leu Met Arg Ser Pro Val Leu Pro Ser Ser Arg Leu Thr Cys Ala Ser
 35 40 45
 Pro Gln Leu Pro Arg Met Trp Thr Trp Ser Ser Trp Leu Lys
 50 55 60
 <210> 83
 <211> 14
 <212> PRT
 <213> Homo sapiens
 <400> 83
 Trp Leu Lys Asn Trp Lys Arg Phe Lys Leu Lys Lys Lys Tyr
 1 5 10
 <210> 84
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 84
 Arg Arg Asn Leu Gln Arg Asn Leu Lys Val Leu
 1 5 10
 <210> 85
 <211> 155
 <212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 85

Tyr Pro Arg Leu Lys Thr Phe Gly Val Pro Leu Gly Ser Ile Leu Cys

1 5 10 15

Leu Ala Gly Ser Leu Ser Thr Met Met Ile Ile Ser Thr Thr Arg Gln

20 25 30

Glu Cys Gly Arg Arg Ala Ser Val Pro Cys Arg Pro Met Ile Gly Ser

35 40 45

Ala Arg Pro Gly Pro Trp Arg Thr Ser Ala Met Pro Ser Ala Met Gly

50 55 60

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

65 70 75 80

Gly Gly Arg Met Pro Gly Ser Gln Ser Ile Met Met Ser Trp Met Pro

85 90 95

Pro Leu Ala Pro Cys Ala Ala Cys Pro Cys Ser Pro Ala Pro Thr Leu

100 105 110

Cys Pro Ala His Pro Ala Arg Ala Pro Thr Ala Val Pro Ala Phe Thr

115 120 125

Pro Leu Ser Ala His Pro Val Pro Val Leu Ser Gly Cys His Leu Ala

130 135 140

Val Arg Thr Ser Met Leu Thr Leu Leu Pro Met

145 150 155

<210> 86

<211> 15

<212> PRT

<213> Homo sapiens

<400> 86

Val Leu Phe Lys Ala Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly

1 5 10 15

<210> 87

<211> 13

<212> PRT

<213> Homo sapiens

<400> 87

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

1 5 10

<210> 88

<211> 10

<212> PRT

<213> Homo sapiens

<400> 88

Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe

1 5 10

<210> 89

<211> 19

<212> PRT

<213> Homo sapiens

<400> 89

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

1 5 10 15

Phe Gly Ser

<210> 90

<211> 50

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 90

Gly Lys Gly Leu Thr His Pro Val Pro Leu Lys Arg Thr Leu Gln Asn

1 5 10 15

Lys Arg Asn Lys Asn Ile Lys Arg Val Asn Gln Lys Lys Gly Asn Ile

20 25 30

Lys Arg Lys Ser Ile Leu Leu His Leu Ile Val Leu Asn Ser Pro Glu

35 40 45

Ser Asn

50

<210> 91

<211> 13

<212> PRT

<213> Homo sapiens

<400> 91

Thr Pro Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala Pro

1 5 10

<210> 92

<211> 10

<212> PRT

<213> Homo sapiens

<400> 92

Met Ser Arg Thr Pro Pro Arg Arg Val Cys

1 5 10

<210> 93

<211> 8

<212> PRT

<213> Homo sapiens

<400> 93

Leu Ala Lys Lys Thr Leu Thr Asn

1 5

<210> 94

<211>

32

<212> PRT

<213> Homo sapiens

<400> 94

Pro Leu Glu Asn Thr Gln Ile Pro Arg Thr Ser Pro Leu Trp Lys Ile

1 5 10 15

Thr Met Val Leu Thr Tyr Pro Asn Cys Val Val His Val Leu Met Phe

20 25 30

<210> 95

<211> 30

<212> PRT

<213> Homo sapiens

<400> 95

Val Ser Val Ile Thr Met Lys Leu Trp Glu Lys His Phe Lys Gly Leu

1 5 10 15

Asn Trp Asn Leu Val Val Trp Ile Leu Asn Leu Lys Met Met

20 25 30

<210> 96

<211> 23

<212> PRT

<213> Homo sapiens

<400> 96

Ile Ile Cys Ile Lys Asn Met Phe Leu Gln Arg Lys Gly Phe Leu Asn

1 5 10 15

Leu Ser His Val Glu Lys Phe

20

<210> 97

<211> 12

<212> PRT

<213> Homo sapiens

<400> 97

Leu Lys Lys Lys Pro Arg Asp Ile Cys Arg Ile Ser

1 5 10

<210> 98

<211> 12

<212> PRT

<213> Homo sapiens

<400> 98

Arg Leu Arg Ile Pro Ser Leu Arg Lys Tyr Arg Gln

1 5 10

<210> 99

<211> 30

<212> PRT

<213> Homo sapiens

<400> 99

Arg Gly Ala Ser Ser Ser Thr Ser Arg Asp Ser Arg Ser Phe Phe Thr

1 5 10 15

Ser Ala His Pro Ser Arg Pro Cys Arg Met Arg Leu Tyr Gln

20 25 30

<210> 100

<211> 24

<212> PRT

<213> Homo sapiens

<400> 100

Asn Pro Arg Arg Lys Thr Trp Lys Met Arg Lys Lys Tyr Ala Gln Lys

1 5 10 15

Pro Ser Gln Lys Asn His Leu Tyr

20

<210> 101

<211> 11

<212> PRT

<213> Homo sapiens

<400> 101

Ile Ala Lys Lys Arg Ile Lys Leu Arg Arg Asn

1 5 10

<210> 102

<211> 10

<212> PRT

<213> Homo sapiens

<400> 102

Phe Asp Lys Lys Gly Phe Val Ile Leu Ser

1 5 10

<210> 103

<211> 12

<212> PRT

<213> Homo sapiens

<400> 103

Gly Ser Pro Pro Leu His Leu Cys Gln Pro Leu Arg

1 5 10

<210> 104

<211> 9

<212> PRT

<213> Homo sapiens

<400> 104

Glu Leu Lys Lys Asn Leu Leu Leu Pro

1 5

<210> 105

<211> 77

<212> PRT

<213> Homo sapiens

<400> 105

Arg His Pro His Arg Ser Pro Pro Thr Ser Cys Pro Pro Leu Leu Glu

1 5 10 15

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

20 25 30

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

35 40 45

Pro Leu Arg Gly Phe Leu Leu His Gln Pro Leu Pro Gly Gln His Leu

50 55 60

Trp Leu Ser His Arg Leu Arg Leu Arg Leu Pro Arg Thr

65 70 75

<210>

106

<211> 13

<212> PRT

<213> Homo sapiens

<400> 106

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

1 5 10

<210> 107

<211> 14

<212> PRT

<213> Homo sapiens

<400> 107

Leu Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser Arg His

1 5 10

<210> 108

<211> 25

<212> PRT

<213> Homo sapiens

<400> 108

Ile Thr His Pro Phe Ala Ser Gln Pro Leu Gly Gln Glu Met Pro Asn

1 5 10 15

Asn Thr Gln Ile Arg Leu Leu Lys Pro

20 25

<210> 109

<211> 20

<212> PRT

<213> Homo sapiens

<400> 109

Arg Ala Phe Ile His Thr Pro Arg Ser Pro Gly Cys Ser Val Tyr Ala

1 5 10 15

Asn Met Cys Trp

20

<210> 110

<211> 18

<212> PRT

<213> Homo sapiens

<400> 110

Met Thr Leu Lys Ala Leu Val Lys Thr Trp Thr Gln Phe Arg Asn Tyr

1 5 10 15

Pro Arg

<210> 111

<211> 19

<212> PRT

<213> Homo sapiens

<400> 111

Ala Phe Trp Lys Pro Pro Ser Gln Gly Ile Ser Ser Cys Leu Met Thr

1 5 10 15

Gly Cys Trp

<210> 112

<211> 10

<212> PRT

<213> Homo sapiens

<400> 112

Phe Glu Lys Lys Arg Pro Glu Trp Leu Ser

1 5 10

<210> 113

<211> 9

<212> PRT

<213> Homo sapiens

<400> 113

Met Ala Lys Lys Ser Gln Gln Pro Leu

1 5

<210> 114

<211> 9

<212> PRT

<213> Homo sapiens

<400> 114

Glu Ala Lys Lys Ser Met Lys Arg Ser

1 5

<210> 115

<211> 125

<212> PRT

<213> Homo sapiens

<400> 115

Arg Lys Arg Met Lys Thr Gly Ala Ile Gln Glu Lys Gly Ala Ile Gln

1 5 10 15

Glu Lys Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe Glu Ala

20 25 30

Cys Arg Glu Met Glu Ser Leu Ser Ala Pro Glu Lys Ile Thr Leu Phe

35 40 45

Glu Ala His Met Ala Arg Cys Thr Ser Ile Asn Val Leu Cys Val Arg

50 55 60

Ala Ser Leu Ile Glu Lys Leu Met Lys Glu Lys Arg Lys Met Lys Arg

65 70 75 80

Asn Gln Val Ala Ser Pro Gln Ile Met Gln Arg Leu Phe Ile Lys Gly

85 90 95

Tyr Gln Asn Asn His Phe Thr Phe His Leu Gln Asn Phe Ala Phe Phe

100 105 110

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

115 120 125

<210> 116

<211> 17

<212> PRT

<213> Homo sapiens

<400> 116

Ala Ser Pro Gln Ile Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr

1 5 10 15

Ile

<210> 117

<211> 35

<212> PRT

<213> Homo sapiens

<400> 117

Ala Ser Pro Gln Ile Met Gln Arg Thr Ser Ala Asp Arg Phe Arg Met

1 5 10 15
Lys Arg Arg Met Gln Asn Leu Asp Asn Leu Gly Val Pro Trp Pro Leu
20 25 30

Leu Pro Gly

35

<210> 118

<211> 45

<212> PRT

<213> Homo sapiens

<400> 118

Gly Asp Cys Pro Arg Thr Met Ala Gly Pro Ser Ala Ser Leu His Pro

1 5 10 15

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

20 25 30

Cys Arg Ala Gly Gly Pro Ala Gly Trp Ala Arg Gln Ala

35 40 45

<210> 119

<211> 12

<212> PRT

<213> Homo sapiens

<400> 119

Gly Glu Lys Leu Lys His Cys Phe Lys Ala Trp Gly

1 5 10

<210> 120

<211> 10

<212> PRT

<213> Homo sapiens

<400> 120

Met Leu Asn Gln Lys Cys Leu Ala Pro Phe

1 5 10

<210> 121

<211> 10

<212> PRT

<213> Homo sapiens

<400> 121

Ser Leu Ile Leu Ser Phe Gln Arg Val Lys

1 5 10

<210> 122

<211> 8

<212> PRT

<213> Homo sapiens

<400> 122

Gly Ala Lys Lys Ile Thr Phe Leu

1 5

<210> 123

<211> 43

<212> PRT

<213> Homo sapiens

<400> 123

Trp Trp Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys Met Cys Lys

1 5 10 15

Val Ser Gly Gly Cys Thr Ala Cys Val Glu Arg Cys Pro Trp Lys Gly

20 25 30

Ile Cys Trp Lys Trp Pro Val Thr Val Ala Ala

35 40

<210> 124

<211> 16

<212> PRT

<213> Homo sapiens

<400> 124

Arg Thr Leu Glu Ser Ala Gly Leu Phe Pro Trp Leu His Thr Gln Cys

1 5 10 15

<210> 125

<211> 12

<212> PRT

<213> Homo sapiens

<400> 125

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

1 5 10

<210> 126

<211> 12

<212> PRT

<213> Homo sapiens

<400> 126

Pro Ile Pro Pro His Leu Arg His Pro Leu Leu Leu

1 5 10

<210> 127

<211> 30

<212> PRT

<213> Homo sapiens

<400> 127

Val Pro Met Ser Leu Ala Cys Ser Ile Thr Val Ser Phe Val Gly Gln

1 5 10 15

Ile Ser Thr Leu Val Leu Asp Val Ser Ser Ile Ser His Trp

20 25 30

<210> 128

<211> 8

<212> PRT

<213> Homo sapiens

<400> 128

Asp Ser Lys Lys Met Thr Gln Lys

1 5

<210> 129

<211> 64

<212> PRT

<213> Homo sapiens

<400> 129

Arg Ser Leu Leu Tyr Ser Arg Met Cys Leu Val Gln Ile Pro Thr His

1 5 10 15

Thr Trp Glu Pro Asp Tyr Phe Val Ser Leu Pro Met Met Phe Ser Trp

20 25 30
Ala Thr Gln Ser Phe Pro Val Gly Ala Val Phe Leu Thr Arg Pro Ala

35 40 45
Ile Pro Cys Cys Ser Cys Thr Ser His Ser Asn Pro Trp Ser Gln Ser

50 55 60

<210> 130

<211> 29

<212> PRT

<213> Homo sapiens

<400> 130

Arg Arg Arg Asn Ser Arg Lys Gln Ser Gln Val Gln Leu Ala Ile Gln

1 5 10 15

Val Leu Leu Val Asp Lys His Lys Tyr Phe Leu Phe Gly

20 25

<210> 131

<211> 11

<212> PRT

<213> Homo sapiens

<400> 131

Arg Leu Asp Phe His Pro Arg Ser Ser Ser Gly

1 5 10

<210> 132

<211> 10

<212> PRT

<213> Homo sapiens

<400> 132

Ile Leu Ala Met Thr Leu Thr Leu Asn Gly

1 5 10

<210> 133

<211> 10

<212> PRT

<213> Homo sapiens

<400> 133

Gln Arg Pro Pro Arg Ser Ile Leu Ser Leu

1 5 10

<210> 134

<211> 11

<212> PRT

<213> Homo sapiens

<400> 134

Leu Glu Lys Lys Ala Thr Trp Met Arg Arg Thr

1 5 10

<210> 135

<211> 44

<212> PRT

<213> Homo sapiens

<400> 135

Gly Ala Ala Ala Ala Ser Cys Gln Ser Pro Pro Ser Pro Arg Glu Thr

1 5 10 15

Thr Pro Ser Ser Asp Ala Thr Arg Arg Thr Arg Pro Ile Ala Ala Gln

20 25 30

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

35 40

<210> 136

<211> 28

<212> PRT

<213> Homo sapiens

<400> 136

Ile Glu Ala Leu Thr Ala Leu Phe Thr Cys Arg Thr Ala Ser Ile Ser

1 5 10 15

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

20 25

<210> 137

<211> 30

<212> PRT

<213> Homo sapiens

<400> 137

Ala Phe Ser Gly Arg Ile Leu His Gln Pro Glu Met Ala Ala Met Arg

1 5 10 15

Leu Met Pro Lys Phe Leu Asn Ser Thr Asn Ser Trp Trp Thr

20 25 30

<210> 138

<211> 17

<212> PRT

<213> Homo sapiens

<400> 138

Ile Leu Phe His Val Arg Asn Ile Val Tyr Gly Ile Gln Val Met Leu

1 5 10 15

Cys

<210> 139

<211> 25

<212> PRT

<213> Homo sapiens

<400> 139

Gln Asn Thr Arg Ser Thr Asn Leu Glu Lys Asn Pro Ser Leu Lys Lys

1 5 10 15

Gln Ser Gln Arg Arg Gly Lys Leu Ser

20 25

<210> 140

<211> 30

<212> PRT

<213> Homo sapiens

<400> 140

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

1 5 10 15

His Ala Leu Ser Cys Arg Thr Arg Arg Arg Trp Ser Ser Lys

20 25 30

<210> 141

<211> 10

<212> PRT

<213> Homo sapiens

<400> 141

Asn Lys Val Arg Gln Asn Phe Lys Arg Asn

1 5 10

<210> 142

<211> 13

<212> PRT

<213> Homo sapiens

<400> 142

Ile Tyr Pro Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly

1 5 10

<210> 143

<211> 12

<212> PRT

<213> Homo sapiens

<400> 143

Val Asp Pro Pro Gly Ser Val Trp Ile Leu Pro Cys

1 5 10

<210> 144

<211> 12

<212> PRT

<213> Homo sapiens

<400> 144

Ile Ile Lys Lys Met Lys Lys Arg Ile Met Val His

1 5 10

<210> 145

<211> 9

<212> PRT

<213> Homo sapiens

<400> 145

Lys Gly Lys Lys Arg Arg Lys Glu Ile

1 5

<210> 146

<211> 11

<212> PRT

<213> Homo sapiens

<400> 146

Leu Ala Asn Gly Leu Trp Phe Asn Leu Ile Phe

1 5 10

<210> 147

<211> 8

<212> PRT

<213> Homo sapiens

<400> 147

Arg Gly Pro Pro Leu His Thr Arg

1 5

<210> 148

<211> 170

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 148

Asn Glu Gly Asn Asn His Trp Pro Arg Val Glu Met Pro Thr Gly Trp

1 5 10 15

Leu Leu Val Gly Tyr Asn Thr Arg Asn Thr Ala Gln Asn Pro Arg Leu

20 25 30

Gln Gln His Leu Lys His Trp Gln Gln Cys Thr Arg Ala Arg Trp Cys

35 40 45

Gln Glu Pro Cys Gln Thr Leu Thr Phe Phe His Phe Phe Phe Phe

50 55 60

Lys Thr Val Ser Leu Cys Cys Pro Gly Trp Ser Lys Gly Gln Pro Pro

65 70 75 80

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

85 90 95

Thr Gly Val Tyr Gln His Val Trp Leu Ile Cys Phe Val Phe Phe Val
100 105 110

Cys Val Glu Thr Gly Phe Cys His Val Ala Gln Val Gly Leu Glu Arg

115 120 125
Leu Val Ser Leu Ser Gly Ile Thr Asp Val Asn His Trp Ala Gln Pro
130 135 140

Lys Pro Ser Pro Ser Lys Gly Thr Gly Met Asn Arg Pro Ile Gly Leu
145 150 155 160

Arg Val Gly Lys Gly Val Trp Ala Arg Leu
165 170

<210> 149

<211> 78

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 149

Arg Arg Met Thr Arg Arg Thr Met Thr Thr Thr Lys Met Met Met Met
1 5 10 15

Arg Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg Arg Met Thr Met Met
20 25 30

Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu Thr Pro Arg Thr
35 40 45

Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile Ser Gln Arg Arg
50 55 60

Pro Ile Gln Thr Pro Pro Gly Thr Ser Leu Ala Ile Trp Gly
65 70 75

<210> 150

<211> 40

<212> PRT

<213> Homo sapiens

<400> 150

Arg Ala Arg Asn Arg Asn Met Lys Lys Thr Met Ser His Leu Ile Ala

1 5 10 15
 His Gln Ala Leu Lys Met Ser Gly Leu Arg Leu Phe His Pro Arg Leu
 20 25 30
 Leu Thr Arg Lys Lys Pro Gly Lys
 35 40

<210> 151

<211> 15

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 151

Arg Arg Ala Arg Pro Thr Ser Cys Ser Thr Cys Arg Met Trp Trp

1 5 10 15

<210> 152

<211> 25

<212> PRT

<213> Homo sapiens

<400> 152

Gln Val Ser Val Tyr Ser Gly Asn Leu Leu Ser Phe Ser Arg Arg Gly

1 5 10 15

Met Lys Ser Ser Val Arg Leu Lys Asn

20 25

<210> 153

<211> 27

<212> PRT

<213> Homo sapiens

<400> 153

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

1 5 10 15

Glu Val Pro Phe Pro Arg Pro Cys Arg Thr Lys

20 25

<210> 154

<211> 30

<212> PRT

<213> Homo sapiens

<400> 154

Trp Leu Pro Met Arg Ser Leu Gly Glu Pro Trp Arg Ala Gly Phe Gln

1 5 10 15

Trp Gly Glu Ser Pro Trp Gln Val Met Ala Ser Leu Thr Gly

20 25 30

<210> 155

<211> 10

<212> PRT

<213> Homo sapiens

<400> 155

Glu Glu Lys Lys Asn Gly Arg Ile Ser Ser

1 5 10

<210> 156

<211> 13

<212> PRT

<213> Homo sapiens

<400> 156

Thr Met Ser Leu Ser Asn Ile Leu Met Lys Phe Arg Leu

1 5 10

<210> 157

<211> 16

<212> PRT

<213> Homo sapiens

<400> 157

Arg Trp Ile Phe Ser Asn Gln Leu Thr Val Gln Met Leu Cys Leu Pro

1 5 10 15

<210> 158

<211> 114

<212> PRT

<213> Homo sapiens

<400> 158

Leu Leu Thr Pro Asp Thr Arg Trp Ile Phe Ser Asn Gln Leu Gln Thr
1 5 10 15
Val Gln Met Leu Cys Leu Pro Pro Leu Lys Gln Gly Glu Arg Ile Ile
20 25 30
Trp Pro Leu Gly Gly Phe Gln Ile Pro Asn Phe Phe Trp Ser Leu Gly
35 40 45
Ile Gly His Thr Gly Ala Trp Trp His Thr Gly Arg Arg Arg Arg Glu
50 55 60
Trp Gly Gly Ser Thr Val Ser Arg Ser Pro Leu Trp Ile Ser Ser Met
65 70 75 80
Ile Tyr Leu Arg Gly Met Ala Phe Ala Ser Asp Ser Ser Ile Arg Thr
85 90 95
Thr Arg Val Ser Trp Cys Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala
100 105 110

Ser Ser

<210> 159

<211> 13

<212> PRT

<213> Homo sapiens

<400> 159

Ile Pro Ser Leu Asn Ala Gln Trp Met Phe Leu Arg Ile

1 5 10

<210> 160

<211> 20

<212> PRT

<213> Homo sapiens

<400> 160

Ser Arg Arg Asn Arg Arg Tyr Arg Lys Ile Tyr Gly Glu Leu Lys Met

1 5 10 15

Ser Leu Gln Ala

20

<210> 161

<211> 16

<212> PRT

<213> Homo sapiens

<400> 161

Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr Asp

1 5 10 15

<210> 162

<211> 13

<212> PRT

<213> Homo sapiens

<400> 162

Phe Leu Pro Ser Arg Phe Pro Trp Gly Pro Pro Pro Leu

1 5 10

<210> 163

<211> 45

<212> PRT

<213> Homo sapiens

<400> 163

Asn Ser Val Ile Val His Lys Ile Val Leu Val Phe Leu Lys Ser Leu

1 5 10 15

Ser Ser Tyr Asn Cys Glu Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala

20 25 30

Ile Glu Phe Ala Val Leu Lys Leu Leu Asn Met Asp Leu

35 40 45

<210> 164

<211> 61

<212> PRT

<213> Homo sapiens

<400> 164

Val Ala Pro Arg Cys Pro Arg Ser Ala Val Asp Ile Ser Pro Gly Pro

1 5 10 15

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

20 25 30
Ala Leu Leu Gly Ala Ser Ala Pro Cys Gly Ala Ala Gly Ala Arg Glu

35 40 45
Ala Gly Arg Phe Ala Val Leu Gly Thr Met Val Met Lys

50 55 60

<210> 165

<211> 27

<212> PRT

<213> Homo sapiens

<400> 165

Ser Pro Leu Trp Asp Cys Ser Thr Thr Thr Gly Thr His His Gly Cys

1 5 10 15

Leu Trp Glu Ile Pro Ser Val Thr Leu Leu Ala

20 25

<210> 166

<211> 26

<212> PRT

<213> Homo sapiens

<400> 166

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

1 5 10 15

Val Thr Ala Ala Pro Ser Gly Gln Tyr Phe

20 25

<210> 167

<211> 46

<212> PRT

<213> Homo sapiens

<400> 167

Leu Leu Leu Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr Gln Lys

1 5 10 15

Gly Glu Cys Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu Phe Ile

20 25 30

Leu Lys Gln Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met

35 40 45

<210> 168

<211> 9

<212> PRT

<213> Homo sapiens

<400> 168

Ser Leu Phe Phe Ser His Cys Leu Cys

1 5

<210> 169

<211> 9

<212> PRT

<213> Homo sapiens

<400> 169

Leu Lys Lys Lys Val Asn Ala Cys Ser

1 5

<210> 170

<211> 12

<212> PRT

<213> Homo sapiens

<400> 170

Asn Ala Lys Lys Met Glu Asp Met Ile Trp Glu Ser

1 5 10

<210> 171

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 171

Gly Ser Cys Gly Arg Ala Cys Ser Cys Gly Arg Gly Cys Gly Thr Pro

1 5 10 15

Arg Gly Asp Trp Lys Arg His Pro Pro Arg Arg

20 25

<210> 172

<211> 14

<212> PRT

<213> Homo sapiens

<400> 172

Met Ile Arg Lys Ile Gln Lys Arg Arg Arg Thr Ala Asn Arg

1 5 10

<210> 173

<211> 10

<212> PRT

<213> Homo sapiens

<400> 173

Thr Tyr Thr Pro His Ile Cys Arg His Thr

1 5 10

<210> 174

<211> 10

<212> PRT

<213> Homo sapiens

<400> 174

Met Lys Lys Lys Asp Ser Thr Ile Phe Ile

1 5 10

<210> 175

<211> 8

<212> PRT

<213> Homo sapiens

<400> 175

Leu Cys Phe Phe Tyr Leu Leu Tyr

1 5

<210> 176

<211> 11

<212> PRT

<213> Homo sapiens

<400> 176

Leu Thr Thr Leu Ser Phe Val Leu Ile Glu Glu

1 5 10

<210> 177

<211> 75

<212> PRT

<213> Homo sapiens

<400> 177

Asn Leu Asp Leu Gln His Gln Arg Arg Arg Lys Lys Lys Lys Asp Lys

1	5	10	15
Val	Glu Ile Arg Asn Arg Ser Pro Lys Ala Asn Ser Thr Glu Cys Gln		
	20	25	30
Gly	Glu His Ser Arg Glu Gln Asn Leu Leu Asn Leu Val Gln Leu Asn		
	35	40	45
Pro	His Ser Pro His His Arg Lys Asp Glu Glu Asp His Gln Lys Arg		
	50	55	60
His	His His His Asn Gln Lys Lys Met Ser Val		
65	70	75	

<210> 178

<211> 55

<212> PRT

<213> Homo sapiens

<400> 178

Ala	Ser Arg Ala Gly Gln Phe Pro Val Trp Arg Arg Thr Ser Arg Gly
1	5 10 15
Met	Ser Leu Gln Trp Lys Ser Gly Asn Ala Cys Thr Pro Leu Arg Cys
	20 25 30
Pro	Ser Arg Ser Pro Ala Thr Phe Leu Thr Ala Leu Asn Gly Trp His
	35 40 45
Arg	Ser Gly Leu Arg Ala Gln
	50 55

<210> 179

<211> 68

<212> PRT

<213> Homo sapiens

<400> 179

Pro Tyr Pro Ile Ser Glu Gly Leu Thr Met Thr Thr Gly Arg Asn Ile

1 5 10 15

Asn Ser Asn Ser Leu Met Thr Asn Cys Leu Phe Ser Pro Ile Phe Leu

20 25 30

Cys His His Ala Ile Met His Arg Lys Met Thr Ser Pro His Phe Arg

35 40 45

Leu Phe Ser Ser Lys Ile Pro His Pro Gln Val Pro Ser Val Val Ala

50 55 60

Leu Cys Lys Phe

65

<210> 180

<211> 24

<212> PRT

<213> Homo sapiens

<400> 180

Leu Lys Leu Ala Pro Leu Gln Val Thr Thr Thr Leu Lys Leu Ile Leu

1 5 10 15

Val Met Leu Glu Ile Val Thr Glu

20

<210> 181

<211> 42

<212> PRT

<213> Homo sapiens

<400> 181

Cys Arg Val Asn Ala Val Glu Glu Leu His Ser Arg Arg Met Ser Val

1 5 10 15

Arg Ile Val Lys Asn Trp Val Ser Cys Cys Tyr Val Arg Leu Ser Ala

20 25 30

Val Gly Leu Ser Thr Trp Ser Ala Leu Asp

35 40

<210> 182

<211> 27

<212> PRT

<213> Homo sapiens

<400> 182

Arg Leu Pro Leu Arg Pro Gln Arg Gly Pro Arg Pro Leu His Arg Trp

1 5 10 15

Leu Gln Gln Thr Thr Gly Cys Ser Gln Arg Arg

20 25

<210> 183

<211> 14

<212> PRT

<213> Homo sapiens

<400> 183

Arg Lys Met Gln Ser Leu Asn His Pro Ser Arg Leu Thr Asn

1 5 10

<210> 184

<211> 19

<212> PRT

<213> Homo sapiens

<400> 184

Ser Arg Lys Lys Gly His Thr Lys Asn Arg Arg Lys Ala Lys Arg Lys

1 5 10 15

Pro Gln Ile

<210> 185

<211> 11

<212> PRT

<213>

> Homo sapiens

<400> 185

Asn Lys Ile Ile Cys Lys Gly His Arg Ile Thr

1 5 10

<210> 186

<211> 9

<212> PRT

<213> Homo sapiens

<400> 186

Ser Ser Phe Phe Tyr Thr Ser Asp Arg

1 5

<210> 187

<211> 9

<212> PRT

<213> Homo sapiens

<400> 187

Gln Lys Lys Gly His Met Ile Phe Ser

1 5

<210> 188

<211> 66

<212> PRT

<213> Homo sapiens

<400> 188

Met Leu Gln Lys Gln Cys Cys Tyr Asn Leu Val Ile Lys His Pro Leu

1 5 10 15

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

20 25 30

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

35 40 45

Phe Phe Ile Cys Leu Leu Met Phe Ile Lys Arg Trp Lys Pro Ala Ala

50 55 60

Thr Lys

65

<210> 189

<211> 146

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 189

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

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

 50 55 60
 Cys Pro Leu Gln Thr Phe His Leu His His Cys Arg Thr Gln Pro Ser
 65 70 75 80
 Ser Cys Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln Trp Ser Gly Ala
 85 90 95
 Val Val Gly Leu Arg Pro Val Ala His His Leu Pro Arg Pro Ile Gln
 100 105 110
 Gly Leu His Cys Pro Gln Ala Pro His Gln Pro Ala Leu Ser Trp Gly

 115 120 125
 Lys Trp Pro Val Gly Met Thr Gly Pro Ala Arg Cys Cys Arg Trp Pro
 130 135 140
 Arg Arg
 145
 <210> 190
 <211> 78
 <212> PRT
 <213> Homo sapiens
 <400> 190
 Arg Thr Arg Leu Thr Leu Thr Gly Thr Arg Ser Ser Gly Thr Arg Ala
 1 5 10 15
 Ser Pro Ser Ala Val Cys Leu Cys Cys Trp Thr Cys Pro Ser Arg Ser
 20 25 30

 Phe Pro Ala Ala Ser Pro Ser Gly Leu Arg Ala Pro Val Gly Ala Gln
 35 40 45
 Ala Pro Pro Glu Val Thr Leu Arg Ala Ser Cys Ala Ser Ser Ala Ser
 50 55 60

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

65 70 75

<210> 191

<211> 52

<212> PRT

<213> Homo sapiens

<400> 191

Cys His Pro Ala Trp Leu Ser Pro Ile Ser Ala Cys Pro Arg Leu Leu

1 5 10 15

Pro Tyr Pro Phe His Val Leu Ala Leu Glu Val Thr Phe Pro Pro Gly

20 25 30

Thr Ala Met Pro Gln Met Gln Leu Gln Ala Leu Ala Met Trp Glu Lys

35 40 45

Gly Trp Asp Lys

50

<210> 192

<211> 44

<212> PRT

<213> Homo sapiens

<400> 192

Met Asp Leu Asp Gly Met Leu Thr Val Ile Gly Gln Gly Leu Val Gly

1 5 10 15

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

20 25 30

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

35 40

<210> 193

<211> 33

<212> PRT

<213> Homo sapiens

<400> 193

Ser Gln Lys Ser Gln His His Cys Ala Leu Arg Lys Ile Glu Trp Ala

1 5 10 15

Thr Lys Leu Ser Leu Gly Gly Lys Ala Gly Pro Gln Ala Gln Glu Lys
 20 25 30

Ala

<210> 194

<211> 29

<212> PRT

<213> Homo sapiens

<400> 194

Ile Arg Met Cys Ala Leu Ser His Pro Ser Phe Tyr Ile Ser Ser Thr
 1 5 10 15

Val Cys Phe Leu Ser Lys His Cys Met Thr Ala Cys Thr
 20 25

<210> 195

<211> 13

<212> PRT

<213> Homo sapiens

<400> 195

Arg Cys Ser Leu Met Glu Gln Ile Pro His Leu Lys Ser
 1 5 10

<210>

> 196

<211> 19

<212> PRT

<213> Homo sapiens

<400> 196

Leu Leu Lys Lys Ser Ser Gln Leu Arg Arg Ser Trp Arg Asn Val Ser
 1 5 10 15

Arg Ile Ser

<210> 197

<211> 19

<212> PRT

<213> Homo sapiens

<400> 197

Ser Ile Pro His Val Pro Lys Ala Thr Ala Ala His Ser Val Thr Val

1 5 10 15

Lys Leu Gln

<210> 198

<211> 11

<212> PRT

<213> Homo sapiens

<400> 198

Thr His Pro Cys Thr Met Leu Leu Pro Gln Gly

1 5 10

<210> 199

<211> 16

<212> PRT

<213> Homo sapiens

<400> 199

Ser Arg Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys Val Lys

1 5 10 15

<210> 200

<211> 9

<212> PRT

<213> Homo sapiens

<400> 200

Trp Leu Lys Lys Ser Thr Lys Ser Arg

1 5

<210> 201

<211> 8

<212> PRT

<213> Homo sapiens

<400> 201

Asp Arg Val Phe Leu Val Lys Ile

1 5

<210> 202

<211> 11

<212> PRT

<213> Homo sapiens

<400> 202

Asn Ile Glu Ile Thr Pro Gln Arg Ser Lys Ala

1 5 10

<210> 203

<211> 106

<212> PRT

<213> Homo sapiens

<400> 203

Gly Ala Leu Arg Ala Thr Ala Pro Ala Thr Ala Ala Pro Gln Ala Gln

1 5 10 15

Thr Pro His Trp Arg Ala Ala Thr Thr Ser Ser Met Ser Ser Ser Pro

20 25 30

Arg Ala Glu Pro Thr Ser Ser Ser Ser Trp Ala Thr Cys Trp Pro Arg

35 40 45

Cys Cys Ser Ser Ser Cys Tyr Trp Ser Leu Ser Ser Trp Pro Pro Ala

50 55 60

Gly Ala Ala Glu Ala Thr Asn Thr Arg Thr Arg Ser Arg Glu Ser Gln

65 70 75 80

Arg Gly Arg Met Leu Thr Trp Arg Ser Ser Leu Trp Leu Gln Gly Thr

85 90 95

Arg Cys Phe Thr Gly Val Arg Thr Ser Ser

100 105

<210> 204

<211> 86

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 204

Gln Ser Ser Pro Phe Leu Ala Arg Ser Trp Asn Thr Met Gln Trp Asn

1 5 10 15
 Asn Lys Lys Met Ala Met Thr Val Ile Ala Gly Ala His His Cys Gln
 20 25 30

Tyr Lys Leu Thr Tyr Thr Lys Val Trp Lys Met Asn Trp Lys Lys Met
 35 40 45

Met Ile Gly Ser Gln His Leu Leu Phe Ser Pro Leu Asp Ser Ser Pro
 50 55 60

Leu Gln Leu Leu Leu His Pro His Gly Lys Arg Cys Asn Pro Cys Cys
 65 70 75 80

Arg Leu Thr Trp Met Ser
 85

<210> 205

<211> 135

<212> PRT

<213> Homo sapiens

<400> 205

Cys Arg Gly Gly Pro Ser Ala Ser Asp Arg Cys Cys Ser Cys Ser Pro
 1 5 10 15

Ser Gly Phe Ser Ala Gly Arg Gly Arg Cys Pro Val Gln Gly Cys Leu
 20 25 30

Arg Pro His Arg Val Gln Leu Leu Arg Arg Trp Gly Pro Gly Ser Pro
 35 40 45

Ala Gly Gln Arg Leu Ser Lys Gly Phe Gln Leu Leu Arg Trp Trp Gly
 50 55 60

Pro Gly Ser Pro Ala Pro Glu Pro Arg Lys Gly Pro Phe Pro Pro Pro
 65 70 75 80

Asp Pro Pro Trp Pro Val Thr Ala Val Thr Val Met Ala Gly Ser Val
 85 90 95

Pro Ser Ala Gln Ser Val Asp Ala Leu Glu Ser Pro Gly Pro Leu Ala
 100 105 110

Leu Glu Gly Pro Ser Ser Pro Arg Asn Leu Leu Trp Arg Glu Met Ser

115 120 125

Ile Phe Leu Pro Gly Ile Phe

130 135

<210> 206

<211> 87

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 206

His Leu Asn Arg Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu

1 5 10 15

Thr Met Met Met Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile

20 25 30

Pro Leu Pro Ser Pro Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His

35 40 45

Pro Pro Pro Pro Cys Leu Leu Leu Leu His His Arg His His Leu Ala

50 55 60

Phe Leu Glu Met Ala Cys Ser Ser Gln His Thr His Ser Ile Lys Ile

65 70 75 80

Trp Ile Ser Phe Ser His Glu

85

<210> 207

<211> 89

<212> PRT

<213> Homo sapiens

<400> 207

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

1 5 10 15

Glu Lys Leu Ser Trp Asn Ile Cys Lys Asn Leu Ser Leu Tyr Leu Asp

20 25 30

Lys Phe Val Gln Arg Leu Leu Tyr Val Tyr Ile Ile Glu Thr Asn Val

35 40 45

Phe Val Leu Asn Leu Phe His Val Pro Val Asn Gln Ile Phe Met Met
 50 55 60
 Ala Phe Tyr Leu Lys Tyr Thr Glu Lys Ala Trp Val Met Glu Leu Glu
 65 70 75 80

Trp Leu Ile Gln Gln Gln Cys Tyr Gln
 85

<210> 208

<211> 53

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 208

Gly Pro Val Tyr Tyr Val Cys Asn Arg Met Asn Val Ser Ser Val Leu
 1 5 10 15

Lys Pro Phe Leu Phe Thr Val Pro Ile Glu Asp Met Arg Glu Cys Thr
 20 25 30

Leu Gly Arg Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Cys Leu

35 40 45

Ile Pro Val Pro Ile

50

<210> 209

<211> 43

<212> PRT

<213> Homo sapiens

<400> 209

Asp Leu Pro Arg Met Leu Pro Ile Ser Ser Pro Leu His Arg Pro Gln
 1 5 10 15

Met Pro Phe Trp Thr Cys Thr Phe Pro Ala Thr Thr Trp Gly Thr Trp
 20 25 30

Glu Thr Pro Ser Thr Trp Gly Trp Arg Thr Phe
 35 40

<210> 210

<211> 58

<212> PRT

<213> Homo sapiens

<400> 210

Val Ile Ala Ile Leu Ser Ser Met Cys Gln Glu Ile Leu Asn Arg His

1 5 10 15

His Arg Arg Lys Glu Val Arg Lys Leu Lys Gln Ile Leu Phe Gln Val

20 25 30

Glu Glu Thr Lys Ser Gly Arg Phe Trp Ile Lys His Asp Leu Val Ser

35 40 45

Cys Leu Gln Ser Tyr Leu Val Met Glu Ala

50

55

<210> 211

<211> 9

<212> PRT

<213> Homo sapiens

<400> 211

Trp Leu Gly Met Ala Leu Ile Phe Gly

1 5

<210> 212

<211> 87

<212> PRT

<213> Homo sapiens

<400> 212

Ala Asn Met Asp Ala Gln Pro Met Met Pro Thr Pro Asn Ile Ile Ala

1 5 10 15

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

20 25 30

Pro Trp Leu Gly Met Ala Leu Ile Pro Leu Pro Gly Met Arg Gln Pro

35 40 45

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

50 55 60

Ala Trp His Ser Arg Ser Met Ala Pro Thr Gln Thr Cys Leu Ala Pro

65 70 75 80

His Pro Lys Pro His Trp Asn

85

<210> 213

<211> 53

<212> PRT

<213> Homo sapiens

<400> 213

Thr Ala Leu Lys Tyr Ile Phe Val Ala Val Arg Ala Ile Cys Val Met

1 5 10 15

Lys Ser Phe Leu Ile Phe Arg Arg Trp Lys Ser His Ser Pro Leu Gln

20 25 30

Ile Gln Leu His Leu Ser His Pro Ile Thr Thr Ser Cys Ser Ile Pro

35 40 45

Trp Cys His Leu Cys

50

<210> 214

<211> 61

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 214

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

1 5 10 15

Thr Ala Pro Cys Pro Cys Ser Ser Ala Glu Gly Trp Thr Ala Trp Pro

20 25 30

Ser Arg Pro Cys Pro Ser Arg Thr Ala Ser Ala Arg Cys Trp Thr Trp

35 40 45

Ser Ser Arg Gly Leu Lys Gly Arg Ser Arg Cys Arg Thr

50 55 60

<210> 215

<211> 35

<212> PRT

<213> Homo sapiens

<400> 215

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

1 5 10 15

Trp Thr Val Ile Leu Leu Asn Pro Cys Gly Asn Leu His Leu Lys Thr

20 25 30

Thr Ser Leu

35

<210> 216

<211> 33

<212> PRT

<213> Homo sapiens

<400> 216

Val Ser Trp Tyr Ser His Gln Lys Lys Leu Thr Val Pro His Ser Leu

1 5 10 15

Leu Phe Arg His Lys Ser Arg Arg Leu Arg Leu Cys Tyr Met Ala Asn

20 25 30

Trp

<210> 217

<211> 12

<212> PRT

<213> Homo sapiens

<400> 217

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

1 5 10

<210> 218

<211> 22

<212> PRT

<213> Homo sapiens

<400> 218

Met Asn Ser Val Asn Leu Ser Ser Pro Lys Ala Arg Asp Trp Thr Val

1 5 10 15

Ser Glu Leu Leu Lys Asn

20

<210> 219

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 219

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

1 5 10 15

Leu Trp Thr Val

20

<210> 220

<211> 17

<212> PRT

<213> Homo sapiens

<400> 220

Gln Arg Lys Pro Lys Arg Ala Asn Cys Val Ile Gln Arg Arg Ala Lys

1 5 10 15

Met

<210> 221

<211> 11

<212> PRT

<213> Homo sapiens

<400> 221

Met Gln Lys Lys Trp Pro Ile Thr Tyr Val Ala

1 5 10

<210> 222

<211> 11

<212> PRT

<213> Homo sapiens

<400> 222

Gly Gly Gly Gly Ser Trp Ser Ser Pro Ser Gly

1 5 10

<210> 223

<211> 16

<212> PRT

<213> Homo sapiens

<400> 223

Gly Lys Asp Arg Tyr Cys Ser Asn Ile Asp Lys His Trp Leu Asn Ser

1 5 10 15

<210> 224

<211> 8

<212> PRT

<213> Homo sapiens

<400> 224

Arg Ala Asp Pro Gln Arg His Thr

1 5

<210> 225

<211> 8

<212> PRT

<213> Homo sapiens

<400> 225

Arg Ala Phe Phe Gly Gly Leu Leu

1 5

<210> 226

<211> 117

<212> PRT

<213> Homo sapiens

<400> 226

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

1 5 10 15

Trp Leu Pro Phe Gly Ile Asn Trp Glu Arg Arg Thr Arg Thr Met Arg

20

25

30

Thr Ser Ser Ser Pro Arg Trp Thr Arg Leu Pro Thr Arg Trp Arg Pro
35 40 45
Ser Lys Cys Thr Ala Ser Pro His Ser Ser Ser Phe Leu Pro Val Pro
50 55 60
Thr Gly Arg Ser Leu Ile Thr Thr Gly Asn Ala Arg Trp Met Val Leu
65 70 75 80
Arg Asn Ser Trp Arg Ala Val Ala Arg Met Gly Gln Gly Met Met Thr
85 90 95
Ile Ser Arg Thr Trp Lys Lys Gln Arg Ser Gln Thr Trp Arg Lys Thr
100 105 110
Met Ile Arg Lys Leu
115
<210> 227
<211> 117
<212> PRT
<213> Homo sapiens
<400> 227
Cys Arg Thr Arg Pro Arg Lys Ala Ala Ser Ala Gln Ser Ser Arg Ser
1 5 10 15
Gly Gly Glu Gly Gly Ser Val Leu Val Gly Met Glu Arg Thr Ala Ser
20 25 30
Thr Gly Glu Thr Val Glu Met Arg Arg Trp Trp Thr Leu Val Met Glu
35 40 45
Trp Lys Ser Ser Tyr Arg Ala Ala Thr Pro Cys Pro Ala Pro Pro Arg
50 55 60
Pro Ala Arg Val Pro Ala His Ala Ser Thr Ser Leu Ser Ser His Ile
65 70 75 80
Thr Leu Lys Pro Val Thr Pro Gln Glu Arg Lys Thr Gln Asp Val Gly
85 90 95
Met Ala Val Ser Met Asp Thr Ile Ser Ile Val Thr Met Trp Gly Glu
100 105 110
Gly Gly Gly Val Gly

115
 <210> 228
 <211> 57
 <212> PRT
 <213> Homo sapiens
 <400> 228
 Val Ala Arg Val Glu Val Ala Ala Gly Pro Pro Met Arg Glu Val Ala
 1 5 10 15
 Glu Ala Ala Ala Val Val Met Val Val Arg Pro Val Ala Thr Leu Ser

20 25 30
 Pro Gly Glu Ala Arg Ala Pro Leu Glu Ser Val Arg Gln Ile Tyr Ser
 35 40 45
 Glu His Asn Tyr Cys Arg Leu Ile Leu
 50 55

<210> 229
 <211> 38
 <212> PRT
 <213> Homo sapiens
 <400> 229
 Arg Leu Pro Gly Leu Thr Cys Lys Val Arg Arg Thr Leu His Gln Leu
 1 5 10 15
 Lys Leu Cys Gln Arg Val Met Ile Leu Ser Val Val Phe Gln Ile Leu

20 25 30
 Met Thr Cys Gln Trp Pro
 35
 <210> 230
 <211> 26
 <212> PRT
 <213> Homo sapiens
 <400> 230
 Cys Leu Glu Ser Gly Thr Asp His Ile Leu Thr Glu Ile Leu Ser Ile
 1 5 10 15
 Ser Cys Lys Lys Met Asn Gln Met Glu Leu

20 25

<210> 231

<211> 27

<212> PRT

<213> Homo sapiens

<400> 231

Arg Gly Gly Ala Pro Leu Pro Ser Trp Ser Pro Pro Cys Gln Ser Leu

1 5 10 15

Arg Gln Ala Val Thr Ser Ser Arg Thr Ser Gly

20 25

<210> 232

<211> 13

<212> PRT

<213> Homo sapiens

<400> 232

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

1 5 10

<210> 233

<211> 11

<212> PRT

<213> Homo sapiens

<400> 233

Glu Cys Cys Ser Ser Trp Leu Arg Arg Ile Glu

1 5 10

<210>

234

<211> 24

<212> PRT

<213> Homo sapiens

<400> 234

Met Glu Cys Ser Lys Leu Lys Leu Phe Asn Leu Phe Trp Thr Trp Gln

1 5 10 15

Arg Glu Pro Val Met Gln Pro Gln

20

<210> 235

<211> 13

<212> PRT

<213> Homo sapiens

<400> 235

Leu Gln Lys Lys Asn Ser Arg Lys Arg Lys Gln Lys Gly

1 5 10

<210> 236

<211> 12

<212> PRT

<213> Homo sapiens

<

400> 236

Leu Val Val Cys Leu Ser Arg Arg Met Lys Arg Cys

1 5 10

<210> 237

<211> 20

<212> PRT

<213> Homo sapiens

<400> 237

Val Asp Ser Ser Ser Tyr His Pro Phe Lys Ile Asn Gln Asn Ile Arg

1 5 10 15

Phe Gln Lys Phe

20

<210> 238

<211> 12

<212> PRT

<213> Homo sapiens

<400> 238

Arg Lys Arg Arg Arg Arg Lys Arg Lys Arg Ala Asn

1 5 10

<210> 239

<211> 20

<212> PRT

<213> Homo sapiens

<400> 239

Pro Tyr Lys Phe Ser Glu Tyr Arg Arg Ala Phe Ser Trp Ser Ala Asp

1 5 10 15

Ile Thr Gly Thr

20

<210> 240

<211> 10

<212> PRT

<213> Homo sapiens

<400> 240

Ile Leu Phe Phe Tyr Met Ala Tyr Leu Trp

1 5 10

<210> 241

<211> 14

<212> PRT

<213> Homo sapiens

<400> 241

Asn Gly Leu Pro Glu Thr Glu Lys Met Pro Gln Leu Met Pro

1 5 10

<210> 242

<211> 12

<212> PRT

<213> Homo sapiens

<400> 242

Tyr Tyr Gln Lys Thr Trp Arg Val Ile Leu Pro Asp

1 5 10

<210> 243

<211> 97

<212> PRT

<213> Homo sapiens

<400> 243

Ser Thr Trp Phe His Val Thr Ser Gly Thr Ser Leu Ser Cys Ala Leu

1 5 10 15

Pro Ser Val Leu Ala Arg Trp Asn Leu Pro Met Cys Ser Gly Pro Gly
20 25 30

Asn Thr Ser Lys Ser Trp Arg Pro Thr Cys Cys Glu Gln Arg Gly Ser
35 40 45

Arg Ser Glu Ala Ser Cys Arg Asn Gln Lys Leu Lys Arg Asp Ile Ser
50 55 60

Glu Asn Trp Asn Lys Lys Gln Ile Asn Ile Ile Leu Pro Ser Trp Asn
65 70 75 80

Ser Ala Val Cys Gly Phe Pro Cys Leu Ser Pro Lys Leu Ser Arg Gly
85 90 95

Leu

<210> 244

<211> 58

<212> PRT

<213> Homo sapiens

<400> 244

Ser Ala Ala Trp Arg Ser Cys Ile Ala Leu Trp Cys Ala Ser Ser Val
1 5 10 15

Thr Glu Arg Thr Arg Cys Ala Gly Arg Trp Leu Trp Tyr Cys Trp Pro
20 25 30

Thr Trp Leu Arg Gly Thr Ala Trp Gln Leu Val Pro Leu Gln Cys Arg
35 40 45

Arg Ala Val Ser Ala Thr Ser Trp Ala Ser

50

55

<210> 245

<211> 60

<212> PRT

<213> Homo sapiens

<400> 245

Ala Val Thr Arg Ala Ser Ala Pro Arg Ala Thr Ala Ala Ala Gly Ala
1 5 10 15

Trp Arg Gly Arg Arg Pro Pro Thr Ala Arg Ser Ser Ala Thr Thr Arg
 20 25 30
 Gly Pro Pro Ser Ser Thr Ser Arg Ala Val Gly Arg Pro Pro Cys Trp
 35 40 45

Arg Gly Pro Gly Ser Thr Thr His Thr Ser Arg Pro
 50 55 60

<210> 246

<211> 25

<212> PRT

<213> Homo sapiens

<400> 246

Thr Ile Lys Ile Ser Gln Ile Gln Asn Gln Ser Val Asn Lys Asn Phe
 1 5 10 15

His Ile His Leu Lys Arg Thr Tyr Gln
 20 25

<210> 247

<211> 77

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 247

Ala Glu Thr Ile Thr Gln Leu Tyr Gly Lys His Tyr Ala Ser Gly Trp

1 5 10 15

Met Met Leu Met Ser Lys Thr Pro Arg Thr Tyr Arg Met Cys Thr Val

20 25 30

Gly Met Pro Arg Ser Val Cys Gly Trp Pro Ser Cys Phe Pro Gly Leu

35 40 45

Ala Gly Ser Ser Gln Gly Pro Thr Leu Arg Ser Gly Ser His Cys Pro

50 55 60

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

65 70 75

<210> 248

<211> 63

<212> PRT

<213> Homo sapiens

<400> 248

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

1 5 10 15

Ser Leu Leu Phe Ser Ile Arg Arg Trp Ser Thr Ile Ser Cys Pro Arg

20 25 30

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

35 40 45

Pro Ala Ser Pro Gly Arg Arg Pro Leu Lys Lys Trp Pro Thr Pro

50 55 60

<210> 249

<211> 67

<212> PRT

<213> Homo sapiens

<400> 249

Ala Ser Pro Leu Lys Arg Asp Pro Gln Gln Gly Gln Phe Ile Pro Ser

1 5 10 15

Gln Pro Pro Thr Leu Pro Trp Thr Leu Arg Lys Gln Pro Gln Gly Pro

20 25 30

Ser Cys Ser Arg Gly Ser Gln Arg Ala Val Arg Gly Thr Ser Pro Ser

35 40 45

Gln Gly Ile Leu Gly Ser Thr Gly Cys Ser Leu Gly Ser Arg Leu His

50 55 60

Ser Trp Cys

65

<210> 250

<211> 58

<212> PRT

<213> Homo sapiens

<400> 250

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

1 5 10 15
 Arg Ser Ser Ser Phe Arg Ser Pro His Thr Ser Pro Phe Phe Gly Pro
 20 25 30

Thr Ser Gly Cys Leu Gly Phe Thr Gln Glu Pro Pro Leu Pro Gln Phe
 35 40 45
 Pro Arg Thr Cys His Phe Met Phe Leu Phe
 50 55

<210> 251

<211> 15

<212> PRT

<213> Homo sapiens

<400> 251

Met Lys Ala Leu Ile Ser Gln Glu Met Phe Ser Gln Ala Leu Leu

1 5 10 15

<210> 252

<211> 33

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 252

Asp Thr Thr Phe Gln Arg Ala Pro Leu Lys Phe Lys Leu Ala Leu Lys

1 5 10 15

Arg Val Cys Arg Lys Ser Val Leu Gly Ser Gly Gly Gln Arg Thr Ser

 20 25 30

Trp

<210> 253

<211> 28

<212> PRT

<213> Homo sapiens

<400> 253

Ser Phe Leu Val Leu Arg Phe Met Ser Gln Ile Ile Leu Ser Glu Phe

1 5 10 15

Trp Met Cys Cys Gly Leu Val Pro Thr Ser Ser Pro

20 25

<210> 254

<211> 39

<212> PRT

<213> Homo sapiens

<400> 254

Thr Arg Gly Thr Gly Trp Pro Leu Ala Gly Gln Gln Pro Gly Ser Cys

1 5 10 15

Pro Ser Gln His Gln Gly Leu Pro Gly Arg Leu Pro Pro Pro Arg Pro

20 25 30

Leu Gln Arg Val Arg His Thr

35

<210> 255

<211> 44

<212> PRT

<213> Homo sapiens

<400>

> 255

Cys Arg Arg Leu Val Ser Thr Leu Asn Phe Ser Ala His Leu Leu Met

1 5 10 15

Trp Thr Pro Cys Thr Val Thr Trp Pro Ile Cys Thr Leu Ser Ser Ser

20 25 30

Lys Thr His Ser Thr Ser Met His Met Gln Gln Ser

35 40

<210> 256

<211> 25

<212> PRT

<213> Homo sapiens

<400> 256

Leu Glu Arg Phe Glu Thr Leu Lys Ile Lys Ser Ser Lys Asn Ile Cys

1 5 10 15

Phe Leu His Val Ser Val Cys Pro Ser

20 25

<210> 257

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 257

Thr Leu Met Met Ser Asn Gly Cys Trp Gly Trp Gln Gln Ser Trp Glu

1 5 10 15

<210> 258

<211> 45

<212> PRT

<213> Homo sapiens

<400> 258

Ser Leu Leu Lys Arg Asn Met Lys Ser Ser Trp Met Phe Ala Lys Ile

1 5 10 15

Phe Asn Gln Phe Ser Val Thr Ser Ala Trp Lys Asn Ser Trp Ile Gln

20 25 30

Leu Phe Gly Leu Arg Ser Asp Trp Leu Ile Arg Ala Val

35 40 45

<210> 259

<211> 27

<212> PRT

<213> Homo sapiens

<400> 259

Ala Gly Ser Thr Gly Ala Ser Arg Pro Leu Arg Thr Arg Arg Thr Arg

1 5 10 15

Ser Gln Cys Arg Arg Ser Trp Ser Pro Ala Arg

20 25

<210> 260

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 260

His Pro Ala Ala Arg Ser Ser Ser Cys Cys Pro Ala Pro Met Ser Leu

1 5 10 15

Ser Trp Gly Thr Ala Leu Met Thr Ser Pro Arg

20 25

<210> 261

<211> 16

<212> PRT

<213> Homo sapiens

<400> 261

Arg Ser Gln Asn His Gln Lys Ser Pro Gln Ala Leu Ala Met Pro Trp

1 5 10 15

<210> 262

<211> 30

<212> PRT

<213> Homo sapiens

<400> 262

Arg Ser Gln Asn His Gln Lys Arg Lys Val Leu Gly Thr Ile Leu Val

1 5 10 15

His Asn His Ile Ile Asp Tyr Ala Trp Val Ile Cys His Leu

20 25 30

<210> 263

<211> 25

<212> PRT

<213> Homo sapiens

<400> 263

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

1 5 10 15

Gln Asn Gly Val Leu Ile Trp Leu Met

20 25

<210> 264

<211> 8

<212> PRT

<213> Homo sapiens

<400> 264

Lys Glu Lys Lys Gly Gly Ser Glu

1 5

<210> 265

<211> 12

<212> PRT

<213> Homo sapiens

<400> 265

Glu Leu Leu His Pro Ser Gln Arg Leu Leu Val Pro

1 5 10

<210> 266

<211> 17

<212> PRT

<213> Homo sapiens

<400> 266

Val Ile Phe Phe Ser Lys Pro Lys Arg Ile Lys Asn Leu Ser Leu Lys

1 5 10 15

Thr

<210> 267

<211> 26

<212> PRT

<213> Homo sapiens

<400> 267

Lys Ser Ala Arg Thr Ala Leu Asn Ser Glu Leu Asp Val Gln Asn Ala

1 5 10 15

Val His Glu Asn Gln Lys Glu Arg Val Phe

20 25

<210> 268

<211> 19

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 268

Ile Ile Leu Asp Thr Ala Lys Leu Leu Thr Ser Pro Gln Ser Leu Leu

1 5 10 15

Pro Ile Arg

<210> 269

<211> 11

<212> PRT

<213> Homo sapiens

<400> 269

Arg Ile Leu Leu Gly Thr Phe Leu Ala Ile Pro

1 5 10

<210> 270

<211> 24

<212> PRT

<213> Homo sapiens

<400> 270

Gly Cys Cys Arg Leu Leu Thr Glu Met Gly Lys Arg Lys Arg Lys Arg

1 5 10 15

Arg Ser His Trp Met Lys Ala Gln

20

<210> 271

<211> 11

<212> PRT

<213> Homo sapiens

<400> 271

Leu Ile Asn Pro Asp Lys Lys Ile Lys Met Ile

1 5 10

<210> 272

<211> 8

<212> PRT

<213> Homo sapiens

<400> 272

Asn Lys Lys Lys Val Asn Lys Asn

1 5

<210> 273

<211> 12

<212> PRT

<213> Homo sapiens

<400> 273

Phe Ile Phe Phe Leu Ile Leu Trp Ser Ser Arg Gln

1 5 10

<210> 274

<211> 12

<212> PRT

<213> Homo sapiens

<400> 274

Met Lys Lys Glu Asn Lys Ile Lys Trp Lys Leu Asn

1 5 10

<210> 275

<211> 13

<212> PRT

<213> Homo sapiens

<400> 275

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

1 5 10

<210> 276

<211> 18

<212> PRT

<213> Homo sapiens

<400> 276

Leu Ala Phe Ser Ser Leu Leu Trp Pro Ser His Leu Asp Met Ser Met

1 5 10 15

Leu Gln

<210> 277

<211> 17

<212> PRT

<213> Homo sapiens

<400> 277

Lys Pro Asn Lys Asn Thr Gln Ile Thr Phe Ser Leu Met Ser Phe Thr

1 5 10 15

Leu

<210> 278

<211> 12

<212> PRT

<213> Homo sapiens

<400> 278

Arg Phe Phe Pro Ser Ile Leu Ile Lys Ser Tyr Ile

1 5 10

<210> 279

<211> 12

<212> PRT

<213> Homo sapiens

<400> 279

Gly Ser Pro Pro Gly Gly Pro Arg Pro Cys Trp Thr

1 5 10

<210> 280

<211> 13

<212> PRT

<213> Homo sapiens

<400> 280

Ser Ile Gly Tyr Leu Thr Gly Phe Cys Ser Pro Asn Ala

1 5 10

<210> 281

<211> 13

<212> PRT

<213> Homo sapiens

<400> 281

Glu Glu Pro Pro Ser Cys Arg Pro Thr Ala His Ile Pro

1 5 10

<210> 282

<211> 13

<212> PRT

<213> Homo sapiens

<400> 282

Glu Gln Lys Thr Glu Trp Glu Trp Lys Leu Gln Ile Glu

1 5 10

<210> 283

<211> 12

<212> PRT

<213> Homo sapiens

<400> 283

Lys Val Ala Phe Leu Cys Glu Lys Glu Gln Ile Val

1 5 10

<210> 284

<211> 8

<212> PRT

<213> Homo sapiens

<400> 284

Gln Leu Lys Lys Ala Val Lys Val

1 5

<210> 285

<211>

> 12

<212> PRT

<213> Homo sapiens

<400> 285

Leu Gln Arg Met Ser Ser Asp Lys Arg Asn Thr Gly

1 5 10

<210> 286

<211> 9

<212> PRT

<213> Homo sapiens

<400> 286

Ile Asn Lys Lys Ile Gln Ala Thr Lys

1 5

<210> 287

<211> 93

<212> PRT

<213> Homo sapiens

<400> 287

Thr Ser Ser Pro Arg Thr Met Ser Trp Leu Cys Cys Leu Gly Gln Ile

1 5 10 15

Met Ala Ser Ala Val Glu Ala Ser Gln Pro Pro Thr Trp Pro Ser Met

20 25 30

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

35 40 45

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

50 55 60

Met Ala Ala Met Thr Thr Ala Ala Ala Pro Cys Ser His Pro Gln Ser

65 70 75 80

Trp Pro Val Ser Leu Ser Arg Trp Arg Cys Ala Ser Val

85 90

<210> 288

<211> 112

<212> PRT

<213> Homo sapiens

<400> 288

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

1 5 10 15

His Thr Gln Glu Arg Asp Pro Leu Ser Ala Val Asn Ala Gly Asn Arg

20 25 30

Leu Val Arg Ser His Thr Ser Met Tyr Ile Glu Lys Cys Thr Gln Glu

35 40 45

Lys Asp Arg Ile Val Ala Glu Asn Val Glu Asn Pro Ser Ala Arg Ser

50 55 60

His Ala Ser Ile Asn Ile Gly Glu Leu Thr Gln Glu Arg Ser Pro Met

65 70 75 80

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

85 90 95

Asp Ile Arg Lys Phe Met Leu Gly Arg Met Pro Thr Gly Met Lys Thr

100 105 110

<210> 289

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 289

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

1 5 10 15

Phe Gln Ile Ser Thr Tyr Gln Ala Gln Leu Arg Ile Ser Leu Arg Lys

20 25 30

Lys Lys Thr Lys Gln Asp Ile Leu Thr His Ile Ile Glu Cys Leu Lys

35 40 45

Lys Met Lys Thr Ser Thr Ser Leu Gly Met Ile

50 55

<210> 290

<211> 94

<212> PRT

<213> Homo sapiens

<400> 290

Val Ala Pro Cys Pro Trp Ser Trp Gly Ser Leu Arg Met Leu Val Gln

1 5 10 15

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

20 25 30

Leu Met Thr His Tyr Cys Ala Met Leu Gly Gln Leu Ser Ala Glu Ala
35 40 45

Lys Leu Arg Gly Arg Arg Gly Gly Gly Ala Ala Pro Gln Pro Val Pro
50 55 60

Ala Ser Asn Arg Val Ala Ala Ala Val Ser Gln Glu Asp Ala Gly Leu
65 70 75 80

Val Glu Glu Pro Met Glu Asp Val Val Glu Asp Gly Pro Gly
85 90

<210> 291

<211> 82

<212> PRT

<213> Homo sapiens

<400> 291

Asn Thr His Leu Gln Leu Thr His Cys Phe Leu Glu Ile Lys Pro Tyr

1 5 10 15

Ser Thr Lys Lys Met Lys Met Ala Cys Gly Lys Arg Ser Leu Leu Gln
20 25 30

Glu Val Lys Lys His Glu Leu Pro Lys Lys Ala Pro Ser Trp Pro Asp
35 40 45

Arg Pro Leu Val Gly Leu Ala Arg Ile Gln Ile Trp Ile Leu His Leu
50 55 60

Leu Gly Leu Arg Pro Pro Ser Leu Leu Ser Val Phe Gln Met Thr Phe

65 70 75 80

Ile Lys

<210> 292

<211> 88

<212> PRT

<213> Homo sapiens

<400> 292

Gly Gly Phe Arg Gln Trp Trp Cys Thr Cys Arg Met Ser Gly Pro Ser

1 5 10 15

Cys Leu Leu Trp Arg Ser Gly Arg Pro Cys Ala Ser Arg Lys Leu Gln
 20 25 30
 Arg Gln Leu Pro Gln Pro Arg Arg His Lys Gly Lys Arg Ser Leu Leu
 35 40 45

Asn Arg His Leu Met Pro Trp Ser Lys Gln Gln Thr Leu Leu Asp Gly
 50 55 60
 Thr Gln Lys Leu Gln Arg Pro Pro His Ser Arg Lys Arg Thr Leu Ile
 65 70 75 80
 Ser Gln Arg Pro Leu His Pro Pro
 85

<210> 293

<211> 62

<212> PRT

<213> Homo sapiens

<400> 293

Leu Ala Gly Leu Leu Cys Pro Ala Leu His Leu Val Lys Pro Arg Val
 1 5 10 15

Leu His Gln Asn Leu Asp Pro Thr Ser Ser Ser Phe Ser Lys Trp Cys
 20 25 30
 Arg Pro Trp Leu Glu Gln Met Leu His Ser Cys Arg Ile Gln Lys Ser
 35 40 45
 Asp Phe Ser Asn Asn Trp Asn Ser Ser Thr Gln Trp Gly Ser
 50 55 60

<210> 294

<211> 127

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 294

Asn Val His Arg Gln Pro Val Gln Ile Ile Lys Asn Met Glu Thr Thr
 1 5 10 15

Val Thr Tyr Arg Lys Lys Gln Ile Gln Ser Gln Ser Ser Thr Ser Ile

20 25 30
 Leu Ser Ala Leu Arg Val Ser Pro Val Arg Asn Ser Pro Cys Ser Met
 35 40 45
 Cys Cys Val Ile Ile Pro Pro Gly Ser Ser His Ala Cys Val Gln Lys
 50 55 60
 Val Thr Ser Ser Leu Gly Ile Arg Ala Gln Gly Thr Arg Arg Ser Ser

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

<210> 295

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 295

Asn Val His Arg Gln Pro Val Gln Gln Ile Gln Ser Gln Ser Ser Thr
 1 5 10 15

<210> 296

<211> 14

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 296

Val His Arg Gln Pro Val Gln Ile Gln Ser Gln Ser Ser Thr
 1 5 10

<210> 297

<211> 30

<212> PRT

<213> Homo sapiens

<400> 297

Ser Arg Pro Gly Trp Lys Arg Thr Gln Gln Arg Pro Pro Trp Arg Thr

1 5 10 15

Ser Arg Gly Gln Ala Gln Asp Thr Ser Gly His Arg Gly Ser

20 25 30

<210> 298

<211> 53

<212> PRT

<213> Homo sapiens

<400> 298

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

1 5 10 15

Ser Arg Ser Thr Thr Ala Pro Val Gly Ser Gln Cys Val Pro Ser Trp

20 25 30

Thr Ala Arg Arg Trp Ser Thr Thr Ala Ser Gly Trp Arg Arg Trp Thr

35 40 45

Thr Ala Arg Pro Pro

50

<210> 299

<211> 37

<212> PRT

<213> Homo sapiens

<400> 299

Leu Ser Ala Ile Arg Lys Met Thr Tyr Phe Thr Ser Trp Ile Leu Asp

1 5 10 15

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

20 25 30

Lys Arg Met Trp Ser

35

<210> 300

<211> 54

<212> PRT

<213> Homo sapiens

<400> 300

Trp Glu Thr Leu Ser Thr Trp Arg Pro Ser Glu Arg Trp Ser Cys Arg

1 5 10 15

Ser Pro Ala Ser Leu Pro Arg Met Trp Cys Trp Cys His Gln Ala Ser

20 25 30

Met Pro Trp Arg Ala Thr Pro Pro Leu Leu Gly Ala Thr Thr Ser Pro

35 40 45

Pro Asp Ala Ser Gly Thr

50

<210> 301

<211> 42

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 301

Tyr Lys Gly Arg Lys Glu Arg Lys Thr Ser Val Gln Gly Ile Thr Thr

1 5 10 15

Val Ile Leu Lys Arg Arg Thr Ser Leu Arg Arg Glu Ser Phe Met Lys

20 25 30

Asn Phe Leu Ala Val Thr Ile Thr Gly Ser

35 40

<210> 302

<211> 67

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 302

Arg Pro Pro Met Thr Thr Trp Pro Arg Met Arg Met Thr Leu Arg Trp

1 5 10 15

Ala Arg Gly Ser Leu Pro Gly Pro Ala Arg Ala Arg Pro Thr Thr Pro

20 25 30

Leu Leu Pro Trp Arg Thr Thr Cys Ser Ser Arg Pro Arg Val Gly Ala

35 40 45

Ser Arg Pro Ala Pro His Arg Pro Gln Arg Ser Ser Arg Arg Tyr Ser

50 55 60

Arg Ser Ala

65

<210> 303

<211> 71

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 303

Arg Ser Thr Gly Leu Thr Gly Glu Gln Thr His Trp Leu Arg Pro Thr

1 5 10 15

Ser Gly Pro Ala Thr Met Ser Pro Trp Tyr Arg Gly Pro Thr Pro Ser

20 25 30

Pro Leu Thr Cys Arg Cys Thr Thr Pro Pro Ala Ser Pro Trp Leu Pro

35 40 45

Ile Pro Val Arg Pro Met Gly Ala Arg Ala Pro Ala Pro Thr Cys Val

50 55 60

Ser Ser Thr Thr Thr Gly Ser

65 70

<210> 304

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 304

Arg Ser Leu Pro Ala Gly Pro Ser Ser Arg Arg Arg Ala Pro Pro Arg

1 5 10 15

Ser Gly Arg Gly Ser Leu Arg Lys Trp Arg Pro Gly Ala Ser Arg Arg

20 25 30

Trp Arg Met Ser Thr Trp Pro Ser

35 40

<210> 305

<211> 43

<212> PRT

<213> Homo sapiens

<400> 305

Val Ser Thr Ser Trp Gly Pro Thr Ala Gly Ala Ala Arg Ala Arg Thr

1 5 10 15

Cys Ser Pro Cys Ser Pro Thr Thr Pro Ser Pro Ala Ser Gly Ser Thr

20 25 30

Ser Arg Arg Thr Arg Pro Asn Arg Val Leu Thr

35 40

<210> 306

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 306

Thr Trp Pro Ala Ala Cys Trp Ala Thr Trp Thr Ser Pro Gly Ala Ala

1 5 10 15

Val Pro Val Ala Leu Arg Pro Ser Ala Ser Trp Ser Arg Cys Thr Cys

20 25 30

Ser Ser Ser Ala Thr Met Trp Arg Ser Thr Thr Pro Arg

35 40 45

<210> 307

<211> 32

<212> PRT

<213> Homo sapiens

<400> 307

Arg Arg Ser Arg Ala Glu Cys Gly Ser Thr Arg Ser Leu Thr Ala Arg

1 5 10 15

Arg Glu Thr Pro Thr Ala Thr Met Cys Ala Ala Pro Arg Val Ser Pro

20 25 30

<210> 308

<211> 57

<212> PRT

<213> Homo sapiens

<400>

308

Met Val Lys Arg Lys Asn Pro Lys Arg Arg Lys Leu Gln Glu Leu Leu

1 5 10 15

Lys Arg Arg Lys Leu Arg Lys Asn Ser Asn Leu Ser His Met Met Ile

20 25 30

Arg Phe Phe Trp Met Glu Met Arg Cys Met Tyr Gly Ser Met Thr Gln

35 40 45

Phe Thr Leu Lys His Leu Ser Trp Asp

50 55

<210> 309

<211> 35

<212>

> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 309

Arg Glu Pro Leu Val Leu Ser Val Gly Asn Leu Ile Gly Leu Pro Ile

1 5 10 15

Met Pro Ser Arg Cys Glu Asn Ser Ser Leu Gly Gly Met Leu Glu Met

20 25 30

Ser Met His

35

<210> 310

<211> 28

<212> PRT

<213> Homo sapiens

<400> 310

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

1 5 10 15

Pro Ala Ala Cys His Pro Ser Leu Arg Thr Gly Thr

20

25

<210> 311

<211> 66

<212> PRT

<213> Homo sapiens

<400> 311

Gly Met Thr Ser Thr Cys Pro Ser Ala Met Thr Trp Ala Thr Ser Ser

1

5

10

15

Pro Cys Ser Ala Thr Glu Arg Ala Thr Ser Ala Gly Val Trp Thr Lys

20

25

30

Met Ala Glu Arg Cys Arg Ala Pro Ala Pro Ser Gln Ala Pro Pro Leu

35

40

45

Arg Val Tyr Pro Pro Ser Leu His Pro Trp Ser Gly Pro Arg Pro Gly

50

55

60

Gln Met

65

<210> 312

<211> 38

<212> PRT

<213> Homo sapiens

<400> 312

Gly Gly Arg Met Leu Leu Glu Met Met Lys Arg Leu Val Arg Lys Asn

1

5

10

15

Leu Lys Lys Thr Met Met Ile Leu Lys Thr Ser Leu Lys Met Ser Phe

20

25

30

Gln Lys Met Arg Lys Arg

35

<210> 313

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 313

Ser His Ile Trp Pro Lys Gly Phe Glu Ala Gln Arg Ala Gln Glu His

1 5 10 15

Arg Ala Gln Leu Val Cys Ser Ala Leu Leu Pro Glu Gly Ile Arg Cys

20 25 30

Arg Pro Gly Ala Pro Ala Ala Val Ser Pro Pro Arg Gly Ser Gln

35 40 45

<210> 314

<211> 50

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 314

Gln Thr Ser His Trp Cys Pro Thr Gln Pro Arg Arg Val Ala Ser Arg

1 5 10 15

Val Trp Pro Ser Thr Thr Thr Leu Ser Cys Pro Pro Arg Ser Ser Thr

20 25 30

Ser Cys Ser Thr Ala Ala Thr Ala Pro Ser Pro Cys Thr Pro Arg Ala

35 40 45

Ala Glu

50

<210> 315

<211> 22

<212> PRT

<213> Homo sapiens

<400> 315

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

1 5 10 15

Thr Val Leu Leu His Leu

20

<210> 316

<211> 36

<212> PRT

<213> Homo sapiens

<400> 316

Asn Asp Gly Gly Gly Ser Arg Ser Trp His Leu Pro Ser His Pro Met

1 5 10 15

Gln Gln Thr Pro Thr Thr Ala Arg Pro Ser Thr Gln Thr Ser Trp Pro

20 25 30

Ser Trp Pro Ser

35

<210> 317

<211> 30

<212> PRT

<213> Homo sapiens

<400> 317

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

1 5 10 15

Asn His Tyr Ser Phe Cys Gln Lys His Glu Gln Ser His Thr

20 25 30

<210> 318

<211> 26

<212> PRT

<213> Homo sapiens

<400> 318

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

1 5 10 15

Glu Met Ala Arg Arg Lys Lys Thr Glu Glu

20 25

<210> 319

<211> 17

<212> PRT

<213> Homo sapiens

<400> 319

Leu Ala Met Thr Asp Asp Gln Arg Met Val Lys Asn Lys Gln Leu Leu

1 5 10 15

Met

<210> 320

<211> 21

<212> PRT

<213> Homo sapiens

<400> 320

Met Leu Thr Gln Thr Asp Ser Ala Trp Asp Leu Glu Ile Ala Glu Val

1 5 10 15

Leu Phe His Ile Gln

20

<210> 321

<211> 34

<212> PRT

<213> Homo sapiens

<400> 321

Ala Phe Arg Asp Arg Asn Thr Arg Ile Leu Gly Arg Val Ser Ala Pro

1 5 10 15

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

20 25 30

Lys Phe

<210> 322

<211> 54

<212> PRT

<213> Homo sapiens

<400> 322

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

1 5 10 15

Pro Trp Gln Pro Gly Arg Asn Ile Thr Thr Lys Leu Ile Gln Arg Pro

20 25 30

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

35 40 45

Leu Gly Glu Glu Glu Leu

50

<210> 323

<211> 26

<212> PRT

<213> Homo sapiens

<400> 323

Ser Ser His Met His Asn Thr Ser Pro Cys Gln Met Met Ser His Leu

1 5 10 15

Asn His Val Gln Phe Val Leu Tyr Lys Leu

20 25

<210> 324

<211> 32

<212> PRT

<213> Homo sapiens

<400> 324

Cys Tyr Leu Ala Gly Ser Lys Met Thr Ser Leu Thr Ser Gly Trp Asn

1 5 10 15

Gly Lys Arg Gln Ser Cys Ser Gln Leu Cys Leu Leu Pro Cys Thr Ile

20 25 30

<210> 325

<211> 73

<212> PRT

<213> Homo sapiens

<400> 325

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

1 5 10 15

Leu His Phe Leu Ala Lys Asp Pro His Pro Met Phe Leu Cys Thr Pro

20 25 30

Arg Ala His Pro Leu Ala Arg Pro Gln Gly His Leu Leu Ala His Pro

35 40 45

Gly Pro Ser Pro Thr Trp Pro Gly Pro Leu Pro Leu Pro Gln Thr Arg

50 55 60
 Leu Asp Leu Ser Ala Gly Pro Thr Ala
 65 70
 <210> 326
 <211> 24
 <212> PRT
 <213> Homo sapiens
 <400> 326
 Ser Ser Ile His Ile Val Glu Lys Gln Leu Lys Leu Arg Glu Arg Pro
 1 5 10 15
 Thr Asn Lys Lys Lys Arg Lys Asn
 20
 <210> 327
 <211> 25
 <212> PRT
 <213> Homo sapiens
 <400> 327
 Leu Gln Lys Lys Ala Pro Gln Lys Arg Ile Lys Leu Leu Arg Met Leu
 1 5 10 15
 Pro Ala Leu Tyr Leu Met Ala Cys Gln
 20 25
 <210> 328
 <211> 40
 <212> PRT
 <213> Artificial Sequence
 <220><223> modified Homo sapiens FSP
 <400> 328
 Ala Ala Gln Met Ser Trp Ser Leu Pro Cys Pro Pro Gly Gly Ala Glu
 1 5 10 15
 Glu Arg Met Glu Ala Pro Ser Val Gly Val Ala Arg Arg Arg Arg Arg
 20 25 30
 Ser Lys Gly Ser Ser Met Arg Cys
 35 40

<210> 329

<211> 24

<212> PRT

<213> Homo sapiens

<400> 329

Met Thr Pro Gly Pro Gly Ala Gly Pro Ala Ala Cys Ser Ser Cys Ala

1 5 10 15

Pro Ala Leu Cys Ala Ala Ala Ala

20

<210> 330

<211> 34

<212> PRT

<213> Homo sapiens

<400> 330

Thr Ser Arg Gly Ser Ser Leu Gln Ala Ser Ser Trp Lys Met Ala Ala

1 5 10 15

Leu Phe Leu Thr Thr Thr Ser Arg Lys Ser Arg Pro Cys Thr Trp Ser

20 25 30

Cys Ala

<210> 331

<211> 10

<212> PRT

<213> Homo sapiens

<400> 331

Phe Glu Phe Phe Leu Gln Cys Pro Ala Lys

1 5 10

<210> 332

<211> 24

<212> PRT

<213> Homo sapiens

<400> 332

Leu Cys Thr Ile Cys Thr Ser Tyr Val Ser Pro Trp Ile Ile Phe Thr

1 5 10 15

Glu Met Glu Tyr Phe Thr Glu Met

20

<210> 333

<211> 33

<212> PRT

<213> Homo sapiens

<400> 333

Cys Gly Lys Ser Ile Trp Trp Leu Lys Glu Leu Arg Val Leu Met Phe

1 5 10 15

Leu His Leu Trp Asp Ser Met Lys Gln Val Ala Leu His Gln Ser Asn

20

25

30

Arg

<210> 334

<211> 23

<212> PRT

<213> Homo sapiens

<400> 334

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

1 5 10 15

Arg Pro Leu Thr Leu Gln Ser

20

<210> 335

<211> 15

<212> PRT

<213> Homo sapiens

<400> 335

Leu Lys Asp Cys Ile Ser Thr Lys Pro Ile Ser Gly Ile Val Pro

1 5 10 15

<210> 336

<211> 25

<212> PRT

<213> Homo sapiens

<400> 336

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

1 5 10 15

Trp Pro Leu Gly Lys Phe Arg Phe Arg

20 25

<210> 337

<211> 35

<212> PRT

<213> Homo sapiens

<400> 337

Lys Phe Cys Asn Phe Ile Leu Leu Phe Ser Leu Ile Leu Ser Ile Lys

1 5 10 15

His Ile Ser Val Phe Phe His Ile Phe Ser Ala Val Ile Leu Thr Gln

20 25 30

Tyr Arg Ser

35

<210> 338

<211> 13

<212> PRT

<213> Artificial Sequence

<

220><223> modified Homo sapiens FSP

<400> 338

Gly Arg Cys Tyr Gln Leu Pro Gln Leu Gln Gly Phe Leu

1 5 10

<210> 339

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 339

Ser Lys Leu Tyr Gly Asp His Phe Leu Leu Leu

1 5 10

<210> 340

<211> 21

<212> PRT

<213> Homo sapiens

<400> 340

Ala Arg Ala Ile Ala Thr Arg Pro Gly Gly Trp Asn Arg Met Gly Glu

1 5 10 15

Pro Arg Gly Phe Cys

20

<210> 341

<211> 13

<212> PRT

<213> Homo sapiens

<400> 341

Glu Glu Leu Phe Leu Leu Val Ser Leu Ala Met Phe Arg

1 5 10

<210> 342

<211> 22

<212> PRT

<213> Homo sapiens

<400> 342

Ile Pro Ser Arg His Met Phe Ser Val Thr Lys Ile Met Leu Lys Glu

1 5 10 15

Thr Phe Lys Arg Arg Lys

20

<210> 343

<211> 22

<212> PRT

<213> Homo sapiens

<400> 343

Arg Arg Lys Ile Ile Pro Asn Cys Phe Trp Gly Lys Thr Glu Ser Pro

1 5 10 15

Ser Ile Phe Thr Thr Cys

20

<210> 344

<211> 41

<212> PRT

<213> Homo sapiens

<400> 344

Arg Thr Thr Thr Thr Ser Leu Lys Glu Glu Glu Gly Ile Ile Leu Ile

1 5 10 15

Thr Glu Ser Arg Ser Leu Ala Leu Leu Phe Gln Ser Leu Met Ile Leu

20 25 30

Ile Cys Ala Gly Thr Lys Glu Pro Phe

35 40

<210> 345

<211> 33

<212> PRT

<213> Homo sapiens

<400> 345

Ser Ser Gly Gly Gly Leu Gly Leu Ile Met Leu Pro Trp Ser Gly Val

1 5 10 15

Glu Ile Ile Ile Cys Leu Lys Arg Ile Val Lys Arg Arg Lys Arg Lys

20 25 30

Asn

<210> 346

<211>

> 11

<212> PRT

<213> Homo sapiens

<400> 346

Thr Thr Lys Lys Ser Met Ile Glu Trp Lys Ile

1 5 10

<210> 347

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 347

Ala Gly Ser Ala Thr Lys Met Ser Thr Asn Ala Ala Arg Arg Thr Gly

1 5 10 15

Ala Ala Ser Arg Ser Ala Thr Thr Ser Arg Val Ala Ser Thr Val Pro

20 25 30

Ala Met Ala Gly Pro Ala Lys Thr

35 40

<210> 348

<211> 9

<212> PRT

<213> Homo sapiens

<400> 348

Gly Ser Lys Lys Thr Gly Ile Met Trp

1 5

<210> 349

<211> 16

<212> PRT

<213> Homo sapiens

<400> 349

Arg Glu Lys Arg Gln Ala Val Asn Met Met Cys Gln His Thr Met Ile

1 5 10 15

<210> 350

<211> 27

<212> PRT

<213> Homo sapiens

<400> 350

Gly Leu Ser Leu Ser Tyr Gly Pro Val Ser Pro Ile Ile Arg Arg Leu

1 5 10 15

Trp Asn Ile Phe Val Arg Asn Gln Glu Lys Ile

20 25

<210> 351

<211> 17

<212> PRT

<213> Homo sapiens

<400> 351

Ser Ser Cys Phe Gln Arg Arg Lys Arg Arg Ile Tyr Gln His Leu Arg

1 5 10 15

Tyr

<210> 352

<211> 68

<212> PRT

<213> Homo sapiens

<400> 352

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

1 5 10 15

Arg Pro Pro Ala Phe Leu Trp Ala Leu Arg Ile Leu Thr Pro Leu Pro

20 25 30

Leu Pro Gln Pro Gln Pro Pro Ala Val Ala Thr Ala Thr Val Ala Ala

35 40 45

Thr Ala Ala Ala Leu Leu Gly Leu Cys Pro Phe Pro His His Pro Ile

50 55 60

Trp Pro Glu Val

65

<210> 353

<211> 13

<212> PRT

<213> Homo sapiens

<400> 353

Ser Pro Ser Leu Gln Thr Gln Trp Arg Leu Lys Arg Ser

1 5 10

<210> 354

<211> 12

<212> PRT

<213> Homo sapiens

<400> 354

Thr Leu Val Met Val Ala Thr Val Lys Leu Phe Leu

1 5 10

<210> 355

<211> 23

<212> PRT

<213> Homo sapiens

<400> 355

Leu Val Cys Ser Ala Leu Ile Ser Leu Thr Leu Lys Gly Asn Leu Phe

1 5 10 15

Thr Leu Leu Thr Leu Leu Met

20

<210> 356

<211> 40

<212> PRT

<213> Homo sapiens

<400> 356

Val Ala Phe His Pro Ser Gln Pro Gly Pro Cys Gly Arg Pro Thr Pro

1 5 10 15

Lys Leu Pro Ser Pro Met Arg Arg Gln Pro Ser Trp Gln Trp Ala Ala

20 25 30

Ser Pro Ser Thr Ala Thr Thr Ser

35 40

<210> 357

<211> 26

<212> PRT

<213> Homo sapiens

<400> 357

Leu Val Ile Pro Lys Leu Ile Ile Leu Met Glu Lys Thr Leu Thr Gly

1 5 10 15

Cys Leu Arg Ala Leu Lys Met Asn Arg Phe

20 25

<210> 358

<211> 14

<212> PRT

<213> Homo sapiens

<400> 358

Thr Lys Ser Gly Lys Lys Gln Glu Leu Thr Phe Leu Leu Leu

1 5 10

<210> 359

<211> 11

<212> PRT

<213> Homo sapiens

<400> 359

Glu Ser Pro Pro Ala Pro Ser Met Pro Arg Cys

1 5 10

<210> 360

<211> 17

<212> PRT

<213> Homo sapiens

<400> 360

Arg Gln Thr Leu Arg Thr Leu Ser Leu Arg Gly Met Val Pro Arg Thr

1 5 10 15

Leu

<210> 361

<211> 10

<212> PRT

<213> Homo sapiens

<400> 361

Thr Thr Ser Gln Ser Gln Leu Ser Ser Glu

1 5 10

<210> 362

<211> 9

<212> PRT

<213> Homo sapiens

<400> 362

Glu Met Lys Lys Thr Thr Phe Ile Ser

1 5

<210> 363

<211> 25

<212> PRT

<213> Homo sapiens

<400> 363

Arg Phe Gln Met Gln Pro Leu Ser Leu Met Pro Ala His Trp Ser Ile

1 5 10 15

Cys Leu Leu Arg Asp Ser Met Ile Trp

20 25

<210> 364

<211> 13

<212> PRT

<213> Homo sapiens

<400> 364

Val Trp Lys Lys Met Lys Ser Lys Thr Ser Cys Val Val

1 5 10

<210> 365

<211> 10

<212> PRT

<213> Homo sapiens

<400> 365

Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys

1 5 10

<210> 366

<211> 18

<212> PRT

<213> Homo sapiens

<400> 366

Thr Trp Pro Thr Gln Thr Trp Thr Arg Leu Pro Arg Arg Ser Cys Cys

1 5 10 15

Ser Arg

<210> 367

<211> 13

<212> PRT

<213> Homo sapiens

<400> 367

His Thr Ser Thr Leu Gly Lys Lys Ser Ile Leu Leu Leu

1 5 10

<210> 368

<211> 26

<212> PRT

<213> Homo sapiens

<400> 368

Gly Ile Tyr Phe Met Leu Gln Thr Pro Thr Ile Thr Arg Leu Lys Leu

1 5 10 15

Trp Ile Gln Lys Gln Lys Thr Val Gln His

20 25

<210> 369

<211> 13

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 369

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

1 5 10

<210> 370

<211> 31

<212> PRT

<213> Homo sapiens

<400> 370

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

1 5 10 15

Cys Leu Leu Ser Gln Ala Pro Pro Ala Gly Ser Gly Gly Arg Arg

20 25 30

<210> 371

<211> 55

<212> PRT

<213> Homo sapiens

<400> 371

Gly Ser Pro Ser Arg Ser Ala Ala Cys Gly Gly Arg Glu Arg Arg Asp

1 5 10 15

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

20 25 30

Trp Pro Cys Pro Ala Val Pro Leu Gly Pro Ala Arg Thr Gly Leu Leu

35 40 45

Pro Gly Glu Ala Ala Pro Ser

50 55

<210> 372

<211> 15

<212> PRT

<213> Homo sapiens

<400> 372

Cys Trp Thr Ser His Leu Met Gln Met Thr Arg Pro Trp Leu Asn

1 5 10 15

<210> 373

<211> 12

<212> PRT

<213> Homo sapiens

<400> 373

Gln Arg Lys Lys Ser Leu Lys Pro Ser Gly Ser Leu

1 5 10

<210> 374

<211> 8

<212> PRT

<213> Homo sapiens

<400> 374

Arg Thr Pro Pro Gly Gly Gly Arg

1 5

<210> 375

<211> 8

<212> PRT

<213> Homo sapiens

<400> 375

Glu Glu Lys Lys Lys Ala His Leu

1 5

<210> 376

<211> 15

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 376

Ala Thr Val Pro Thr Cys Ser Pro Arg Thr Leu Arg Cys Leu Pro

1 5 10 15

<210> 377

<211> 11

<212> PRT

<213> Homo sapiens

<400> 377

Ile Gly Asp Arg Glu Gln Val Lys Lys Thr Met

1 5 10

<210> 378

<211> 9

<212> PRT

<213> Homo sapiens

<400> 378

Leu Ser Lys Lys Glu Lys Met Thr Arg

1 5

<210> 379

<211> 28

<212> PRT

<213> Homo sapiens

<400> 379

Leu Ser Ile Asn Asn Tyr Arg Phe Gln Met Lys Phe Tyr Phe Arg Phe

1 5 10 15

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

20 25

<210> 380

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 380

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

1 5 10 15

Ser Cys Gln Thr Thr Pro Pro Ile Thr Leu Ser Ser Thr Pro Arg

20 25 30

<210> 381

<211> 8

<212> PRT

<213> Homo sapiens

<400> 381

Asp Tyr Lys Lys Asn Thr Gly Ile

1 5

<210> 382

<211> 10

<212> PRT

<213> Homo sapiens

<400> 382

Ile Val Ala Leu Met Ser Ser Thr Ile Ile

1 5 10

<210> 383

<211> 12

<212> PRT

<213> Homo sapiens

<400> 383

Ile Pro Phe Phe Thr Gly Leu Thr Arg Met Met Arg

1 5 10

<210> 384

<211> 25

<212> PRT

<213> Homo sapiens

<400> 384

Glu Gly Arg Ser Ser Thr Asn Ala Arg Ser Ala Thr Val Cys Leu Thr

1 5 10 15

Ala Gly Thr Ser Ser Lys Ile Thr Trp

20 25

<210> 385

<211> 14

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 385

Ser Phe Ile Ala Leu Ile Gly Arg Leu Met Phe Gln Ala Cys

1 5 10

<210> 386

<211> 17

<212> PRT

<213> Homo sapiens

<400> 386

Asn Thr Met Lys Trp Trp Glu Leu Tyr Leu Val Ile Leu Ser His Ile

1 5 10 15

Ala

<210> 387

<211> 13

<212> PRT

<213> Homo sapiens

<400> 387

Ser Lys Pro Lys Arg Ile Lys Asn Leu Ser Leu Lys Thr

1 5 10

<210> 388

<211> 14

<212> PRT

<213> Homo sapiens

<400> 388

Ser Leu Asn Gln Arg Ser Tyr Ala Arg Pro Ser Cys Gln Pro

1 5 10

<210> 389

<211> 16

<212> PRT

<213> Homo sapiens

<400> 389

Met Ser Pro Pro Phe Met Pro Ser Arg Val Leu Phe Met Ser Arg Arg

1 5 10 15

<210> 390

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 390

Ile Arg Val Ile Glu Val Ala Arg His Lys Pro Leu Leu Arg Asn Leu

1 5 10 15

Lys Lys Lys Lys Ala Arg Ile Leu Arg Lys

20 25

<210> 391

<211> 13

<212> PRT

<213> Homo sapiens

<400> 391

Pro Ala Gly Trp Pro Gln Ala Ala Pro Arg Pro Ser Ala

1 5 10

<210> 392

<211> 16

<212> PRT

<213> Homo sapiens

<400> 392

Met Ala Thr Ser Ser His Arg Phe Leu Glu Asp Met Leu Pro Ala Lys

1 5 10 15

<210> 393

<211> 9

<212> PRT

<213>

> Homo sapiens

<400> 393

Glu Ser Pro Pro Ala Ser Leu Lys Asn

1 5

<210> 394

<211> 12

<212> PRT

<213> Homo sapiens

<400> 394

Gly Pro Pro Pro Ala Pro Pro Ile Ser Leu Ala Ser

1 5 10

<210> 395

<211> 10

<212> PRT

<213> Homo sapiens

<400> 395

Thr Gln Lys Lys Ser Tyr Pro Ile Lys Thr

1 5 10

<210> 396

<211> 11

<212> PRT

<213> Homo sapiens

<400> 396

Asn Trp Ile Ser Lys Lys Leu Asn Leu Thr Met

1 5 10

<210> 397

<211> 9

<212> PRT

<213> Homo sapiens

<400> 397

Leu Tyr Lys Lys Asn Ser Arg Arg Leu

1 5

<210> 398

<211> 14

<212> PRT

<213> Homo sapiens

<400> 398

Ser Ile Phe Leu Ala Lys Glu Ser Ser Gly Arg Ala Tyr Val

1 5 10

<210> 399

<211> 13

<212> PRT

<213> Homo sapiens

<400> 399

His Gln Arg Cys Ala Ala Ser Gln Gln Ser Ala Ser Phe

1 5 10

<210> 400

<211> 9

<212> PRT

<213> Homo sapiens

<400> 400

Asp Leu Lys Lys Arg Arg Ser Ala Val

1 5

<210> 401

<211> 17

<212> PRT

<213> Homo sapiens

<400> 401

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

1 5 10 15

Gly

<210> 402

<211> 14

<212> PRT

<213> Homo sapiens

<400> 402

Asn Tyr Asn Lys Glu Phe Leu His Gln Gly Gln Leu Glu Asn

1 5 10

<210> 403

<211> 15

<212> PRT

<213> Homo sapiens

<400> 403

Leu Gln Thr Trp Lys Lys Asn His Leu Thr Gln Thr Thr Leu Lys

1 5 10 15

<210> 404

<211> 10

<212> PRT

<213> Homo sapiens

<400> 404

His Ile Thr Gly Gly Thr Gly Leu Leu Leu

1 5 10

<210> 405

<211> 10

<212> PRT

<213> Homo sapiens

<400> 405

Glu Glu Gly Gly Cys Ala Ser Gly Thr Trp

1 5 10

<210> 406

<211> 29

<212> PRT

<213> Homo sapiens

<400> 406

Asn Gln Glu Arg Ser Pro Asp Pro Ser Pro Asp Leu His Thr Gly Leu

1 5 10 15

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

20 25

<210> 407

<211> 12

<212> PRT

<213> Homo sapiens

<400> 407

Ala His Gln Lys Arg Lys Gln Ser Cys Arg Cys Ser

1 5 10

<210> 408

<211> 9

<212> PRT

<213> Homo sapiens

<400> 408

Cys His Lys Lys Thr Ser Gln Leu Asp

1 5

<210> 409

<211> 16

<212> PRT

<213> Homo sapiens

<400> 409

Arg Glu Phe Ile Asn Leu Lys Met Ile Lys Trp Thr Leu Leu Lys Ser

1 5 10 15

<210> 410

<211> 12

<212> PRT

<213> Homo sapiens

<400> 410

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

1 5 10

<210> 411

<211> 13

<212> PRT

<213> Homo sapiens

<400> 411

Ser Leu Ser Pro Gly Pro Lys Arg Thr Gln Ile Trp Ser

1 5 10

<210> 412

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 412

Asn Trp Met Thr Met Gln Thr Ile Ile Lys Asn Arg Thr Glu Ala Met

1 5 10 15

Pro Arg Glu His Leu Leu

20

<210> 413

<211> 11

<212> PRT

<213> Homo sapiens

<400> 413

Glu Phe Phe Phe Thr Ile Gly Ile Thr Trp Ile

1 5 10

<210> 414

<211> 11

<212> PRT

<213> Homo sapiens

<400> 414

Phe Pro Phe Phe Ser Ser Leu Glu Gln Cys Pro

1 5 10

<210> 415

<211> 8

<212> PRT

<213> Homo sapiens

<400> 415

Leu Tyr Lys Lys Ile Glu Lys Asn

1 5

<210> 416

<211> 21

<212> PRT

<213> Homo sapiens

<400>

416

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

1 5 10 15

Thr Ser Ser Ser Leu

20

<210> 417

<211> 12

<212> PRT

<213> Homo sapiens

<400> 417

Leu Pro Leu Gln Pro Tyr Leu Leu Pro Cys Leu Leu

1 5 10

<210> 418

<211> 11

<212> PRT

<213> Homo sapiens

<400> 418

Leu Ile Glu Gln Asn Leu Ile Gly Lys Lys Asn

1 5 10

<210> 419

<211> 11

<212> PRT

<213> Homo sapiens

<400> 419

Glu His Gly Gly Pro Pro Ser Ser Met Pro Leu

1 5 10

<210> 420

<211> 11

<212> PRT

<213> Homo sapiens

<400> 420

Thr His Trp Lys Arg Asn Pro Lys Ala Ile Trp

1 5 10

<210> 421

<211> 13

<212> PRT

<213> Homo sapiens

<400> 421

Gly Tyr Thr Pro Gln Met Glu Ala Gly Ala Gly Gln Trp

1 5 10

<210> 422

<211> 11

<212> PRT

<213> Homo sapiens

<400> 422

Leu Thr Lys Lys Ile Arg Asn Ser Cys Leu Ile

1 5 10

<210> 423

<211> 10

<212> PRT

<213> Homo sapiens

<400> 423

Gln Pro Pro Arg Arg Pro Ser Thr Ala Asn

1 5 10

<210> 424

<211> 10

<212> PRT

<213> Homo sapiens

<400> 424

Ala Pro Lys Lys Thr Leu Leu Lys Cys Trp

1 5 10

<210> 425

<211> 9

<212> PRT

<213> Homo sapiens

<400> 425

Asp Met Lys Lys Asn Cys Gly Ser Leu

1 5

<210> 426

<211> 9

<212> PRT

<213> Homo sapiens

<400> 426

Trp Thr Thr Gly Val Pro Pro Ser Ser

1 5

<210> 427

<211> 11

<212> PRT

<213> Homo sapiens

<400> 427

Asp Ser Leu Lys Met Val Lys Asn Phe Leu Ser

1 5 10

<210> 428

<211> 9

<212> PRT

<213> Homo sapiens

<400> 428

Phe Leu Asn Pro Arg Lys Leu Gly Pro

1 5

<210> 429

<211> 9

<212> PRT

<213> Homo sapiens

<400> 429

Lys Thr Pro Pro Gly Gly Tyr Pro Leu

1 5

<210> 430

<211> 14

<212> PRT

<213> Homo sapiens

<400> 430

Ser Pro Cys Trp Ala Trp Thr Pro Gly Gly Trp Ala Ala Ser

1 5 10

<210> 431

<211> 8

<212> PRT

<213> Homo sapiens

<400> 431

Gln Val Pro Pro Ser Ile Leu His

1 5

<210> 432

<211> 11

<212> PRT

<213> Homo sapiens

<400> 432

Val Lys Pro Thr Leu Trp Glu Glu Gly Thr Ser

1 5 10

<210> 433

<211> 8

<212> PRT

<213> Homo sapiens

<400> 433

Tyr Trp Ala Pro His Val Thr Pro

1 5

<210> 434

<211> 11

<212> PRT

<213> Homo sapiens

<400> 434

Leu Leu His Phe Leu Val Met Leu Arg Ile Ile

1 5 10

<210> 435

<211> 11

<212> PRT

<213>

> Homo sapiens

<400> 435

Asn Thr Leu Lys Asn Ser Phe Leu Leu Trp Pro

1 5 10

<210> 436

<211> 11

<212> PRT

<213> Homo sapiens

<400> 436

Glu Arg Gln Lys Ile Lys Lys Lys Pro Lys Arg

1 5 10

<210> 437

<211> 42

<212> PRT

<213> Homo sapiens

<400> 437

Gly Arg Arg Lys Arg Ser Glu Gly Gly Val Lys Arg Lys Lys Glu Asn

1 5 10 15

Val Cys Lys Arg Arg Lys Arg Asn Val Gly Glu Lys Lys Arg Lys Gly

20 25 30

Phe Asp Gly Arg Lys Arg Lys Gly Asp Gly

35 40

<210> 438

<211> 24

<212> PRT

<213> Homo sapiens

<400> 438

Tyr Met Lys Lys Asn Leu Thr Pro Ser Phe Ala Met Lys Tyr Leu Pro

1 5 10 15

Pro Ile Cys Thr Leu Gly Asp Gln

20

<210> 439

<211> 13

<212> PRT

<213> Homo sapiens

<400> 439

Tyr Ser Ala Ser Gly His Gly Val Arg Ile Thr Lys Ser

1 5 10

<210> 440

<211> 19

<212> PRT

<213> Homo sapiens

<400> 440

Glu Met Phe Val Leu Asn Pro Cys Leu Pro Ser Ile Met Leu Thr Ser

1 5 10 15

His Asn Met

<210> 441

<211> 14

<212> PRT

<213> Homo sapiens

<400> 441

Val Pro Ala Leu Lys Lys Leu Arg Ser Pro Leu Trp Ile Phe

1 5 10

<210> 442

<211> 55

<212> PRT

<213> Homo sapiens

<400> 442

Arg Gln Pro Glu Ala Ala Thr Lys Ser Cys Val Arg Ser Ser Cys Gly

1 5 10 15

Gly Pro Ser Gly Asp Glu Pro Pro Pro Cys Leu Gln Gln Pro Asp Pro

20 25 30

Arg Ala Leu Ser Gln Ala Phe Ser Arg Ser Phe Pro Leu Phe Pro Ser

35 40 45

Leu Ala Gly Lys Ser Met Ile

50 55

<210> 443

<211>

48

<212> PRT

<213> Homo sapiens

<400> 443

Arg Thr Pro Thr Ser Pro Ala Ala Thr Lys Ser His Ser Leu Arg Val

1 5 10 15

Phe Gly Trp Ala Asp Ala Leu Leu Asn Leu Val Ala Arg Val Pro Ser

20 25 30

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

35 40 45

<210> 444

<211> 32

<212> PRT

<213> Homo sapiens

<400> 444

Arg Glu Pro Arg Glu Arg Leu Tyr Gln Asp Thr Ser Leu Met Met Ile
1 5 10 15

Val Leu Thr Ile Gln Asn Ala Ala Phe Leu Ser Asn Ile Arg Met Ala
20 25 30

<210> 445

<211> 29

<212> PRT

<213> Homo sapiens

<400> 445

Ser Lys Thr Gln Arg Arg Tyr Lys Leu Ser Ser Leu Lys Glu Asp Leu
1 5 10 15

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

20 25

<210> 446

<211> 45

<212> PRT

<213> Homo sapiens

<400> 446

Pro Gly Leu Arg Pro Ser Gln His Leu Leu Leu Tyr Ile Thr Leu Arg
1 5 10 15

Val Val Lys Trp Ile Pro Ala Leu Ala Thr Ala Ser Ala Trp Pro Ala
20 25 30

Pro Ser Ala Lys Thr Val Trp His Pro Thr Leu Leu Ile
35 40 45

<210> 447

<211> 28

<212> PRT

<213> Homo sapiens

<400> 447

Cys His Leu Ala Ser Cys Pro Gln Cys Phe His Gln Trp Gly Arg His
1 5 10 15

His His Ser His Arg Tyr Gln Glu Trp Tyr Leu Arg
20 25

<210> 448
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 448
 Gly Ala Thr Pro Gln Ala Ala Pro Thr Thr Ser
 1 5 10

<210> 449
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 449
 Val Leu Thr Lys Gln Lys Val Leu Tyr Lys
 1 5 10

<210> 450
 <211> 10
 <212> PRT
 <213> Homo sapiens
 <400> 450

Ile Lys Ala Leu Leu Thr Leu Asn Ser Leu
 1 5 10

<210> 451
 <211> 9
 <212> PRT
 <213> Homo sapiens
 <400> 451

Gly Thr Pro Pro Trp Met Pro Phe Arg
 1 5

<210> 452
 <211> 49
 <212> PRT
 <213> Homo sapiens
 <400> 452

His Arg Pro Pro His Ser Gln Gln Pro Phe His Ser His Cys Pro Ser

1 5 10 15
Arg Ser Pro Gln Pro Ser Leu Arg Pro His Pro His Pro Leu Arg Ala
20 25 30
Gln Gly Cys Asn Pro Ser Leu Ser Thr Thr His Arg Trp Tyr Ser Trp
35 40 45
Gly

<210> 453

<211> 64

<212> PRT

<213> Homo sapiens

<400> 453

Asn Tyr Gly His Cys Asn Ser Pro Leu Ala Phe Leu Thr Gln Leu Leu

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

<210> 454

<211> 51

<212> PRT

<213> Homo sapiens

<400> 454

Arg Lys His Cys Cys Lys Arg Ile Thr Leu Arg Ser Ser Cys Ser Leu

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

Ala Pro Thr

50

<210> 455

<211> 47

<212> PRT

<213> Homo sapiens

<400> 455

Asn Ser Gly Ser Gln Ser Gly Thr Lys Met Lys Ala Thr His Ser Gly

1 5 10 15

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

20 25 30

Gln Lys Phe Asn Leu Asp Leu Lys Ala Cys Ser Ile Pro Glu Asp

35 40 45

<210> 456

<211> 28

<212> PRT

<213> Homo sapiens

<400> 456

Arg Asp Gln Cys Phe Gln Met Met Glu Gly Lys Ala Phe Leu Pro Glu

1 5 10 15

Arg Lys Cys Phe Pro Gly Asn Gln His Pro Leu Gly

20 25

<210> 457

<211> 43

<212> PRT

<213> Homo sapiens

<400> 457

Ala Met Arg Arg Pro Ser Ser Arg His Ala Ala His Arg Pro Leu Cys

1 5 10 15

Gln Arg Phe Pro Thr Leu Thr Val Ser Arg Trp Met Thr Ser Leu Ile

20 25 30

Ser Ser Leu Arg Val Glu Arg Ser Pro Ser Pro

35 40

<210> 458

<211> 25

<212>

PRT

<213> Homo sapiens

<400> 458

Cys Ile Trp Gln Pro Val Met Asp Thr Val Ile Leu Tyr Arg Ser Tyr

1 5 10 15

Cys Ser Thr Arg Gln Thr Ser Met Gln

20 25

<210> 459

<211> 17

<212> PRT

<213> Homo sapiens

<400> 459

Asn Ser Leu Ala Leu Cys Trp Val Pro Ala Cys Trp Val Thr Cys Leu

1 5 10 15

His

<210> 460

<211> 21

<212> PRT

<213>

> Homo sapiens

<400> 460

Leu Leu Gln Pro Cys Leu Lys Ala Leu Ser Val Pro Leu Trp Lys Met

1 5 10 15

Pro Ser Arg Ala Ser

20

<210> 461

<211> 13

<212> PRT

<213> Homo sapiens

<400> 461

Asn Pro Pro Leu Arg Phe Asn Leu Ile Leu Met Met Tyr

1 5 10

<210> 462

<211> 19

<212> PRT

<213> Homo sapiens

<400> 462

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

1 5 10 15

Leu Arg Thr

<210> 463

<211> 12

<212> PRT

<213> Homo sapiens

<400> 463

Asp Ala Lys Lys Leu Val Leu Leu Asn Trp Leu Pro

1 5 10

<210> 464

<211> 14

<212> PRT

<213> Homo sapiens

<400> 464

Gly Gly Arg Met Arg Asn Ile Phe Thr Pro Ala Gly His Lys

1 5 10

<210> 465

<211> 10

<212> PRT

<213> Homo sapiens

<400> 465

Leu Cys Arg Asn Met Lys Gln Gln Ile Tyr

1 5 10

<210> 466

<211> 20

<212> PRT

<213> Homo sapiens

<400> 466

Gly Glu Trp Ala Ala Leu Gly Pro Cys Trp Lys Ser Ala Cys Arg Ala

1 5 10 15

Ser Arg Ser Ala

20

<210> 467

<211> 8

<212> PRT

<213> Homo sapiens

<400> 467

Cys Pro Gly Gly Ala Leu Gln Trp

1 5

<210> 468

<211> 10

<212> PRT

<213> Homo sapiens

<400> 468

Glu Ala Lys Lys Arg Ile Met Trp Leu Leu

1 5 10

<210> 469

<211> 13

<212> PRT

<213> Homo sapiens

<400> 469

His Thr Ser Trp Asn Phe Arg Pro Leu Asn Trp Arg Ser

1 5 10

<210> 470

<211> 36

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 470

Val Gly Ala Gln Leu Met Leu Thr Ser Thr Ser Cys Ser Thr Met Ser
1 5 10 15

Cys Leu Ser Arg Pro Gly Trp Ala Ala Leu Gln Arg Leu Thr Trp Val
20 25 30

Cys Arg Arg Pro
35

<210> 471

<211> 87

<212> PRT

<213> Homo sapiens

<400> 471

Arg Ala Pro Pro Lys Thr Ala Pro Glu Thr Ala Ala Lys Phe Leu Lys
1 5 10 15

Glu Gly Thr Glu Arg Asn Thr Ala Glu Ser Leu Gln Glu Lys Leu Gly
20 25 30

Val Thr Pro Gly Ser Trp Trp Met His Leu Arg Ser Arg Phe Leu Ser

35 40 45

Ala Asn Ala Ala Cys Glu Cys Val Arg Arg Leu Pro Cys Asp Gly Asn
50 55 60

Thr Leu Pro Arg Arg Thr Ser Asn Phe Tyr Val Asp Val His Glu Ala
65 70 75 80

Leu Val Phe Asp Val Cys Leu
85

<210> 472

<211> 29

<212> PRT

<213> Homo sapiens

<400> 472

Gln Leu Leu Ser Gln Thr Pro Arg Leu Pro Pro Cys Leu His Thr Glu

1 5 10 15

Glu Pro Ser His Trp Thr Gly Gly Pro Arg Ser Pro Pro
20 25

<210> 473

<211> 29

<212> PRT

<213> Homo sapiens

<400> 473

Ile Ala Phe His Ile Lys Ser Ile Ala Ala Ala Leu Lys Arg His Phe

1 5 10 15

Thr Val Asn Met Ser Lys Val Glu Thr Gly Leu His Val

20 25

<210> 474

<211> 31

<212> PRT

<213> Homo sapiens

<400> 474

Trp Lys Lys Thr Gln Ala Asp Cys Phe Phe Gly Leu Leu Lys Lys Ile

1 5 10 15

Gly Leu Pro Gln Cys Gly Asp Ser Phe Leu Lys Arg Pro Leu Thr

20 25 30

<210> 475

<211> 23

<212> PRT

<213> Homo sapiens

<400> 475

Ala Val Phe Ala Ser Ser Arg Pro Thr Ser Pro Ala Ser Cys Arg Arg

1 5 10 15

Pro Pro Ser Ser Trp Trp Arg

20

<210> 476

<211> 24

<212> PRT

<213> Homo sapiens

<400> 476

Thr Gln Arg Arg Leu Lys Asn Trp Lys Glu Lys Lys Cys Ile Glu Leu

1 5 10 15
 Asn Ile Leu Ile Ser Trp Arg Ile
 20
 <210> 477
 <211> 38
 <212> PRT
 <213> Homo sapiens
 <400> 477
 Arg His Asn Asp Gly Lys Asn Glu Lys Asn Trp Pro Asn Ser Met Lys
 1 5 10 15
 Pro Ser Tyr Gly Ser Val Ala Thr Ala Ala Ser Ser Gly His Cys Ile
 20 25 30
 Leu Cys Leu Val Trp Arg
 35
 <210> 478
 <211> 46
 <212> PRT
 <213> Homo sapiens
 <400> 478
 Thr Arg Glu Lys Ile Lys Gln Pro Val Ala Gln Trp Val Met Ile Thr
 1 5 10 15
 Lys Arg Pro Lys Glu Asn His Gln Arg Lys Arg Arg Asn Val Asn Ile
 20 25 30
 Lys Lys Arg Leu Arg Ile Pro Ser Leu Arg Lys Tyr Arg Gln
 35 40 45
 <210> 479
 <211> 50
 <212> PRT
 <213> Homo sapiens
 <400> 479
 Leu Pro Thr Pro Phe Cys Thr Thr Leu Arg Asn Phe Phe Leu Ser Ser
 1 5 10 15
 Leu Ile Leu Ala Val Leu Cys Thr Asn Cys Ile Phe Arg Tyr Thr Ala

20 25 30
 Ser Phe Leu Gln Ala Phe Met Leu Pro Gly Phe Leu Lys His Thr Lys
 35 40 45

Arg Lys

50

<210> 480

<211> 33

<212> PRT

<213> Homo sapiens

<400> 480

Leu Pro Ile Leu Met Met Pro Ser Lys Lys Leu Ile Leu Tyr Leu Phe

1 5 10 15

Leu Cys Cys Pro Thr Leu Ser Phe Trp Gln Arg Glu Gln Pro Ser Arg

20 25 30

Thr

<210> 481

<211> 29

<212> PRT

<213> Homo sapiens

<400> 481

Leu Ser Met Ile Met Tyr Ser Leu Pro Leu Thr Tyr Ser Asn Leu His

1 5 10 15

Thr Leu Thr Ile Leu Lys Lys Tyr Met Leu Ser Gln Asn

20 25

<210> 482

<211> 28

<212> PRT

<213> Homo sapiens

<400> 482

Cys Thr Pro Phe Cys Thr Leu Ser Ala Lys His Val Pro Leu Ser Ile

1 5 10 15

Ser Gly Ser Pro Ala Leu Glu Leu Leu Gly Pro Trp

20 25

<210> 483

<211> 11

<212> PRT

<213> Homo sapiens

<400> 483

Leu Asn Gln Lys Asn Ile Pro Asp Leu Ser Ile

1 5 10

<210> 484

<211> 15

<212> PRT

<213> Homo sapiens

<400> 484

Val Ser Pro Leu Ala Pro Cys Pro Pro Leu Glu Val His Leu His

1 5 10 15

<210> 485

<211> 14

<212> PRT

<213> Homo sapiens

<400> 485

Ser Thr Gly Arg Leu Thr Ala Arg Arg Met Pro Pro Cys Leu

1 5 10

<210> 486

<211> 8

<212> PRT

<213> Homo sapiens

<400> 486

Arg Pro Lys Lys Arg Thr Val Leu

1 5

<210> 487

<211> 21

<212> PRT

<213> Homo sapiens

<400> 487

Val Val Lys Val Trp Met Arg Val Lys Tyr Thr Lys Glu Val Ile Met

1 5 10 15

Asp Leu Thr Asn Val

20

<210> 488

<211> 13

<212> PRT

<213> Homo sapiens

<400> 488

Phe Arg Phe Phe Arg Met Arg Lys Trp Arg Asp Gln Ile

1 5 10

<210> 489

<211> 18

<212> PRT

<213> Homo sapiens

<400> 489

His Phe Trp Asn Ser Thr Lys Lys Arg Leu Arg Thr Met Lys Ile Lys

1 5 10 15

Cys Ser

<210> 490

<211> 13

<212> PRT

<213> Homo sapiens

<400> 490

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

1 5 10

<210> 491

<211> 13

<212> PRT

<213> Homo sapiens

<400> 491

Met Thr Lys Lys Glu Asn Ala Asn Met Ile Phe Lys Lys

1 5 10

<210> 492

<211> 12

<212> PRT

<213> Homo sapiens

<400> 492

Ala Leu Lys Lys Pro Leu Arg Lys Val Arg Arg Leu

1 5 10

<210> 493

<211> 10

<212> PRT

<213> Homo sapiens

<400> 493

Asp Gln Phe Phe Trp Lys Met Gln Leu Leu

1 5 10

<210> 494

<211> 196

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 494

Ala Pro Thr Val Leu Gly Gly Pro Arg Trp Leu Cys Cys Thr Gln Asn

1 5 10 15

Val Ala Ser Gly Asn Gly Pro Leu Leu Ala Arg Pro Ala Gly Lys Pro

20 25 30

Arg Ala Ala Ser Leu Ser Ser Trp Lys Ala Leu Gly Pro Ser Ala Ala

35 40 45

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

50 55 60

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

65 70 75 80

Phe Cys Gly Gln Thr Trp Pro Gly Ser Trp Gly Ser Gln Glu Ser Phe

85 90 95
 Ile Cys Cys Ala Asp Ile Ser Thr Ala Leu Pro Leu Gly Ser Ser Arg
 100 105 110
 Pro Ala Pro Ala Pro Arg His Arg Glu His Glu His Gly His Gln Ala
 115 120 125
 Arg Pro Pro Arg Leu Leu Phe Thr Ser Leu Met Gln Leu Leu Trp Thr
 130 135 140
 Gln Leu Thr Arg His Ser Pro Pro Thr Leu His Thr Gly Pro His Pro
 145 150 155 160
 Ser Leu His Val Ala Ala Leu Ser Leu Leu Arg Met Asp Ser Thr Leu
 165 170 175
 Arg Gln Gly Ala Ser Leu Phe Ser Leu Thr Leu Gly Gly Pro Gly Pro
 180 185 190
 Trp Lys Asp Pro
 195
 <210> 495

<211> 120

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 495

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

50 55 60
 Gln Arg Ser Leu Asn His Leu Leu Ser Ser Trp Lys Thr Gly Ala Trp
 65 70 75 80
 Lys Thr Leu Thr Thr Cys Ser Gln Arg Arg Ile Ile Glu Pro Ser Pro

85 90 95
 Thr Thr Arg Pro Ser Ala Ser Leu Ser Asp Pro Ser Leu Leu Pro Lys
 100 105 110
 Ile Pro Arg Leu Leu Ser Pro Arg
 115 120

<210> 496

<211> 9

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 496

Arg Ser Trp Gly Thr Ala Leu Gly Arg

1 5

<210> 497

<211> 104

<212> PRT

<213> Homo sapiens

<400> 497

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

1 5 10 15

Thr Arg Asn Pro Arg Arg Ser Leu Ala Ser Pro Thr Arg Gly Lys Gly

20 25 30

Ser Ala Arg Gly Cys Gly Arg Ser Arg Thr Thr Leu Leu Ser Arg Leu

35 40 45

Pro Ala Ile Ser Pro Pro Arg Lys Arg Ala Val Trp Lys Ser Leu Asn

50 55 60

Gln Ser Pro Lys Leu Gln Arg Val Thr Val Ile Arg Arg Gly Met Gln

65 70 75 80

Arg Ala Ala Ala Thr Arg Lys Gly Ser Trp Ser Leu Met Ser Gln Pro

85 90 95

Arg Arg Arg Thr Arg Lys Glu Arg

100

<210> 498

<211> 57

<212> PRT

<213> Homo sapiens

<400> 498

His Leu Thr Thr Lys Gly Glu Gly Trp Val His Gln Trp Gly Val Thr

1 5 10 15

Val Gly Ala Gln Val Ala Thr Ala Pro Ser Met Gly Thr Pro His Pro

20 25 30

Leu Pro His His Pro Ser Met Ala Leu Thr Pro Thr Ala Leu Cys Ser

35 40 45

Trp Ser Met Ala Trp Ile Asn Leu Arg

50 55

<210> 499

<211> 64

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 499

Thr Cys Arg Ala Ile Val Thr Met Thr Ser Cys Leu Tyr Leu Arg Thr

1 5 10 15

Thr Glu Gly His Pro Val Gly Ala Ile Pro Pro His Ser Ala Ser Tyr

20 25 30

Pro Thr Tyr Pro Thr His Phe Ser Thr Trp Glu Pro Val Pro Ser Asp

35 40 45

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

50 55 60

<210> 500

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 500

Arg Arg Arg Lys Arg Arg Asp Ile Gln Glu Asn Gln Arg Thr Leu Leu
 1 5 10 15
 Lys Ile Gln Asn Cys Thr Tyr Pro Gly Ser Pro Ala Trp Arg Leu Val

 20 25 30
 Ala Phe Leu Ser Leu Val Ala Arg Leu Trp Lys Ala Ser Asp Leu Ser
 35 40 45
 Val Arg Lys Arg Asn Thr Tyr Gly Trp Lys Leu Ser Met Ala Arg Val
 50 55 60

Ile Glu Asn Ser Ala Ser Lys Gln Lys Ile His

65 70 75

<210> 501

<211> 60

<212> PRT

<213> Homo sapiens

<400> 501

Gly Cys Phe Trp Pro Cys Leu Trp Asn Ser Leu Leu Arg Phe Cys Pro

1 5 10 15
 Ala Ser Cys Ser Gly Cys Tyr Ser Trp Thr Ile Pro Pro Thr Gly Ser

 20 25 30
 Pro Phe Ser Cys Thr Thr Thr Arg Ser Ser Met Asn Pro Thr Ser Leu

 35 40 45

Thr Pro Gly Arg Ser Ser Arg Thr Thr Ser Gln Leu

 50 55 60

<210> 502

<211> 52

<212> PRT

<213> Homo sapiens

<400> 502

Cys Thr Thr Ser Arg Gly His Cys Thr Gly Ser Pro Arg Pro Cys Thr

1 5 10 15
 Pro Phe Ala Ile Ser Cys Thr Ala His Lys Trp Asn Gly Lys Thr Pro

 20 25 30

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

35

40

45

Cys Cys Arg Arg

50

<210> 503

<211> 33

<212> PRT

<213> Homo sapiens

<400> 503

Lys Gln Thr Arg Arg Arg Lys Leu Leu Leu Leu Cys Lys Lys Asn Gln

1

5

10

15

Ile Leu Lys Lys Lys Gly Glu Lys Leu Lys His Cys Phe Lys Ala Trp

20

25

30

Gly

<210> 504

<211> 33

<212> PRT

<213> Homo sapiens

<400> 504

Cys Pro Leu Leu Leu Val Tyr Ile Met Ser Thr Thr Gly Trp Leu Glu

1

5

10

15

Arg Ala Tyr Gly Arg Leu Trp Arg Pro Thr Ala Ile Arg Gln Thr Leu

20

25

30

Tyr

<210> 505

<211>

> 52

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 505

Ser Leu Leu Val Pro Arg Arg Leu Leu Pro Tyr Thr Leu Pro His Ser

1 5 10 15
 Ala His Gly Ser Arg Arg Thr Ser Thr Cys Gln His Pro Thr Thr Thr
 20 25 30
 Asn Thr Ser Ser Ser Ser Ser Ser Gln Met Trp Cys Arg Pro Arg Ser
 35 40 45
 Ser Cys Ile Arg

50

<210> 506

<211> 45

<212> PRT

<213> Homo sapiens

<400> 506

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

<210> 507

<211> 71

<212> PRT

<213> Homo sapiens

<400> 507

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

Ala Leu Cys Ile Glu Pro Asn

65 70

<210> 508

<211> 41

<212> PRT

<213> Homo sapiens

<400> 508

Met Lys Leu Thr Leu Ala Val Leu Pro Thr Leu Arg Asn Leu His Cys

1 5 10 15

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

20 25 30

Met Asn Leu Glu Ile Leu Leu Gly Val

35 40

<210> 509

<211> 27

<212> PRT

<213> Homo sapiens

<400> 509

Cys Ser Ile Lys Pro Pro Leu Pro Arg Arg Trp Thr Thr Val Leu Arg

1 5 10 15

Glu Pro Trp His Gly Met Gln Glu Ile Arg Pro

20 25

<210> 510

<211> 15

<212> PRT

<213> Homo sapiens

<400> 510

Arg Thr Gly Pro Trp Thr Pro Leu Leu Pro Pro Ser Cys Pro Trp

1 5 10 15

<210> 511

<211> 32

<212> PRT

<213> Homo sapiens

<400> 511

Asn Met Glu Thr Phe Gln Ser Met Ser Trp Pro Ile Leu Thr Ile Phe

1 5 10 15

Leu Thr Ser Met Arg Thr Ile Ile Pro Glu Phe Cys Leu Asn Glu Phe

20 25 30

<210> 512

<211> 16

<212> PRT

<213> Homo sapiens

<400> 512

Leu Gly Gln Ile Ile Met Lys Lys Met Arg Arg Pro Val Cys Tyr Lys

1 5 10 15

<210> 513

<211> 37

<212>

> PRT

<213> Homo sapiens

<400> 513

Leu Pro Pro Pro Ser His Arg Ala Pro His Ser Pro Pro Pro Ser Gln

1 5 10 15

His Arg Arg Ala Gln Asp Gln Pro His Ser Cys Leu Cys Pro Arg Arg

20 25 30

Thr Gly Cys Cys Val

35

<210> 514

<211> 22

<212> PRT

<213> Homo sapiens

<400> 514

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

1 5 10 15

Arg Arg Met Arg Arg Gln

20

<210> 515

<211> 15

<212> PRT

<213> Homo sapiens

<400> 515

Leu Gln Lys Lys Glu Ile Ala Lys Asn Val Phe Val Gln Asn Ile

1 5 10 15

<210> 516

<211> 11

<212> PRT

<213> Homo sapiens

<400> 516

Ile Ile Lys Lys Asn Pro Ala Leu Pro Lys His

1 5 10

<210> 517

<211> 14

<212> PRT

<213> Homo sapiens

<400> 517

Gly Phe Lys Met Gln Ser Arg Arg Arg Lys Trp Ala Gly Asn

1 5 10

<210> 518

<211> 19

<212> PRT

<213> Homo sapiens

<400> 518

Ser Ala Thr Thr Thr Thr Val Ile Leu Glu Ile Ile Ile Met Asp Arg

1 5 10 15

Val Ile Pro

<210> 519

<211> 12

<212> PRT

<213> Homo sapiens

<400> 519

Ala Ala Ser Gly Ala Ala Glu Ala Ala Glu Leu Leu

1 5 10

<210> 520

<211> 12

<212> PRT

<213> Homo sapiens

<400> 520

Ile Thr Lys Lys Arg Asn Trp Leu Arg Ser Trp Leu

1 5 10

<210> 521

<211> 14

<212> PRT

<213> Homo sapiens

<400> 521

Arg Arg Lys Asn Lys Lys Gln Pro Thr Phe Phe Leu Trp Gln

1 5 10

<210> 522

<211> 16

<212> PRT

<213> Homo sapiens

<400> 522

Val Thr Ile Arg Ile Gln Lys Gln Lys Phe Arg Ile Leu Lys Arg Ile

1 5 10 15

<210>

> 523

<211> 14

<212> PRT

<213> Homo sapiens

<400> 523

Arg Lys Glu Asn Thr Val Lys Arg Pro Asn Leu Pro His Leu

1 5 10

<210> 524

<211> 9

<212> PRT

<213> Homo sapiens

<400> 524

Ile Glu Lys Lys Glu Arg Lys Asn Leu

1 5

<210> 525

<211> 10

<212> PRT

<213> Homo sapiens

<400> 525

Leu Thr Leu Phe Ser Leu Lys Val Trp Glu

1 5 10

<210> 526

<211> 11

<212> PRT

<213> Homo sapiens

<400> 526

Ile Leu Ile Val Cys Arg Lys Ser Phe Tyr Ser

1 5 10

<210> 527

<211> 11

<212> PRT

<213> Homo sapiens

<400> 527

Leu Ile Ser His Leu Met Lys Trp Ala His Pro

1 5 10

<210> 528

<211> 8

<212> PRT

<213> Homo sapiens

<400> 528

Ser Leu Phe Phe Ser Tyr Cys Phe

1 5

<210> 529

<211> 11

<212> PRT

<213> Homo sapiens

<400>

529

Thr Leu Asn Trp Lys Arg Asn Leu Leu Phe Gly

1 5 10

<210> 530

<211> 13

<212> PRT

<213> Homo sapiens

<400> 530

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

1 5 10

<210> 531

<211> 48

<212> PRT

<213> Homo sapiens

<400> 531

Thr Leu Asn Trp Lys Arg Glu Pro Arg Leu Ser Tyr Leu Lys Thr Met

1 5 10 15

Tyr Ser Ser Leu Phe Trp Ser Gln Phe Pro Phe Leu Gln Cys Cys His

20 25 30

His His His Leu His His His Tyr His His Val Leu Asn Lys Tyr Ile

35 40 45

<210> 532

<211> 226

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 532

Gln Thr Gln Leu Pro Lys Val Trp Asp Pro Val Phe Phe Gly Ala Ala

1 5 10 15

Ser Pro Pro Ser Cys Thr Trp Ala Asp Trp Leu Cys Gly Ala Trp Ala

20 25 30

Cys Ala Ala Thr Cys Ser Gln Pro Ser Ser Ser Arg Gln His Arg Ser
 35 40 45
 Ala Leu Met Thr Phe Leu Leu Ala Ser Trp Cys Val Pro Lys Val Ser
 50 55 60
 Cys Gln Gly Val Arg Arg Pro Trp Asn Ser Leu Pro Arg Ser Thr Trp
 65 70 75 80
 His Ser Val Leu Met Cys His Gln Leu Cys Ser Asp Thr Ser Ser Ile
 85 90 95
 Val Ala Gly Gln Ala Thr His Gln Trp Pro Gly Ser Cys Pro Arg Cys
 100 105 110
 Ala Ser Arg Pro Arg Arg Glu Arg Thr Ala Ala Trp Gln Leu Cys Cys
 115 120 125
 Arg Arg Pro Ser Arg Thr Thr Phe Arg Ser Gln Gln Pro Ser Trp Gln
 130 135 140
 Gly Cys Cys Pro Gly Ser Thr Gly Ala Cys Trp Leu Ser Ala Arg His
 145 150 155 160
 Leu Arg Arg Pro Cys Ser Gly Ala Arg Pro Val Pro Ala Gly Val Trp
 165 170 175
 Pro Ala Ala Ser Ala Ser Thr Ser Thr Pro Ser Arg Gln Leu His Arg
 180 185 190
 Val Arg Pro Arg Ala Cys Met Pro Cys Pro Gly Ser Ser Gly Ser Ser
 195 200 205
 Gly Ala Cys Thr Arg Cys Arg Arg Ser Gly Trp Leu Gly Arg Leu His
 210 215 220
 Val Ala
 225
 <210> 533
 <211> 88
 <212> PRT
 <213> Homo sapiens
 <400> 533
 His His Leu Val Pro Leu Phe Ile Trp Thr Pro Trp Arg Lys Ser Gly

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

 Val Pro Cys Pro Asn Leu Leu Pro Ala Pro Ser Ala Leu Val Leu Leu
 50 55 60
 Ala Pro Ala Thr Pro Pro Phe Gly Leu Ile Pro Arg Leu Pro Thr Gly
 65 70 75 80
 Leu Tyr Cys Phe Pro Ser Ser Asp
 85

<210> 534

<211> 66

<212> PRT

<213> Homo sapiens

<400> 534

Leu Lys Arg Gln Met Gly Ser Ser Leu Leu Val Ser Met Lys Asn Pro
 1 5 10 15

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

Ser Ala

65

<210> 535

<211> 63

<212> PRT

<213> Homo sapiens

<400> 535

Ile Phe His Ser Gly Met Leu Pro Leu Glu Ile Ala Leu Thr Ile Ser

1 5 10 15
Pro Phe Ser Thr Val Cys Arg Glu Ser Glu Arg Asp Tyr Asn Met Asp
20 25 30
Phe Leu Thr Leu Arg His Leu Met Trp Met Asn Met Asn Ile Met Ser
35 40 45
Glu Leu Lys Met Val Thr Ser Thr Gly Leu Phe Gln Glu Asn Phe
50 55 60
<210> 536
<211> 115
<212> PRT
<213> Homo sapiens

<400> 536
Pro Met Phe Tyr Val Gly Pro Leu Met Cys Leu Leu Thr Gly Val Phe
1 5 10 15
Val Ile Ser Gly Ser His Leu Phe Cys Thr Ala Pro Ala Met Ser Asp
20 25 30
Ser Ser Pro Ser Val Thr Cys Cys Arg Val Gln Pro Ser Trp Trp Leu
35 40 45
Ser Pro Thr Ala Gly Phe Trp Arg Pro Trp Pro Ala Pro Cys Thr Leu
50 55 60

Ser Ser Ser Ala Thr Cys Cys Ser Leu Met Trp Leu Leu Ser Ser His
65 70 75 80
Phe Gly Ser Cys Cys Ile Ser Ser Phe Thr Met Gly Leu Ser Val Lys
85 90 95
Cys Arg Tyr Thr Pro Gly Leu Cys Leu Ser Gln Pro Phe Ser Ser Leu
100 105 110
Phe Ser Pro
115

<210> 537
<211> 105
<212> PRT
<213> Homo sapiens
<400> 537

Gly Ser Leu Leu Ser Pro Pro Glu Arg Arg Cys Gly Ser Arg Leu Trp

1 5 10 15

Arg Ala Trp Arg Arg Phe Pro Leu Leu Met Met Trp Arg Thr Pro Met

20 25 30

Thr Thr Arg Leu Arg Thr Gln Ala Cys Arg Arg Asn Ser Ser Arg Pro

35 40 45

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

50 55 60

Arg Arg Thr Gly Gly Cys Leu Leu Trp Arg Gly Arg Cys Ser His Arg

65 70 75 80

Arg Gly Gly Cys Pro Trp Cys Pro Arg Lys Pro Arg Ser Trp Pro Arg

85 90 95

Ser Ala Cys Glu Pro Gly Arg Ser Pro

100 105

<210> 538

<211> 140

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 538

Ser Arg Ala Ser Trp Val Pro Pro Gln Pro Cys Arg Cys Ser Met Gly

1 5 10 15

Gln Pro Cys Pro Arg Arg Cys Cys Ser Ser Pro Cys Arg Pro Arg Ala

20 25 30

Arg Arg Ser Pro Ala Ser Trp Glu Thr His Pro Trp Ala Pro Ser Ser

35 40 45

Leu Gly Pro Ser Gln Pro Thr Pro Ser Ser Gly Ser Cys Leu Gln Glu

50 55 60

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

65 70 75 80

Cys Cys His Pro Cys Leu Ala Leu Leu Gly Val Thr Gly Arg Pro Trp

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

<210> 539

<

211> 48

<212> PRT

<213> Homo sapiens

<400> 539

Ala Ala Leu Thr Ser Ser Ala Ile Ser Gly Pro Gly Trp Thr Pro Arg
 1 5 10 15
 Pro Pro Thr Phe Leu Ser Pro Trp Pro Ser Pro Ala Ile Pro Leu Leu
 20 25 30
 Thr Pro Arg Met Ser Trp Cys Ser Ser Leu Thr Thr Trp Pro Asn Ser
 35 40 45

<210> 540

<211> 80

<212> PRT

<213> Homo sapiens

<400> 540

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

Arg Arg Leu Pro Ser Val Ile Pro Thr Arg Thr Ala Arg Trp Pro Arg

[illegible]

<210> 542

<211> 102

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 542

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

Arg Val His Ile Asn Ser Ile Leu Thr Gln Ser Cys Phe Leu Asp Phe

50

55

60

Gly Val Glu Ala Phe Tyr Arg Lys Glu Ser Ser Asp Val Ile Leu Ala

65

70

75

80

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

85

90

95

Pro Ala Trp Pro Thr Trp

100

<210> 543

<211> 87

<212> PRT

<213> Homo sapiens

<400> 543

Tyr Ile Gln Val Lys Lys Leu Ile Ser Val Lys Asn Val Glu Asn Val

1

5

10

15

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

20

25

30

Glu Arg Lys Cys Gly Lys Asn Ile Lys Gln His Phe Ile Asn Val Met

35

40

45

Phe Val Arg Lys Phe Leu Lys Ala Asn Gln Val Trp Lys Cys Ile Phe

50

55

60

Glu Arg Ile Gln Val Lys Asn His Thr Ser Val Lys Phe Ala Ile Ser

65

70

75

80

Leu Leu Glu Leu Arg Lys His

85

<210> 544

<211> 50

<212> PRT

<213> Homo sapiens

<400> 544

Gln Gly Gln Ala Arg Asp Leu Arg Cys Pro Leu Thr Ala Pro Leu Ala

1

5

10

15

Cys Leu His Leu Pro Ser Pro Pro Val Arg Ser Thr Val Cys Ala Met

20 25 30

Asp Ser Leu Arg Pro Val Arg Leu Gln Lys Tyr Pro Gln Ala Ala Ala

35 40 45

Val Pro

50

<210> 545

<211> 93

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 545

Ala Ser Leu Leu Ser Arg Ser Ser Met Ser Leu Val Arg Thr Trp Ser

1 5 10 15

Ser Lys Leu Asn Arg His Gln Ser Leu Ala Leu Pro Val Pro Gln Gly

20 25 30

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

35 40 45

Lys Gly Pro Gly Lys Val Lys Val Ser Pro Leu Gly Asp Ser Cys Ser

50 55 60

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

65 70 75 80

Phe Trp Ser Ala Arg Arg Ser Leu Val Ser Pro Gly Trp

85 90

<210> 546

<211> 45

<212> PRT

<213> Homo sapiens

<400> 546

Arg Arg Trp Pro Arg Pro Arg Arg Ser Ala Val Ser Cys Phe Arg Ile

1 5 10 15

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

20 25 30
Val Leu Pro Ala Ser Pro Arg Thr Ser Pro Trp Ser Pro
35 40 45
<210> 547
<211> 60
<212> PRT
<213> Homo sapiens
<400> 547
Ser Arg Ser Ser Ala Thr Leu Pro Gly Arg Arg Arg Arg Arg Trp Leu

1 5 10 15
Arg Arg Arg Arg Gln Pro Ile Ser Val Ala Pro Ala Gly Pro Pro Arg
20 25 30
Arg Pro Asn Gln Lys Pro Asn Pro Pro Gly Gly Ala Arg Cys Val Ile
35 40 45
Met Arg Pro Thr Trp Pro Gly Thr Ser Ala Phe Thr
50 55 60
<210> 548
<211> 30
<212> PRT
<213> Homo sapiens
<400> 548

Arg Glu Ser Arg Ala Met Ile Ser Leu Gly Ala Leu Arg Glu Asp Trp

1 5 10 15
Asn Gln Lys Arg Ser Leu Gly Gln Gln Ile Pro Val Val Ile
20 25 30
<210> 549
<211> 57
<212> PRT
<213> Homo sapiens
<400> 549

Arg Ser Ile Asn Thr Glu Val Asn Ile Arg Asn Ile Asn Ile Pro Gln
1 5 10 15
Lys Lys Thr Arg Ile Lys Asn Ile Asn Ile Ser Ile Asn Ile Arg Asn

20 25 30

Thr Lys Glu Lys Arg Leu Leu Met Leu Leu Ile Lys Arg Val Cys Leu

35 40 45

Gln Gln Lys Glu Leu Asn Leu Met Ile

50 55

<210> 550

<211> 94

<212> PRT

<213> Homo sapiens

<400> 550

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

1 5 10 15

Thr Pro Ala Leu Cys Ser Leu Arg Arg Leu Arg Pro Ser Met Ser Ser

20 25 30

Thr Gly Arg His Thr Pro Cys Glu His Arg Thr Gln Ala Thr Leu Ala

35 40 45

Cys Pro Gly Ala Arg Arg Gln Leu Pro Arg Asn Phe Leu Gly Glu Arg

50 55 60

Ala Leu Gly Leu Pro Ser Pro Leu Arg Val Ser Lys Trp Asp Asp Ser

65 70 75 80

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

85 90

<210> 551

<211> 76

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 551

Trp Ser Pro Pro Gln Pro Arg Pro Pro Arg Asp Ala Ala Gly Phe Ser

1 5 10 15

Val Ser Val Arg Asp Ser Arg Glu Glu Pro Gly Gly Ser Ser Pro Arg

20 25 30

Gly Ala Met Leu Arg Ala Gly Leu Ser Ser Val Thr Ile Pro Ala Cys
35 40 45

Asn Ile Ser Val Asn Ser Glu Met Asp Leu Gly Pro Leu Thr Pro Arg
50 55 60

Thr Gln Pro Trp Ala Arg Ala Arg Gly Arg Arg Lys
65 70 75

<210> 552

<211> 39

<212> PRT

<213> Homo sapiens

<400> 552

Gln Pro Pro Lys Ala Leu Gln Pro Pro Arg Ala Pro Gln Leu Pro Asn
1 5 10 15

Ala Pro Gln Pro Pro Ser Ile Pro Gln Pro Pro Arg Ala Pro Gln Pro
20 25 30

Leu Lys Leu Leu Gln Cys Leu
35

<210> 553

<211> 29

<212> PRT

<213> Homo sapiens

<400> 553

Gly Leu Thr Met Ser Pro Leu Trp Pro Ser Cys Pro Trp Thr Gly Cys
1 5 10 15

Arg Cys Trp Lys Pro Cys Ala Gly Thr Gly Leu Ala Pro
20 25

<210> 554

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 554

Thr Leu Glu Ser Ala Leu Glu Lys Gly Phe Met Asn Leu Ala Asn Val

1 5 10 15

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

20 25 30

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

35 40 45

<210> 555

<211> 38

<212> PRT

<213> Homo sapiens

<400> 555

Leu Leu Lys Asn Ser Leu Gln Arg Leu Phe Val Leu Glu Leu Gly Val

1 5 10 15

Ser Leu Ile Gln Met Thr Cys Arg Gly Trp His Thr Phe Trp Ser Thr

20 25 30

Trp Tyr Ser Trp Val Val

35

<210> 556

<211> 16

<212> PRT

<213> Homo sapiens

<400> 556

Leu Leu Lys Asn Ser Asn Cys Arg Ala Cys Phe Cys Cys Gly Gln Ser

1 5 10 15

<210> 557

<211> 18

<212> PRT

<213> Homo sapiens

<400> 557

His Leu Leu Leu Ser Leu His Pro Ser Leu Pro Lys Leu Pro Gln Asn

1 5 10 15

Pro Leu

<210> 558

<211> 51

<212> PRT

<213> Homo sapiens

<400> 558

Arg Glu Ile Arg Cys Val Gln Ala Val Val Ile Leu Cys Ser Glu Leu

1 5 10 15

Ser Ser Val His Glu Val Leu Ser Ser Cys Val Ala Leu Phe Lys Gly

20 25 30

Ala Arg Glu His Ile Cys Leu Arg Glu Thr Tyr Arg Leu Ile Ser Thr

35 40 45

Ile Ala Ile

50

<210> 559

<211> 30

<212> PRT

<213> Homo sapiens

<400> 559

Asn Val Lys Asn Pro Lys Val Ile Leu Ile Phe Leu Met Lys Lys Gln

1 5 10 15

Pro Ser Lys Val Arg Arg Lys Glu Ala His Gly Leu Pro Leu

20 25 30

<210> 560

<211> 32

<212> PRT

<213> Homo sapiens

<400> 560

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

1 5 10 15

Arg Arg Ser Ser Thr Ala Ser Thr Ser Trp Glu Gly Trp Pro Pro Gly

20 25 30

<210> 561

<211> 48

<212> PRT

<213> Homo sapiens

<400> 561

Ile Cys Pro Trp Lys Arg Gln Pro Gly Ala Val Ala Gln Arg Ile Gly

1 5 10 15

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

20 25 30

Gly Lys Thr Val Arg Arg Thr Val Leu Glu Trp Arg Leu Thr Cys Trp

35 40 45

<210> 562

<211> 36

<212> PRT

<213> Homo sapiens

<400> 562

Gln Thr Leu Arg Pro Trp Leu Trp Leu Thr Ala Trp Ala Ala Ser Thr

1 5 10 15

Gly Ala Cys Gly Arg Arg Gln Leu Gly Ala Asn Ala Arg Cys Ser Ser

20 25 30

Gly Met Arg Cys

35

<210> 563

<211> 33

<212> PRT

<213> Homo sapiens

<400> 563

Arg Arg Thr Lys Pro Ala Ala Leu Ser Pro Val Met Val Pro Arg Gln

1 5 10 15

Lys Tyr Gln Gln Arg Val Lys Arg Ser Ser Ala Asp Pro Leu Pro Leu

20 25 30

Cys

<210> 564

<211> 17

<212> PRT

<213> Homo sapiens

<400> 564

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

1 5 10 15

Asn

<210> 565

<211>

> 17

<212> PRT

<213> Homo sapiens

<400> 565

Leu Asp Pro Met Ala Pro His Arg Ser Pro Thr Asn Lys Leu Leu Pro

1 5 10 15

Gln

<210> 566

<211> 25

<212> PRT

<213> Homo sapiens

<400> 566

Asn Ser Lys Lys Pro Pro Gln Ser Lys Arg Thr Asn Gly Met Lys Met

1 5 10 15

Asn Met Lys Gly Pro Glu Gly Arg Arg

20 25

<210> 567

<211> 56

<212>

> PRT

<213> Homo sapiens

<400> 567

Leu Pro Val Asn Val His Leu Val Ser His Ser Ile Thr Leu Leu Val

1 5 10 15

Ser Thr Thr Thr Asn Val Gly Leu Asn Leu Arg Phe Val Glu Gln Arg
20 25 30
Glu Ser Val Lys Thr Leu Gln Ala Val Ser Ala Val Asn Ala Lys Glu
35 40 45
Gly Ser Leu Leu Met Pro Pro Asp
50 55
<
210> 568
<211> 24
<212> PRT
<213> Homo sapiens
<400> 568
Ser Arg Gly Gln Arg Ser Leu Val Ser Ala Asp Glu Ser Thr Thr His
1 5 10 15
Leu Arg Asn Ala Arg Lys Thr Lys
20
<210> 569
<211> 16
<212> PRT
<213> Homo sapiens
<400> 569
Phe Val Lys Trp Leu Lys Lys Glu Glu Lys Glu Val Gln Leu Gln Asp
1 5 10 15
<210> 570
<211> 33
<212> PRT
<213> Homo sapiens
<400> 570
Gly Leu Gln Thr Lys Arg Thr Leu Arg Ile Arg Lys Pro Arg Val Leu
1 5 10 15
Lys Pro Leu Gln Phe Arg Leu Ala Ser Gln Ile Leu Pro Thr Leu Ser
20 25 30
Lys

<210> 571

<211> 12

<212> PRT

<213> Homo sapiens

<400> 571

Gln Thr Glu Ile Val Ser Gly Ile Leu Ala Tyr Cys

1 5 10

<210> 572

<211> 22

<212> PRT

<213> Homo sapiens

<400> 572

Val Ala Thr Pro Gly Arg Pro Trp Pro Pro Ser Phe Ser Ala Pro Cys

1 5 10 15

Cys Trp Arg Leu Trp Pro

20

<210> 573

<211> 33

<212> PRT

<213> Homo sapiens

<400> 573

Ala Ser Ser Pro Ser Leu Leu Val Gly Ala Asn Arg Ser Ser Ala Met

1 5 10 15

Gly Arg Thr Gly Gly Gly Cys Gln Trp Trp His His Phe Trp Val Pro

20 25 30

Ile

<210> 574

<211> 11

<212> PRT

<213> Homo sapiens

<400> 574

Ser Tyr Ala Leu Ser Asn Lys Asn Leu Leu Ile

1 5 10

<210> 575

<211> 62

<212> PRT

<213> Homo sapiens

<400> 575

Met Ala Leu His Gly Val Gln Leu Arg Lys Ser Lys Asp Leu His Phe

1 5 10 15

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

20 25 30

Gln Leu Ile Ala Ala Leu Met Thr Ile Trp Met Asn Ile Pro Leu Glu

35 40 45

Lys Met Trp Gln Leu Thr Val Val Leu Asn Gly Ser Gly Leu

50 55 60

<210> 576

<211> 18

<212> PRT

<213> Homo sapiens

<400> 576

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

1 5 10 15

Ile Phe

<210> 577

<211> 12

<212> PRT

<213> Homo sapiens

<400> 577

Lys Met Leu Lys Arg Thr Lys Cys Phe Thr Phe Gly

1 5 10

<210> 578

<211> 21

<212> PRT

<213> Homo sapiens

<400> 578

Arg Glu Arg Thr Arg Ile Asn Arg Lys Glu Leu Arg Leu Tyr His Pro

1 5 10 15

Asp Thr His His Ala

20

<210> 579

<211> 13

<212> PRT

<213> Homo sapiens

<400> 579

Arg Ile Pro Pro His His Pro Arg Cys Leu Arg Asp Ala

1 5 10

<210> 580

<211> 19

<212> PRT

<213> Homo sapiens

<400> 580

His His His Gln Cys Gln Pro Trp Ser Pro Thr Leu Pro Arg Thr Pro

1 5 10 15

Leu Leu Pro

<210> 581

<211> 21

<212> PRT

<213> Homo sapiens

<400> 581

Met Gln Lys Lys Lys Ser Ser Arg Glu Ile Arg Lys Arg Arg Arg Met

1 5 10 15

Met Met Met Arg Arg

20

<210> 582

<211> 13

<212> PRT

<213> Homo sapiens

<400> 582

Trp Met Arg Arg Leu Glu Glu Arg Trp Glu Asn Lys Leu

1 5 10

<210> 583

<211> 8

<212> PRT

<213> Homo sapiens

<400> 583

Ala Gln Lys Lys Asn Arg Arg His

1 5

<210> 584

<211> 20

<212> PRT

<213> Homo sapiens

<400> 584

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

1 5 10 15

Met Arg Arg Thr

20

<210> 585

<211> 8

<212> PRT

<213> Homo sapiens

<400> 585

Ser Leu Lys Lys Gln Tyr Pro Lys

1 5

<210> 586

<211> 21

<212> PRT

<213> Homo sapiens

<400> 586

Lys Leu Phe Leu Val Arg Glu Val Gln Arg Gly Glu Lys Gln Glu Leu

1 5 10 15

Arg Arg Ile Lys Gln

20

<210> 587

<211> 18

<212> PRT

<213> Homo sapiens

<400> 587

Leu Val Ala Ile Ser Phe Lys Thr Val Phe Lys Ala Ser His Ala Ala

1 5 10 15

Lys Thr

<210> 588

<211> 22

<212> PRT

<213> Homo sapiens

<400> 588

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

1 5 10 15

Ile Tyr Gln Glu Ala Thr

20

<210> 589

<211> 18

<212> PRT

<213> Homo sapiens

<400> 589

Asn Ser Asp Gln Asn Leu Phe Thr Glu Ile Ile Leu Asn Pro Pro Lys

1 5 10 15

His Gln

<210> 590

<211> 10

<212> PRT

<213> Homo sapiens

<400> 590

Ser Arg Lys Arg Ala Val Ser Asn Ser Arg

1 5 10

<210> 591

<211> 18

<212> PRT

<213> Homo sapiens

<400> 591

Met Ala Pro Ser Ser Ala Ala Ala Asp Gln Asp Ser Gly Cys Trp Met

1 5 10 15

Thr Trp

<210> 592

<211> 18

<212> PRT

<213> Homo sapiens

<400> 592

His Asn Gly Tyr Val Leu Gln Lys Lys Leu His Phe Thr Phe Tyr Thr

1 5 10 15

Cys Leu

<210> 593

<211> 13

<212> PRT

<213> Homo sapiens

<400> 593

Gln Pro Pro Pro Arg Ser Glu Val Leu Ser Cys Pro Leu

1 5 10

<210> 594

<211> 13

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 594

Arg Ala Leu Ala Ala Leu Pro Ser Ser Ser Thr Leu Arg

1 5 10

<210> 595

<

211> 11

<212> PRT

<213> Homo sapiens

<400> 595

Asp His Lys Lys Met Tyr Ser Ala His Ser Cys

1 5 10

<210> 596

<211> 11

<212> PRT

<213> Homo sapiens

<400> 596

Ser Ser Lys Lys Ile Ser Lys Met Ile Phe Val

1 5 10

<210> 597

<211> 18

<212> PRT

<213> Homo sapiens

<400> 597

Gln Ser His Arg Pro Pro Arg Ala Ser Ser Ala Gly Asp Leu Gln Cys

1 5 10 15

Gln Ala

<210> 598

<211> 23

<212> PRT

<213> Homo sapiens

<400> 598

Ser Val Gly Cys Leu Gly Cys Pro Gly Ser Arg Leu Pro Arg Ser Ala

1 5 10 15

Pro Ser Pro Met Ser Met Arg

20

<210> 599

<211> 20

<212> PRT

<213> Homo sapiens

<400> 599

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

1 5 10 15

Lys Arg Arg Asn

20

<210> 600

<211> 26

<212> PRT

<213> Homo sapiens

<400> 600

Ala Ala Lys Phe Ala Arg Cys Ala Thr Ala Leu Glu His Val Ser Ser

1 5 10 15

Ser Leu Arg Leu Arg Thr Arg Thr Arg Thr

20

25

<210> 601

<211> 30

<212> PRT

<213> Homo sapiens

<400> 601

Thr Ser Ala Leu Asp Val Ser Ala Pro Ala Ala Met Ile Ala Ala Cys

1 5 10 15

Ser Ala Ala Leu Leu Ser Ala Trp Ala Arg Trp Asn Val Cys

20

25

30

<210> 602

<211> 11

<212> PRT

<213> Homo sapiens

<400> 602

Gln Asp Arg Ile Phe Arg Val Phe Gln Asn His

1 5 10

<210> 603

<211> 20

<212> PRT

<213> Homo sapiens

<400> 603

Glu Thr Asp Thr Ser Ser Ala Phe Ser Ser Leu Leu Pro Leu Arg Asn

1 5 10 15

Leu Ser Gln Leu

20

<210> 604

<211> 15

<212> PRT

<213> Homo sapiens

<400> 604

Met Glu Lys Thr Gln Gln Met Gly Arg Arg Met Glu His Ile Leu

1 5 10 15

<210> 605

<211> 12

<212> PRT

<213> Homo sapiens

<400> 605

Arg Lys Leu Phe Ser Ser Lys Arg Lys Lys Lys Lys

1 5 10

<210> 606

<211> 13

<212> PRT

<213> Homo sapiens

<400> 606

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

1 5 10

<210> 607

<211> 14

<212> PRT

<213> Homo sapiens

<400> 607

Arg Arg Lys Asn Gln Arg Cys Leu Thr Phe Gln Pro Phe Thr

1 5 10

<210> 608

<211> 11

<212> PRT

<213> Homo sapiens

<400> 608

Lys Thr Val Phe Leu Asn His Trp Arg Gly Ser

1 5 10

<210> 609

<211> 12

<212> PRT

<213> Homo sapiens

<400> 609

Lys Lys Lys Lys Asn Met Lys Pro Ser Leu Leu Leu

1 5 10

<210> 610

<211> 9

<212> PRT

<213> Homo sapiens

<400> 610

Cys Gly Pro Pro Ala Trp Ala Leu Cys

1 5

<210> 611

<211> 10

<212> PRT

<213> Homo sapiens

<400> 611

Arg Arg Tyr Phe Trp Lys Arg Gln Glu Met

1 5 10

<210> 612

<211> 11

<212> PRT

<213> Homo sapiens

<400> 612

Asp Gly Trp Gly Ala Thr Ala Pro Thr Arg Gly

1 5 10

<210> 613

<211> 10

<212> PRT

<213> Homo sapiens

<400> 613

Arg Gly Gly Ile Leu Leu Ser Met Phe Leu

1 5 10

<210> 614

<211> 9

<212> PRT

<213> Homo sapiens

<400> 614

Gln Glu Ser Pro Arg Ser Pro Leu Leu

1 5

<210> 615

<211> 10

<212> PRT

<213> Homo sapiens

<400> 615

Lys Arg Lys Lys Ala Ala Arg Lys Leu Thr

1 5 10

<210> 616

<211> 9

<212> PRT

<213> Homo sapiens

<400> 616

Thr His Phe Phe Thr Phe Phe Asn Leu

1 5

<210> 617

<211> 11

<212> PRT

<213> Homo sapiens

<400> 617

Glu Val Val Phe Trp Met Thr Ser Gly Leu Ile

1 5 10

<210> 618

<211> 12

<212> PRT

<213> Homo sapiens

<400> 618

Met Arg Lys Leu Ala Phe Pro Gln Phe Ser Ser Cys

1 5 10

<210> 619

<211> 8

<212> PRT

<213> Homo sapiens

<400> 619

Val Ser Lys Lys Asp Leu Ser Pro

1 5

<210> 620

<211> 9

<212> PRT

<213> Homo sapiens

<400> 620

Ser Ile Gly Phe Leu Leu Gln Asn Leu

1 5

<210> 621

<211> 10

<212> PRT

<213> Homo sapiens

<400> 621

Glu Val Lys Lys Pro Pro Val Cys Ser Arg

1 5 10

<210> 622

<211> 21

<212> PRT

<213> Homo sapiens

<400> 622

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

1 5 10 15

Gln Leu Phe Arg Gly

20

<210> 623

<211> 13

<212> PRT

<213> Homo sapiens

<400> 623

Ala Val Pro Pro His Val Lys Arg His Ala Val Asn Leu

1 5 10

<210> 624

<211> 38

<212> PRT

<213> Homo sapiens

<400> 624

Thr Cys Ser Pro Gln Ser Leu Leu Ser Ser Trp Arg Ser Thr Gln Pro

1 5 10 15

His Val Pro Pro Ser Thr Leu Trp Gly Val Arg Met Thr Ser Leu Ser

20 25 30

Ala Ser Thr Ser Leu Trp

35

<210> 625

<211> 11

<212> PRT

<213> Homo sapiens

<400> 625

Val Asn Leu Phe Leu Thr Lys Met Met Arg Met

1 5 10

<210> 626

<211> 12

<212> PRT

<213> Homo sapiens

<400> 626

Ala Leu Lys Lys Arg Arg Met Val Leu Leu Lys Ser

1 5 10

<210> 627

<211> 233

<212> PRT

<213> Homo sapiens

<400> 627

Trp Leu Ala Pro Pro Glu Ala Gly Ala Ala Arg Gly Ala Glu Ala Ala

1 5 10 15

Ala Val Val Thr Ala Ala Phe Thr Lys Glu Ala Ser Lys Lys Ala Met

20 25 30

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

35 40 45

Met Thr Glu Ala Arg Gly Gly Leu Arg Ser Gln Gln Gly Gly Met Glu

50 55 60

His Asp Val Ala Leu Arg Arg Glu Gly Leu Ala Gln Gly Arg Ser Thr

65 70 75 80

Pro Ala Gln Thr Ala Arg Thr Gly Ala Pro Tyr Gly Arg Asn Arg Arg

85 90 95

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

100 105 110

Ala Thr Ala Gly Ala Pro Pro Ala Leu Met Val Val Pro Ala Leu Leu

115 120 125

Ala Gly Gly Asn Met Gly Asn Gly Gly Ala Ser Leu Asn Leu Ile Cys

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

195 200 205
 Pro Arg Ser Pro Phe Leu Arg Ser Arg Ser Trp Thr Ser Lys Gly Trp
 210 215 220
 Arg Arg Arg Arg Asn Leu Pro Lys Gly
 225 230

<210> 628

<211> 70

<212> PRT

<213> Homo sapiens

<400> 628

Asn Asp Leu Arg Lys Asn Lys Glu Gln Pro Ala Lys Thr Gly Pro Ser
 1 5 10 15
 Gln Lys Arg Thr Gly Arg Arg Gly Gly Ser Ile Lys Val Leu Ile Pro

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

<210> 629

<211> 78

<212> PRT

<213> Homo sapiens

<400> 629

Tyr Cys His Leu Arg Leu Pro Ser Gln Ala Pro Leu Lys Gly Lys Arg

1 5 10 15
Ala Gln Asn Gln Ala Gln Pro Asn Leu Leu Pro Gln Asn Gln His His
20 25 30
Leu Leu Arg Gln Trp Thr Gln Thr Val Gln Ala Pro Arg Phe Pro Leu
35 40 45
Leu Lys Ser Arg Ser Ser Trp Ile Gln Pro Leu Trp Ser Gln Glu Leu
50 55 60
Trp Met Pro Ser Gln Trp Arg Val Leu Glu Ile Leu Thr Asn

65 70 75

<210> 630

<211> 38

<212> PRT

<213> Homo sapiens

<400> 630

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

<210> 631

<211> 23

<212> PRT

<213> Homo sapiens

<400>

> 631

Met Phe Leu Ile Gln Arg Glu Leu Leu Lys Thr Leu Asn Met Ile Gln
1 5 10 15
Val Leu Met Ser Val Val His
20

<210> 632

<211> 15

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 632

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

1 5 10 15

<210> 633

<211> 11

<212> PRT

<213> Homo sapiens

<400>

633

Met Gly Glu Lys Asn Gln Ser Leu Trp Thr Ser

1 5 10

<210> 634

<211> 24

<212> PRT

<213> Homo sapiens

<400> 634

Leu Pro Val Tyr Arg Gln Thr His Trp Arg Leu Tyr Pro Lys Pro Phe

1 5 10 15

Ala Gly Leu Phe Pro Leu Lys Pro

20

<210> 635

<211> 97

<212> PRT

<213> Homo sapiens

<400> 635

Gln Pro Ala Arg Gln Ala Arg Ala Gln Asp Arg Trp Arg Thr Gln Arg

1 5 10 15

Pro Gly Pro Ala Ser Ser Pro Gly Ser Arg Ser Pro Ser His Val Arg

20 25 30

His Leu His His Gly Trp Ala Ser Val Pro Gly Leu Pro Lys Val Ala
35 40 45

Met Ala Pro Gly Thr Pro Gly Ile Arg Gly Pro His Ala Pro Pro Thr
50 55 60

Trp Leu Pro Ala Arg Pro Ser Arg Leu Pro Gly Ser Ala Ala Ala Pro

65 70 75 80
Thr Leu Pro Arg Ala Leu Ala Arg Leu Pro Pro Ala Val Gly Gly Cys
85 90 95

Val

<210> 636

<211> 24

<212> PRT

<213> Homo sapiens

<400> 636

Arg Ser Val Lys Arg Cys Lys Arg Ser Leu Pro Lys Gly Ile Val Lys

1 5 10 15

Leu Thr Leu Gln Ile Tyr Asn Ile

20

<210> 637

<211> 14

<212> PRT

<213> Homo sapiens

<400> 637

Gly Asn Phe Gln Arg Thr Thr Cys His Ser Ile Leu Ser Ser

1 5 10

<210> 638

<211> 15

<212> PRT

<213> Homo sapiens

<400> 638

Leu Lys Pro Tyr Arg Ser Val Leu Val Leu Ile Lys Met Phe Phe

1 5 10 15

<210> 639

<211> 8

<212> PRT

<213> Homo sapiens

<400> 639

Asp Glu Lys Lys Arg Lys Gln Lys

1 5

<210> 640

<211> 23

<212> PRT

<213> Homo sapiens

<400> 640

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

1 5 10 15

Lys Arg Val Thr Ser Ile Arg

20

<210> 641

<211> 19

<212> PRT

<213> Homo sapiens

<400> 641

Ser Trp Cys Leu Cys Cys Arg Leu Ile Ala Met Lys Glu Met Thr Trp

1 5 10 15

Thr Lys Ile

<210> 642

<211> 12

<212> PRT

<213> Homo sapiens

<400> 642

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

1 5 10

<210> 643

<211> 82

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 643

Val Thr Pro Pro Val Ala Arg Met Gly Arg Ser Pro Thr Ser Lys Pro

1 5 10 15

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

20 25 30

Pro Lys Gln Ser Pro Asp Ala Ser Pro Pro Val Ala Pro Pro Ala Trp

35 40 45

Thr Arg Pro Gly Ser Thr Ala Val Ser His Pro Gly Ser Thr Pro Gly

50 55 60

Ala Pro Ser Leu Ala Thr Ala Val Pro Ser Pro Leu Asp Ser Ser Ala

65 70 75 80

Met Ser

<210> 644

<211> 48

<212> PRT

<213> Homo sapiens

<400> 644

Ala Asn Pro Gln Leu Leu Cys Gln Asn Pro Glu Lys Leu Ala Leu Lys

1 5 10 15

Glu Asp Leu Leu Tyr Leu Arg Thr Ser Gly Glu Pro Trp Asp Thr Glu

20 25 30

Arg Asn Leu Arg Pro Leu Ser Leu Gln Cys Gln Ser Leu Ala Leu Pro

35 40 45

<210> 645

<211> 40

<212> PRT

<213> Homo sapiens

<400> 645

Asn Pro His Phe Arg Pro Pro Arg Thr Trp Arg Ala Thr Thr Ser Ala
1 5 10 15

Gln Leu Ala Arg Cys Ser Pro Trp Ala Thr Leu Pro His Met Pro Arg
20 25 30

Ala Arg Ser Ser Thr Ala Ala Ala
35 40

<210> 646

<211> 37

<212> PRT

<213> Homo sapiens

<400> 646

Thr Thr Ala Gln Thr Ala Pro Pro Ser Thr Arg Met Met Ala Thr Cys
1 5 10 15

Pro Cys Pro Gln Gly Trp Pro Gln Cys Pro Val Ala Glu Arg Ala Val
20 25 30

Glu Thr Ile Cys Pro
35

<210> 647

<211> 41

<212> PRT

<213> Homo sapiens

<400> 647

His Pro Leu Pro Thr Leu Thr Cys Pro Thr Met Pro Gly Arg Thr Pro
1 5 10 15

Thr Ala Asn Pro Pro Thr Pro Ser Ala Ala Ser Tyr Leu Trp Pro Ser
20 25 30

Arg Thr Leu Gln Pro Ser Ala Cys Gln
35 40

<210> 648

<211> 29

<212> PRT

<213> Homo sapiens

<400> 648

Glu Ala Thr Ser Asn Gln Asp Leu Leu Gln Met Val Pro Cys Ser Met

1 5 10 15

Gln Asp Pro Leu Leu Ser Leu Trp Thr Leu Phe Thr Glu

20 25

<210> 649

<211> 38

<212> PRT

<213> Homo sapiens

<400> 649

Asn Val Asn Val Cys Ser Pro Lys Ile Leu Ile Leu Lys His Gln Lys

1 5 10 15

Met Ile Arg Asp Phe Arg Arg Asn Leu Arg Lys Trp Leu Lys Ser Tyr

20 25 30

Lys Gly Lys Lys Gln Ile

35

<210> 650

<211> 36

<212> PRT

<213> Homo sapiens

<400> 650

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

1 5 10 15

Val Gly Cys Val Ile Leu Lys Met Thr Val Val Met Ala Ala Met Lys

20 25 30

Lys Ile Ala Gln

35

<210> 651

<211>

> 16

<212> PRT

<213> Homo sapiens

<400> 651

Ala Ala Pro Met Met Ser Ser Met Ala Cys Gly Ser Ala Glu Ser Ser

1 5 10 15
 <210> 652
 <211> 24
 <212> PRT
 <213> Homo sapiens
 <400> 652
 Arg Leu Phe Trp Met Arg Arg Leu Trp Cys Phe Arg Gln Leu Ser Gly

1 5 10 15
 Asp Ile Ser Arg Gly Gln Ser Ser

20
 <210> 653
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 653
 Glu Gln Lys Lys Ile Ser Pro Phe Ile Tyr Phe Phe Leu

1 5 10
 <210> 654
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 654
 Lys Leu Lys Lys Ala Ser Val Leu Leu Phe Ser

1 5 10
 <210> 655
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 655
 Asp Thr Gln Ile Pro Arg Thr Ser Arg Trp Cys

1 5 10
 <210> 656
 <211> 9
 <212> PRT

<213> Homo sapiens

<400> 656

Ser Val Lys Lys Arg Met Ile Ile Phe

1 5

<210> 657

<211> 10

<212> PRT

<213> Homo sapiens

<400> 657

Arg Val Pro Phe Leu Phe Val Val Gln Val

1 5 10

<210> 658

<211> 8

<212> PRT

<213> Homo sapiens

<400> 658

Leu Glu Val Gly Ala Thr Ser Ser

1 5

<210> 659

<211> 94

<212> PRT

<213> Homo sapiens

<400> 659

Ser Arg Ser Pro Lys Ser Met Ser Pro Pro Gly Arg Thr Gln Leu Pro

1 5 10 15

Pro Ser Gln Leu Pro Gln Pro His Arg His Arg Lys Thr Cys Ser Arg

20 25 30

Arg Ala Thr Pro Leu Ser Ser Leu Ala Ala Ala Pro Gly Ala Arg Ala

35 40 45

Gly Ala Arg His Pro Pro Pro Thr Arg Arg Gln Arg Ser Leu Cys Ser

50 55 60

Ser Gln Pro Ser Gln Pro Arg Pro Arg Ser Cys Leu Gly Thr Pro Leu

65 70 75 80

Ala Gly Leu Pro Ala Cys Pro Ser Pro Cys Pro Pro Val Arg

85 90

 $\langle 210 \rangle$ 660

<211> 16

<212> PRT

<213> Homo sapiens

<400> 660

Arg His Pro Pro Pro Thr Arg Arg Pro Ser Gln Pro Arg Pro Arg Ser

1 5 10 15

<210> 661

<211> 70

<212> PRT

<213> Homo sapiens

<400> 661

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

1 5 10 15

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

20 25 30

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

35 40 45

Pro Thr Gln Gln Leu Pro His Ala Leu Leu Ala Pro Ser Leu Gln Asp

50 55 60

Leu Ala Lys Arg Pro Pro

65 70

<210> 662

<211> 17

<212> PRT

<213> Homo sapiens

<400> 662

Arg Ala Trp Ala Pro Ala Pro Pro Thr Arg Cys Val Trp Gln Gln Pro

1 5 10 15

Ser

<210> 663

<211> 30

<212> PRT

<213> Homo sapiens

<400> 663

Thr Arg Lys Ala Ser Ala Ala Ser Cys Ala Ser Gly Val Thr Thr Ser

1 5 10 15

Thr His Arg Pro Ala Ser Ala Trp Thr Ser Met His Gln Thr

20 25 30

<210> 664

<211> 36

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 664

Val Leu Thr Val Ala Cys Arg Ser Ala Gln Pro Pro Arg Pro Trp Asp

1 5 10 15

His Ala Ala Pro Val Thr Cys Thr Cys Gly Arg Thr Arg Gly Leu Gly

20 25 30

Gly Gly Thr Thr

35

<210> 665

<211> 44

<212> PRT

<213> Homo sapiens

<400> 665

Lys Thr Lys Asn Leu Pro Leu Lys Thr Lys Leu Lys Lys Lys Glu Asn

1 5 10 15

Lys Thr Thr Leu Asn Leu Gln Met Ala Glu His His Leu Leu Cys Pro

20 25 30

Arg Ile Met Asn Lys Ala Gln Pro Tyr Gly Ile Cys

35 40

<210> 666

<211> 43

<212> PRT

<213> Homo sapiens

<400> 666

His Pro Ile His Ile Gly Cys Thr Gln Thr Met Val Met Gly Ile Ile

1 5 10 15

Phe Met Cys Leu Arg Leu Cys Pro His Ile Leu Asp Arg Leu Gln Arg

20 25 30

Gly Leu Pro Gly Asn Trp Glu Leu Lys Leu Glu

35 40

<210> 667

<211> 35

<212> PRT

<213> Homo sapiens

<400> 667

Val Ser Ser Thr His Ser Thr Thr Thr Gly Ser His Trp Lys Gln Pro

1 5 10 15

Thr Asp Gly Ala Val Cys Thr Arg Thr Ser Met Arg Ser Phe Pro Thr

20 25 30

Arg Ser Thr

35

<210> 668

<211> 27

<212> PRT

<213> Homo sapiens

<400> 668

His Thr Trp Asn Gly Pro Arg Ile Gly Val Asn Val Gly Phe Ser Gly

1 5 10 15

Gln Thr Phe Glu Leu Leu Leu Met Leu Met Tyr

20 25

<210> 669

<211> 21

<212> PRT

<213> Homo sapiens

<400> 669

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

1 5 10 15

Ser Ile Glu Glu Leu

20

<210> 670

<211> 21

<212> PRT

<213> Homo sapiens

<400> 670

Val Thr Trp Met Lys Arg Arg Arg Arg Asn Leu Ile Leu Arg Lys Pro

1 5 10 15

Glu Trp Ile Phe Lys

20

<210> 671

<211> 10

<212> PRT

<213> Homo sapiens

<400> 671

Leu Glu Lys Lys Glu Ser Glu Lys Trp Met

1 5 10

<210> 672

<211> 18

<212> PRT

<213> Homo sapiens

<400> 672

Val Ser Asn Trp Arg Val Lys Ser Leu Pro Cys Leu Pro Phe Phe Ser

1 5 10 15

Val Leu

<210> 673

<211> 9

<212> PRT

<213> Homo sapiens

<400> 673

Gly Cys Thr Pro Gln Leu Cys Trp Thr

1 5

<210> 674

<211> 20

<212> PRT

<213> Homo sapiens

<400> 674

Thr Phe Leu Leu Trp Lys Asn Trp Lys Arg Ala Leu Ser Thr Arg Lys

1 5 10 15

Ile Cys Ser Lys

20

<210> 675

<211> 10

<212> PRT

<213> Homo sapiens

<400> 675

Glu Glu Lys Lys Thr Glu His Tyr Ala Tyr

1 5 10

<210> 676

<211> 12

<212> PRT

<213> Homo sapiens

<400> 676

Phe Leu Gln Gly Val Ala Leu Ala Val Gln Ala Ser

1 5 10

<210> 677

<211> 9

<212> PRT

<213> Homo sapiens

<400> 677

Leu Met Phe Phe Cys Gly His Gln Asn

1 5

<210> 678

<211> 10

<212> PRT

<213> Homo sapiens

<400> 678

Ile Arg Lys Lys Ala Asp Leu His Thr Gln

1 5 10

<210> 679

<211> 48

<212> PRT

<213> Homo sapiens

<400> 679

Gly Ala Pro Arg Ser Pro Ser Ser Val Ala Gly Ser Ser Ser Ala Thr

1 5 10 15

Trp Gln Ser Gly Ala Met Trp Val Gln Pro Pro Trp Glu Gln Leu Pro

20 25 30

Gly Gly Ser Cys Thr Leu Arg Met Gly Leu Met Ser Thr Thr Ala Ser

35 40 45

<210> 680

<211> 126

<212> PRT

<213> Homo sapiens

<400> 680

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

1 5 10 15

Trp Pro Val His Thr Arg Pro Arg Ser Ser Pro Gly Met Asn Ser Glu

20 25 30

His Ser Gly Ser Ala Gly Val Val Ala Leu Ser Arg Leu Ala Met Val

35 40 45

Gln Ser His Pro Met Ser Leu Ser Leu Trp Pro Gly Pro Ser Arg Gly

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

Glu Pro Pro Pro Pro Ser Ser Gly Thr Ser Trp Gly Gln Pro
 115 120 125

<210> 681

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 681

Thr Leu Trp Thr Leu Cys Ser Ser Thr Pro Thr Cys Leu Arg Thr Cys
 1 5 10 15
 His Leu Met Arg Ser Leu Trp Pro Pro Gln Arg Pro Ser Asn Ser Arg
 20 25 30
 Lys Phe Gly Trp Gln Met Arg Ala Ser Thr Pro Ala Pro Cys Leu Thr

35 40 45
 His Cys Thr Phe Trp Thr Arg Leu

50 55

<210> 682

<211> 27

<212> PRT

<213> Homo sapiens

<400> 682

Pro Pro Pro Gly Trp Leu Pro Arg Leu Thr Arg Glu Arg Ala Ala Ala
 1 5 10 15
 Ala Leu Arg Ala Val Gly Thr Gln Ile Ser Ile
 20 25

<210> 683

<211> 76

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 683

Ser Ile Lys Lys Lys Lys Asn Lys Glu Gly Val Gly Arg Glu Val Leu

1 5 10 15

Val Val Val Val Pro Val Ala Ile Ala Glu Leu Val Val Leu Val Val

20 25 30

Leu Ser Leu Ala Leu His Thr Val Leu Ala Gln Val Val Leu Leu Lys

35 40 45

Gly Lys Arg Asp Thr Val Gly Val Asp Leu Gln Gln Ser Lys Leu Asp

50 55 60

Val Ala Gly Val Glu Ala Ile Leu Ala Glu Leu Lys

65 70 75

<210> 684

<211> 20

<212> PRT

<213> Homo sapiens

<400> 684

Leu Gln Asp Gly Ser Leu Asp Arg Asn Leu Gly Ser Pro Leu Met Ser

1 5 10 15

Glu Phe Arg Lys

20

<210> 685

<211> 30

<212> PRT

<213> Homo sapiens

<400> 685

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

1 5 10 15

Ile Leu Gln Thr Gly Ala Pro Gly Met Asn Ile Lys Glu Thr

20 25 30

<210> 686

<211> 43

<212> PRT

<213> Homo sapiens

<400> 686

Thr Leu Ser His Gln Ile Lys Ser Ser Phe Gly Gln Lys Met Gly Lys

1 5 10 15

Val Ile Phe Thr Asn Tyr Leu Pro Val Ala Phe Gln Leu Val Ile His

20 25 30

Ser Ala Val Met Trp Gly Arg Gln Leu Lys Ile

35 40

<210> 687

<211> 21

<212> PRT

<213> Homo sapiens

<400> 687

Leu His Tyr Leu Met Arg Trp Pro Ile Asn Leu Ile Arg Arg Trp Thr

1 5 10 15

Ser Phe Trp Glu Ile

20

<210> 688

<211> 28

<212> PRT

<213> Homo sapiens

<400> 688

Thr Gly Thr Lys His Glu Ser Gly Leu Leu Lys Thr Ser Gln Lys Leu

1 5 10 15

Ser Leu Lys Lys Met Thr Gln Gly Pro Cys Leu Gly

20 25

<210> 689

<211> 24

<212> PRT

<213> Homo sapiens

<400> 689

Arg His Pro Pro Gly Ser Thr Arg Tyr Pro Ser Phe Pro Leu Arg Leu

1 5 10 15

Val Pro Leu Ser Leu Ile Gly Pro

20

<210> 690

<211> 35

<212> PRT

<213> Homo sapiens

<400> 690

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

1 5 10 15

His Ser Pro Pro Arg Gly Trp Cys Ser Ala Ala Trp Pro Pro Arg His

20

25

30

Gly Trp Cys

35

<210> 691

<211> 44

<212> PRT

<213> Homo sapiens

<400> 691

Thr Ser Arg Pro Cys Thr Ser Thr Ser Thr Thr Ser Leu Leu Pro Met

1 5 10 15

Ala Leu Leu Cys Val Lys Arg Gly Arg Arg Cys Thr Lys Ala Lys Ala

20

25

30

Thr Ala Val Ser Ala Ala Val Ser Thr Glu Gln Ile

35

40

<210> 692

<211> 13

<212> PRT

<213> Homo sapiens

<400> 692

Trp Phe Ala Phe Leu Ser Ile Lys Lys Arg Ala Ala Arg

1 5 10

<210> 693

<211> 25

<212> PRT

<213> Homo sapiens

<400> 693

Leu Arg Met Ser Leu Ile Leu Ser Val Ile Cys Ser Cys Ser Trp Glu

1 5 10 15

Leu Trp Gly Tyr Met Ile Cys His Ile

20 25

<210> 694

<211> 26

<212> PRT

<213> Homo sapiens

<400> 694

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

1 5 10 15

Pro Ser Thr Thr Gly Arg Trp Cys Ala Leu

20 25

<210> 695

<211> 13

<212> PRT

<213> Homo sapiens

<400> 695

Tyr Ile Thr Leu Leu Tyr Leu Arg Lys Ile Phe Lys Val

1 5 10

<210> 696

<211> 19

<212> PRT

<213> Homo sapiens

<400> 696

Gln Asp Thr Leu Arg Asn Leu Leu Leu Gln Thr Thr Leu Thr Cys Trp

1 5 10 15

Trp Ile His

<210> 697

<211> 20

<212> PRT

<213> Homo sapiens

<400> 697

Asn Thr His Pro Leu Leu Gln Ala Cys Ser Pro Ser Ala Cys Arg Cys

1 5 10 15

Pro Cys His Gln

20

<210> 698

<211> 14

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 698

Asn Leu Gln Ile Arg Arg Leu Pro Arg Gln Arg Leu Leu Ser

1 5 10

<210> 699

<211> 26

<212> PRT

<213> Homo sapiens

<400> 699

Cys Ile His Ile Thr Gly Met Ser Leu Leu Gly Leu His Gly Thr Met

1 5 10 15

Glu Lys Ser Glu Gly Met Lys Ser Phe His

20

25

<210> 700

<211> 20

<212> PRT

<213> Homo sapiens

<400> 700

Gly Asn Thr Ala Asn Gly Pro Gly Ile Gly Arg Lys Ser Leu Met Pro

1 5 10 15

Met Gln Val Thr

20

<210> 701

<211> 36

<212> PRT

<213> Homo sapiens

<400> 701

Glu Ala Phe Thr Leu Thr Met Val Gly Phe Ser Lys Leu Ile Ser His

1 5 10 15

Val Leu Leu Ser Tyr Lys Pro Phe Ser Lys Gly Lys Glu His Glu Arg

20 25 30

Ile Pro Glu Ser

35

<210> 702

<211> 11

<212> PRT

<213> Homo sapiens

<400> 702

Gly Ser Trp Gly Val Pro Trp Met Thr Ser Met

1 5 10

<210> 703

<211> 13

<212> PRT

<213> Homo sapiens

<400> 703

Thr Ser Gly Thr Lys Ser Ser Arg Lys Ser Met Asn Ser

1 5 10

<210> 704

<211> 13

<212> PRT

<213> Homo sapiens

<400> 704

Ser Ser Lys Lys Arg Lys Lys Gly Asn Met Trp Thr Thr

1 5 10

<210> 705

<211> 19

<212> PRT

<213> Homo sapiens

<400> 705

Asp Val Ala Gly Glu Glu Asn Glu Gly Pro Pro Arg Pro Ser Leu Met

1 5 10 15

Cys Pro Arg

<210> 706

<211> 12

<212> PRT

<213> Homo sapiens

<400> 706

Pro Glu Ile Phe Leu Arg Met Asn Trp Cys Val Ser

1 5 10

<210> 707

<211> 22

<212> PRT

<213> Homo sapiens

<400> 707

His Leu His Arg Met Leu Tyr Met Asn Arg Leu Gln Pro Ser Thr Gln

1 5 10 15

Trp Tyr Lys Ile Thr Ala

20

<210> 708

<211> 12

<212> PRT

<213> Homo sapiens

<400> 708

Gly Leu Pro Gln Lys Glu Leu Lys Gly Ile Gln Leu

1 5 10

<210> 709

<211> 11

<212> PRT

<213> Homo sapiens

<400> 709

Lys Lys Lys Lys Ser Asn Ile Pro Lys Thr Pro

1 5 10

<210> 710

<211> 21

<212> PRT

<213> Homo sapiens

<400> 710

Val Ser Pro Ala Phe Leu Asn Phe Met Asp Leu Leu Leu Thr Ile Lys

1 5 10 15

Leu Glu Leu Cys Val

20

<210> 711

<211> 9

<212> PRT

<213> Homo sapiens

<400> 711

Asn Ile Ile Phe Leu Ser Asp Pro Gly

1 5

<210> 712

<211> 14

<212> PRT

<213> Homo sapiens

<400> 712

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

1 5 10

<210> 713

<211> 12

<212> PRT

<213> Homo sapiens

<400> 713

Asn Met Val Lys Met Leu Val Phe Ile Leu Lys Leu

1 5 10

<210> 714

<211> 10

<212> PRT

<213> Homo sapiens

<400> 714

Ile Ala Met Thr Met Asp Gln Tyr Pro Phe

1 5 10

<210> 715

<211> 13

<212> PRT

<213> Homo sapiens

<400> 715

Pro Pro Phe Phe Thr Ile Asp Leu Val Thr Thr Cys Ile

1 5 10

<210> 716

<211> 8

<212> PRT

<213> Homo sapiens

<400> 716

Cys Lys Lys Lys Asn Asp Gly Thr

1 5

<210> 717

<211> 10

<212> PRT

<213> Homo sapiens

<400> 717

Met Thr Gly Phe Leu Thr Pro Arg Asp Phe

1 5 10

<210> 718

<211> 13

<212> PRT

<213> Homo sapiens

<400> 718

Leu Pro Pro Pro Trp Thr Ala Gln Leu Pro Cys Ile Ser

1 5 10

<210> 719

<211> 11

<212> PRT

<213> Homo sapiens

<400> 719

Arg Leu Ile Glu Ile Lys Val Pro Ser Gln Lys

1 5 10

<210> 720

<211> 11

<212> PRT

<213> Homo sapiens

<400> 720

Gly Glu Lys Lys Tyr Asn Val Phe His Met Lys

1 5 10

<210> 721

<211> 8

<212> PRT

<213> Homo sapiens

<400> 721

Lys Ala Phe Phe Leu Pro Val Arg

1 5

<210> 722

<211> 109

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 722

Ala His Pro Arg Pro Pro Ala Leu Ser Leu Arg Ser Leu Gln Arg Ser
1 5 10 15
Pro Ala Leu Arg Ala Arg Trp Ser Thr Ser Phe Cys Leu Ala Pro Lys
20 25 30
Arg Pro Leu Leu Leu Thr Pro Arg Glu Gln Thr Trp Leu Asp Pro Asp
35 40 45
Pro Ala Asn Ala Pro Cys Arg Cys Ser Ala Pro Ala Asn Gln Pro Arg
50 55 60
Thr Glu Ser Pro Pro Pro Leu Pro Ala Asp Leu Pro His Ser Ser Gly
65 70 75 80
Leu Ala Leu Cys Gly Ile Val Ser Thr Ser Ser His Leu Ile Leu Leu
85 90 95
Trp Leu Leu Gly Ser Arg Met Ala His Pro Arg Leu Pro
100 105
<210> 723
<211> 131
<212> PRT
<213> Artificial Sequence
<220><223> modified Homo sapiens FSP
<400> 723
Ser Thr Ala Thr Ala Pro Trp Thr Ser Ala Ser Ser Thr Arg Ser Ala
1 5 10 15
Lys Trp Ala Thr Ser Thr Gly Ala Arg Cys Leu Thr Ser Gly Ala Ala
20 25 30
Ala Ala Cys Trp Arg Arg Cys Ser Ala Thr Ser Arg Gly Arg Ala Arg
35 40 45
Ser Pro Arg Val Arg Ser Arg Thr Leu Pro Lys Leu Cys Leu Trp Trp
50 55 60
Met Thr Asn Leu Thr Thr Arg Arg Ser Thr Arg Arg Ser Cys Trp Thr
65 70 75 80
Ser Pro Gly Met His Thr Gln Thr Ser Arg Ala Pro Gln Pro Ser Arg

85

90

95

Ala Gln Thr Trp Arg Thr Ser Pro His Cys Gly Ile Asp Thr Pro Val

100

105

110

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

115

120

125

Gly Leu Cys

130

<210> 724

<211> 70

<212> PRT

<213> Homo sapiens

<400> 724

Val Lys Thr Gly Ser Ser Trp Thr Gly Ser Cys Arg Gln Gly Trp Arg

1

5

10

15

Trp Ser Gly Ser Asp Cys Gly Ile Ser Ile Thr Thr Thr Thr Pro Arg

20

25

30

Gly Ala Cys Gly Ala Ser Ala Ala Gly Arg Ala Leu Ala Arg Gly Arg

35

40

45

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

50

55

60

Leu Leu Gly Ala Gly Leu

65

70

<210> 725

<211> 13

<212> PRT

<213> Homo sapiens

<400> 725

Ser Ala Thr Arg Met Pro Gly Pro Val Pro Ala Pro Ser

1

5

10

<210> 726

<211> 40

<212> PRT

<213> Homo sapiens

<400> 726

Gly Pro Pro Thr Ala Gln Cys Gln His Pro Pro Glu Pro Leu Phe Leu

1 5 10 15

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

20 25 30

Ser Cys His Pro His His Gln Phe

35 40

<210> 727

<211> 57

<212> PRT

<213> Homo sapiens

<400> 727

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

1 5 10 15

Pro Pro Thr Ser Thr Thr Leu Trp Ser Ser Ala Phe Ser Ala Thr Arg

20 25 30

Met Pro Gly Ile Pro Ala Gly Leu Gly Leu Gly Phe Gly Arg Ala Glu

35 40 45

Gly Ala Gln Glu Gly Lys Ala Arg Val

50 55

<210> 728

<211> 81

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 728

Thr Gly Gly Arg Arg Met Thr Arg Arg Thr Met Thr Thr Thr Lys Met

1 5 10 15

Met Met Met Arg Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg Arg Met

20 25 30

Thr Met Met Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu Thr

35 40 45

Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile Ser

50 55 60

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

65 70 75 80

Gly

<210> 729

<211> 68

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 729

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

1 5 10 15

Pro Glu Arg Arg Cys Leu Leu Pro Leu Pro Ser Cys Ala Gly Pro Gly

20 25 30

Asp Gln Ala Arg Met Arg Thr Ser Ala Val Ser Cys Cys Arg Ser Pro

35 40 45

Trp Thr Pro Cys Glu His Phe Pro Arg Pro Arg Ser Cys Gly Trp Arg

50 55 60

Trp Trp Arg Glu

65

<210> 730

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 730

Thr Tyr Gly Ala Trp Ala Ser Arg Trp Trp Ser Trp Gln Gln Asp Ser

1 5 10 15

<210> 731

<211> 117

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 731

Gln Thr Pro Pro Ser Arg Thr Met Thr Ser Gly Pro Thr Tyr Gly Ala

1 5 10 15

Trp Ala Ser Arg Cys Pro Ala Arg Leu Pro Pro Arg Trp Ser Trp Gln

20 25 30

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

35 40 45

Pro Lys Ser Tyr Arg Lys Ser Pro Arg Phe Cys Pro Asp Thr Trp Ala

50 55 60

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

65 70 75 80

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

85 90 95

Thr Trp Arg Pro Gly Ser Arg Met Ser Trp Arg Arg Leu Ser His Arg

100 105 110

Gly Leu Ala Ala Ser

115

<210> 732

<211> 32

<212> PRT

<213> Homo sapiens

<400> 732

Trp Val Leu Ile Cys Leu Asp Leu Phe Arg Gln Lys Phe Arg Lys Pro

1 5 10 15

Leu Met Leu Gln Glu Ser Leu Phe Gln Met Ile Phe Ser Ser Ile Phe

20 25 30

<210> 733

<211> 95

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 733

Leu Pro Met Pro Pro Pro Pro Arg Arg Pro Leu Pro Pro Pro Pro Arg

1 5 10 15

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

20 25 30

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

35 40 45

Glu Asp Ser Arg Lys Ala Lys Pro Asp Phe Trp Lys Val Gln Asn Ser

50 55 60

Phe Gly Ser Leu Val Pro Glu Arg Glu Lys Met Leu Val Pro Gly Gly

65 70 75 80

Thr Arg Val Cys Gln His Ala Lys Ile Gly Pro Cys Tyr Met Lys

85 90 95

<210> 734

<211> 64

<212> PRT

<213> Homo sapiens

<400> 734

Asn Arg Phe Arg Leu Cys Ile Thr Ile Leu Pro Gly Met Lys Met Ser

1 5 10 15

Trp Ser Ser Glu Lys Val Met Ser Leu Met Ser Trp Lys Ser Val Met

20 25 30

Thr Ala Gly Leu Trp Gly Pro Gln Glu Glu Pro Asn Ser Leu Val Leu

35 40 45

Ser Pro Glu Thr Thr Ser Arg Gly Cys Glu Leu Arg Ser Leu Leu Leu

50 55 60

<210> 735

<211> 66

<212> PRT

<213> Homo sapiens

<400> 735

Leu Leu Leu Arg Ile Leu Arg Leu Arg Arg His Leu Pro Pro Ala Ala

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

65

<210> 736

<211> 81

<

212> PRT

<213> Homo sapiens

<400> 736

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

65	70	75	80
Gly	Leu	Met	Ala
Ala	Asp	Arg	Ala
Trp	Gly	Leu	Phe
Thr	Pro	Ala	Pro
Thr			

<210> 737

<211> 42

<212> PRT

<213> Homo sapiens

<400> 737

Asp Gln Trp Cys Pro Asp Gly Ser His Leu Gly Gln Pro Arg Gln Leu

1 5 10 15

Pro Arg Asp Arg Arg Pro Arg Thr Ser His Ile Ser Ala Leu Ile Ala

20 25 30

Ala Arg Gly Leu Cys Ser Ala Ala Ala Ser

35 40

<210> 738

<211> 23

<212> PRT

<213> Homo sapiens

<400> 738

Asn Leu Ala Ile Val Glu Glu Glu Met Phe Leu Val Met Gly Glu Leu

1 5 10 15

Asn Tyr Val Pro Leu Ala Leu

20

<210> 739

<211> 52

<212> PRT

<213> Homo sapiens

<400> 739

Pro Tyr Phe Trp Arg Thr Leu Gln Pro Met Glu Met His Phe Phe Phe

1 5 10 15

Cys Gln His Phe Pro Ser Gly Pro Thr Arg Val Pro Leu Ser Lys Tyr

20 25 30

Thr Thr Arg Ser Lys Ser Leu Lys Gln Asp Lys Arg Phe Tyr Phe Ser

35 40 45

Ile Pro Ser Thr

50

<210> 740

<211> 44

<212> PRT

<213> Homo sapiens

<400> 740

Arg Arg Cys Glu Val Gln His Ser Ser Val Thr Arg Glu Lys Thr Gly

1 5 10 15

Cys Gly Phe Ser Ala Val Asn Lys Thr Gln Glu Val Phe Trp Trp Lys

20 25 30

Asn Thr Leu Tyr Leu Ile Lys Ile His Tyr Met Lys

35 40

<210> 741

<211> 22

<212> PRT

<213> Homo sapiens

<400> 741

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

1 5 10 15

Arg Met Arg His Arg Val

20

<210> 742

<211> 52

<212> PRT

<213> Homo sapiens

<400> 742

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

1 5 10 15

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

20 25 30

Ile Lys Asp Ile Phe Leu Met Lys Arg Phe Leu Thr Leu Ala Ser Ala

35 40 45

His Val Gly Val

50

<210> 743

<211> 42

<212> PRT

<213> Homo sapiens

<400> 743

Gly Ser Leu Leu Gly Leu Ser Leu Ala Gln Pro Glu Ala Leu Lys Val
1 5 10 15

Ala Ala Arg Leu Arg Cys Gln His Pro Gln His His His Arg Arg Arg
20 25 30
Val Gln Cys Ser Leu Ser Arg Val Arg Arg
35 40

<210> 744

<211> 30

<212> PRT

<213> Homo sapiens

<400> 744

Gly Ser Asn Ser Asn Leu Gly Met Lys Cys Gly Ile Gln Asn Gln Met
1 5 10 15
Leu Val Ile Gln Gln Glu Ala Gly Phe Gly Ile Leu His Thr
20 25 30

<210> 745

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 745

Gln Ser Gln Gly Gly Gly Ala Gly Gly Glu Ser Gln Arg Ala Asn Ser
1 5 10 15
Ala Arg Arg Pro Leu Gly Arg Ile Gln Gly Arg Cys Arg Ala Ala Gly
20 25 30
Pro Ala Cys Gly Arg Gly Arg Ala
35 40

<210> 746

<211> 31

<212> PRT

<213> Homo sapiens

<400> 746

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

1 5 10 15

Leu Gly Lys Leu Glu Met Val Lys Ala Val Gln Leu Arg Val Ala

20 25 30

<210> 747

<211> 58

<212> PRT

<213> Homo sapiens

<400> 747

Phe Met Arg Asn Phe Leu Asn Met Leu Cys Phe Glu Asn Ile Leu Leu

1 5 10 15

His Leu His Gln Ile Met Lys Phe Leu Leu Arg Gln Pro Gly Gln Gly

20 25 30

Ile Trp Lys Leu Arg Leu Ile Gln Pro Ser Leu Trp Leu Ser Leu Trp

35 40 45

Ile Arg Pro Asn Leu Leu Leu Phe His Ile

50 55

<210> 748

<211> 32

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 748

His Pro Gln Ser His Leu His Pro Leu Gly Leu Pro His Leu Pro His

1 5 10 15

Pro His Cys Gln Thr Thr Arg Ala Pro Cys Gln Asp Trp Pro Leu Pro

20 25 30

<210> 749

<211> 62

<212> PRT

<213> Homo sapiens

<400> 749

Pro Pro Ala Gly Lys Asn Leu Met Lys Ser Pro Gln Trp Trp Gly Ser
1 5 10 15

Ser Val His Leu Ala Trp Ser Ser Gln Ser Leu Ser Leu His Gly Ser
20 25 30

Ala Val Arg Glu Asn His Pro Ser Leu Thr Arg Leu Leu His Thr Ser

35 40 45

Leu Cys Met Cys Leu Arg Glu Leu Ile Phe Thr Leu Lys Thr

50 55 60

<210> 750

<211> 53

<212> PRT

<213> Homo sapiens

<400> 750

Met Glu Tyr Cys Pro Pro Leu Asn Ser Cys Ala Ser Val Cys Ala Ser

1 5 10 15

Trp Ser Leu Asp Gly Cys His Pro Leu Trp Ser Trp His Ser Ser Arg

20 25 30

Ala Gly Arg Ala Gly Gly Gln Gly Ala Gln Asp Cys Pro Cys Ile Ala

35 40 45

Glu Leu Trp Gln Cys

50

<210> 751

<211> 44

<212> PRT

<213> Homo sapiens

<400> 751

Leu Trp Leu Trp Ala Gly Trp Thr Val Trp Trp Ser Cys Gly Pro Gly

1 5 10 15

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

20 25 30

Leu Leu Arg Phe Ser Cys Met Arg Val Ala Ser Tyr

35 40

<210> 752

<211> 44

<212> PRT

<213> Homo sapiens

<400> 752

Val Met Pro Leu His His Gly Leu Thr Gln Lys Met Ile Ser Glu Thr

1 5 10 15

Cys Ser Val Arg Ser Phe Met Asp Leu Lys Ile Lys Leu Ala Met Lys

20 25 30

Ile Gly Gly Val Ser Leu Thr Ser Phe Leu Phe Pro

35 40

<210> 753

<211> 29

<212> PRT

<213> Homo sapiens

<400> 753

Ala Ala Ala Thr Thr Leu Thr Ser Ala Ala Ser Ser Ala Gly Ser Ser

1 5 10 15

Trp Thr Pro Gly Arg Arg Gly Gly Thr Cys Ala Ser Ser

20 25

<210> 754

<211> 22

<212> PRT

<213> Homo sapiens

<400> 754

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

1 5 10 15

His Gln Gln Leu Pro Arg

20

<210> 755

<211> 27

<212> PRT

<213> Homo sapiens

<400> 755

Trp Arg Glu Ala Trp Arg Arg Ser Ser Trp Pro Arg Trp Thr Met Ala

1 5 10 15

Trp Ala Gln His Gly Ser Pro Ala Ile Gly Gly

20 25

<210> 756

<211> 54

<212> PRT

<213> Homo sapiens

<400> 756

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

1 5 10 15

Gln Leu Gly Phe Thr Leu Lys Arg Tyr Arg Ser Phe Leu Asn Ile Glu

20 25 30

Phe Leu Gln Thr Pro Lys Leu Thr Arg Lys Leu Ser Glu Trp Ser Arg

35 40 45

Arg Lys Leu Leu Thr Cys

50

<210> 757

<211> 32

<212> PRT

<213> Homo sapiens

<400> 757

Val Val Lys Thr Val Ala Leu Gly His Leu Thr Ile Arg Asn Val Ala

1 5 10 15

Ser Val Asp Pro Gly Gln Thr Val Leu Trp Met Glu Ser Leu Cys Leu

20 25 30

<210> 758

<211> 9

<212> PRT

<213> Homo sapiens

<400> 758

Cys His Trp Gly Ala Ala Pro Gly Ser

1 5
 <210> 759
 <211> 25
 <212> PRT
 <213> Artificial Sequence
 <220><223> modified Homo sapiens FSP
 <400> 759
 Gly Pro Val Tyr Tyr Val Cys Asn His Met Asn Val Ser Ser Val Leu
 1 5 10 15

Lys Pro Ser Leu Phe Thr Val Pro Ile
 20 25
 <210> 760
 <211> 30
 <212> PRT
 <213> Homo sapiens
 <400> 760
 Thr Ser Gln Arg Ile Pro Cys Ser Leu Gln Lys Lys Met His Leu Lys
 1 5 10 15
 Tyr Gly Leu Phe Ser Thr Phe Tyr Leu Arg Thr Ser Ile His
 20 25 30

<210> 761
 <211> 27
 <212> PRT
 <213> Homo sapiens
 <400> 761
 Ala Leu Gln Val Phe Ser Ser Thr Gly Leu Lys Arg Thr Leu Ile Glu

1 5 10 15
 Arg Val Ser Met Asp Thr Ala Phe Arg Glu Ser
 20 25
 <210> 762
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 762

Pro Ala Pro Ala Thr Gln Ala Pro Cys Met Met Thr

1 5 10

<210> 763

<211> 31

<212> PRT

<213> Homo sapiens

<400> 763

Lys Thr Ala Lys Thr Leu Cys Gly His Arg Met Asp Pro Gln Pro Arg

1 5 10 15

Ser Cys Ser Ser Leu Trp Ser Trp Gln Leu Lys Pro Cys Pro Cys

20 25 30

<210> 764

<211> 34

<212> PRT

<213> Homo sapiens

<400> 764

Leu Val Lys Val Gln Thr His Ile Ser Val Ile Pro Ser Leu Glu Ser

1 5 10 15

Ser Pro Leu Gly Val Gln Asp Trp Gly Asn Pro Ser Ala Leu Ile Gln

20 25 30

Asn Ser

<210> 765

<211> 32

<212>

> PRT

<213> Homo sapiens

<400> 765

Leu Leu Trp Glu Asp Arg Ala Lys Asn Thr Gln Ala Leu Pro Leu Pro

1 5 10 15

Leu Ser Gly Glu Ala Leu Ser Ile Gly Pro Ala Leu Gln Leu Lys Val

20 25 30

<210> 766

<211> 28

<212> PRT

<213> Homo sapiens

<400> 766

Arg Lys Ser Leu Ile Leu Cys Lys Thr Asn Leu Leu Val Phe Ile Asn

1 5 10 15

Asp Ser Arg Arg His Leu Asp Ser Met Glu Lys Phe

20 25

<210> 767

<211> 22

<212> PRT

<213> Homo sapiens

<400> 767

Trp Thr Arg Ser Gln Lys Gly Lys Ala Ser Leu Thr Ile Gly Gly Trp

1 5 10 15

Arg Ile Cys Cys Ser Leu

20

<210> 768

<211> 24

<212> PRT

<213> Homo sapiens

<400> 768

Arg His Pro Leu Gln Ser Leu His His Pro Pro Cys Ser Leu Ser Ala

1 5 10 15

Ala Thr Gln Ala Ile Pro Pro Arg

20

<210> 769

<211> 40

<212> PRT

<213> Homo sapiens

<400> 769

Val Arg Ile Leu Glu Ile Ser Ser His Phe Leu His Ile Leu Arg Ser

1 5 10 15

Gln Lys Met Ile Gln Leu Asn Leu Thr Val Met Lys Lys Ile Leu Leu
20 25 30

Leu Phe Phe His His His Leu Val
35 40

<210> 770

<211> 38

<212> PRT

<213> Homo sapiens

<400> 770

Asn Leu Arg Asn Gln Ser Val Ala Met Ala Asp Trp Arg Glu Met Lys
1 5 10 15

Ser Val Ile Val Val Leu Arg Leu Asn Val Asp Leu Gln Ala Val Val
20 25 30

Ile Phe Glu Leu Val Tyr
35

<210> 771

<211> 25

<212> PRT

<213> Homo sapiens

<400> 771

Arg Ile Lys Ala Ser Ser Met Pro Gln Thr Pro Glu Arg Gln Thr Leu
1 5 10 15

Pro His Leu Thr Ser Leu Pro Ser Arg
20 25

<210> 772

<211> 20

<212> PRT

<213> Homo sapiens

<400> 772

Leu Arg Thr Lys Leu Cys Phe Ala Pro Cys Thr Asn Gln Arg Glu Phe
1 5 10 15

Met Ser Lys Asn
20

<210> 773

<211> 44

<212> PRT

<213> Homo sapiens

<400> 773

Arg Lys Ser Pro Val Thr Gly Asn Met Arg His Trp Pro Cys Leu Lys

1 5 10 15

Asp Arg Lys Gln Ala Glu Arg Pro Gly Leu Ile Cys Arg Asn Pro Ser

20 25 30

Leu Leu Trp Ala Trp Met Met Lys Leu His Asn Tyr

35 40

<210> 774

<211> 13

<212> PRT

<213> Homo sapiens

<400> 774

Val Ile Pro Pro Ile Gln Cys Phe Ile Leu Met Tyr Phe

1 5 10

<210> 775

<211> 13

<212> PRT

<213> Homo sapiens

<400> 775

Lys Glu Lys Lys Ser Arg Thr Leu Met Lys Met Ile Ser

1 5 10

<210> 776

<211> 24

<212> PRT

<213> Homo sapiens

<400> 776

His Pro Leu Pro Lys Met Asn Thr Thr Arg Met Gly Ile Trp Ile Ser

1 5 10 15

Pro Gly Ala Gly Pro Gly Leu His

20

<210> 777

<211> 12

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 777

Asn Lys Trp Asn Ala Met Val Val Leu Asn Lys Gly

1 5 10

<210> 778

<211> 19

<212> PRT

<213> Homo sapiens

<400> 778

Gln Arg Pro Leu Pro Gly Asn Gly Val Arg Lys Ala Gln Asn Gly Trp

1 5 10 15

Cys Arg His

<210> 779

<211> 21

<212> PRT

<213> Homo sapiens

<400> 779

Leu Trp Ser Ser Arg His Thr Ser Leu Arg Ile Thr His Lys Arg His

1 5 10 15

Gly Ser Ile Pro Leu

20

<210> 780

<211> 13

<212>

> PRT

<213> Homo sapiens

<400> 780

Ser Gln Glu Ile Leu Val Ile Ala Leu Leu Leu Lys Arg

1 5 10

<210> 781

<211> 15

<212> PRT

<213> Homo sapiens

<400> 781

Thr Trp Arg Lys Leu Ala Asp Ser Leu Val Cys Ser Trp Ile Thr

1 5 10 15

<210> 782

<211> 12

<212> PRT

<213> Homo sapiens

<400> 782

Cys His Leu Val Ser Thr Cys Gln Thr Ile Pro Ser

1 5 10

<210> 783

<211> 11

<212> PRT

<213> Homo sapiens

<400> 783

Leu Glu Ile Leu Arg Arg Ser Ser Leu Gly Arg

1 5 10

<210> 784

<211> 27

<212> PRT

<213> Homo sapiens

<400> 784

Leu Glu Asn Leu Asp Ser Arg Gln Lys Phe Pro Phe Asp Leu Ile Ile

1 5 10 15

Met Ala Asn Met Tyr Gln Trp Ile Arg Val Arg

20 25

<210> 785

<211> 16

<212> PRT

<213> Homo sapiens

<400> 785

Leu Pro Ile Met Pro Cys Trp Ser Pro Cys Leu Ala Gly Ser Leu Trp

1 5 10 15

<210> 786

<211> 11

<212> PRT

<213> Homo sapiens

<400> 786

Met Ser Leu Leu Gln Arg Thr Val Ser Gln Gln

1 5 10

<210> 787

<211> 8

<212> PRT

<213> Homo sapiens

<400> 787

Lys Gln Lys Lys Asn Trp Gln Ser

1 5

<210> 788

<211> 19

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 788

Met Leu Lys Asn Val Arg Gly Asn Asn Ser Lys Leu Lys Tyr Arg Arg

1 5 10 15

Lys Arg Lys

<210> 789

<211> 22

<212> PRT

<213> Homo sapiens

<400> 789

Ser Ala Ile Lys Gln Arg Lys Gln Arg Thr Met Trp Ser Gly Lys Pro

1 5 10 15

Ser Leu Trp Ser Ser Gly

20

<210> 790

<211> 13

<212> PRT

<

213> Homo sapiens

<400> 790

Lys Glu Lys Lys Leu Arg Leu Ala Val Leu Val Asn Asn

1 5 10

<210> 791

<211> 14

<212> PRT

<213> Homo sapiens

<400> 791

Gly Leu Ala Ser Pro Leu Ala Ala Cys Arg Leu Thr Ser Pro

1 5 10

<210> 792

<211> 11

<212> PRT

<213> Homo sapiens

<400> 792

Ile Ser Lys Lys Gln Asn Ala Leu Ala Glu His

1 5 10

<210> 793

<

211> 13

<212> PRT

<213> Homo sapiens

<400> 793

Gly Gln Lys Lys Ile Arg Lys Thr Ser Gln Val Leu Thr

1 5 10

<210> 794

<211> 11

<212> PRT

<213> Homo sapiens

<400> 794

Ser Glu Lys Cys Arg Ser Ser Leu Asp Trp Arg

1 5 10

<210> 795

<211> 10

<212> PRT

<213> Homo sapiens

<400> 795

Glu Lys Met Cys Trp Phe Arg Thr Gly Met

1 5 10

<210> 796

<211> 13

<212> PRT

<213> Homo sapiens

<400> 796

Ala His Lys Lys Ala Met Lys Lys Ala Thr Lys Ser Ser

1 5 10

<210> 797

<211> 10

<212> PRT

<213> Homo sapiens

<400> 797

Phe Thr Pro Phe Leu Val His Lys Met Phe

1 5 10

<210> 798

<211> 20

<212> PRT

<213> Homo sapiens

<400> 798

Ala Gly Arg Ala Ala Pro Ala Pro Ser Pro Arg Thr Ala Ala Ala Cys

1 5 10 15

Pro Thr Pro Val

20

<210> 799

<211> 9

<212> PRT

<213> Homo sapiens

<400> 799

Val Arg Tyr Pro Arg Ala Arg Pro Arg

1 5

<210> 800

<211> 9

<212> PRT

<213> Homo sapiens

<400> 800

Gln Leu Leu Lys Met Arg Ser Trp Asn

1 5

<210> 801

<211> 11

<212> PRT

<213> Homo sapiens

<400> 801

Val Ile His Phe Lys Lys Ser Lys Ile Ile Trp

1 5 10

<210> 802

<211> 12

<212> PRT

<213> Homo sapiens

<400> 802

Gly Pro Thr Pro Leu Leu Leu Ser Ser Gly Phe Tyr

1 5 10

<210> 803

<211> 10

<212> PRT

<213> Homo sapiens

<400> 803

Asn Gln Leu Thr Arg Asp Trp Lys Ala Ser

1 5 10

<210> 804

<211> 11

<212> PRT

<213> Homo sapiens

<400> 804

Leu Ile Glu Glu Phe Thr His Leu Cys Ser Leu

1 5 10

<210> 805

<211> 12

<212>

> PRT

<213> Homo sapiens

<400> 805

Ala Val Glu Lys Ser Pro His Leu Arg Trp Leu Ile

1 5 10

<210> 806

<211> 12

<212> PRT

<213> Homo sapiens

<400> 806

Ser Leu Pro Asn Leu Lys His Cys Leu Met Met Ser

1 5 10

<210> 807

<211> 10

<212> PRT

<213> Homo sapiens

<400> 807

Ala Gly Ser Gly Ser Asp Thr Gln Arg Asp

1 5 10

<210> 808

<211> 8

<212> PRT

<213> Homo sapiens

<400> 808

Thr Asp Lys Lys Val Trp Leu Met

1 5

<210> 809

<211> 11

<212> PRT

<213> Homo sapiens

<400> 809

Ile Val Lys Lys Gly Glu Glu Gly Gly Arg Met

1 5 10

<210> 810

<211> 15

<212> PRT

<213> Homo sapiens

<400> 810

Thr Ser Met Thr Ser Thr Trp Thr Gly Leu Leu Arg Ser Arg Cys

1 5 10 15

<210> 811

<211> 8

<212> PRT

<213> Homo sapiens

<400> 811

Asp Cys Gln Lys Ser His Ser Ser

1 5

<210> 812

<211> 9

<212> PRT

<213> Homo sapiens

<400> 812

Arg Ala Phe Phe Ile Ser His Ser Leu

1 5

<210> 813

<211> 8

<212> PRT

<213> Homo sapiens

<400> 813

Leu Asn Gln Lys Asn Ser Val Ile

1 5

<210> 814

<211> 11

<212> PRT

<213> Homo sapiens

<400> 814

Gln Leu Gln Lys Thr Ala Pro Gly Leu Asn Ile

1 5 10

<210> 815

<211> 12

<212> PRT

<213> Homo sapiens

<400> 815

Lys Gly Lys Lys Asn Val Leu Arg Leu Thr Ser Cys

1 5 10

<210> 816

<211> 10

<212> PRT

<213> Homo sapiens

<400> 816

Leu Lys Lys Ile Leu Gln Asp Tyr Gln Ser

1 5 10

<210> 817

<211> 10

<212> PRT

<213> Homo sapiens

<400> 817

Phe Phe Thr Thr Cys Gly Asn Arg Arg Ser

1 5 10

<210> 818

<211> 11

<212> PRT

<213> Homo sapiens

<400> 818

Leu Ala Gln Trp Ala Pro Ala Ala Ser Pro Ala

1 5 10

<210> 819

<211> 10

<212> PRT

<213> Homo sapiens

<400> 819

Leu Ala Gly Arg Ala Met Gly Arg Ala Pro

1 5 10

<210> 820

<211> 8

<212> PRT

<213> Homo sapiens

<400> 820

Thr Gly Lys Lys Asn Cys Ser Ile

1 5

<210> 821

<211> 10

<212> PRT

<213> Homo sapiens

<400> 821

Lys Asp Leu Phe Cys Arg Gly Ile Ser Leu

1 5 10

<210> 822

<211> 8

<212> PRT

<213> Homo sapiens

<400> 822

Gly Thr Pro Pro Ser Pro Val Ser

1 5

<210> 823

<211> 36

<212> PRT

<213> Homo sapiens

<400> 823

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

1 5 10 15

Val Val Thr Phe Phe Ala Ala Gly Ser Ala Lys Met Ser Cys Gln Ser

20 25 30

Trp Leu Ala Pro

35

<210> 824

<211> 23

<212> PRT

<213> Homo sapiens

<400> 824

Ser Thr Ser Ala Ser Cys Ser Ser Ser Phe Ser Leu Val Met Thr Leu

1 5 10 15

Thr Leu Asp Thr Trp Arg Leu

20

<210> 825

<211> 15

<212> PRT

<213> Homo sapiens

<400> 825

Arg Pro Glu Asn Ser Gln Ile Asn Ser Ser Leu Cys Asn Glu Ala

1 5 10 15

<210> 826

<211> 8

<212> PRT

<213> Homo sapiens

<400> 826

Ile Arg Lys Lys Arg Cys Val Tyr

1 5

<210> 827

<211> 58

<212> PRT

<213> Homo sapiens

<400> 827

Thr Thr Leu Ala Phe Gln Lys Ser Leu Pro Trp Pro Lys Leu Leu Pro

1 5 10 15

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

20 25 30

Leu Leu Gly Pro Leu Thr Gln Ile His Gln Ile Leu Leu Ser Lys Phe

35 40 45

Ser Phe Phe Gln Leu Leu Cys Thr Arg Asp

50 55

<210> 828

<211> 11

<212> PRT

<213> Homo sapiens

<400> 828

Met Asn Leu Pro Phe Gly Ser Phe Met Ser Gln

1 5 10

<210> 829

<211> 8

<212> PRT

<213> Homo sapiens

<400> 829

Pro Asp Pro Pro Thr Gly Ile Gly

1 5

<210> 830

<211> 11

<212> PRT

<213> Homo sapiens

<400> 830

Leu Cys Lys Lys Ile Met Met Arg Ser Ile Gln

1 5 10

<210> 831

<211> 10

<212> PRT

<213> Homo sapiens

<400> 831

Thr Pro Arg Thr Gly Gly Pro Arg Cys Trp

1 5 10

<210> 832

<211> 11

<212> PRT

<213> Homo sapiens

<400> 832

Pro Thr Phe Phe Ile Ser Pro Asn Lys Thr His

1 5 10

<210> 833

<211> 18

<212> PRT

<213> Homo sapiens

<400> 833

His Lys Trp Leu Lys Phe Cys Leu Leu Arg Val Val Lys Glu Ser Phe

1 5 10 15

His Glu

<210> 834

<211> 214

<212> PRT

<213> Homo sapiens

<400> 834

Val Ala Ala Pro Ser Pro Gly Cys Thr Leu Ala Arg Ala Pro Ser Thr
1 5 10 15
Pro Val Lys Thr Val Trp Ala Thr His Arg Ala Arg Val Pro Pro Ala
20 25 30
Cys Leu Leu His Ser Trp Ile Ser Leu Lys Ser Ser Cys Gln Phe Asn
35 40 45
Lys Met Ala Ser Thr His Tyr His Thr Ser Glu Gly Gln Gln Gly Gln
50 55 60
Gly Pro Gly Gln Arg Gln Gly Arg Ala Leu Pro Gln Ser Pro Ala Val
65 70 75 80
Arg Ala Leu Ala Ala Ser Gly Thr Trp Phe Ile Leu Cys Arg Ser Ser
85 90 95
Leu Pro Ser Pro Thr Leu Trp Arg Arg Arg Gly Ser Gly Thr Ile Met
100 105 110
Gly Pro Arg Leu Arg Glu Glu Val Ala Leu Glu Glu Thr Ala Thr Pro
115 120 125
Ala Arg Ala Leu Glu Ala Pro Thr Pro Pro Ile Thr Thr Ile Thr Thr
130 135 140
Thr Ile Thr Thr Thr Thr Ser Pro Gly Thr Ala Arg Gly Ala Arg Ala
145 150 155 160
Arg Thr Ala Arg Gly Met Gly Gly Thr Arg Pro Ser Pro Gln Ala Gly
165 170 175
Gly Val Pro Met Thr Thr Trp Thr Val Ile Ala Ala Ser Trp Arg Val
180 185 190
Gly Gly Pro Leu Gly Ser Leu Val Val Pro Ser Ala Trp Arg Val Gln
195 200 205
Met Gly Pro Thr Gly Thr
210
<210> 835
<211> 140
<212> PRT
<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 835

Ser Leu Arg Lys Lys Arg Arg Lys Ser Pro Ile Thr Arg Asn Leu Arg
1 5 10 15

His Trp Pro Cys Leu Lys Asp His Lys Trp Ala Val Arg Leu Gly Leu
20 25 30

Ile Cys Arg Asn Pro Gly Leu Leu Trp Ala Cys Met Val Lys Leu Gln
35 40 45

Glu Tyr Gln His Leu Leu Ile Lys Thr Ser Leu Arg Lys Lys Arg Lys
50 55 60

Ser Pro Ile Thr Arg Asn Leu Arg Gln Trp Pro Cys Leu Arg Ala Ser
65 70 75 80

Arg Val His Thr Leu Lys Asp His Arg Trp Ala Val Arg Leu Gly Leu
85 90 95

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

Arg Arg Ser Ser Lys Gly His Glu Cys Leu Val Met Ile Phe Gln Cys
115 120 125

Pro Val Arg Thr Leu Arg Ala His Ser Leu Ile Gln
130 135 140

<210> 836

<

211> 90

<212> PRT

<213> Homo sapiens

<400> 836

Gln His Cys Pro Pro Val Pro Gly Ser Ala Ser Leu Phe His Arg Arg
1 5 10 15

Arg Thr Gln Gly His Pro Ala Leu His Gln Cys Leu Ser Leu Thr Met
20 25 30

Ser Ser Ala Trp Pro Pro Thr Val Thr Ile Trp Met Cys Arg His Pro
35 40 45

Arg Pro Gln Leu Ser Leu Thr Leu Pro Gln Leu Ser Leu Thr Gln Pro

50

55

60

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

65

70

75

80

Pro Arg Arg Ala Pro Gln Gly Val Asn Pro

85

90

<210> 837

<211> 39

<212> PRT

<213> Homo sapiens

<400> 837

Leu Gly Ser Ile Arg Gly Leu Asn Gly Asn Gln Met Arg Met Glu Ser

1

5

10

15

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

20

25

30

Leu Arg Lys Thr Trp Ser Phe

35

<210> 838

<211> 14

<212> PRT

<213> Homo sapiens

<400> 838

Thr Val Leu Ser Leu Val Thr Ile Ser Arg Phe Val Leu Ser

1

5

10

<210> 839

<211> 19

<212> PRT

<213> Homo sapiens

<400> 839

Asn Ser Asn Ile Gln Leu Met Thr Thr Arg Asn Phe Trp Pro Met Ala

1

5

10

15

Ser Ala Ile

<210> 840

<211> 13

<212> PRT

<213> Homo sapiens

<400> 840

Trp Glu Lys Lys Arg Gly Thr Lys Ser Met Lys Val Thr

1 5 10

<210> 841

<211> 12

<212> PRT

<213> Homo sapiens

<400> 841

Ser Thr Phe Phe His Glu Asp Leu Val Arg Ile Pro

1 5 10

<210> 842

<211> 8

<212> PRT

<213> Homo sapiens

<400> 842

Trp Glu Lys Lys Trp Val Arg Ser

1 5

<210> 843

<211> 11

<212> PRT

<213> Homo sapiens

<400> 843

Asn Val Pro Leu Thr Lys Leu Ser Glu Val Phe

1 5 10

<210> 844

<211> 17

<212> PRT

<213> Homo sapiens

<400> 844

Leu Trp Asp Pro Ser Arg Arg Arg Thr Thr Thr Val Pro Ile Ser Thr

1 5 10 15

Ser

<210> 845

<211> 11

<212> PRT

<213> Homo sapiens

<400> 845

Leu Gln Lys Lys Ile Ser Trp Asn Leu Ser Leu

1 5 10

<210> 846

<211> 9

<212> PRT

<213> Homo sapiens

<400> 846

Lys Glu Lys Lys Gln Trp Lys Lys Asn

1 5

<210> 847

<211> 154

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 847

Val Pro Leu Pro Arg Ser Leu Leu Arg Gln Pro Val Gln Leu Arg Thr

1 5 10 15

Glu Pro Ala Arg Ser Ser Cys Ile Ser Thr Ala Ser Thr Thr Glu Ser

20 25 30

Thr Pro Thr Ala Ser Ser Ala Met Ala Val Thr Arg Ser Ser Arg Gly

35 40 45

Cys Trp Pro Ala Pro Ser Arg Pro Thr Ala Ser Thr Pro Ala Gly Arg

50 55 60

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

65 70 75 80
Ala Pro Trp Pro Ser Gly Pro Arg Thr Ser Thr Ala Val Pro Gly Ser
85 90 95

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

<210> 848

<211> 29

<212

> PRT

<213> Homo sapiens

<400> 848

Gln Glu Leu Lys Glu Ala Val Lys Phe Ser Ile Val Lys Asn Asn Ser

1 5 10 15

Asn Asn Lys Cys Gly Ile Gln Pro Gly Leu Pro Ile Leu
20 25

<210> 849

<211> 16

<212> PRT

<213> Homo sapiens

<400> 849

Val Ser Gly Ser Trp Ser Leu Gly His Pro Trp Cys Cys Leu Gly Leu

1 5 10 15

<210> 850

<211> 22

<212> PRT

<213> Homo sapiens

<400> 850

Leu Thr Leu Asn Ser Leu Arg Trp Pro Leu Gln Leu Ser Asn Leu Ala

1 5 10 15

Gly Ser Gln Ile Ser Trp

20

<210> 851

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 851

Ser Glu Arg Cys Leu Leu Val Cys Leu Leu Ser Leu Cys Lys Met Gly

1 5 10 15

Pro Thr Ile Leu Leu Thr Phe Gly Val His Gln Met Gly

20

25

<210> 852

<211> 12

<212> PRT

<213> Homo sapiens

<400> 852

Arg Pro Cys Trp Ser Arg Cys Ser Leu Arg Gln Met

1 5 10

<210> 853

<211> 34

<212> PRT

<213> Homo sapiens

<400> 853

Cys Val Gly Cys Gln Phe Ile Val Pro Thr Arg Gly Ala Pro Leu Met

1 5 10 15

Ala Arg Val His Thr Glu His Ser Arg Val Leu Leu Ser Pro Ser Phe

20

25

30

Thr Cys

<210> 854

<211> 19
 <212> PRT
 <213> Homo sapiens
 <400> 854
 Asn Tyr Arg Lys Leu Tyr Gln Lys Gln Leu Glu Lys Arg Ile Lys His
 1 5 10 15
 Leu Cys Ser

<210> 855
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 855
 Ser Ala Thr Pro Leu Pro His Tyr Leu Ala His
 1 5 10

<210> 856
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 856
 Thr Ser Ser Leu Thr Met Glu Ser Ser Gly His

1 5 10
 <210> 857
 <211> 12
 <212> PRT
 <213> Homo sapiens
 <400> 857

Leu Met Phe Phe Gly Asn Gln Ser Ile Ile Thr Leu
 1 5 10
 <210> 858
 <211> 11
 <212> PRT
 <213> Homo sapiens
 <400> 858

Leu Asn His Gln Lys Gly Lys Phe Met Asn Phe

1 5 10

<210> 859

<211> 160

<212> PRT

<213> Homo sapiens

<400> 859

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

1 5 10 15

Ala Ser Gly Gly Val Ser Arg Tyr Ile Ser Arg Cys Ala Pro Pro Ala

20 25 30

Thr Ala Trp Thr Ser Trp Pro Thr Ala Thr Trp Trp Ala Cys Ala Thr

35 40 45

Arg Arg Met Lys Leu Arg Ser Trp Leu Arg Arg Trp Arg Phe Lys Thr

50 55 60

Ala Pro Met Lys Met Gly Arg Cys Ser Cys Gly Gln Gly Ser Cys Ser

65 70 75 80

Thr Ile Ser Gln Asn His Thr Pro Thr Val Arg Leu Leu Glu Leu Pro

85 90 95

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

100 105 110

Met Val Val Arg Thr Thr Ser Ser Pro Cys Ser Arg Ala Thr Ala Ser

115 120 125

His Pro Pro Gly Cys His Cys Gly Lys Val Ser Thr Ser Thr Pro Thr

130 135 140

Phe Leu Ala Arg Pro Leu Pro Trp Pro Leu Pro Ser Thr Gln Met Ser

145 150 155 160

<210> 860

<211> 85

<212> PRT

<213> Homo sapiens

<400> 860

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

Gly Ser Arg Arg Cys Cys Leu Arg Thr Ser Cys Gly Ala Ala Arg Pro
 35 40 45
 Arg Arg Thr Arg Ser Ala Trp Gly Asp Trp Val Ala Ser Pro Pro Thr
 50 55 60
 Arg Ser Ser Ser Arg Thr Ala Cys Gly Ala Ala Ser Pro Pro Ala Arg
 65 70 75 80
 Ser Trp Ser Ala Pro
 85

<210> 861
 <211> 60
 <212> PRT
 <213> Homo sapiens
 <400> 861

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

<210> 862
 <211> 105
 <212> PRT
 <213> Homo sapiens
 <400> 862

His Thr Ala Thr Lys Ala Tyr Thr Ser Pro His Ala Glu Gly Glu Phe
 1 5 10 15

Cys Pro Gly Glu Thr Asp Thr Pro Asp Met Gly Glu Gly Leu Ser Gly
 20 25 30
 Asn Thr Glu Thr Lys Arg Glu Arg Gly Phe Arg Thr Ser Pro Pro Phe
 35 40 45
 Ile Ser Lys Pro Gln Arg Ala Leu Trp Ser Pro Pro Cys Pro Ser Pro

50 55 60
 Gly Pro Pro Ser Leu Thr Ser Gly Leu Ser Cys Ser Trp Cys Ala Pro
 65 70 75 80
 Cys Thr Gly Ala Gly Trp Val Gly Lys Trp Ala Gly Leu Gln Leu Pro
 85 90 95
 Phe Tyr Pro Gln Trp Gln Leu Pro Pro
 100 105

<210> 863

<211> 63

<212> PRT

<213> Homo sapiens

<400> 863

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

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

<210> 864

<211> 35

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 864

Ala Ala Ala Arg Trp Lys Ala Cys Leu Trp Pro Val Ala Pro Arg Cys

1 5 10 15
Ser Arg Trp Pro Pro Ala Ile Leu Pro Ala Ser Thr Pro Pro Ser Ala
20 25 30

Pro Pro Thr

35

<210> 865

<211> 31

<212> PRT

<213> Homo sapiens

<400> 865

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

1 5 10 15

Gly Asn Gly Leu Gln Ser Gln Ala Gly Ala Leu Arg Met Ile Ser

20 25 30

<210> 866

<211> 23

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 866

Gln Gln Val Pro Gly Leu Met Lys Thr Gly Pro Ser Trp Met Glu Ala

1 5 10 15

Trp Asn Gln Met Gly Pro Thr

20

<210> 867

<211> 25

<212> PRT

<213> Homo sapiens

<400> 867

Ala Ser Arg Trp Asn Pro Leu Arg Arg Thr Arg Ala Leu Arg Gly Pro

1 5 10 15

Pro Arg Gln Arg Ala Ala Ala Pro His

20 25

<210> 868

<211> 21

<212> PRT

<213> Homo sapiens

<400> 868

Tyr Ser Tyr Pro Ser Ser Leu Ser Val Phe Ser Val Pro Gly Tyr His

1 5 10 15

Leu Tyr Tyr Phe Arg

20

<210> 869

<211> 21

<212> PRT

<213> Homo sapiens

<400> 869

Ile Phe Tyr Ile Phe Ser Trp Ile Cys Pro Pro Thr Lys Lys Gln Arg

1 5 10 15

His Lys Ile Gln Leu

20

<210> 870

<211> 19

<212> PRT

<213> Homo sapiens

<400> 870

Ser Ile Gln His Leu Gln Ala Pro Ser Pro Ser Leu Trp Pro Trp Asn

1 5 10 15

Met Leu Cys

<210> 871

<211> 12

<212> PRT

<213> Homo sapiens

<400> 871

Ser Ala Ser Lys Asn Gly Asn Lys Lys Asn Ser Arg

1 5 10

<210> 872

<211> 9

<212> PRT

<213> Homo sapiens

<400> 872

Glu Ser Leu Lys Asn Thr Leu Asn Gln

1 5

<210> 873

<211> 12

<212> PRT

<213> Homo sapiens

<400> 873

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

1 5 10

<210> 874

<211> 19

<212> PRT

<213> Homo sapiens

<400> 874

Leu Thr Asp Phe Phe Val Leu Trp Lys Ala Ser Gly Thr Ile Gln Phe

1 5 10 15

Asn Cys Lys

<210> 875

<211> 10

<212> PRT

<213> Homo sapiens

<400> 875

Leu Ala Ala Phe Leu Asn Phe Val Met His

1 5 10

<210> 876

<211> 12

<212> PRT

<213> Homo sapiens

<400> 876

Pro Pro Lys Lys Phe Ser Ile Leu Pro Ser Ser Arg

1 5 10

<210> 877

<211> 22

<212> PRT

<213> Homo sapiens

<400> 877

Trp Asp Gln Arg Lys Arg Lys Met Gly Lys Val Ile Ser Lys Gly Asn

1 5 10 15

Asp Leu Ser Lys Thr Gly

20

<210> 878

<211> 10

<212> PRT

<213> Homo sapiens

<400> 878

Trp Ala Ser Thr Ile Arg Asp Arg Cys Val

1 5 10

<210> 879

<211> 11

<212> PRT

<213> Homo sapiens

<400> 879

Cys Gln Leu Ile Glu Asn Val Pro Leu Leu Leu

1 5 10

<210> 880

<211> 12

<212> PRT

<213> Homo sapiens

<400> 880

Lys Thr Pro Pro Gly Leu Leu Arg Asn Thr Gln Gln

1 5 10

<210> 881

<211> 10

<212> PRT

<213> Homo sapiens

<400> 881

Ala Gly Ala Arg Gly Glu Ile Ala Val Met

1 5 10

<210> 882

<211> 10

<212> PRT

<213> Homo sapiens

<400> 882

Glu Lys Ile Pro Arg Gly Pro Ser Ala Ser

1 5 10

<210> 883

<211> 10

<212> PRT

<213> Homo sapiens

<400> 883

Gln Leu Pro Lys Met Ala Pro Phe Met Met

1 5 10

<210> 884

<211> 9

<212> PRT

<213>

> Homo sapiens

<400> 884

Lys Asp Lys Lys Gln Ile Met Lys Cys

1 5

<210> 885

<211> 165

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 885

Thr Asn Ala Leu Thr Leu Ala Gln Trp Ser Pro Val Ile Ala Ala Ser

1 5 10 15

Pro Ser Ala Ser Thr Gln Ala Arg Cys Ala Thr Ser Ala Ala Ala Thr

20 25 30

Thr Ser Pro Pro Thr Ser Ala Pro Thr Gln Ala Lys Ser Pro Ser Pro

35 40 45

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

50 55 60

Ile Pro Arg Ser Thr Cys Gly Arg Arg Thr Arg Lys Gln Thr Lys Val

65 70 75 80

Leu Trp Pro Leu Arg Pro Pro Pro Leu Ser Leu Pro Thr Arg Pro Arg

85 90 95

Leu Leu Pro Leu Thr Arg Pro Arg Leu Leu Pro Leu Ile His Pro Arg

100 105 110

Pro Pro Pro His Thr His Leu Pro Ala Pro Arg Pro Thr His Pro Leu

115 120 125

Cys Thr Val Ala Ser Pro Pro Arg Arg Trp Pro Pro Arg Thr Pro Leu

130 135 140

Phe Pro Leu Leu Ser Arg Pro Arg Ser Ala Ala Ser Leu Ala Pro Pro

145 150 155 160

Gln Gly Phe Arg Thr

165

<210

> 886

<211> 49

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 886

Gly Ala Trp Glu Leu Gly Gly Leu Ala Arg Trp Gly Pro Leu Cys Thr

1 5 10 15

His Pro Gln Cys Gln Val Leu Leu Leu Val Glu Asp Val Leu Cys Ala
 20 25 30
 Lys Trp Phe Ile Cys Pro Ala Ser Phe Asn Pro Gln Asn Asp Ser Met
 35 40 45

Arg

<210> 887

<211> 34

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 887

Arg Asn Leu Ile Leu Met Ile Lys Val His Lys Phe Leu His Asn Leu
 1 5 10 15
 Ser Lys Tyr Thr Asp Lys Leu Gln Lys Ala Arg Met Leu Leu Pro Pro
 20 25 30

Lys Ala

<210> 888

<211> 80

<212> PRT

<213> Homo sapiens

<400> 888

Arg Lys Gln Leu Tyr Ile Gln Asn Ala Leu Asn Leu Ser Arg Pro His

1 5 10 15
 Ser Ala Arg Leu Thr Ala Ser Asp Thr Thr Arg Thr Arg Thr Cys Arg
 20 25 30

Thr Trp Arg Arg Ser Ser Ala Ser Ala Ala Ser Ala Trp Arg Arg Ser
 35 40 45

Phe Ala Ala Ser Cys Thr Arg Gly Thr Ser Cys Thr Pro Trp Arg Ala
 50 55 60

Lys Ile Ser Thr Met Ser Thr Tyr Arg Glu Lys Leu Ser Gly Phe Pro

65				70				75				80			
<210> 889															
<211> 100															
<212> PRT															
<213> Homo sapiens															
<400> 889															
Leu	Pro	Trp	Met	Val	Pro	Trp	Gly	Met	Glu	Ala	Leu	Gly	Ser	Trp	Gly
1				5				10				15			
Gln	Thr	Asp	Leu	Thr	Val	Leu	Gly	Gln	Pro	Gly	Val	Arg	Ala	Leu	Gly
20				25				30							
Lys	Trp	Leu	Gln	Trp	Pro	His	Pro	Asp	Pro	Ala	Gly	Ser	Pro	Arg	Pro
35				40				45							
Gly	Pro	Arg	Gly	Gly	His	Pro	Gln	Pro	Arg	Pro	Ser	Thr	Pro	Ala	Ser
50				55				60							
Pro	Gly	Asn	Arg	Gly	Leu	Pro	Leu	Pro	Pro	Pro	Val	Trp	Ala	Val	Leu
65				70				75				80			
Ala	Trp	Ala	Arg	Ala	His	Leu	Ala	Val	Glu	Ala	Cys	Leu	Arg	Thr	His
85				90				95							
Gly	Cys	Ser	Gly												
100															
<210> 890															
<211> 35															
<212> PRT															
<213> Homo sapiens															
<400> 890															
Ser	Arg	Pro	Arg	His	Arg	Val	Arg	Lys	Arg	Arg	Cys	Pro	His	Cys	Arg
1				5				10				15			
Ser	Ser	Leu	Pro	Gly	Arg	His	Arg	Leu	Gln	Ser	Cys	Arg	Pro	Ser	Pro
20				25				30							
Asp	Pro	Arg													
35															
<210> 891															
<211> 40															

<212> PRT

<213> Homo sapiens

<400> 891

Ala Pro Ala Cys His Trp Leu Ala Arg Leu Gly Trp Arg Val Ser Glu

1 5 10 15

Glu Pro Val Leu Ser Ser Leu Thr Ser Leu Arg Ile Glu Leu Leu Leu

20 25 30

Ser Ser Cys Ser Ser Arg Trp Gly

35 40

<210> 892

<211> 62

<212> PRT

<213> Homo sapiens

<400> 892

Met Lys Met Ala Cys Gly Lys Arg Ser Leu Leu Gln Glu Val Lys Lys

1 5 10 15

His Glu Leu Pro Lys Lys Ala Pro Ser Trp Pro Asp Arg Pro Leu Val

20 25 30

Gly Leu Ala Arg Ile Gln Ile Trp Ile Leu His Leu Leu Gly Leu Arg

35 40 45

Pro Pro Ser Leu Leu Ser Val Phe Gln Met Thr Phe Ile Lys

50 55 60

<210> 893

<211> 42

<212> PRT

<213> Homo sapiens

<400> 893

Ala Ala Ala Pro Arg Ser Thr Pro Arg Ala Thr Arg Pro Ser Cys Ala

1 5 10 15

Gly Pro Ser Arg Arg Ala Ala Arg Ala Ser Thr Ala Lys Ser Ala Ser

20 25 30

Ser Arg Met Ala Ser Thr Ser Cys Ala Ala

35

40

<210> 894

<211> 38

<212> PRT

<213> Homo sapiens

<400> 894

Arg Ala Gly Asn Phe Ala Ile Met Glu Ile Gln Cys Pro Ala Leu Arg

1 5 10 15

Lys Thr Leu Pro Ile Leu Phe Gly Ser Leu Arg Arg Gln Asn Met Ser

20 25 30

Leu Glu Met Trp Cys Arg

35

<210> 895

<211> 38

<212> PRT

<213> Homo sapiens

<400> 895

Arg Val Trp Ser Phe Leu Phe Leu Arg Gln Arg Ala Thr Ser Thr Ile

1 5 10 15

Thr Ile Ala Cys Thr Lys Glu Ser Leu Asn Ser Gln Asn Ser Ser Phe

20 25 30

Ile Phe Ser Leu Leu Ile

35

<210> 896

<211> 17

<212> PRT

<213> Homo sapiens

<400> 896

Lys Asp Gln Arg Ile Ile Lys Val Ala Pro Leu Val Glu Asp Lys Met

1 5 10 15

Ile

<210> 897

<211> 34
 <212> PRT
 <213>
 > Homo sapiens
 <400> 897
 Ile Ala Gln Leu Met Lys Asp Gln Arg Ile Ile Lys Val Pro Gln Ile
 1 5 10 15
 Val Cys Gly Leu Arg Ile Val Leu Arg Lys Lys Arg Thr Val Phe Leu
 20 25 30
 Arg Gln

<210> 898
 <211> 31
 <212> PRT
 <213> Homo sapiens
 <400> 898
 Ile Gln Asp Gln Asp Gln Glu Leu Ala Thr Val Leu Leu Gln Ser Ala
 1 5 10 15
 Leu Asp Cys Ile Phe Gly Val Glu Glu Met Ala Thr Lys Lys His
 20 25 30

<210> 899
 <211> 58
 <212> PRT
 <213> Homo sapiens
 <400> 899
 Pro Ser Leu Asn Leu Ile Ser His Gln Ser Ser Val Gly Cys Ser Lys
 1 5 10 15
 Gly Ile Trp Arg Ala Pro Glu Met Thr Leu Phe Ser Thr Pro Thr Phe
 20 25 30
 Ala Ala Ser Ser Pro Trp Ala Ser Met Ser Trp Val Ser Ser Gly Cys

35 40 45
 Ser Leu Pro Leu Trp Ser Ser Ser Cys Cys
 50 55

<210> 900

<211> 42

<212> PRT

<213> Homo sapiens

<400> 900

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

1 5 10 15

Gly Val Pro Val Ile Pro Pro Leu Val Ile Ser Trp Trp Ala Gly Thr

20 25 30

Arg Ser Leu Trp Leu Leu Leu Pro Val Gly

35 40

<210> 901

<211> 40

<212> PRT

<213> Homo sapiens

<400> 901

Gly Gly Thr Gly Thr Asp Met Thr Thr Gln Lys Leu Met Met Val Pro

1 5 10 15

Asn Gln Cys Lys Leu Glu Leu Glu Leu Ser Leu Arg Asn Tyr Ala Leu

20 25 30

Glu Ser Ser Gln Val Pro Met Lys

35 40

<210> 902

<211> 28

<212> PRT

<213> Homo sapiens

<400>

> 902

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

1 5 10 15

Asp Ser Lys Arg Asn His Gly His Pro Gln Leu Thr

20 25

<210> 903

<211> 23

<212> PRT

<213> Homo sapiens

<400> 903

Asn Val Leu Cys Lys Gln Gln Asn Gly Leu Pro Ala Pro Glu His Val

1 5 10 15

Gly Trp Glu Tyr Leu Thr Gly

20

<210

> 904

<211> 17

<212> PRT

<213> Homo sapiens

<400> 904

Gly Lys Gly Met Lys Lys Ile Lys Lys Cys Leu His Ala Asn Gln Gln

1 5 10 15

Glu

<210> 905

<211> 18

<212> PRT

<213> Homo sapiens

<400> 905

Asn Asn Leu Cys Gln Arg Leu His Trp Arg Leu Arg His Val Ile Val

1 5 10 15

Leu Ile

<210> 906

<211> 13

<212> PRT

<213> Homo sapiens

<400> 906

Glu Gln Leu Phe Leu Lys Leu Gln Glu Ala Asn Gly Ile

1 5 10

<210> 907

<211> 27

<212> PRT

<213> Homo sapiens

<400> 907

Met Leu Thr Ala Leu Pro Pro Ala Met Thr Ala Met Cys Gly Tyr Gly

1 5 10 15

Ile Arg Gly Asn Pro Val Gln Gln Trp Asn Ile

20 25

<210> 908

<211> 19

<212> PRT

<213> Homo sapiens

<400> 908

Leu Asn Val Thr Cys Phe Val Ile Phe Arg Arg Val Arg Asn Glu Leu

1 5 10 15

Gln Lys Trp

<210> 909

<211> 28

<212> PRT

<213> Homo sapiens

<400> 909

Val Ile Met Ser Ile Thr Gly Lys Lys Glu Glu Ser Asn Arg Ser Lys

1 5 10 15

Ala Leu Ser Glu Ala Thr Pro Phe His Trp Ile Thr

20 25

<210> 910

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400>

> 910

Leu Ala Val Ser Ala Val Thr Gly Arg Ala Arg Ser Leu Gly Leu Ser

1 5 10 15

Lys Val Ser Ser Glu Pro Gly Leu Met Ser Thr

20 25

<210> 911

<211> 16

<212> PRT

<213> Homo sapiens

<400> 911

Leu Lys Thr Phe His Met Lys Cys Phe Leu Asn Leu Ser Gln Met Glu

1 5 10 15

<210> 912

<211> 8

<212> PRT

<213> Homo sapiens

<400> 912

Pro Asp Lys Lys Ser Arg Asn Cys

1 5

<210> 913

<211> 9

<212> PRT

<213> Homo sapiens

<400> 913

Asn Ile Arg Ala Arg Gln Glu Gly Asn

1 5

<210> 914

<211> 13

<212> PRT

<213> Homo sapiens

<400> 914

Leu Ser Asn Ile Arg Ala Arg Gln Glu Gly Lys Ser Gly

1 5 10

<210> 915

<211> 21

<212> PRT

<213> Homo sapiens

<400> 915

Ala Arg Gly Thr Ser Pro Ile Arg His Cys Ser His Ser Ser Ser Cys

1 5 10 15

Ser Gly Pro Ser Ser

20

<210> 916

<211> 20

<212> PRT

<213> Homo sapiens

<400> 916

Phe Arg Glu Lys Arg Asn Tyr Val Lys Lys Lys Ser Lys Leu Lys Lys

1 5 10 15

Lys Glu Lys Lys

20

<210> 917

<211> 22

<212> PRT

<213> Homo sapiens

<400> 917

Ser Arg Thr Ala Leu Ile Thr His Thr Leu Cys Cys Trp Leu Thr Trp

1 5 10 15

Ala Gln Val Ser Ala Phe

20

<210> 918

<211> 21

<212> PRT

<213> Homo sapiens

<400> 918

Arg Arg Arg Ser Leu Pro Cys Gly Trp Thr Leu Leu Tyr Leu Ser Ser

1 5 10 15

Ala Trp Arg Met Lys

20

<210> 919

<211> 9

<212> PRT

<213> Homo sapiens

<400> 919

Leu Arg Pro Pro Trp Pro Ser Trp Ser

1 5

<210> 920

<211> 18

<212> PRT

<213> Homo sapiens

<400> 920

Ile Gln Ala Ser Thr Ser Pro Ser Ser Gln His Gly Cys Met Arg Asp

1 5 10 15

Leu Pro

<210> 921

<211> 10

<212> PRT

<213> Homo sapiens

<400> 921

Glu Val Thr Arg Cys Cys Phe Phe His Lys

1 5 10

<210> 922

<211> 20

<212> PRT

<213> Homo sapiens

<400> 922

Ala Pro Ser Leu Thr Phe Ser Pro Ser Gly Leu Met Glu Ile Trp Ile

1 5 10 15

Ser Ala Ser Val

20

<210> 923

<211> 15

<212> PRT

<213> Homo sapiens

<400> 923

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

1 5 10 15

<210> 924

<211> 12

<212> PRT

<213> Homo sapiens

<400> 924

Ile Ser Lys Lys Cys Ser Leu Ser His Gln Glu Lys

1 5 10

<210> 925

<211> 18

<212> PRT

<213> Homo sapiens

<400> 925

Leu Arg Phe Leu Arg Thr Met Lys Gln Trp Pro Lys Phe Cys Ser Ala

1 5 10 15

Gly Ile

<210> 926

<211> 11

<212> PRT

<213> Homo sapiens

<400> 926

Thr Pro Leu Lys Asn Glu Asp Phe Ile Ser Cys

1 5 10

<210> 927

<211> 10

<212> PRT

<213> Homo sapiens

<400> 927

Trp Thr Cys Leu Lys Met Ser Ile Gly Ala

1 5 10

<210> 928

<211> 11

<212> PRT

<213> Homo sapiens

<400> 928

Asp Gly Trp Gly Ala Met Ala Leu Thr Arg Gly

1 5 10

<210> 929

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 929

Ala Trp Lys Ala Val Leu Val Glu Arg Gly Pro

1 5 10

<210> 930

<211> 16

<212> PRT

<213> Homo sapiens

<400> 930

Asn Ser Leu Gly Ile Ile Trp Pro Lys Ser Gly Leu Ile Leu Thr Ala

1 5 10 15

<210> 931

<211> 14

<212> PRT

<213> Homo sapiens

<400> 931

Pro Trp Lys Asn Ser Glu Ser Met Lys Lys Val Lys Cys Ile

1 5 10

<210> 932

<211> 12

<212> PRT

<213> Homo sapiens

<400> 932

Ile Tyr Ile Phe Cys Leu His Tyr Gly Thr Gln Leu

1 5 10

<210> 933

<211> 9

<212> PRT

<213> Homo sapiens

<400> 933

Phe Ser Lys Lys Ala Arg Lys Gln Ser

1 5

<210> 934

<211> 12

<212> PRT

<213> Homo sapiens

<400> 934

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

1 5 10

<210> 935

<211> 10

<212> PRT

<213> Homo sapiens

<400> 935

Ser Gln Lys Thr Val Ser Ser Gly Lys Val

1 5 10

<210> 936

<211> 10

<212> PRT

<213> Homo sapiens

<400> 936

Tyr Ser Lys Lys Ala Lys Glu Arg Gln Asn

1 5 10

<210> 937

<211> 11

<212> PRT

<213> Homo sapiens

<400> 937

Ile Asn Lys Lys Thr Ser Arg Ile Phe Pro Ala

1 5 10

<210> 938

<211> 11

<212> PRT

<213> Homo sapiens

<400> 938

Leu Asn Lys Met Asn Ser Gly Trp Ser Leu Lys

1 5 10

<210> 939

<211> 9

<212> PRT

<213> Homo sapiens

<400> 939

Leu Ala Phe Phe Thr Thr Tyr Met Ala

1 5

<210> 940

<211> 10

<212> PRT

<213> Homo sapiens

<400> 940

Arg Ser Gln Gly Ala Gly Pro Val Ala Thr

1 5 10

<210> 941

<211> 11

<212> PRT

<213> Homo sapiens

<400> 941

Lys Val Lys Lys Gln Asp Pro Lys Pro Ile Asn

1 5 10

<210> 942

<211> 10

<212> PRT

<213> Homo sapiens

<400> 942

Leu Val Gly Gly Ala Gly His Gly Arg Trp

1 5 10

<210> 943

<211> 193

<212> PRT

<213> Homo sapiens

<400> 943

Ser Val Ser Cys Gly Ser Asn Thr Thr Thr Cys Ile Trp Leu Pro His

1 5 10 15

Pro Arg Arg Thr Arg Ala Cys Arg Trp Ser Phe Leu Ser Ser Ile Arg

20 25 30

Trp Cys Arg Cys Phe Pro Ser Thr Ser Arg Ser Trp Arg Arg Arg Ala

35 40 45

Ser Gly Thr Thr Leu Leu Ser Ser Thr Ser Cys Trp Thr Ser Ser Trp

50 55 60

Thr Ser Ala Thr Pro Arg Pro Pro Thr Ala Arg Ser Cys Arg Ser Thr

65 70 75 80

Ser Leu Arg Lys Ala Thr Ser Trp Lys Gln Gly Pro Arg Gly His Gln

85 90 95

Pro Pro Ser Pro Thr Arg Cys Pro Gly Gly Pro Lys Ala Ser Ser Ile

100 105 110

Gly Arg Met Arg Cys Ser Trp Thr Ser Ser Ser Leu Ser Thr Ser Trp

115 120 125

Val Asn Thr Gln Glu Trp Asp Gly Trp Val Thr Arg Ser Ala Pro Thr

130 135 140

Ala Met Ser Cys Ala Ala Arg Ser Trp Ala Pro Ser Arg Cys Glu Ser

145 150 155 160
 Ser Ser Arg Ala Cys Pro Ser Cys Ala Trp Ala Ser Thr Thr Arg Ser
 165 170 175
 Ser Leu Thr Thr Arg Ala Ala Ala Lys Ala Asn Pro Trp Ser Trp Arg
 180 185 190

Met

<210> 944

<211> 16

<212> PRT

<213> Homo sapiens

<400> 944

Ser Ser Ser Leu Ser Thr Ser Trp Ser Ala Pro Thr Ala Met Ser Cys

1 5 10 15

<210> 945

<211> 82

<212> PRT

<213> Homo sapiens

<400> 945

Arg Thr Pro Ala Ser Cys Val Arg Thr Leu Thr Trp Thr Trp Gln Trp

1 5 10 15

Ser Val Pro Ile Arg Glu Cys Ser Ser Thr Lys Ala Ser Val Ala Arg

20 25 30

Gln Pro Pro Gly Cys Ser Trp Arg Ser Arg Ser Thr Leu Ser Leu Ser

35 40 45

Gly Gly Ala Trp Ser Met Pro Arg Asn Gly Pro Trp Glu Thr Pro Ser

50 55 60

Met Ser Lys Gln Asn Arg Gly Leu Arg Leu Ile Lys Ser Ser Ser Thr

65 70 75 80

Lys Ser

<210> 946

<211> 174

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 946

Ser Ser Ser Arg Thr Pro Arg Arg Gln Arg Ser Ser Thr Thr Pro Pro

1 5 10 15

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

20 25 30

Cys Gly Ser Ala Thr Gly Trp Trp Thr Pro Trp Ser Pro Leu Ser Thr

35 40 45

Thr Pro Trp Thr Arg Ala Asn Ala Arg Thr Arg Ala Trp Arg Thr Arg

50 55 60

Cys Ala Ser Cys Gly Thr Cys Pro Thr Ala Ser Thr Thr Arg Cys Arg

65 70 75 80

Arg Pro Arg Cys Ser Gly Trp Arg Val Ala Ala Ala Gly Thr Trp Arg

85 90 95

Gly Arg Arg Arg Glu Arg Ser Trp Ala Ala Ser Arg Arg Arg Ala Gly

100 105 110

Gly Cys Ala Ser Cys Pro Ser Pro Pro Met Arg Ser Pro Ser Arg Arg

115 120 125

Cys Pro Arg Thr Pro Arg Ala Ser Ser Gly Cys Gly Ala Pro Arg Ser

130 135 140

Trp Gly Cys Thr Thr Gly Cys Cys Ser Ala Ala Arg Pro Pro Gly Arg

145 150 155 160

Cys Arg Thr Ser Arg Gln Ala Thr Ala Gly Gly Arg Gly Cys

165 170

<210> 947

<211> 60

<212> PRT

<213> Homo sapiens

<400> 947

Gly Pro Ser Trp Thr Trp Gly Arg Ala Pro Arg Thr Glu Ser Ser Gln

1 5 10 15
Pro Arg Gly Ser Ser Ser Cys Ser Ala Arg Trp Cys Leu Gly Arg Cys

20 25 30
Cys Cys Ser Gly Asn Asp Gly Arg Thr Arg Ser Ser Gly Trp Met Pro

35 40 45
Gly Met Asn Met Lys Met Lys Thr Phe Met Lys Ala

50 55 60
<210> 948

<211> 163

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 948

Ser Leu Leu Val Trp Pro Val Gly Arg Asn Trp Gln Leu Ala Gly Pro
1 5 10 15

Leu Thr Pro Thr Arg Gly Leu Thr Arg Thr Thr His Pro Gly Val Pro
20 25 30

Arg Gly Ser Leu Met Thr Trp Pro Leu Thr Gly His Gln Arg Gly Ala
35 40 45

Trp Pro Pro Gly Leu Pro Pro Glu Pro Glu Val Pro Pro Ala Leu Glu
50 55 60

Cys Trp Asp Pro Thr Pro Gln Ser Pro Ser Trp Pro Leu Gln Phe Leu
65 70 75 80

Gly Pro Leu Ala Pro Ala His His Ser Gly Ser His Ser Glu Tyr Pro
85 90 95

Met Ser Ser Ser Gly Leu Pro Cys Ser Trp Trp Trp Thr Gln Ala Thr
100 105 110

Pro Ala Pro Thr Trp Thr Thr Ser Ser Arg Leu Ala Arg Ala Pro Arg
115 120 125

Ala Ser Cys Ala Ser Pro Pro Cys Ala Ala Arg Ala Ser Trp Trp Pro
130 135 140

Ser Arg Arg Trp Thr Cys Ala Ser Ser Arg Gly Ala Ser Cys Ser Ser
 145 150 155 160
 Thr Arg Trp

<210> 949

<211> 74

<212> PRT

<213> Homo sapiens

<400> 949

Met Asp Thr Leu Ala Leu His Asp Pro His Pro Met Ala Thr Ser Gly
 1 5 10 15
 Gly Leu Ser Leu His Pro Asp Pro Leu Pro Gly His Gln Phe Pro Leu
 20 25 30
 Glu Ala His Phe Glu Ala Leu Ser Leu Ser Lys Phe Thr Phe Ser Phe

35 40 45
 Leu Leu Leu His Phe Pro Asn Ile Phe Ser Ile Pro Trp Thr Asn Gln
 50 55 60
 Arg Cys Cys Ser Ser Leu Gly Gln Arg Tyr
 65 70

<210> 950

<211> 52

<212> PRT

<213> Homo sapiens

<400> 950

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

<210> 951

<211> 38

<212> PRT

<213> Homo sapiens

<400> 951

Cys His Pro Leu Trp Glu Gln Leu Asp Thr Glu Pro Thr Pro Arg Leu

1 5 10 15

Cys Ser Ala Arg Lys Glu Asn Gln Arg Trp Ser Leu Arg Pro Ala Ala

20 25 30

Arg Arg Pro Trp Arg Ser

35

<210> 952

<211> 58

<212> PRT

<213> Homo sapiens

<400> 952

Cys Tyr Leu His His Trp Asn Tyr Leu Ser Phe Leu Lys Gly Gln Ile

1 5 10 15

Ile Arg Glu Met Ser Phe His Leu Leu Asn Tyr Arg Thr Ser Asn Ile

20 25 30

Ser His Gln Trp Ile Arg Leu His Phe Gln Lys Ala Leu Glu Ile Lys

35 40 45

His Ile Ser Lys Gly Val His Arg Val Gly

50 55

<210> 953

<211> 103

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 953

Trp Cys Ser Pro Asp Ser Ser Ser Ser Pro Arg Thr Arg Ser Ser Gly

1 5 10 15

Cys Pro Ser Tyr Ala Gly Arg Arg Pro Thr Gln Ser Leu Ser Gln Pro

20 25 30

Gly Trp Cys Pro Leu Ser Arg Pro Ser Trp Pro Pro Leu Pro Ala Thr

35 40 45

Ser Ser Pro Pro Pro Ala Ser Thr Ser Leu Met Thr Asn Thr Gly Cys

50 55 60

Pro Leu Pro Thr Arg Asn Leu Leu Cys Pro Cys Ser Ser Val Thr Gly

65 70 75 80

Thr Ser Thr Arg Ser Lys Gly Met Glu Gly Thr Thr Glu Arg Pro Glu

85 90 95

Pro Arg Ala Ala Arg Gly Pro

100

<210> 954

<211> 64

<212> PRT

<213> Homo sapiens

<400> 954

His Leu Leu Pro Cys Leu Glu Lys Gln Glu Cys His Leu Leu Leu Pro

1 5 10 15

Leu Phe Leu Val Val Leu Glu Ser Leu His Leu Leu His Phe Pro Glu

20 25 30

Ala Leu Ala Phe Leu His Leu His Pro Glu Trp Val Cys Leu His Leu

35 40 45

Pro His Leu Asp Leu Glu Phe Leu Gln Pro Gln Phe Cys His Leu Asp

50 55 60

<210> 955

<211> 45

<212> PRT

<213> Homo sapiens

<400> 955

His Ala Gly Ala Cys Thr Glu Glu Ile Ala Ile Leu Met Arg Leu Thr

1 5 10 15

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

20 25 30

Trp Arg Phe Gln Lys Ala Ser Leu Gln Glu Gln Pro Gln
 35 40 45

<210> 956

<211> 41

<212> PRT

<213> Homo sapiens

<400> 956

Trp Ile Gln Leu Asp Phe Asp Phe Arg Leu Met Arg Lys Glu Asn Pro
 1 5 10 15
 Lys Leu His Thr Trp Cys Ser Trp Arg Ser Leu Lys Lys Lys Asp Ser
 20 25 30

Trp His His Ile Glu Gly Gly Phe Gln
 35 40

<210> 957

<211> 14

<212> PRT

<213> Homo sapiens

<400> 957

Ile Gln Leu Asp Phe Asp Phe Arg Glu Trp Leu Met Cys Cys

1 5 10

<210> 958

<211> 78

<212> PRT

<213> Homo sapiens

<400> 958

Ala Asp Phe Thr Glu Pro Gly Gln Ala Ile Ser Pro His Pro Thr Leu
 1 5 10 15
 Glu Leu Ser Pro Ala Thr Ser Asn Pro His Pro Leu Gly Pro Gln Ile
 20 25 30

Trp Pro Pro Gly Leu Pro Pro Ser His Met Leu Pro Ser Pro His Leu
 35 40 45

Ala Thr Arg Val Ser Arg Leu Thr Cys Asp Ile Phe Pro Met Glu Glu

50 55 60
Ser Trp Asp Leu Gln Leu Ala Ile Met Asp Cys Ser Asp Phe

65 70 75

<210> 959

<211> 74

<212> PRT

<213> Homo sapiens

<400> 959

Arg Trp Leu Pro Gly Gly Gly Ser Pro Trp Thr Ser Arg Arg Gly Pro

1 5 10 15

Pro Trp Ser Ser Thr Thr Pro Cys Thr Gln Gly Val Arg Glu Gly Thr

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

35 40 45
Val Thr Ser Met Ser Pro Gly Pro Pro Cys Arg Gly Ser Gly Ala Ser

50 55 60
Ser Phe Ile Arg His Thr Gly Asn Pro Pro

65 70

<210> 960

<211> 49

<212> PRT

<213> Homo sapiens

<400> 960

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

1 5 10 15
Ser His Ser Ser Arg Pro Gly Ser His Pro Arg Arg His Ile Gln Ser

20 25 30
Gln Leu Ser Gln Ala Leu Glu Leu Gly Gln Pro Ser Thr Asp Phe Ile

35 40 45
Leu

<210> 961

<211> 45

<212> PRT

<213> Homo sapiens

<400> 961

Val Gly Pro Lys Lys Gly Ala Arg His Arg Trp Pro Val Pro Ala Pro

1 5 10 15

Leu Leu Ser Ala Ser Ala Ser Thr Ser Leu Pro Ser Pro Ser Ser Cys

20 25 30

Pro His Thr Leu Phe Arg Lys Asn Pro Leu Trp Arg Cys

35 40 45

<210> 962

<211> 56

<212> PRT

<213> Homo sapiens

<400> 962

Ala Thr Met Thr His Pro Arg Thr Ala Thr Ser Leu Asp Ile Met Thr

1 5 10 15

Cys Leu Gln Tyr Gly Ile Pro His His Leu His Phe Asp Ala Arg Thr

20 25 30

Val Glu Glu Pro Gly Trp Tyr Gly Arg Gly Gln His Thr Trp Leu Leu

35 40 45

Leu Leu Lys Ala Gly Asp Arg Ala

50 55

<210> 963

<211> 78

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 963

Ala Gln Gly Ser Val Met Ile Ser Ser Pro Ala Ser Ser Gln Arg Trp

1 5 10 15

Pro Pro Pro Arg Trp Met Ser Ser Glu Val Thr Arg Leu Trp Ser Ser

20 25 30

Ser Gly Ala Gly Lys Ser Glu Thr Cys Gly Ser Cys Ala Arg Ser Ile
 35 40 45
 Ser Gly Arg Gln Ser Pro Ser Pro Ala Ala Cys Trp Met Ala Trp Leu
 50 55 60
 Arg His Arg Leu Arg Ala Gly Ala Gly Cys Gly Gln Val Pro
 65 70 75

<210> 964

<211> 59

<212> PRT

<213> Homo sapiens

<400> 964

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

50

55

<210> 965

<211> 34

<212> PRT

<213> Homo sapiens

<400> 965

Leu Glu Ile Arg Gln Leu Ser Ser Lys Ser Leu Trp Arg Val Gly Pro
 1 5 10 15
 Lys Thr Arg Val Leu Asn Ser Ser Lys Pro Pro Leu Ser Gln Ile Pro
 20 25 30
 Leu Arg

<210> 966

<211> 24

<212> PRT

<213> Homo sapiens

<400> 966

Leu Trp Thr Ile Arg Asn Tyr Leu Leu His Lys Leu Leu Lys Leu Phe

1 5 10 15

Arg Ile Tyr Asn Ser Gly Asp Phe

20

<210> 967

<211> 23

<212> PRT

<213> Homo sapiens

<400> 967

Ser Gln Gly Ser Gln Asn Phe Ala Leu Thr Lys His His Trp Leu Ile

1 5 10 15

Leu Glu Ser Ile Cys Ala Lys

20

<210> 968

<211> 59

<212> PRT

<213> Homo sapiens

<400> 968

His Pro Thr Thr Trp Asn Ala Cys Pro Trp Gly Gln Leu Pro Thr Gly

1 5 10 15

Glu Gln Ile Arg Pro Gly Arg His Pro Pro Leu Arg Pro Gln Arg Pro

20 25 30

Ser Pro Arg Pro Arg Leu Leu Thr Met Pro Thr Gly Leu Gln Ser Arg

35 40 45

Leu Phe Ser Ala Glu Lys Thr Pro Leu Pro Leu

50 55

<210> 969

<211> 24

<212> PRT

<213> Homo sapiens

<400> 969

Asn Ser Pro Phe Gly Ser Ser Cys Leu Gln Thr Ser Asn Asn Asn Met

1 5 10 15

Glu Lys Val Thr Leu Lys Lys Val

20

<210> 970

<211> 34

<212> PRT

<213> Homo sapiens

<400> 970

Ile Ser Phe Arg Val Leu Ala Ser Ser Trp Tyr Ala Ser Leu Pro Ser

1 5 10 15

Pro Ser Cys Asn Leu Trp Met Pro Ser Thr Lys Ile Arg Leu Phe Thr

20 25 30

Ala Ile

<210> 971

<211>

> 27

<212> PRT

<213> Homo sapiens

<400> 971

Ser Leu Phe Leu Pro Gly Ser Thr Pro Ser Leu His Phe Leu Cys Trp

1 5 10 15

Ser Leu Arg Ser Ser Gly Gly Cys Arg Ser Ala

20 25

<210> 972

<211> 30

<212> PRT

<213> Homo sapiens

<400> 972

Leu Glu Ser Leu Pro Ala Phe Leu Arg Cys His Leu Lys Thr Glu Val

1 5 10 15

Pro Cys Gly Leu Trp Leu Arg Ser Met Gly Glu Ile Ala Ser

20 25 30

<210> 973

<211> 38

<212> PRT

<213> Homo sapiens

<400> 973

Val Gly Glu Leu Cys Gly Gly Ser Glu Pro Gln Thr Gln Ser Trp Cys

1 5 10 15

Val Gln Leu Gly Val Gly Met Gly Leu Lys Lys Pro Ser Cys Trp Cys

20 25 30

Trp Thr Leu Met Trp Thr

35

<210> 974

<211> 35

<212> PRT

<213> Homo sapiens

<400>

> 974

Arg Arg Arg Thr Pro Thr Ala Met Gly Arg Asn His Ser Cys Thr Ser

1 5 10 15

Arg Ser Pro Ser Ser Ser Trp Met Ser Ser Glu Ser Trp Arg Ser Arg

20 25 30

Thr Cys Arg

35

<210> 975

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 975

His Trp Ser Pro Ser Pro Leu His His His Ala His Cys Leu Pro Thr

1 5 10 15

Pro Glu Trp Pro Arg Ala Trp Val Leu Gln Gln Tyr Pro His

20 25 30

<210> 976

<211> 20

<212> PRT

<213> Homo sapiens

<400> 976

His His His Arg Arg Ala Pro Gly Gln Gly Ser Ala Thr Ala Ser Pro

1 5 10 15

Ala Arg Cys Thr

20

<210> 977

<211> 29

<212> PRT

<213> Homo sapiens

<400> 977

Trp Ser Arg Ser Trp Arg Ser Ser Arg Cys Pro Cys Cys Gly Trp Ser

1 5 10 15

Thr Thr Ala Arg Pro Ala Cys Ser Met Arg Leu Thr Ser

20

25

<210> 978

<211> 19

<212> PRT

<213> Homo sapiens

<400> 978

Asn Gly Asn Pro Val Gln Glu Ser Pro Gln His Gln Met Ile Gln Asp

1 5 10 15

Ala Gln Gly

<210> 979

<211> 22

<212> PRT

<213> Homo sapiens

<400> 979

Cys Pro Met Met Asn Phe Leu Arg Tyr Tyr Leu Arg Leu Lys Ile Pro

1 5 10 15

Leu Gly Cys Asn Leu Thr

20

<210> 980

<211> 26

<212> PRT

<213> Homo sapiens

<400> 980

Leu Thr Lys Leu Met Val Trp Leu Gln Tyr Gly Gln Ala Gly Lys Ile

1 5 10 15

Arg Phe Thr Val Leu Leu Phe Pro Pro Cys

20

25

<210> 981

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 981

Ala Ser Thr Ser Ser Val Thr Ala Ser Cys Ala Ser Thr Thr Ser Arg

1 5 10 15

Gly Met Trp Asn

20

<210> 982

<211> 27

<212> PRT

<213> Homo sapiens

<400> 982

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

1 5 10 15

Val Trp Arg Pro Pro Leu Arg Met Gly Leu Trp

20

25

<210> 983

<211> 27

<212> PRT

<213> Homo sapiens

<400> 983

Leu Gly Gly Gly Cys Ile Thr Leu Ala His Val Cys Gln Ala Trp Pro

1 5 10 15

Val Tyr Gly Leu His Leu Thr Asp Leu Phe Val

20 25

<210> 984

<211> 18

<212> PRT

<213> Homo sapiens

<400> 984

Leu Ser Arg Asn Ser Thr Leu Leu Ile Glu Glu Asn Leu His His Ser

1 5 10 15

Lys Asn

<210> 985

<211> 14

<212> PRT

<213> Homo sapiens

<400> 985

Asn Thr Gly Pro Arg Lys Asn Arg Ser Gly Lys Lys Trp Lys

1 5 10

<210> 986

<211> 11

<212> PRT

<213> Homo sapiens

<400> 986

Pro Pro Val Trp Ser Arg Cys Gly Arg Arg Cys

1 5 10

<210> 987

<211> 15

<212> PRT

<213> Homo sapiens

<400> 987

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

1 5 10 15

<210> 988

<211> 21

<212> PRT

<213> Homo sapiens

<400> 988

Gln Leu Asp Leu Leu Leu Pro Ser Glu Tyr Tyr Met Phe Pro Ala Trp

1 5 10 15

Gly Ser Val Phe Trp

20

<210> 989

<211> 13

<212> PRT

<213> Homo sapiens

<400> 989

Ser Met Lys Lys Ile Glu Ser Trp Thr Ser Leu His Pro

1 5 10

<210> 990

<211> 10

<212> PRT

<213> Homo sapiens

<400> 990

Ser Leu Phe Arg Glu Thr Gln Ser Asn Arg

1 5 10

<210> 991

<211> 21

<212> PRT

<213> Homo sapiens

<

400> 991

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

1 5 10 15

Gly Lys Ser Val Leu

20

<210> 992

<211> 13

<212> PRT

<213> Homo sapiens

<400> 992

Pro Phe Leu Pro Ile Gln Lys Ala Ala Ser Gly Arg Gly

1 5 10

<210> 993

<211> 13

<212> PRT

<213> Homo sapiens

<400> 993

Ser Asp Ala Pro Leu Glu Ala Leu Thr Gly Gln Gly Met

1 5 10

<210> 994

<211> 10

<212> PRT

<213> Homo sapiens

<400> 994

Lys Lys Lys Lys Arg Thr Arg Ile Ile Met

1 5 10

<210> 995

<211> 10

<212> PRT

<213> Homo sapiens

<400> 995

Arg Met Lys Lys Val Ile Ile Lys Trp Ala

1 5 10

<210> 996

<211> 11

<212> PRT

<213> Homo sapiens

<400> 996

Ile Asn Glu Lys Arg Leu Thr Cys Ser Ile Leu

1 5 10

<210> 997

<211> 19

<212> PRT

<213> Homo sapiens

<400> 997

Ala Thr Ser Thr Pro Gly Arg Leu Ser Ser Ser Pro Arg Cys Pro Gly

1 5 10 15

Asn Gly Gly

<210> 998

<211> 15

<212> PRT

<213> Homo sapiens

<400> 998

Asn Val Gly Arg Pro Leu Asp Thr Val Gln Pro Leu Lys Cys Ile

1 5 10 15

<210> 999

<211> 10

<212> PRT

<213> Homo sapiens

<400> 999

Asp Glu Lys Lys Arg Glu Lys Val Ile Ser

1 5 10

<210> 1000

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1000

Ser Asn Lys Lys Trp Lys Lys Met Lys Arg Ser

1 5 10

<210> 1001

<211> 8

<212> PRT

<213> Homo sapiens

<400> 1001

Thr Met Lys Lys Ile Val Met Tyr

1 5

<210> 1002

<211> 21

<212> PRT

<213> Homo sapiens

<400> 1002

Gly Gly Gly Thr Gln Asp Ser Val Trp Gln Ala Cys Arg Lys Ser Gln

1 5 10 15

Val Pro Leu Leu Ser

20

<210> 1003

<211> 12

<212> PRT

<213> Homo sapiens

<400> 1003

Phe Ser Pro Pro Pro Ala Ala Cys Ser Pro Ala Lys

1 5 10

<210> 1004

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1004

Thr Val Gln Lys Met Gln Asn Thr Cys Val

1 5 10

<210> 1005

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1005

Asn Pro Lys Lys Asp Gln Leu Leu Lys Asp Phe

1 5 10

<210> 1006

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1006

Arg Met Gly Gly Ser Gln Leu Ser Arg Ile

1 5 10

<210> 1007

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1007

Thr Asn Lys Lys Gln Leu Met Arg Lys Lys Ser

1 5 10

<210> 1008

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1008

Glu Leu Lys Lys Ile Thr Val Asn Tyr Leu Gln

1 5 10

<210> 1009

<211>

> 13

<212> PRT

<213> Homo sapiens

<400> 1009

Phe Ile Glu Lys Asn Ser Lys Met Thr Gln Ile Ile Gln

1 5 10

<210> 1010

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1010

Glu Ala Lys Glu Val Phe Pro Lys Met Leu

1 5 10

<210> 1011

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1011

Arg Val Leu Ala Thr His Pro Gln Ala Thr

1 5 10

<210> 1012

<211> 8

<212>

> PRT

<213> Homo sapiens

<400> 1012

Ala Ala Gly Gly Thr Gly Arg Arg

1 5

<210> 1013

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1013

Ala Gln Pro Gly Ser Gly Leu Glu Thr Cys

1 5 10

<210> 1014

<211> 13

<212> PRT

<213> Homo sapiens

<400> 1014

Lys Gly Lys Lys Ala Ile Gln Arg Gln Ser Gln Met Arg

1 5 10

<210> 1015

<211> 37

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1015

Cys Trp Ser Pro Leu Gln Pro Arg Ala Arg Gln Arg Gln Thr Arg Cys

1 5 10 15

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

20 25 30

Ser Arg Ser Pro Arg

35

<210> 1016

<211> 34

<212> PRT

<213> Homo sapiens

<400> 1016

Arg Arg Ser Cys Leu Pro His Gln Leu His Pro Trp Gly Pro Ser Cys

1 5 10 15

Leu Leu Cys Leu Gly Thr Ile Val Pro Leu Pro Cys Ala Pro Ser Ser

20 25 30

Pro Gly

<210> 1017

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1017

Pro Gly Ala Leu Leu Asn Pro Ser Arg Gly

1 5 10

<210> 1018

<211> 13

<212> PRT

<213> Homo sapiens

<400> 1018

Cys His Pro His His Pro Gln Val Pro His His Pro Leu

1 5 10

<210> 1019

<

211> 11

<212> PRT

<213> Homo sapiens

<400> 1019

Leu Gly Leu Asn Met Lys Arg Asn Ser Lys Pro

1 5 10

<210> 1020

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1020

Glu Pro Lys Lys Ser Leu Ile Pro Leu Ser Gly

1 5 10

<210> 1021

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1021

Gly Trp His Trp Ala Phe Arg Lys Glu

1 5

<210> 1022

<211> 49

<212> PRT

<213

> Homo sapiens

<400> 1022

Gly Lys Thr Ser Thr Pro Leu Thr Ser Ile Ser Pro Arg Trp Pro Ser

1 5 10 15

Leu Leu Thr Cys Ser Trp Leu Gly Trp His Trp Ala Phe Arg Lys Gly

20 25 30
 Ser Pro Arg Arg Cys Trp Ala Cys Val Gln Ala Gln Arg Trp Cys Gly
 35 40 45
 Trp

<210> 1023
 <211> 10
 <212> PRT
 <213> Homo sapiens
 <400> 1023

Val Asn Phe Val Lys Ile Leu Met Ile Gln
 1 5 10

<210> 1024
 <211> 38
 <212> PRT
 <213> Artificial Sequence
 <220><223> modified Homo sapiens FSP
 <400> 1024

Gly Ser Gly Ser Ala Pro Cys Arg Arg Val Arg Gly Pro Ala Ser Pro
 1 5 10 15
 Met Gly Met Arg Arg Arg Ala Gln Pro Ser Ala Ser Thr Arg Arg Cys
 20 25 30
 Ser Ala Cys Ser Thr Ser
 35

<210> 1025
 <211> 42
 <212> PRT
 <213> Homo sapiens
 <400> 1025

Ala Leu Ser Val Tyr Gln Phe Phe Ile Pro Gln Arg Glu Val Lys Ile
 1 5 10 15
 Ser Thr Ile Ile Leu Pro Ser Asn Lys Pro Phe Lys Pro Leu Thr Lys
 20 25 30

Arg Ile Leu Val Leu Leu Gly Ser Ile Lys

35

40

<210> 1026

<211> 34

<212> PRT

<213> Homo sapiens

<400> 1026

Ala Arg Pro Ala Arg Pro Cys Pro Thr Gly His Ser Leu Val Gln Met

1

5

10

15

Glu Pro Leu Thr Thr Ala Arg Pro Thr Ser Ser Ser Thr Thr Cys Pro

20

25

30

Arg Thr

<210> 1027

<211> 18

<212> PRT

<213> Homo sapiens

<400> 1027

Ala Thr Arg Met Pro Glu Pro His Arg Ala Leu Pro Thr Arg Val Pro

1

5

10

15

Phe Pro

<210> 1028

<211> 11

<212> PRT

<213> Homo sapiens

<400>

> 1028

Ser Leu Val Met Lys Gly Gln Ile Pro Val Arg

1

5

10

<210> 1029

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1029

Tyr Tyr Lys Tyr Val Thr Asn Ala Cys Leu

1 5 10

<210> 1030

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1030

Ser Leu Pro Pro Ala Pro Leu Leu His Glu

1 5 10

<210> 1031

<211> 24

<212> PRT

<213> Homo sapiens

<400> 1031

Ile Leu Thr Met Arg Gln Trp Leu Lys Asn Arg Ser Leu Glu Arg Thr

1 5 10 15

His Leu Leu Ile Ile Gln Asn Ile

20

<210> 1032

<211> 14

<212> PRT

<213> Homo sapiens

<400> 1032

Thr Pro Trp Ser Thr Thr Arg Pro Thr Thr Pro Trp Leu Thr

1 5 10

<210> 1033

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1033

Leu Thr Ile Lys Ile Thr Ser Thr Phe Ile Ser

1 5 10

<210> 1034

<211

> 15

<212> PRT

<213> Homo sapiens

<400> 1034

Arg Arg Pro Cys Thr His Ser Gly Ser Thr Thr Arg Ser His Ser

1 5 10 15

<210> 1035

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1035

Val Ile Glu Lys Asn Leu Met Val Gly Gly

1 5 10

<210> 1036

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1036

Thr Ala Glu Lys Arg Ile Lys Met Ser Thr

1 5 10

<210> 1037

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1037

Thr Pro Met Asp Ser His Arg Ser Ser Gln Asp Lys Thr Leu Thr His

1 5 10 15

Pro Ser Met Glu Thr Thr Arg Arg Arg Val Pro His Pro Thr Met Thr

20 25 30

Thr Arg Thr Ser Leu Pro Pro Thr Gly Met Thr Arg Ala Ser Asp Arg

35 40 45

Pro Ser Ser Ala Arg Cys Ser

50

55

<210> 1038

<211> 42

<212> PRT

<213> Homo sapiens

<400> 1038

Leu Ser Thr Val Thr Thr His Trp Ser Ser Gly Trp Thr Leu Cys Trp

1 5 10 15

Ala Leu Pro Lys Arg Ala Ser Asn Trp Thr Ser Arg Thr Ser Arg Gln

20 25 30

Trp Ala Pro Pro Trp Thr Ser Cys Gly Ser

35 40

<210> 1039

<211> 39

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1039

Leu Pro Gln Pro Cys Gly Pro Ala Ser Cys Ser Thr Pro Ser Trp Pro

1 5 10 15

Met Ala Val Pro Thr Ser Arg Ser Cys Met Ala Arg Ser Pro Arg Pro

20 25 30

Ser Ala Cys Gln Leu Pro Arg

35

<210> 1040

<211> 28

<212> PRT

<213> Homo sapiens

<400> 1040

Val Val Asn Leu Gly His Ser Cys Cys Leu Asp Pro Glu Thr Arg Leu

1 5 10 15

Leu Arg Cys Gly Met Ser Val Leu Ala Cys Ala Leu

20 25

<210> 1041

<211> 23

<212> PRT

<213> Homo sapiens

<400> 1041

Leu Leu His Phe Leu Glu Lys Ser Pro Leu Glu Glu Trp Asn Gln Trp

1 5 10 15

Val Met His Leu Cys Trp His

20

<210> 1042

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1042

Arg Ile Ser Leu Phe Leu Gly Ser His Pro Phe Arg Ala Arg Ile Leu

1 5 10 15

Cys Leu Thr Pro Cys Lys Pro Arg Ser Ser

20 25

<210> 1043

<211> 17

<212> PRT

<213> Homo sapiens

<400> 1043

Asn Leu Trp Leu Ile Val Leu Thr Gln Leu Val Leu Asn Leu Val Gln

1 5 10 15

Glu

<210> 1044

<211> 16

<212> PRT

<213> Homo sapiens

<400> 1044

Pro Thr Thr Gln His Met Thr Thr Ser Ala Gly Ser Leu Ser Pro Thr

1 5 10 15

<210> 1045

<211> 16

<212> PRT

<213> Homo sapiens

<400> 1045

Leu Leu Lys Arg Thr Ile Gln Met Pro Pro Ala Ser Pro Ala Ser Ser

1 5 10 15

<210> 1046

<211> 13

<212> PRT

<213> Homo sapiens

<400> 1046

Arg Glu Arg Phe Leu Ser Asn Arg Met Lys Trp Lys Tyr

1 5 10

<210> 1047

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1047

Lys Pro Ile Phe Leu Asn Arg Tyr Leu Leu Gln

1 5 10

<210> 1048

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1048

His Asn Pro Phe Leu Ala Ser Cys Arg Trp

1 5 10

<210> 1049

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1049

Gln Cys Pro Ser Cys Met Pro Ser Gly Thr

1 5 10

<210> 1050

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1050

Glu Thr Ala Pro His Leu His Leu Leu

1 5

<210> 1051

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1051

Pro Gln Trp Cys Gly Trp Val Arg Tyr Glu Gly Pro Arg Ala Glu Pro

1 5 10 15

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

20 25 30

Thr Leu Tyr Ile Phe Thr Asp Lys Ser Lys Asn Leu Tyr Ser Leu Cys

35 40 45

Gly Ser Thr Leu Val Ser Leu Gln Val Ser

50 55

<210> 1052

<211> 74

<212> PRT

<213> Homo sapiens

<400> 1052

Cys Ser Gln Arg Arg Trp Ile His Leu Met Arg Tyr Ala Thr Ala Phe

1 5 10 15

Leu Cys Asn Ser Val Asp Asn Met Ile Ser Gln Cys Leu Gln Phe Glu

20 25 30

Cys Phe Leu Lys Cys Arg Lys Leu Val Leu Thr Pro Met Pro Leu Leu
35 40 45

Met Val Ile Ile Ile Arg Leu Phe Trp Lys Val Pro Gly Leu Gln Glu
50 55 60

Val Val Val Ala Ile Phe Phe Gly Gln Lys
65 70

<210> 1053

<211> 53

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1053

Arg Gly Ala Ala Leu Ala Ile Ser Met Gly Val Arg Val Met Trp Ala
1 5 10 15

Ser Phe Lys His Ser Thr Leu Ala Leu Ala Val Cys His Ile Ile Ser

20 25 30

Arg Ile Thr Leu Gly Leu Ser Leu Gln Gly Val Leu Ser Thr Asn Ser

35 40 45

Ser Lys Ser Ser Ser

50

<210> 1054

<211> 84

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1054

Arg Arg Ser Cys Pro Thr Leu Arg Ala Cys Ala Asn Ser Trp Ser Thr

1 5 10 15

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

20 25 30

Trp Ala Gly Pro Ala Ala Thr Ser Ser Leu Glu Ala Ser Gly Met Pro

35 40 45

Pro Ser Ser Pro Ser Met Ala Ser Leu Cys Trp Ser Thr Val Ala Gln
 50 55 60
 Thr Pro Ser Pro Val Ser Gly Ser Trp Cys Gly Thr Trp Thr Ala Trp
 65 70 75 80
 Met Pro Cys Trp

<210> 1055

<211> 54

<212> PRT

<213> Homo sapiens

<400> 1055

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

<210> 1056

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1056

Arg Arg Lys Ser Trp Lys Met Lys Ser Pro Val Asp Thr Val Leu Ser
 1 5 10 15
 Lys Glu Asn Gln Ile Cys Lys Val Lys Thr Ile Leu Ala Pro Ala Pro
 20 25 30
 His Ala Leu Ser Leu Pro Arg Pro Gln Pro Phe Phe Arg Ala Ile Asp
 35 40 45
 Lys Asp Arg
 50

<210> 1057

<211> 41

<212> PRT

<213> Homo sapiens

<400> 1057

Ser Arg Leu Ser Pro Pro Glu Ala Ala Phe Gln Arg Met Leu Ala Met

1 5 10 15

Glu Leu Arg Ser Pro Asp His Pro Arg Ala Glu Tyr Pro Asp Phe Ser

20 25 30

Pro Ser Pro Gly Pro Val Ala Gly Leu

35 40

<210> 1058

<211> 38

<212> PRT

<213> Homo sapiens

<400> 1058

Pro Arg Pro Leu Pro Gly Leu Pro Ala Pro Pro Gln Arg Ser Ser Trp

1 5 10 15

Met Gly Ser Ser Cys Ser Ser Cys Gly Thr Arg Pro Met Ser Ser Trp

20 25 30

Leu Cys Ala Trp Gly Glu

35

<210> 1059

<211> 15

<212> PRT

<213> Homo sapiens

<400> 1059

Ser Trp Met Gly Ser Ser Cys Ser Cys Gly Thr Arg Pro Met Ser

1 5 10 15

<210> 1060

<211> 34

<212> PRT

<213> Homo sapiens

<400> 1060

Asn Trp Ile Leu Val Asn Leu Phe Ser Gly Thr Ser Lys Ala Pro Phe
 1 5 10 15
 Leu Cys Gly Gly Ile Asp Gln Thr Ser Gln Pro Ser Ala Gly Pro Arg
 20 25 30
 Gly Thr

<210> 1061

<211> 28

<212> PRT

<213> Homo sapiens

<400> 1061

Val Gly Arg Ser Gly Trp Gly Val Pro Ala Ser Cys Thr Ala Ala Pro
 1 5 10 15
 Pro Thr Ser Arg Trp Met Ser Trp Gln Asp Cys Ser

20 25

<210> 1062

<211> 30

<212> PRT

<213> Homo sapiens

<400> 1062

Ser Ala Gly Val Leu Arg Gly Ser Lys Arg Thr Gly Pro Ala Cys Met
 1 5 10 15
 Pro Thr Lys Arg Arg Thr Val Met Lys Ser Thr Trp Arg Ser
 20 25 30

<210> 1063

<211> 25

<212> PRT

<213> Homo sapiens

<400> 1063

Ile Trp Trp Ile Val Gln Asn Ser Phe Leu Leu Pro Phe Arg Met Ser

1 5 10 15

Ser Phe Pro Lys Lys Phe Phe Phe Leu

20 25

<210> 1064

<211> 24

<212> PRT

<213> Homo sapiens

<400> 1064

Ala Asn Ser Lys Leu Ser Ser Ser Leu Leu Leu Arg Lys His Ser Cys

1 5 10 15

Gly Gln Lys His Leu Thr Ser Cys

20

<210> 1065

<211> 21

<212> PRT

<213> Homo sapiens

<400> 1065

Ile Ser Ser Trp Gln Val Leu Phe Met Asn Ile Gln Glu Asp Ile Leu

1 5 10 15

Ser Leu Leu Ser Gln

20

<210> 1066

<211> 17

<212> PRT

<213> Homo sapiens

<400> 1066

Leu Glu Trp Gln Ala Leu Asp Tyr Ser Arg Ser Trp Leu Trp Thr Asp

1 5 10 15

Thr

<210> 1067

<211> 12

<212> PRT

<213> Homo sapiens

<400> 1067

Leu Leu Arg Gln Gly Lys Cys Gln Ser Ala Trp Ser

1 5 10

<210

> 1068

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1068

Pro Arg Ser Tyr Met Pro Thr Leu Cys Ala Ala Ser Thr Met Pro Trp

1 5 10 15

Gln Lys Thr Phe Pro Ser Asn His Trp Cys Arg Trp Gln Pro Gly Ala

20 25 30

Leu Gly Ser Met Gly Thr Ser Cys Trp Gln Gly Thr Ala Arg Arg Leu

35 40 45

Ser Pro Phe Arg Trp Thr Lys Arg Lys Cys Trp His Cys Trp Lys Arg

50 55 60

Cys Cys Ser Pro Thr Cys Pro Cys Gln Pro Leu Glu Asp Met Pro Ser

65 70 75 80

Gln Pro Ser

<210> 1069

<211> 46

<212> PRT

<213> Homo sapiens

<400> 1069

Gln Leu Ala Leu Lys His Gln Leu Arg His Pro Leu His Pro Pro His

1 5 10 15

Leu Val Pro Lys Leu Gln Arg Arg Gln Phe Leu Ala Lys Gln Gly Gln

20 25 30

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

35 40 45

<210> 1070

<211> 61

<212> PRT

<213> Homo sapiens

<400> 1070

His Pro Val Arg Pro Pro Pro Pro Asn Val Arg Ala Trp Val Gly Gln

1 5 10 15

Gln Pro Pro Met Pro Leu Gly Arg Pro Leu Gly Leu Glu Gly Gln Gly

20 25 30

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

35 40 45

Pro Thr Gly Lys Gly Leu Glu Gly Gly Arg His Arg Thr

50 55 60

<210> 1071

<211> 42

<212> PRT

<213> Homo sapiens

<400> 1071

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

1 5 10 15

Arg Thr Pro Arg Gly Ser Ser Ser Met Arg Ser Leu Ser Met Thr Ser

20 25 30

Leu His Ser Ala Leu Thr Gln Ser Leu Ser

35 40

<210> 1072

<211> 57

<212> PRT

<213> Homo sapiens

<400> 1072

Glu Ala Pro Ser Thr Arg Ala Ala Pro Pro Ser Leu Arg Ala Ala Arg

1 5 10 15

Ala His Gln Arg Thr Gly Arg Gln His Pro Pro Pro Ala Lys His Ser

20 25 30

Ser Ser Gln Cys Thr Gln Gly Arg Arg Trp Gly Ala Trp His Pro Gly

35

40

45

Ser Trp Pro Val Ala Gln Arg Met Gly

50

55

<210> 1073

<211> 30

<212> PRT

<213> Homo sapiens

<400> 1073

Arg Pro Trp Asn Ser Ser Thr Arg Gly Cys Cys Arg Pro Val Gly Arg

1

5

10

15

Pro Arg Pro Arg Gly Gly Trp Val Trp Trp Ala Pro Arg Ala

20

25

30

<210> 1074

<211> 25

<212> PRT

<213> Homo sapiens

<400> 1074

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

1

5

10

15

Gly Asn Asn Met Gln Pro Asn Ser Ile

20

25

<210> 1075

<211> 22

<212> PRT

<213> Homo sapiens

<400> 1075

Leu Ala Pro Pro Asp Trp Pro Gly Ile Trp Met Asp Ser Cys Arg Arg

1

5

10

15

Pro Ala Pro Gln Asp Cys

20

<210> 1076

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> modified Homo sapiens FSP

<400> 1076

Arg Pro Cys Ser Ser Cys Trp Gly Leu Val Leu Pro Thr Cys Leu Leu

1 5 10 15

Ala Ser Trp Gln Pro Gly Gly Cys Arg

20 25

<210> 1077

<211> 24

<212> PRT

<213> Homo sapiens

<400> 1077

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

1 5 10 15

Thr Ser Leu Phe Thr Ile Pro Ser

20

<210> 1078

<211> 17

<212> PRT

<213> Homo sapiens

<400> 1078

Arg Pro Ala Ser Ser Trp Cys Ser Pro Ser Arg Ser Val Pro Ser Ala

1 5 10 15

Ser

<210> 1079

<211> 19

<212> PRT

<213> Homo sapiens

<400> 1079

Arg Ser Ile Phe Arg Gly His Arg Ser Trp Asp Leu Pro Ile Ile Val

1 5 10 15

Asn Leu Ser

<210> 1080

<211> 10

<212> PRT

<213> Homo sapiens

<400> 1080

Glu Ser Glu Lys Asn Trp Trp Lys Asn Leu

1 5 10

<210> 1081

<211> 14

<212> PRT

<213> Homo sapiens

<400> 1081

Asp Ile Thr Ile Thr Leu Glu Leu Arg Thr Ile Trp Ile Val

1 5 10

<210> 1082

<211> 11

<212> PRT

<213> Homo sapiens

<400> 1082

Pro Gln Pro Pro Gly Cys Cys Pro Trp Pro Ala

1 5 10

<210> 1083

<211> 13

<212> PRT

<213> Homo sapiens

<400> 1083

Arg Ser Phe Phe Pro Lys Ser Ser Pro Leu Phe Arg Met

1 5 10

<210> 1084

<211> 13

<212> PRT

<213> Homo sapiens

<400> 1084

Leu Leu Gly Gly Cys Ser Gly Leu Pro Trp Pro Arg Arg

1 5 10

<210> 1085

<211> 9

<212> PRT

<213> Homo sapiens

<400> 1085

Arg Cys Pro Pro Arg Trp Ser Pro Cys

1 5

<210> 1086

<211> 8

<212> PRT

<213> Homo sapiens

<400> 1086

Thr Leu Arg Phe Leu His Leu Ser

1 5

<210> 1087

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1087

His Pro Gln Val Cys Pro Leu Arg Gly Ser Gln Leu Gln Arg Thr Glu

1 5 10 15

Gln Gly Glu Asp His Pro Leu His Pro Leu Ser Arg Gln His Arg Ala

20 25 30

Leu Val Val Gly Glu Leu Gly Pro Gln Ala Trp Pro Gln Leu Leu Leu

35 40 45

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

50 55 60

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

65 70 75 80

Trp Lys Arg

<210> 1088

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 1A

<400> 1088

Thr Glu Ile Gln Leu Thr Met Asn Asp Ser Lys His Lys Leu Glu Ser

1 5 10 15

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

20 25 30

Gln Thr Pro Gln Asp Ser Arg Gln Val Leu Ala Leu Ala Lys Lys Thr

35 40 45

Leu Thr Asn Ala Ser Arg Ala Gly Gln Phe Pro Val Trp Arg Arg Thr

50 55 60

Ser Arg Gly Met Ser Leu Gln Trp Lys Ser Gly Asn Ala Cys Thr Pro

65 70 75 80

Leu Arg Cys Pro Ser Arg Ser Pro Ala Thr Phe Leu Thr Ala Leu Asn

85 90 95

Gly Trp His Arg Ser Gly Leu Arg Ala Gln Met Pro Ser Ser Trp Ser

100 105 110

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

115 120 125

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

130 135 140

Leu Tyr Ser Arg Met Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu

145 150 155 160

Pro Asp Tyr Phe Val Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln

165 170 175

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

180 185 190

Cys Ser Cys Thr Ser His Ser Asn Pro Trp Ser Gln Ser Asn Gln Gln

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

Ser Leu Glu Lys Met Pro Leu Met Arg Arg Ala Arg Pro Thr Ser Cys
450 455 460

Ser Thr Cys Arg Met Trp Trp Lys Gly Lys Lys Arg Arg Lys Glu Ile
465 470 475 480

Val Pro Met Ser Leu Ala Cys Ser Ile Thr Val Ser Phe Val Gly Gln
485 490 495

Ile Ser Thr Leu Val Leu Asp Val Ser Ser Ile Ser His Trp Arg Leu
500 505 510

Pro Cys Lys Val Thr Glu Ser Ser Ser Ser Phe Phe Tyr Thr Ser Asp
515 520 525

Arg Thr Pro Leu Ser Ile Ser Arg Pro Thr Ser Arg Ala Arg Gln Ser
530 535 540

Cys Cys Leu Pro Gly Leu Thr His Pro Ala His Gln Pro Leu Gly Ser
545 550 555 560

Met Ser Thr Arg Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro
565 570 575

Gly Pro Trp Arg Ala Ala Leu Gly Lys Glu Val Lys Arg Ser Gln Ser
580 585 590

Lys Leu Arg Leu Arg Asn Thr Ser Pro Gly Glu Lys Asn Asp Leu Gln
595 600 605

Leu Phe Val Met Ser Asp Thr Thr Tyr Lys Ile Tyr Trp Thr Val Ile
610 615 620

Leu Leu Asn Pro Cys Gly Asn Leu His Leu Lys Thr Thr Ser Leu Gln
625 630 635 640

Arg Pro Pro Arg Ser Ile Leu Ser Leu Asn Gly Ile Trp Glu Val Met
645 650 655

Pro Arg Thr Leu Glu Gly Cys Ile Ser Val Lys Asp His Arg Thr Ser
660 665 670

Gln Asn His Ser Lys Cys Ile Thr Glu Cys Val Arg Thr Ala Leu Asn
675 680 685

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

690	695	700	
Ile Phe Ile Asn Lys Val Arg Gln Asn Phe Lys Arg Asn Phe Lys Lys			
705	710	715	720
Lys Lys Pro Leu Thr Phe Ser Pro Ser Arg Arg Met Thr Arg Arg Thr			
	725	730	735
Met Thr Thr Thr Lys Met Met Met Met Arg Arg Thr Lys Arg Arg Arg			
	740	745	750
Arg Lys Arg Arg Arg Met Thr Met Met Thr Arg Arg Thr Leu Leu Thr			
	755	760	765
Lys Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu			
770	775	780	
Pro Arg Gln Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro Gly			
785	790	795	800
Thr Ser Leu Ala Ile Trp Gly Arg Thr Arg Leu Thr Leu Thr Gly Thr			
	805	810	815
Arg Ser Ser Gly Thr Arg Ala Ser Pro Ser Ala Val Cys Leu Cys Cys			
	820	825	830
Trp Thr Cys Pro Ser Arg Ser Phe Pro Ala Ala Ser Pro Ser Gly Leu			
835	840	845	
Arg Ala Pro Val Gly Ala Gln Ala Pro Pro Glu Val Thr Leu Arg Ala			
850	855	860	
Ser Cys Ala Ser Ser Ala Ser Lys Ala Cys Ala Gly Leu Trp Pro Trp			
865	870	875	880
Gly Ala Gln Val Arg Val Gly Ala Gly Thr Gly Gly Gly Pro Ala Cys			
	885	890	895
Val Pro Val Ala Glu Ala Ser Thr Gly Ala Trp Thr Ala Glu Gly Ala			
900	905	910	
Ala Gly Thr Arg Cys Arg Ala Ser Arg Ala Pro Cys Arg Gln Leu Pro			
915	920	925	
Ala Ser Ser Pro Thr Lys Cys Glu Ile Cys Val Lys Arg Arg Arg Arg			
930	935	940	

Arg Lys Arg Ser Ser Gln Ser Arg Ser Pro Val Pro Lys Lys Arg Glu
 945 950 955 960
 Arg Met Met Leu Pro Val Arg Ala Arg Thr Ala Arg Ser Ala Leu Pro
 965 970 975

Gln Gly Arg Ala Pro Leu Glu Gly Met Leu Leu Pro Arg Ala Leu Pro
 980 985 990
 Ser Leu Leu Ser Arg Met Pro Ala Arg Arg Glu Ser Arg Phe Trp Leu
 995 1000 1005
 Ala Leu Gln Ala Leu Gly Leu Arg Pro Pro His Leu Pro Ser Cys
 1010 1015 1020
 His Pro Leu Pro Gln Leu Leu Gly Pro Pro Pro Pro His Gln Ala
 1025 1030 1035

Pro Met Thr Leu Lys Ala Leu Val Lys Thr Trp Thr Gln Phe Arg
 1040 1045 1050
 Asn Tyr Pro Arg Ala Asp Lys Lys Asn Val Arg Ser Thr Ala Phe
 1055 1060 1065
 Phe Leu Leu Asp Ile Ile Leu Gly Asp Cys Pro Arg Thr Met Ala
 1070 1075 1080
 Gly Pro Ser Ala Ser Leu His Pro Ala Ser Gly Arg Ala Ser Arg
 1085 1090 1095

Lys Thr Trp Gln Arg Arg Leu Arg Ala Cys Arg Ala Gly Gly Pro
 1100 1105 1110
 Ala Gly Trp Ala Arg Gln Ala Tyr Pro Arg Leu Lys Thr Phe Gly
 1115 1120 1125
 Val Pro Leu Gly Ser Ile Leu Cys Leu Ala Gly Ser Leu Ser Thr
 1130 1135 1140
 Met Met Ile Ile Ser Thr Thr Arg Gln Glu Cys Gly Arg Arg Ala
 1145 1150 1155

Ser Val Pro Cys Arg Pro Met Ile Gly Ser Ala Arg Pro Gly Pro
 1160 1165 1170
 Trp Arg Thr Ser Ala Met Pro Ser Ala Met Gly Val Ala Leu Pro

1175	1180	1185
Thr Ser Cys Glu Ser Gly Arg	Ser Pro Pro Ala Thr	Gly Gly Arg
1190	1195	1200
Met Pro Gly Ser Gln Ser Ile	Met Met Ser Trp Met	Pro Pro Leu
1205	1210	1215
Ala Pro Cys Ala Ala Cys Pro	Cys Ser Pro Ala Pro	Thr Leu Cys
1220	1225	1230
Pro Ala His Pro Ala Arg Ala	Pro Thr Ala Val Pro	Ala Phe Thr
1235	1240	1245
Pro Leu Ser Ala His Pro Val	Pro Val Leu Ser Gly	Cys His Leu
1250	1255	1260
Ala Val Arg Thr Ser Met Leu	Thr Leu Leu Pro Met	Glu Ala Lys
1265	1270	1275
Lys Ser Met Lys Arg Ser Asn	Ala Lys Lys Met Glu	Asp Met Ile
1280	1285	1290
Trp Glu Ser Arg Leu Pro Leu	Arg Pro Gln Arg Gly	Pro Arg Pro
1295	1300	1305
Leu His Arg Trp Leu Gln Gln	Thr Thr Gly Cys Ser	Gln Arg Arg
1310	1315	1320
Ile Val Phe Phe Leu Ala Pro	Tyr Phe Pro Arg His	Pro His Arg
1325	1330	1335
Ser Pro Pro Thr Ser Cys Pro	Pro Leu Leu Glu Ala	Phe Pro Leu
1340	1345	1350
Pro Arg Ala Ser Leu Arg Ala	Thr Val Pro Arg His	Ser Ser Val
1355	1360	1365
Leu Ala Thr Gly Leu His Leu	His Arg Gln Ile Ser	Leu Pro Leu
1370	1375	1380
Arg Gly Phe Leu Leu His Gln	Pro Leu Pro Gly Gln	His Leu Trp
1385	1390	1395
Leu Ser His Arg Leu Arg Leu	Arg Leu Pro Arg Thr	Gln Pro Ser
1400	1405	1410

Leu Pro Gly Pro Cys Ala Ser Leu Leu Ser Thr Leu Ser Gln Pro
 1415 1420 1425
 Pro Pro Gln Ala Pro Ser Gln Val Trp Thr Ala Ala Thr Leu Arg
 1430 1435 1440
 Cys Pro Ala Val Pro Ala Ala Ala Cys Pro Pro Ala Leu Arg Ser
 1445 1450 1455

Met Pro Lys Ser Arg Asn Gln Val Leu Phe Arg Arg Asn Leu Thr
 1460 1465 1470
 Pro Ser Gln Leu Arg Thr Leu Ala Pro Pro Tyr Met Leu Leu Pro
 1475 1480 1485
 Gln Ser Leu Ser Gln Ser Leu Ser Arg Lys Gln Ile Pro Ser Gln
 1490 1495 1500
 Ser Met Leu Val
 1505

<210> 1089

<211> 1501

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 2A

<400> 1089

Arg Lys Met Gln Ser Leu Asn His Pro Ser Arg Leu Thr Asn Gly Ser
 1 5 10 15
 Pro Pro Leu His Leu Cys Gln Pro Leu Arg Met Ser Arg Thr Pro Pro
 20 25 30
 Arg Arg Val Cys Ala Ala Pro Pro His Arg Leu Leu Gly Pro Ser Arg
 35 40 45
 Trp Asn Pro Arg Arg Lys Thr Trp Lys Met Arg Lys Lys Tyr Ala Gln
 50 55 60
 Lys Pro Ser Gln Lys Asn His Leu Tyr Gly Gly Lys Lys Arg Ser Lys
 65 70 75 80
 Phe Ser Arg Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys Val
 85 90 95

Lys Val Leu Phe Lys Ala Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly
 100 105 110
 Arg Cys Ser Leu Met Glu Gln Ile Pro His Leu Lys Ser Arg Arg Lys
 115 120 125

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

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

 Ile Cys Trp Lys Trp Pro Val Thr Val Ala Ala Ile Arg Met Cys Ala
 260 265 270
 Leu Ser His Pro Ser Phe Tyr Ile Ser Ser Thr Val Cys Phe Leu Ser
 275 280 285
 Lys His Cys Met Thr Ala Cys Thr Arg Lys Arg Met Lys Thr Gly Ala
 290 295 300
 Ile Gln Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg
 305 310 315 320

 Ile Cys Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser
 325 330 335
 Ala Pro Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr

340	345	350
Ser Ile Asn Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met		
355	360	365
Lys Glu Lys Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile		
370	375	380
Met Gln Arg Leu Phe Ile Lys Gly Tyr Gln Asn Asn His Phe Thr Phe		
385	390	395
His Leu Gln Asn Phe Ala Phe Phe Ser Ser Phe Gly Asn Asn Lys Tyr		
405	410	415
Ile Asn Ile Leu Thr Ile Leu Phe His Val Arg Asn Ile Val Tyr Gly		
420	425	430
Ile Gln Val Met Leu Cys Ala Ser Pro Gln Ile Met Gln Arg Thr Ser		
435	440	445
Ala Asp Arg Phe Arg Met Lys Arg Arg Met Gln Asn Leu Asp Asn Leu		
450	455	460
Gly Val Pro Trp Pro Leu Leu Pro Gly Ile Pro Ser Leu Asn Ala Gln		
465	470	475
Trp Met Phe Leu Arg Ile Ala Ser Pro Gln Ile Met Gln Arg Met Ser		
485	490	495
Ala Val Asn Phe Glu Thr Ile Arg Ala Arg Asn Arg Asn Met Lys Lys		
500	505	510
Thr Met Ser His Leu Ile Ala His Gln Ala Leu Lys Met Ser Gly Leu		
515	520	525
Arg Leu Phe His Pro Arg Leu Leu Thr Arg Lys Lys Pro Gly Lys Leu		
530	535	540
Leu Leu Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr Gln Lys Gly		
545	550	555
Glu Cys Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu Phe Ile Leu		
565	570	575
Lys Gln Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met Gly His Arg		
580	585	590

Glu Gly Ser Glu Ser Asp Asn Leu Gly Leu Leu Tyr Ser Phe Pro Pro
 595 600 605
 Pro Tyr Pro Ile Ser Glu Gly Leu Thr Met Thr Thr Gly Arg Asn Ile
 610 615 620
 Asn Ser Asn Ser Leu Met Thr Asn Cys Leu Phe Ser Pro Ile Phe Leu
 625 630 635 640

 Cys His His Ala Ile Met His Arg Lys Met Thr Ser Pro His Phe Arg
 645 650 655
 Leu Phe Ser Ser Lys Ile Pro His Pro Gln Val Pro Ser Val Val Ala
 660 665 670
 Leu Cys Lys Phe Arg Ala Phe Ile His Thr Pro Arg Ser Pro Gly Cys
 675 680 685
 Ser Val Tyr Ala Asn Met Cys Trp Pro Lys Phe Phe Leu Thr Phe Ser
 690 695 700

 Gln Gln Trp Ser Ser Val Thr Ser Leu Glu Trp Thr Ala Gln Glu Arg
 705 710 715 720
 Gly Cys Ser Ser Trp Leu Met Lys Gln Thr Trp Met Lys Ser Trp Ser
 725 730 735
 Leu Arg Asp Pro Ser Tyr Arg Ser Ile Leu Glu Tyr Val Ser Thr Arg
 740 745 750
 Val Leu Trp Met Pro Thr Ser Thr Val Leu Gln Ala His Pro Gln Val
 755 760 765

 Pro Ala Leu Ala Pro Gln Ala Trp Trp Pro Ala Arg Arg Gly Pro Leu
 770 775 780
 Thr Ser Ala Pro Ser Ala Gln Gln Ser Leu Thr Arg Glu Lys Ile Ile
 785 790 795 800
 Asn Pro Thr Ile Ser Cys Pro Phe Gln Ser Pro Thr Lys Arg Leu Ile
 805 810 815
 Tyr Pro Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly Phe Leu Pro Ser
 820 825 830

 Arg Phe Pro Trp Gly Pro Pro Pro Leu Asn Ser Val Ile Val His Lys

835	840	845	
Ile Val Leu Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn Cys Glu Arg			
850	855	860	
Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile Glu Phe Ala Val Leu Lys			
865	870	875	880
Leu Leu Asn Met Asp Leu Pro Leu Glu Asn Thr Gln Ile Pro Arg Thr			
885	890	895	
Ser Pro Leu Trp Lys Ile Thr Met Val Leu Thr Tyr Pro Asn Cys Val			
900	905	910	
Val His Val Leu Met Phe Gly Ala Leu Arg Ala Thr Ala Pro Ala Thr			
915	920	925	
Ala Ala Pro Gln Ala Gln Thr Pro His Trp Arg Ala Ala Thr Thr Ser			
930	935	940	
Ser Met Ser Ser Ser Pro Arg Ala Glu Pro Thr Ser Ser Ser Ser Trp			
945	950	955	960
Ala Thr Cys Trp Pro Arg Cys Cys Ser Ser Ser Cys Tyr Trp Ser Leu			
965	970	975	
Ser Ser Trp Pro Pro Ala Gly Ala Ala Glu Ala Thr Asn Thr Arg Thr			
980	985	990	
Arg Ser Arg Glu Ser Gln Arg Gly Arg Met Leu Thr Trp Arg Ser Ser			
995	1000	1005	
Leu Trp Leu Gln Gly Thr Arg Cys Phe Thr Gly Val Arg Thr Ser			
1010	1015	1020	
Ser Arg Tyr Lys Lys Arg Gly Val Ile Ala Trp Arg Arg Gln Ile			
1025	1030	1035	
Asn Arg Arg Lys Leu Gln Arg Lys Lys His Trp Asn Ser Ala Tyr			
1040	1045	1050	
Leu Gly Arg Thr Leu Leu Val Thr Cys Ile Leu Tyr His Arg Trp			
1055	1060	1065	
Ile Val Thr Ser Met Cys Gln Ser Gln Arg Trp Leu Thr Ser Thr			
1070	1075	1080	

Thr Ser Arg Ser Ser Ala Leu Met Trp Thr Glu Leu Ser Leu Glu		
1085	1090	1095
Pro Trp Ile Pro Tyr Leu His Gln Gln Lys Thr Gln Arg Thr Leu		
1100	1105	1110
Glu Ser Ala Gly Leu Phe Pro Trp Leu His Thr Gln Cys Gln Glu		
1115	1120	1125
Lys Lys Ser Arg Lys Leu Met Ser Ser Cys Thr His Pro Cys Thr		
1130	1135	1140
Met Leu Leu Pro Gln Gly Cys His Pro Ala Trp Leu Ser Pro Ile		
1145	1150	1155
Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe His Val Leu Ala		
1160	1165	1170
Leu Glu Val Thr Phe Pro Pro Gly Thr Ala Met Pro Gln Met Gln		
1175	1180	1185
Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp Lys Pro Gly		
1190	1195	1200
Thr Ser Leu Gln Cys Tyr Leu Asn Arg Arg Arg Asn Ser Arg Lys		
1205	1210	1215
Gln Ser Gln Val Gln Leu Ala Ile Gln Val Leu Leu Val Asp Lys		
1220	1225	1230
His Lys Tyr Phe Leu Phe Gly Gln Lys Lys Gly His Met Ile Phe		
1235	1240	1245
Ser Leu Ala Asn Gly Leu Trp Phe Asn Leu Ile Phe Asn Ser Arg		
1250	1255	1260
Lys Lys Leu Leu Glu Asp Met Lys Gln Asn Gly Phe Thr Gly Lys		
1265	1270	1275
Gly Leu Thr His Pro Val Pro Leu Lys Arg Thr Leu Gln Asn Lys		
1280	1285	1290
Arg Asn Lys Asn Ile Lys Arg Val Asn Gln Lys Lys Gly Asn Ile		
1295	1300	1305
Lys Arg Lys Ser Ile Leu Leu His Leu Ile Val Leu Asn Ser Pro		

1310	1315	1320
Glu Ser Asn Leu Ile Leu Ile	Gln His Gly Gly Ile	Phe Thr Phe
1325	1330	1335
Arg Phe Trp Val Glu Lys Leu	Ser Trp Asn Ile Cys	Lys Asn Leu
1340	1345	1350
Ser Leu Tyr Leu Asp Lys Phe	Val Gln Arg Leu Leu	Tyr Val Tyr
1355	1360	1365
Ile Ile Glu Thr Asn Val Phe	Val Leu Asn Leu Phe	His Val Pro
1370	1375	1380
Val Asn Gln Ile Phe Met Met	Ala Phe Tyr Leu Lys	Tyr Thr Glu
1385	1390	1395
Lys Ala Trp Val Met Glu Leu	Glu Trp Leu Ile Gln	Gln Gln Cys
1400	1405	1410
Tyr Gln Gly Ser Cys Gly Arg	Ala Cys Ser Cys Gly	Arg Gly Cys
1415	1420	1425
Gly Thr Pro Arg Gly Asp Trp	Lys Arg His Pro Pro	Arg Arg Ala
1430	1435	1440
Phe Trp Lys Pro Pro Ser Gln	Gly Ile Ser Ser Cys	Leu Met Thr
1445	1450	1455
Gly Cys Trp Leu Glu Lys Lys	Ala Thr Trp Met Arg	Arg Thr Arg
1460	1465	1470
Arg Lys Lys Arg Glu Asp His	Cys Gly Leu Arg His	Pro Ser Trp
1475	1480	1485
Pro Trp Thr Arg Cys Leu Arg	Met Arg Pro Pro Arg	Ser
1490	1495	1500
<210>		
1090		
<211> 1506		
<212> PRT		
<213> Artificial Sequence		
<220><223> Assembled poly-FSP polypeptide 3A		
<400> 1090		

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

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

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

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

 Leu Trp Glu Lys His Phe Lys Gly Leu Asn Trp Asn Leu Val Val Trp

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

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

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

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

Gly Pro Cys Pro Pro Pro Val Thr Pro Leu Arg Val Gln Ser Val Leu
 500 505 510
 Leu Leu Gly Val Pro Gln Thr Ala Ala Arg Gln Pro Ser Arg Pro Thr
 515 520 525
 Gly Arg Thr Pro Thr Thr Arg Leu Met Ala Pro Val Gly Ser Val Met
 530 535 540
 Ser Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr Met
 545 550 555 560

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

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

 Arg Glu Ala Gly Arg Phe Ala Val Leu Gly Thr Met Val Met Lys His
 690 695 700
 Leu Asn Arg Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu Thr
 705 710 715 720
 Met Met Met Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile Pro
 725 730 735
 Leu Pro Ser Pro Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His Pro

740	745	750	
Pro Pro Pro Cys Leu Leu Leu Leu His His Arg His His Leu Ala Phe			
755	760	765	
Leu Glu Met Ala Cys Ser Ser Gln His Thr His Ser Ile Lys Ile Trp			
770	775	780	
Ile Ser Phe Ser His Glu Gln Ser Ser Pro Phe Leu Ala Arg Ser Trp			
785	790	795	800
Asn Thr Met Gln Trp Asn Asn Lys Lys Met Ala Met Thr Val Ile Ala			
805	810	815	
Gly Ala His His Cys Gln Tyr Lys Leu Thr Tyr Thr Lys Val Trp Lys			
820	825	830	
Met Asn Trp Lys Lys Met Met Ile Gly Ser Gln His Leu Leu Phe Ser			
835	840	845	
Pro Leu Asp Ser Ser Pro Leu Gln Leu Leu Leu His Pro His Gly Lys			
850	855	860	
Arg Cys Asn Pro Cys Cys Arg Leu Thr Trp Met Ser Met Leu Gln Lys			
865	870	875	880
Gln Cys Cys Tyr Asn Leu Val Ile Lys His Pro Leu Ile Phe Arg Ile			
885	890	895	
Asn Leu Arg Arg Gln Gly Lys Thr Lys Asp Gly Val Val Gln Ser Leu			
900	905	910	
Gly Phe Leu Asn Gln Gln Ile Ile Leu Gln Lys Glu Phe Phe Ile Cys			
915	920	925	
Leu Leu Met Phe Ile Lys Arg Trp Lys Pro Ala Ala Thr Lys Arg Glu			
930	935	940	
Trp Glu Lys Arg Lys Gln Ile Leu Gly Gly Gly Gly Lys Tyr Lys Glu			
945	950	955	960
Tyr Phe Leu Lys Arg Ile Leu Ile Arg Lys Ala Met Thr Val Leu Ala			
965	970	975	
Gly Asp Lys Lys Gly Leu Gly Arg Phe Met Arg Cys Val Gln Ser Glu			
980	985	990	

Thr	Lys	Ala	Val	Ser	Leu	Gln	Leu	Pro	Leu	Gly	Arg	Gly	Pro	Val	Tyr
995				1000				1005							
Tyr	Val	Cys	Asn	Arg	Met	Asn	Val	Ser	Ser	Val	Leu	Lys	Pro	Phe	
1010				1015				1020							
Leu	Phe	Thr	Val	Pro	Ile	Glu	Asp	Met	Arg	Glu	Cys	Thr	Leu	Gly	
1025				1030				1035							
Arg	Asn	Arg	Met	Asn	Val	Ser	Ser	Val	Leu	Lys	Pro	Cys	Leu	Ile	
1040				1045				1050							
Pro	Val	Pro	Ile	Asp	Leu	Pro	Arg	Met	Leu	Pro	Ile	Ser	Ser	Pro	
1055				1060				1065							
Leu	His	Arg	Pro	Gln	Met	Pro	Phe	Trp	Thr	Cys	Thr	Phe	Pro	Ala	
1070				1075				1080							
Thr	Thr	Trp	Gly	Thr	Trp	Glu	Thr	Pro	Ser	Thr	Trp	Gly	Trp	Arg	
1085				1090				1095							
Thr	Phe	Arg	Gly	Pro	Arg	Arg	Lys	Val	Leu	Met	Val	Leu	Trp	Leu	
1100				1105				1110							
Pro	Ala	Asn	Gln	Ser	Leu	Gln	Lys	Ser	Gln	Val	Phe	Gln	Trp	Val	
1115				1120				1125							
Leu	Arg	Thr	Glu	Asn	Ile	Arg	Lys	Leu	Ile	Trp	Thr	Lys	Gln	Arg	
1130				1135				1140							
Ser	Phe	Leu	Ser	Leu	Phe	Pro	Lys	Leu	Arg	Ala	Thr	Glu	Gln	Met	
1145				1150				1155							
Thr	Asn	Val	Gly	Cys	Ala	Phe	Ser	Gly	Arg	Ile	Leu	His	Gln	Pro	
1160				1165				1170							
Glu	Met	Ala	Ala	Met	Arg	Leu	Met	Pro	Lys	Phe	Leu	Asn	Ser	Thr	
1175				1180				1185							
Asn	Ser	Trp	Trp	Thr	Cys	Thr	Asn	Leu	Ser	Val	Pro	Met	Met	Leu	
1190				1195				1200							
Thr	Ile	Leu	Ile	Trp	Lys	Arg	Val	Phe	Ile	Leu	Leu	Leu	Ser	Asp	
1205				1210				1215							
Lys	Lys	Leu	Leu	Lys	Lys	Ser	Ser	Gln	Leu	Arg	Arg	Ser	Trp	Arg	

1220	1225	1230
Asn Val Ser Arg Ile Ser His Gln Met Lys Cys Leu Thr Ala Val		
1235	1240	1245
Asp Cys Leu Gln Ala Phe Trp Asp Met Asn Met Glu His Arg Leu		
1250	1255	1260
Thr Met Asp Ser Ala Leu Ser Leu Thr Lys Arg Glu Gly Pro Glu		
1265	1270	1275
Thr Cys Lys Lys Lys Leu Leu Leu Lys Leu Leu Thr Met Ser Leu		
1280	1285	1290
Ser Asn Ile Leu Met Lys Phe Arg Leu Arg Leu Arg Ile Pro Ser		
1295	1300	1305
Leu Arg Lys Tyr Arg Gln His Leu Lys Lys Thr Ser Ala Lys Gly		
1310	1315	1320
Glu Lys Leu Lys His Cys Phe Lys Ala Trp Gly Arg Gly Pro Pro		
1325	1330	1335
Leu His Thr Arg Ser Gln Lys Lys Asp Pro Ala Gly Lys Leu Lys		
1340	1345	1350
Lys Leu Thr Thr Leu Ser Phe Val Leu Ile Glu Glu Arg Arg Asn		
1355	1360	1365
Leu Gln Arg Asn Leu Lys Val Leu Trp Leu Lys Lys Ser Thr Lys		
1370	1375	1380
Ser Arg Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe Phe Glu Lys		
1385	1390	1395
Lys Arg Pro Glu Trp Leu Ser Ser Arg Lys Lys Gly His Thr Lys		
1400	1405	1410
Asn Arg Arg Lys Ala Lys Arg Lys Pro Gln Ile Val His Lys Lys		
1415	1420	1425
Arg Gly Leu Phe Leu Lys Lys Lys Tyr Leu Val Gln Gly Ala Lys		
1430	1435	1440
Lys Ile Thr Phe Leu Ser Asn Gly Met Glu Ala Cys Gly Thr His		
1445	1450	1455

Pro Thr Pro Arg Leu Ser Asp Arg Val Phe Leu Val Lys Ile Thr
1460 1465 1470

Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg Ala Arg
1475 1480 1485

Gly Gly Thr Thr Ile Gly Glu Val Thr Ser Leu Cys Phe Phe Tyr
1490 1495 1500

Leu Leu Tyr
1505

<210> 1091

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 4A

<400> 1091

Ile Gln Lys Lys Lys Gln Lys Ser Met Ala Lys Lys Ser Gln Gln Pro

1 5 10 15

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

20 25 30

Arg Gln Arg Asn Asn Ala Lys Lys Met Pro Phe Gln Glu Glu Lys Lys

35 40 45

Asn Gly Arg Ile Ser Ser Ser Leu Ile Leu Ser Phe Gln Arg Val Lys

50 55 60

Asp Ser Lys Lys Met Thr Gln Lys Met Cys Ser Ser Leu Ala Leu Pro

65 70 75 80

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

85 90 95

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

100 105 110

Ser Ser Arg Leu Thr Cys Ala Ser Pro Gln Leu Pro Arg Met Trp Thr

115 120 125

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

130 135 140

Thr Thr Ser Leu Lys Gly Ser Arg Thr Ser Cys Cys Pro Arg Ser His
145 150 155 160

Pro Arg Leu Pro Arg Thr Lys Trp Pro Leu Gln Cys Leu Leu His Ser
165 170 175

Leu Gly Thr Thr Gly Thr Leu Val Trp Glu Arg Gly Val Leu Gln Met
180 185 190

Arg Ser Leu Glu Ala His Cys Pro Leu Gln Thr Phe His Leu His His
195 200 205

Cys Arg Thr Gln Pro Ser Ser Cys Pro Pro Ala Trp Ile Leu Tyr Gln
210 215 220

Gly Gln Trp Ser Gly Ala Val Val Gly Leu Arg Pro Val Ala His His
225 230 235 240

Leu Pro Arg Pro Ile Gln Gly Leu His Cys Pro Gln Ala Pro His Gln
245 250 255

Pro Ala Leu Ser Trp Gly Lys Trp Pro Val Gly Met Thr Gly Pro Ala
260 265 270

Arg Cys Cys Arg Trp Pro Arg Arg Ser Gln Lys Ser Gln His His Cys
275 280 285

Ala Leu Arg Lys Ile Glu Trp Ala Thr Lys Leu Ser Leu Gly Gly Lys
290 295 300

Ala Gly Pro Gln Ala Gln Glu Lys Ala Arg Pro Ser Pro Cys Leu Ser
305 310 315 320

Trp Ser Ser Arg Ile Val Ala Pro Gly His Ala Leu Ser Cys Arg Thr
325 330 335

Arg Arg Arg Trp Ser Ser Lys Cys Arg Gly Gly Pro Ser Ala Ser Asp
340 345 350

Arg Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly Arg
355 360 365

Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu Arg
370 375 380

Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly Phe

385 390 395 400
 Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro Arg
 405 410 415

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

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

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

 Pro Cys Gln Thr Leu Thr Phe Phe His Phe Phe Phe Phe Lys Thr
 610 615 620
 Val Ser Leu Cys Cys Pro Gly Trp Ser Lys Gly Gln Pro Pro Pro Pro
 625 630 635 640

Gly Leu Lys Pro Ser Ser Leu Ala Ser Gln Val Ala Arg Thr Thr Gly
 645 650 655
 Val Tyr Gln His Val Trp Leu Ile Cys Phe Val Phe Phe Val Cys Val
 660 665 670

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

 Cys Arg Ile Ser Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys His
 740 745 750
 Arg Lys Thr Asp Arg Ala Ser Val Ser Phe Trp Thr Leu Leu Pro Thr
 755 760 765
 Thr Gly Val Arg Thr Arg Gly Ser Pro Leu Arg Leu Thr Leu Trp Pro
 770 775 780
 Pro Arg Cys Arg Cys Arg Arg Glu Tyr Arg Val Thr Met Asn Ile Leu
 785 790 795 800

 Asn Ser Leu Pro Ser Ser Met Glu Ile Ala Val Leu Gln Glu Thr Ala
 805 810 815
 Lys Lys Ser Pro Thr Ser Phe Cys Cys Asn Leu Asp Leu Gln His Gln
 820 825 830
 Arg Arg Arg Lys Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser
 835 840 845
 Pro Lys Ala Asn Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln
 850 855 860

 Asn Leu Leu Asn Leu Val Gln Leu Asn Pro His Ser Pro His His Arg
 865 870 875 880
 Lys Asp Glu Glu Asp His Gln Lys Arg His His His His Asn Gln Lys

	885		890		895
Lys Met Ser Val Pro Leu Phe Phe His Gly Asp Leu Cys Arg Glu Ser					
	900		905		910
Thr Leu Gly Asn Phe Trp Met Lys Leu Leu Gln Leu Pro Gln Arg Pro					
	915		920		925
Pro Leu Gln Pro Val Thr Gly Met Glu Ile Leu Leu Trp Ile Leu Leu					
	930		935		940
Lys Met Glu Ile Gln Ile Phe Lys Ile Cys Leu Gly Glu Met Gln Leu					
945		950		955	960
Cys Thr Ser Arg Ile Leu Asn Leu Gln Val Leu Lys Lys Ile Leu Arg					
	965		970		975
Ser Phe Met Lys Leu Tyr His Ser Leu Val Met Cys Leu Arg Leu Arg					
	980		985		990
Thr Lys Leu Glu Lys Ala Leu Ser Ala Leu Phe Ile Trp Pro Gln His					
	995		1000		1005
Ser Tyr Lys Ile Thr His Pro Phe Ala Ser Gln Pro Leu Gly Gln					
	1010		1015		1020
Glu Met Pro Asn Asn Thr Gln Ile Arg Leu Leu Lys Pro Asp Lys					
	1025		1030		1035
Lys Lys Lys Ser Thr Glu Lys Thr Lys Gly Gln Ala Phe Gly Ser					
	1040		1045		1050
Phe Ser Ala Asp Phe Ser Ala Pro Gln Gly Gln Ala Phe Gly Ser					
	1055		1060		1065
Leu Cys Gln Leu Val Ser Ala Asp Phe Ser Ala Pro Gln Val Thr					
	1070		1075		1080
Arg Leu Arg Ser Leu Asn His Leu Leu Ile Trp Leu Lys Asn Trp					
	1085		1090		1095
Lys Arg Phe Lys Leu Lys Lys Lys Tyr Gln Ala Pro Leu Arg Leu					
	1100		1105		1110
Trp Ser Trp Cys Gly Thr Ser Gln Thr Tyr Phe Gly Ser Ile Ile					
	1115		1120		1125

Cys Ile	Lys Asn Met Phe Leu	Gln Arg Lys Gly Phe	Leu Asn Leu
1130	1135	1140	
Ser His	Val Glu Lys Phe Glu	Leu Lys Lys Asn Leu	Leu Leu Pro
1145	1150	1155	
Val Val	Ile Asn Leu Lys Arg	Leu Gln Lys Phe Met	Leu Asn Gln
1160	1165	1170	
Lys Cys	Leu Ala Pro Phe Pro	Ala Cys Thr Ser Lys	Ala Trp Thr
1175	1180	1185	
Pro Arg	Lys Leu Val Gly Arg	Ala Val Arg Arg Lys	Gly Ile Leu
1190	1195	1200	
Ala Met	Thr Leu Thr Leu Asn	Gly Ile Glu Ala Leu	Thr Ala Leu
1205	1210	1215	
Phe Thr	Cys Arg Thr Ala Ser	Ile Ser Val Asn Ile	Ser Thr Leu
1220	1225	1230	
Met Ser	Ile Leu Glu Ala Ile	Ile Lys Lys Met Lys	Lys Arg Ile
1235	1240	1245	
Met Val	His Arg Trp Ile Phe	Ser Asn Gln Leu Thr	Val Gln Met
1250	1255	1260	
Leu Cys	Leu Pro Leu Leu Thr	Pro Asp Thr Arg Trp	Ile Phe Ser
1265	1270	1275	
Asn Gln	Leu Gln Thr Val Gln	Met Leu Cys Leu Pro	Pro Leu Lys
1280	1285	1290	
Gln Gly	Glu Arg Ile Ile Trp	Pro Leu Gly Gly Phe	Gln Ile Pro
1295	1300	1305	
Asn Phe	Phe Trp Ser Leu Gly	Ile Gly His Thr Gly	Ala Trp Trp
1310	1315	1320	
His Thr	Gly Arg Arg Arg Arg	Glu Trp Gly Gly Ser	Thr Val Ser
1325	1330	1335	
Arg Ser	Pro Leu Trp Ile Ser	Ser Met Ile Tyr Leu	Arg Gly Met
1340	1345	1350	
Ala Phe	Ala Ser Asp Ser Ser	Ile Arg Thr Thr Arg	Val Ser Trp

1355 1360 1365
 Cys Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala Ser Ser Ser Pro
 1370 1375 1380
 Leu Trp Asp Cys Ser Thr Thr Thr Gly Thr His His Gly Cys Leu
 1385 1390 1395
 Trp Glu Ile Pro Ser Val Thr Leu Leu Ala Asn Leu His Leu Cys
 1400 1405 1410

Tyr Tyr His Ser Gln Ser Asn Arg Asn Lys Ser Arg Gln Met Glu
 1415 1420 1425
 Ser Leu Gly Met Lys Leu Gln Leu Lys Lys Lys Val Asn Ala Cys
 1430 1435 1440
 Ser Thr Tyr Thr Pro His Ile Cys Arg His Thr Cys Arg Val Asn
 1445 1450 1455
 Ala Val Glu Glu Leu His Ser Arg Arg Met Ser Val Arg Ile Val
 1460 1465 1470

Lys Asn Trp Val Ser Cys Cys Tyr Val Arg Leu Ser Ala Val Gly
 1475 1480 1485
 Leu Ser Thr Trp Ser Ala Leu Asp Asn Lys Ile Ile Cys Lys Gly
 1490 1495 1500
 His Arg Ile Thr
 1505

<210> 1092

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 1B

<400> 1092

Thr Glu Ile Gln Leu Thr Met Asn Asp Ser Lys His Lys Leu Glu Ser
 1 5 10 15

Pro Ala Leu Lys Gln Val Ser Pro Ala Ser Pro Pro Thr Gln Gln Pro
 20 25 30

Gln Thr Pro Gln Asp Ser Arg Gln Val Leu Ala Met Pro Ser Ser Trp

35	40	45
Ser Ser Ser Gly Arg Thr Gln Arg Lys Val Val Lys Asn Pro Ser Gln		
50	55	60
Pro Val Pro Leu Arg Asn Asp Gly Ile Thr Asn Gly Asn Asp Ser Thr		
65	70	75
		80
Arg Ser Cys Ser Ile Ser Leu Lys Lys Ser Leu Glu Lys Met Pro Leu		
85	90	95
Met Met Lys Lys Lys Asp Ser Thr Ile Phe Ile Val Pro Met Ser Leu		
100	105	110
Ala Cys Ser Ile Thr Val Ser Phe Val Gly Gln Ile Ser Thr Leu Val		
115	120	125
Leu Asp Val Ser Ser Ile Ser His Trp Asn Lys Val Arg Gln Asn Phe		
130	135	140
Lys Arg Asn Ala Asp Lys Lys Asn Val Arg Ser Gly Glu Lys Asn Asp		
145	150	155
Leu Gln Leu Phe Val Met Ser Asp Thr Thr Tyr Lys Ile Tyr Trp Thr		
165	170	175
Val Ile Leu Leu Asn Pro Cys Gly Asn Leu His Leu Lys Thr Thr Ser		
180	185	190
Leu Gly Asp Cys Pro Arg Thr Met Ala Gly Pro Ser Ala Ser Leu His		
195	200	205
Pro Ala Ser Gly Arg Ala Ser Arg Lys Thr Trp Gln Arg Arg Leu Arg		
210	215	220
Ala Cys Arg Ala Gly Gly Pro Ala Gly Trp Ala Arg Gln Ala Phe Asp		
225	230	235
Lys Lys Gly Phe Val Ile Leu Ser Val Gly Ala Gly Thr Gly Gly Gly		
245	250	255
Pro Ala Cys Val Pro Val Ala Glu Ala Ser Thr Gly Ala Trp Thr Ala		
260	265	270
Glu Gly Ala Ala Gly Thr Arg Cys Arg Ala Ser Arg Ala Pro Cys Arg		
275	280	285

Gln Leu Pro Ala Ser Ser Pro Thr Lys Cys Glu Ile Cys Val Lys Arg
290 295 300

Arg Arg Arg Arg Lys Arg Ser Ser Gln Ser Arg Ser Pro Val Pro Lys
305 310 315 320

Lys Arg Glu Arg Met Met Leu Pro Val Arg Ala Arg Thr Ala Arg Ser
325 330 335

Ala Leu Pro Gln Gly Arg Ala Pro Leu Glu Gly Met Leu Leu Pro Arg
340 345 350

Ala Leu Pro Ser Leu Leu Ser Arg Met Pro Ala Arg Arg Glu Ser Arg
355 360 365

Phe Trp Leu Ala Leu Gln Ala Leu Gly Leu Arg Pro Pro His Leu Pro
370 375 380

Ser Cys His Pro Leu Pro Gln Leu Leu Gly Pro Pro Pro Pro His Gln
385 390 395 400

Ala Pro Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu Arg Leu Pro Cys
405 410 415

Lys Val Thr Glu Ser Ser Asn Met Gly Gly Asn Arg Ser Ile Cys Leu
420 425 430

Thr Asn Ala Lys Lys Met Glu Asp Met Ile Trp Glu Ser Thr Pro Leu
435 440 445

Ser Ile Ser Arg Pro Thr Ser Arg Ala Arg Gln Ser Cys Cys Leu Pro
450 455 460

Gly Leu Thr His Pro Ala His Gln Pro Leu Gly Ser Met Thr Leu Ala
465 470 475 480

Ile Arg Phe Ile Ser Ala Pro Gln Pro Ser Ser Ser Thr Val Thr Ala
485 490 495

Ala Pro Ser Gly Gln Tyr Phe Lys Gly Lys Lys Arg Arg Lys Glu Ile
500 505 510

Phe Lys Lys Lys Lys Pro Leu Thr Phe Ser Pro Ser Leu Ala Lys Lys
515 520 525

Thr Leu Thr Asn Ser Ser Phe Phe Tyr Thr Ser Asp Arg Glu Ala Lys

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

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

 Ala Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser
 660 665 670
 Arg Lys Gln Ile Pro Ser Gln Ser Met Leu Val Ala Ser Arg Ala Gly
 675 680 685
 Gln Phe Pro Val Trp Arg Arg Thr Ser Arg Gly Met Ser Leu Gln Trp
 690 695 700
 Lys Ser Gly Asn Ala Cys Thr Pro Leu Arg Cys Pro Ser Arg Ser Pro
 705 710 715 720

 Ala Thr Phe Leu Thr Ala Leu Asn Gly Trp His Arg Ser Gly Leu Arg
 725 730 735
 Ala Gln Arg Lys Arg Lys Arg Glu Lys Arg Ser Gln Lys Ser Arg Gln
 740 745 750
 Asn His Leu Gln Leu Lys Ser Cys Arg Arg Lys Ile Ser Asn Trp Ser
 755 760 765
 Lys Leu Arg Ser Pro Trp Ile Phe Val Ser Lys Lys Arg Leu Pro Lys
 770 775 780

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

 Gly Gly Arg Arg Glu Lys Lys Gly Cys Arg Glu Arg Ser Leu Leu Tyr
 850 855 860
 Ser Arg Met Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro Asp
 865 870 875 880
 Tyr Phe Val Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser Phe
 885 890 895
 Pro Val Gly Ala Val Phe Leu Thr Arg Pro Ala Ile Pro Cys Cys Ser
 900 905 910

 Cys Thr Ser His Ser Asn Pro Trp Ser Gln Ser Arg His Pro His Arg
 915 920 925
 Ser Pro Pro Thr Ser Cys Pro Pro Leu Leu Glu Ala Phe Pro Leu Pro
 930 935 940
 Arg Ala Ser Leu Arg Ala Thr Val Pro Arg His Ser Ser Val Leu Ala
 945 950 955 960
 Thr Gly Leu His Leu His Arg Gln Ile Ser Leu Pro Leu Arg Gly Phe
 965 970 975

 Leu Leu His Gln Pro Leu Pro Gly Gln His Leu Trp Leu Ser His Arg
 980 985 990
 Leu Arg Leu Arg Leu Pro Arg Thr Gln Arg Pro Pro Arg Ser Ile Leu
 995 1000 1005
 Ser Leu Arg Leu Pro Leu Arg Pro Gln Arg Gly Pro Arg Pro Leu
 1010 1015 1020
 His Arg Trp Leu Gln Gln Thr Thr Gly Cys Ser Gln Arg Arg Tyr

1025	1030	1035
Pro Arg Leu Lys Thr Phe Gly Val Pro Leu Gly Ser Ile Leu Cys		
1040	1045	1050
Leu Ala Gly Ser Leu Ser Thr Met Met Ile Ile Ser Thr Thr Arg		
1055	1060	1065
Gln Glu Cys Gly Arg Arg Ala Ser Val Pro Cys Arg Pro Met Ile		
1070	1075	1080
Gly Ser Ala Arg Pro Gly Pro Trp Arg Thr Ser Ala Met Pro Ser		
1085	1090	1095
Ala Met Gly Val Ala Leu Pro Thr Ser Cys Glu Ser Gly Arg Ser		
1100	1105	1110
Pro Pro Ala Thr Gly Gly Arg Met Pro Gly Ser Gln Ser Ile Met		
1115	1120	1125
Met Ser Trp Met Pro Pro Leu Ala Pro Cys Ala Ala Cys Pro Cys		
1130	1135	1140
Ser Pro Ala Pro Thr Leu Cys Pro Ala His Pro Ala Arg Ala Pro		
1145	1150	1155
Thr Ala Val Pro Ala Phe Thr Pro Leu Ser Ala His Pro Val Pro		
1160	1165	1170
Val Leu Ser Gly Cys His Leu Ala Val Arg Thr Ser Met Leu Thr		
1175	1180	1185
Leu Leu Pro Met Leu Lys Leu Ala Pro Leu Gln Val Thr Thr Thr		
1190	1195	1200
Leu Lys Leu Ile Leu Val Met Leu Glu Ile Val Thr Glu Ser Thr		
1205	1210	1215
Arg Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro Gly Pro		
1220	1225	1230
Trp Arg Ala Ala Leu Gly Lys Glu Val Lys Arg Ser Gln Ser Lys		
1235	1240	1245
Leu Arg Leu Arg Asn Thr Ser Pro Ile Val Phe Phe Leu Ala Pro		
1250	1255	1260

Tyr Phe Pro Arg Arg Met Thr	Arg Arg Thr Met Thr	Thr Thr Lys
1265	1270	1275
Met Met Met Met Arg Arg Thr	Lys Arg Arg Arg Arg	Lys Arg Arg
1280	1285	1290
Arg Met Thr Met Met Thr Arg	Arg Thr Leu Leu Thr	Lys Lys Thr
1295	1300	1305
Cys Leu Thr Pro Arg Thr Ser	Ala Ala Thr Lys Ala	Leu Pro Arg
1310	1315	1320
Gln Thr Ile Ser Gln Arg Arg	Pro Ile Gln Thr Pro	Pro Gly Thr
1325	1330	1335
Ser Leu Ala Ile Trp Gly Asn	Gln Gln Leu Lys Trp	Thr Pro His
1340	1345	1350
Ile Leu Lys Ser Ala Ser Arg	Arg Ala Arg Pro Thr	Ser Cys Ser
1355	1360	1365
Thr Cys Arg Met Trp Trp Ile	Ala Lys Lys Arg Ile	Lys Leu Arg
1370	1375	1380
Arg Asn Arg Thr Arg Leu Thr	Leu Thr Gly Thr Arg	Ser Ser Gly
1385	1390	1395
Thr Arg Ala Ser Pro Ser Ala	Val Cys Leu Cys Cys	Trp Thr Cys
1400	1405	1410
Pro Ser Arg Ser Phe Pro Ala	Ala Ser Pro Ser Gly	Leu Arg Ala
1415	1420	1425
Pro Val Gly Ala Gln Ala Pro	Pro Glu Val Thr Leu	Arg Ala Ser
1430	1435	1440
Cys Ala Ser Ser Ala Ser Lys	Ala Cys Ala Gly Leu	Trp Pro Trp
1445	1450	1455
Gly Ala Gln Val Arg Gln Pro	Ser Leu Pro Gly Pro	Cys Ala Ser
1460	1465	1470
Leu Leu Ser Thr Leu Ser Gln	Pro Pro Pro Gln Ala	Pro Ser Gln
1475	1480	1485
Val Trp Thr Ala Ala Thr Leu	Arg Cys Pro Ala Val	Pro Ala Ala

1490 1495 1500

Ala Cys Pro Pro

1505

<210> 1093

<211> 1501

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 2B

<400> 1093

Arg Lys Met Gln Ser Leu Asn His Pro Ser Arg Leu Thr Asn Met Ser

1 5 10 15

Arg Thr Pro Pro Arg Arg Val Cys Asn Pro Arg Arg Lys Thr Trp Lys

20 25 30

Met Arg Lys Lys Tyr Ala Gln Lys Pro Ser Gln Lys Asn His Leu Tyr

35 40 45

Asn Ser Arg Lys Lys Leu Leu Glu Asp Met Lys Gln Asn Gly Phe Thr

50 55 60

Gly His Arg Glu Gly Ser Glu Ser Asp Asn Leu Gly Leu Leu Tyr Ser

65 70 75 80

Phe Pro Pro Ile Arg Met Cys Ala Leu Ser His Pro Ser Phe Tyr Ile

85 90 95

Ser Ser Thr Val Cys Phe Leu Ser Lys His Cys Met Thr Ala Cys Thr

100 105 110

Gln Lys Lys Gly His Met Ile Phe Ser Arg Glu Lys Ile Ile Asn Pro

115 120 125

Thr Ile Ser Cys Pro Phe Gln Ser Pro Thr Lys Arg Leu Glu Leu Ser

130 135 140

Leu Glu Pro Trp Ile Pro Tyr Leu His Gln Gln Lys Thr Gln Gly Gly

145 150 155 160

Lys Lys Arg Ser Lys Phe Pro Gly Thr Ser Leu Gln Cys Tyr Leu Asn

165 170 175

Arg Cys Ser Leu Met Glu Gln Ile Pro His Leu Lys Ser Ala Ser Pro

180	185	190	
Gln Ile Met Gln Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg Arg			
195	200	205	
Met Gln Asn Leu Asp Asn Leu Gly Val Pro Trp Pro Leu Leu Pro Gly			
210	215	220	
Pro Leu Glu Asn Thr Gln Ile Pro Arg Thr Ser Pro Leu Trp Lys Ile			
225	230	235	240
Thr Met Val Leu Thr Tyr Pro Asn Cys Val Val His Val Leu Met Phe			
245	250	255	
Trp Leu Pro Met Arg Ser Leu Gly Glu Pro Trp Arg Ala Gly Phe Gln			
260	265	270	
Trp Gly Glu Ser Pro Trp Gln Val Met Ala Ser Leu Thr Gly Pro Tyr			
275	280	285	
Pro Ile Ser Glu Gly Leu Thr Met Thr Thr Gly Arg Asn Ile Asn Ser			
290	295	300	
Asn Ser Leu Met Thr Asn Cys Leu Phe Ser Pro Ile Phe Leu Cys His			
305	310	315	320
His Ala Ile Met His Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe			
325	330	335	
Ser Ser Lys Ile Pro His Pro Gln Val Pro Ser Val Val Ala Leu Cys			
340	345	350	
Lys Phe Arg Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro			
355	360	365	
Gln Ala Arg Leu Cys Leu Ile Val Ser Arg Thr Leu Leu Leu Val Gln			
370	375	380	
Ser Ala Ala Pro Pro His Arg Leu Leu Gly Pro Ser Arg Trp Ser Arg			
385	390	395	400
Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys Val Lys Leu Ala			
405	410	415	
Asn Gly Leu Trp Phe Asn Leu Ile Phe Val Leu Phe Lys Ala Asp Gln			
420	425	430	

Ser Glu Ser Ser Leu Ser Ser Gly Arg Asn Lys Lys Thr Lys Leu Trp
435 440 445

Phe Ser Leu Ile Asn Ile His His Arg Lys Asn Pro Leu Leu Pro Met
450 455 460

Arg Ile Pro Ser Leu Asn Ala Gln Trp Met Phe Leu Arg Ile Leu Leu
465 470 475 480

Leu Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr Gln Lys Gly Glu
485 490 495

Cys Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu Phe Ile Leu Lys
500 505 510

Gln Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met Leu Gln Ala His
515 520 525

Pro Gln Val Pro Ala Leu Ala Pro Gln Ala Trp Trp Pro Ala Arg Arg
530 535 540

Gly Pro Leu Thr Ser Ala Pro Ser Ala Gln Gln Ser Leu Thr Ala Ser
545 550 555 560

Pro Gln Ile Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr Ile Ile
565 570 575

Tyr Pro Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly Arg Thr Leu Glu
580 585 590

Ser Ala Gly Leu Phe Pro Trp Leu His Thr Gln Cys Thr His Pro Cys
595 600 605

Thr Met Leu Leu Pro Gln Gly Trp Trp Cys Thr Arg Gly Gly Gly Lys
610 615 620

Arg Lys Lys Lys Met Cys Lys Val Ser Gly Gly Cys Thr Ala Cys Val
625 630 635 640

Glu Arg Cys Pro Trp Lys Gly Ile Cys Trp Lys Trp Pro Val Thr Val
645 650 655

Ala Ala Gln Trp Ser Ser Val Thr Ser Leu Glu Trp Thr Ala Gln Glu
660 665 670

Arg Gly Cys Ser Ser Trp Leu Met Lys Gln Thr Trp Met Lys Ser Trp

675 680 685
 Ser Leu Arg Asp Pro Ser Tyr Arg Ser Ile Leu Glu Tyr Val Ser Thr
 690 695 700

 Arg Val Leu Trp Met Pro Thr Ser Thr Val Arg Arg Arg Asn Ser Arg
 705 710 715 720
 Lys Gln Ser Gln Val Gln Leu Ala Ile Gln Val Leu Leu Val Asp Lys
 725 730 735
 His Lys Tyr Phe Leu Phe Gly Arg Ala Arg Asn Arg Asn Met Lys Lys
 740 745 750
 Thr Met Ser His Leu Ile Ala His Gln Ala Leu Lys Met Ser Gly Leu
 755 760 765

 Arg Leu Phe His Pro Arg Leu Leu Thr Arg Lys Lys Pro Gly Lys Phe
 770 775 780
 Leu Pro Ser Arg Phe Pro Trp Gly Pro Pro Pro Leu Cys His Pro Ala
 785 790 795 800
 Trp Leu Ser Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe
 805 810 815
 His Val Leu Ala Leu Glu Val Thr Phe Pro Pro Gly Thr Ala Met Pro
 820 825 830

 Gln Met Gln Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp Lys
 835 840 845
 Arg Lys Arg Met Lys Thr Gly Ala Ile Gln Glu Lys Gly Ala Ile Gln
 850 855 860
 Glu Lys Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe Glu Ala
 865 870 875 880
 Cys Arg Glu Met Glu Ser Leu Ser Ala Pro Glu Lys Ile Thr Leu Phe
 885 890 895

 Glu Ala His Met Ala Arg Cys Thr Ser Ile Asn Val Leu Cys Val Arg
 900 905 910
 Ala Ser Leu Ile Glu Lys Leu Met Lys Glu Lys Arg Lys Met Lys Arg
 915 920 925

Asn Gln Val Ala Ser Pro Gln Ile Met Gln Arg Leu Phe Ile Lys Gly
 930 935 940
 Tyr Gln Asn Asn His Phe Thr Phe His Leu Gln Asn Phe Ala Phe Phe
 945 950 955 960

 Ser Ser Phe Gly Asn Asn Lys Tyr Ile Asn Ile Leu Thr Arg Arg Lys
 965 970 975
 Lys Arg Glu Asp His Cys Gly Leu Leu Ile Leu Ile Gln His Gly Gly
 980 985 990
 Ile Phe Thr Phe Arg Phe Trp Val Glu Lys Leu Ser Trp Asn Ile Cys
 995 1000 1005
 Lys Asn Leu Ser Leu Tyr Leu Asp Lys Phe Val Gln Arg Leu Leu
 1010 1015 1020

 Tyr Val Tyr Ile Ile Glu Thr Asn Val Phe Val Leu Asn Leu Phe
 1025 1030 1035
 His Val Pro Val Asn Gln Ile Phe Met Met Ala Phe Tyr Leu Lys
 1040 1045 1050
 Tyr Thr Glu Lys Ala Trp Val Met Glu Leu Glu Trp Leu Ile Gln
 1055 1060 1065
 Gln Gln Cys Tyr Gln Gln Glu Lys Lys Ser Arg Lys Leu Met Ser
 1070 1075 1080

 Ser Cys Arg Ala Phe Ile His Thr Pro Arg Ser Pro Gly Cys Ser
 1085 1090 1095
 Val Tyr Ala Asn Met Cys Trp Ala Phe Trp Lys Pro Pro Ser Gln
 1100 1105 1110
 Gly Ile Ser Ser Cys Leu Met Thr Gly Cys Trp Gly Ser Pro Pro
 1115 1120 1125
 Leu His Leu Cys Gln Pro Leu Arg Arg Tyr Lys Lys Arg Gly Val
 1130 1135 1140

 Ile Ala Trp Arg Arg Arg Lys Trp Gln Ile Arg His Val Leu Lys
 1145 1150 1155
 Asn Leu Ile Leu Phe His Val Arg Asn Ile Val Tyr Gly Ile Gln

1160	1165	1170
Val Met Leu Cys Gly Lys Gly	Leu Thr His Pro Val	Pro Leu Lys
1175	1180	1185
Arg Thr Leu Gln Asn Lys Arg	Asn Lys Asn Ile Lys	Arg Val Asn
1190	1195	1200
Gln Lys Lys Gly Asn Ile Lys	Arg Lys Ser Ile Leu	Leu His Leu
1205	1210	1215
Ile Val Leu Asn Ser Pro Glu	Ser Asn Pro Lys Phe	Phe Leu Thr
1220	1225	1230
Phe Ser Gln Leu Glu Lys Lys	Ala Thr Trp Met Arg	Arg Thr Gly
1235	1240	1245
Ala Leu Arg Ala Thr Ala Pro	Ala Thr Ala Ala Pro	Gln Ala Gln
1250	1255	1260
Thr Pro His Trp Arg Ala Ala	Thr Thr Ser Ser Met	Ser Ser Ser
1265	1270	1275
Pro Arg Ala Glu Pro Thr Ser	Ser Ser Ser Trp Ala	Thr Cys Trp
1280	1285	1290
Pro Arg Cys Cys Ser Ser Ser	Cys Tyr Trp Ser Leu	Ser Ser Trp
1295	1300	1305
Pro Pro Ala Gly Ala Ala Glu	Ala Thr Asn Thr Arg	Thr Arg Ser
1310	1315	1320
Arg Glu Ser Gln Arg Gly Arg	Met Leu Thr Trp Arg	Ser Ser Leu
1325	1330	1335
Trp Leu Gln Gly Thr Arg Cys	Phe Thr Gly Val Arg	Thr Ser Ser
1340	1345	1350
Gly Ser Cys Gly Arg Ala Cys	Ser Cys Gly Arg Gly	Cys Gly Thr
1355	1360	1365
Pro Arg Gly Asp Trp Lys Arg	His Pro Pro Arg Arg	Asn Ser Val
1370	1375	1380
Ile Val His Lys Ile Val Leu	Val Phe Leu Lys Ser	Leu Ser Ser
1385	1390	1395

Tyr Asn Cys Glu Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile
 1400 1405 1410
 Glu Phe Ala Val Leu Lys Leu Leu Asn Met Asp Leu His Trp Asn
 1415 1420 1425
 Ser Ala Tyr Leu Gly Arg Thr Leu Leu Val Thr Cys Ile Leu Tyr
 1430 1435 1440

His Arg Trp Ile Val Thr Ser Met Cys Gln Ser Gln Arg Trp Leu
 1445 1450 1455
 Thr Ser Thr Thr Ser Arg Ser Ser Ala Leu Met Trp Thr Arg Gln
 1460 1465 1470
 Ile Asn Arg Arg Lys Leu Gln Arg Lys Lys Arg His Pro Ser Trp
 1475 1480 1485
 Pro Trp Thr Arg Cys Leu Arg Met Arg Pro Pro Arg Ser
 1490 1495 1500

<210>

1094

<211> 1506

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 3B

<400> 1094

Gly Ala Ala Ala Ala Ser Cys Gln Ser Pro Pro Ser Pro Arg Glu Thr
 1 5 10 15
 Thr Pro Ser Ser Asp Ala Thr Arg Arg Thr Arg Pro Ile Ala Ala Gln
 20 25 30
 Ser Lys Lys Thr Met Thr Ala Ala Gly Leu Thr Pro Lys Asn Lys Lys
 35 40 45
 Arg Arg Lys Leu Arg Pro Lys Met Ile Arg Lys Ile Gln Lys Arg Arg
 50 55 60
 Arg Thr Ala Asn Arg Arg Asn Ser Arg Arg Ala Thr Pro Thr Ser Lys
 65 70 75 80
 Gly Ser Leu Arg Arg Lys Tyr Leu Arg Val Arg Gly Pro Pro Leu His
 85 90 95

Thr Arg Asn Ile Arg Lys Leu Ile Trp Thr Lys Gln Arg Ser Phe Leu
100 105 110

Ser Leu Phe Pro Lys Leu Arg Ala Thr Glu Gln Met Thr Asn Val Gly
115 120 125

Cys Ser Ile Pro His Val Pro Lys Ala Thr Ala Ala His Ser Val Thr
130 135 140

Val Lys Leu Gln Leu Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser
145 150 155 160

Arg His Thr Met Ser Leu Ser Asn Ile Leu Met Lys Phe Arg Leu Gln
165 170 175

Ser Ser Pro Phe Leu Ala Arg Ser Trp Asn Thr Met Gln Trp Asn Asn
180 185 190

Lys Lys Met Ala Met Thr Val Ile Ala Gly Ala His His Cys Gln Tyr
195 200 205

Lys Leu Thr Tyr Thr Lys Val Trp Lys Met Asn Trp Lys Lys Met Met
210 215 220

Ile Gly Ser Gln His Leu Leu Phe Ser Pro Leu Asp Ser Ser Pro Leu
225 230 235 240

Gln Leu Leu Leu His Pro His Gly Lys Arg Cys Asn Pro Cys Cys Arg
245 250 255

Leu Thr Trp Met Ser Gln Asn Thr Arg Ser Thr Asn Leu Glu Lys Asn
260 265 270

Pro Ser Leu Lys Lys Gln Ser Gln Arg Arg Gly Lys Leu Ser Ala Phe
275 280 285

Ser Gly Arg Ile Leu His Gln Pro Glu Met Ala Ala Met Arg Leu Met
290 295 300

Pro Lys Phe Leu Asn Ser Thr Asn Ser Trp Trp Thr Leu Thr Thr Leu
305 310 315 320

Ser Phe Val Leu Ile Glu Glu Ala Arg Gln Pro Ser Arg Pro Thr Gly
325 330 335

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

340	345	350
Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr Met Pro		
355	360	365
Pro Leu Leu His Pro Gln Trp Ala Pro His Ser Ala Gly Leu Ser Pro		
370	375	380
Gly Ala Cys Arg Pro Ala Cys Thr Cys Ile Ser Met Thr Thr Ile Ser		
385	390	395
Arg Ala Thr Trp Gly Pro Val Tyr Tyr Val Cys Asn Arg Met Asn Val		
405	410	415
Ser Ser Val Leu Lys Pro Phe Leu Phe Thr Val Pro Ile Glu Asp Met		
420	425	430
Arg Glu Cys Thr Leu Gly Arg Asn Arg Met Asn Val Ser Ser Val Leu		
435	440	445
Lys Pro Cys Leu Ile Pro Val Pro Ile Ser Glu Lys Lys Arg Lys Leu		
450	455	460
Pro Asn Ile Glu Ile Thr Pro Gln Arg Ser Lys Ala Met Leu Gln Lys		
465	470	475
Gln Cys Cys Tyr Asn Leu Val Ile Lys His Pro Leu Ile Phe Arg Ile		
485	490	495
Asn Leu Arg Arg Gln Gly Lys Thr Lys Asp Gly Val Val Gln Ser Leu		
500	505	510
Gly Phe Leu Asn Gln Gln Ile Ile Leu Gln Lys Glu Phe Phe Ile Cys		
515	520	525
Leu Leu Met Phe Ile Lys Arg Trp Lys Pro Ala Ala Thr Lys Ser Arg		
530	535	540
Lys Lys Gly His Thr Lys Asn Arg Arg Lys Ala Lys Arg Lys Pro Gln		
545	550	555
Ile Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe His Leu Lys Lys Thr		
565	570	575
Ser Ala Lys Trp Leu Lys Lys Ser Thr Lys Ser Arg Ser Asn Gly Met		
580	585	590

Glu Ala Cys Gly Thr His Pro Thr Pro Arg Leu Ser Cys Leu Arg Val
 595 600 605
 Arg Cys Gly Gly Trp Leu Cys Gly Trp Thr Pro Arg Gly Arg Lys Ser
 610 615 620

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

 Gly Glu Lys Leu Lys His Cys Phe Lys Ala Trp Gly Ser Arg Arg Asn
 690 695 700
 Arg Arg Tyr Arg Lys Ile Tyr Gly Glu Leu Lys Met Ser Leu Gln Ala
 705 710 715 720
 Phe Leu Ile His Leu Arg Lys Val Asp Thr His His Leu Gln Val Val
 725 730 735
 Thr Lys Thr Val Thr Ala Thr Thr Ala Asp Gly Gln Arg Met Arg Arg
 740 745 750

 Leu Lys Cys Lys Ala Cys Arg Leu Arg Trp Ala Arg Pro Glu Pro Ala
 755 760 765
 Ala Gln Ala Pro Pro Lys Ser His Phe Pro Pro His Pro Ser Gly Pro
 770 775 780
 Ser Arg Thr Ser Ser Leu Gln Leu Arg Ser Leu Phe Phe Ser His Cys
 785 790 795 800
 Leu Cys Ser Gln Lys Lys Asp Pro Ala Gly Lys Leu Lys Lys Leu Leu
 805 810 815

 Lys Lys Ser Ser Gln Leu Arg Arg Ser Trp Arg Asn Val Ser Arg Ile
 820 825 830
 Ser Thr Pro Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala Pro Val Ser

835	840	845	
Val Ile Thr Met Lys Leu Trp Glu Lys His Phe Lys Gly Leu Asn Trp			
850	855	860	
Asn Leu Val Val Trp Ile Leu Asn Leu Lys Met Met Thr Tyr Met Glu			
865	870	875	880
Met His Tyr Gly His Gln Ala Pro Gln Val Ala Met Leu Pro Lys Leu			
885	890	895	
Leu Cys Arg Gln Met Leu Pro Thr Leu Ser Thr Leu Gln Gln Arg His			
900	905	910	
Pro Gln Gly Pro Cys Pro Pro Pro Val Thr Pro Leu Arg Val Gln Ser			
915	920	925	
Val Leu Leu Leu Gly Val Pro Gln Thr Ala Arg Gly Pro Arg Arg Lys			
930	935	940	
Val Leu Met Val Leu Trp Leu Pro Ala Asn Gln Ser Leu Gln Lys Ser			
945	950	955	960
Gln Val Phe Gln Trp Val Leu Arg Thr Glu Val Ala Pro Arg Cys Pro			
965	970	975	
Arg Ser Ala Val Asp Ile Ser Pro Gly Pro Thr Ser Pro Ser Leu Ala			
980	985	990	
Ser Cys Ala Ser Val Ala Ile Gly Lys Leu Ala Leu Leu Gly Ala Ser			
995	1000	1005	
Ala Pro Cys Gly Ala Ala Gly Ala Arg Glu Ala Gly Arg Phe Ala			
1010	1015	1020	
Val Leu Gly Thr Met Val Met Lys Leu Cys Phe Phe Tyr Leu Leu			
1025	1030	1035	
Tyr Arg Leu Arg Ile Pro Ser Leu Arg Lys Tyr Arg Gln His Leu			
1040	1045	1050	
Asn Arg Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu Thr			
1055	1060	1065	
Met Met Met Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile			
1070	1075	1080	

Pro Leu	Pro Ser	Pro Arg	Gln	His Leu	Leu Pro	Gln	Tyr Pro	Leu
1085			1090				1095	
His Pro	Pro Pro	Pro Cys	Leu	Leu Leu	Leu His	His	Arg His	His
1100			1105				1110	
Leu Ala	Phe Leu	Glu Met	Ala	Cys Ser	Ser Gln	His	Thr His	Ser
1115			1120				1125	
Ile Lys	Ile Trp	Ile Ser	Phe	Ser His	Glu Val	Asp	Pro Pro	Gly
1130			1135				1140	
Ser Val	Trp Ile	Leu Pro	Cys	Asp Leu	Pro Arg	Met	Leu Pro	Ile
1145			1150				1155	
Ser Ser	Pro Leu	His Arg	Pro	Gln Met	Pro Phe	Trp	Thr Cys	Thr
1160			1165				1170	
Phe Pro	Ala Thr	Thr Trp	Gly	Thr Trp	Glu Thr	Pro	Ser Thr	Trp
1175			1180				1185	
Gly Trp	Arg Thr	Phe Arg	Gly	Ala Ser	Ser Ser	Thr	Ser Arg	Asp
1190			1195				1200	
Ser Arg	Ser Phe	Phe Thr	Ser	Ala His	Pro Ser	Arg	Pro Cys	Arg
1205			1210				1215	
Met Arg	Leu Tyr	Gln Cys	Lys	Lys Lys	Leu Leu	Leu	Lys Leu	Leu
1220			1225				1230	
Thr Thr	Thr Thr	Ser Ser	Pro	Arg Arg	Ser Pro	Ala	Leu Arg	Ala
1235			1240				1245	
Arg Gly	Gly Thr	Thr Ile	Gly	Glu Val	Thr Ser	Cys	Thr Asn	Leu
1250			1255				1260	
Ser Val	Pro Met	Met Leu	Thr	Ile Leu	Ile Trp	Lys	Arg Val	Phe
1265			1270				1275	
Ile Leu	Leu Leu	Ser Asp	Lys	Lys Gly	Ala Lys	Lys	Ile Thr	Phe
1280			1285				1290	
Leu Pro	Ile Pro	Pro His	Leu	Arg His	Pro Leu	Leu	Leu Phe	Glu
1295			1300				1305	
Lys Lys	Arg Pro	Glu Trp	Leu	Ser Met	Asp Leu	Asp	Gly Met	Leu

1310	1315	1320
Thr Val Ile Gly Gln Gly Leu	Val Gly Met Thr Pro	Arg Asp Leu
1325	1330	1335
Gly Thr Val Ala Gly Ala Thr	Ala Gln Ile Gln Arg	Pro Ile Gln
1340	1345	1350
Val Gln Thr Gly Gly Arg Leu	Arg Arg Asn Leu Gln	Arg Asn Leu
1355	1360	1365

Lys Val Leu Gln Val Ser Val	Tyr Ser Gly Asn Leu	Leu Ser Phe
1370	1375	1380
Ser Arg Arg Gly Met Lys Ser	Ser Val Arg Leu Lys	Asn Arg Glu
1385	1390	1395
Trp Glu Lys Arg Lys Gln Ile	Leu Gly Gly Gly Gly	Lys Tyr Lys
1400	1405	1410
Glu Tyr Phe Leu Lys Arg Ile	Leu Ile Arg Lys Ala	Met Thr Val
1415	1420	1425

Leu Ala Gly Asp Lys Lys Gly	Leu Gly Arg Phe Met	Arg Cys Val
1430	1435	1440
Gln Ser Glu Thr Lys Ala Val	Ser Leu Gln Leu Pro	Leu Gly Arg
1445	1450	1455
Asn Met Glu His Arg Leu Thr	Met Asp Ser Ala Leu	Ser Leu Thr
1460	1465	1470
Lys Arg Glu Gly Pro Glu Thr	Leu Lys Lys Lys Tyr	Leu Val Gln
1475	1480	1485

His Gln Met Lys Cys Leu Thr	Ala Val Asp Cys Leu	Gln Ala Phe
1490	1495	1500
Trp Asp Met		
1505		

<210> 1095

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 4B

<400> 1095

Ile Gln Lys Lys Lys Gln Lys Ser Asn Leu Asp Leu Gln His Gln Arg

1 5 10 15

Arg Arg Lys Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro

20 25 30

Lys Ala Asn Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln Asn

35 40 45

Leu Leu Asn Leu Val Gln Leu Asn Pro His Ser Pro His His Arg Lys

50 55 60

Asp Glu Glu Asp His Gln Lys Arg His His His His Asn Gln Lys Lys

65 70 75 80

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

85 90 95

Gly Ser Leu Cys Gln Leu Val Ser Ala Asp Phe Ser Ala Pro Gln Val

100 105 110

Thr Arg Leu Arg Ser Leu Asn His Leu Leu Ile Asn Glu Gly Asn Asn

115 120 125

His Trp Pro Arg Val Glu Met Pro Thr Gly Trp Leu Leu Val Gly Tyr

130 135 140

Asn Thr Arg Asn Thr Ala Gln Asn Pro Arg Leu Gln Gln His Leu Lys

145 150 155 160

His Trp Gln Gln Cys Thr Arg Ala Arg Trp Cys Gln Glu Pro Cys Gln

165 170 175

Thr Leu Thr Phe Phe His Phe Phe Phe Phe Phe Lys Thr Val Ser Leu

180 185 190

Cys Cys Pro Gly Trp Ser Lys Gly Gln Pro Pro Pro Pro Gly Leu Lys

195 200 205

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

210 215 220

His Val Trp Leu Ile Cys Phe Val Phe Phe Val Cys Val Glu Thr Gly

225 230 235 240

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

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

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

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

 Lys Leu Ser Leu Gly Gly Lys Ala Gly Pro Gln Ala Gln Glu Lys Ala

	485		490		495										
Asn	Ala	Lys	Lys	Met	Pro	Phe	Gln	Arg	Trp	Ile	Phe	Ser	Asn	Gln	Leu
	500		505		510										
Thr	Val	Gln	Met	Leu	Cys	Leu	Pro	Ile	Glu	Ala	Leu	Thr	Ala	Leu	Phe
	515		520		525										
Thr	Cys	Arg	Thr	Ala	Ser	Ile	Ser	Val	Asn	Ile	Ser	Thr	Leu	Met	Ser
	530		535		540										
Ile	Leu	Glu	Ala	Pro	Leu	Phe	Phe	His	Gly	Asp	Leu	Cys	Glu	Glu	Lys
545			550		555				560						
Lys	Asn	Gly	Arg	Ile	Ser	Ser	Gln	Ala	Pro	Leu	Arg	Leu	Trp	Ser	Trp
	565		570		575										
Cys	Gly	Thr	Ser	Gln	Thr	Tyr	Phe	Gly	Ser	Thr	Ala	Lys	Lys	Ser	Pro
	580		585		590										
Thr	Ser	Phe	Cys	Cys	Glu	Trp	Gly	Gly	Gln	Ala	His	Arg	Gln	Arg	Asn
	595		600		605										
Thr	Gly	Met	Glu	Ile	Leu	Leu	Trp	Ile	Leu	Leu	Lys	Met	Glu	Ile	Gln
	610		615		620										
Ile	Phe	Lys	Ile	Cys	Leu	Gly	Glu	Met	Gln	Leu	Cys	Thr	Tyr	Thr	Pro
625			630		635				640						
His	Ile	Cys	Arg	His	Thr	Cys	Arg	Gly	Gly	Pro	Ser	Ala	Ser	Asp	Arg
	645		650		655										
Cys	Cys	Ser	Cys	Ser	Pro	Ser	Gly	Phe	Ser	Ala	Gly	Arg	Gly	Arg	Cys
	660		665		670										
Pro	Val	Gln	Gly	Cys	Leu	Arg	Pro	His	Arg	Val	Gln	Leu	Leu	Arg	Arg
	675		680		685										
Trp	Gly	Pro	Gly	Ser	Pro	Ala	Gly	Gln	Arg	Leu	Ser	Lys	Gly	Phe	Gln
	690		695		700										
Leu	Leu	Arg	Trp	Trp	Gly	Pro	Gly	Ser	Pro	Ala	Pro	Glu	Pro	Arg	Lys
705			710		715				720						
Gly	Pro	Phe	Pro	Pro	Pro	Asp	Pro	Pro	Trp	Pro	Val	Thr	Ala	Val	Thr
	725		730		735										

Val Met Ala Gly Ser Val Pro Ser Ala Gln Ser Val Asp Ala Leu Glu
740 745 750

Ser Pro Gly Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro Arg Asn Leu
755 760 765

Leu Trp Arg Glu Met Ser Ile Phe Leu Pro Gly Ile Phe Thr Ser Arg
770 775 780

Ile Leu Asn Leu Gln Val Leu Lys Lys Ile Leu Arg Ser Phe Met Lys
785 790 795 800

Leu Tyr His Ser Leu Val Met Cys Leu Arg Leu Arg Thr Lys Leu Glu
805 810 815

Lys Ala Leu Ser Ala Leu Phe Ile Trp Pro Gln His Ser Tyr Lys Gln
820 825 830

Arg Pro Pro Leu Gln Pro Val Gln Val Val Leu Arg Leu Gly Asn Leu
835 840 845

Pro Pro Phe Phe Arg Gly Ser Glu Val Pro Phe Pro Arg Pro Cys Arg
850 855 860

Thr Lys Met Leu Asn Gln Lys Cys Leu Ala Pro Phe Ile Thr His Pro
865 870 875 880

Phe Ala Ser Gln Pro Leu Gly Gln Glu Met Pro Asn Asn Thr Gln Ile
885 890 895

Arg Leu Leu Lys Pro Leu Leu Thr Pro Asp Thr Arg Trp Ile Phe Ser
900 905 910

Asn Gln Leu Gln Thr Val Gln Met Leu Cys Leu Pro Pro Leu Lys Gln
915 920 925

Gly Glu Arg Ile Ile Trp Pro Leu Gly Gly Phe Gln Ile Pro Asn Phe
930 935 940

Phe Trp Ser Leu Gly Ile Gly His Thr Gly Ala Trp Trp His Thr Gly
945 950 955 960

Arg Arg Arg Arg Glu Trp Gly Gly Ser Thr Val Ser Arg Ser Pro Leu
965 970 975

Trp Ile Ser Ser Met Ile Tyr Leu Arg Gly Met Ala Phe Ala Ser Asp

980	985	990
Ser Ser Ile Arg Thr Thr Arg Val	Ser Trp Cys Arg Arg	Cys Gly Ala
995	1000	1005
Lys Ser Ala Ala Ala Ser Ser	Leu Lys Lys Lys Pro	Arg Asp Ile
1010	1015	1020
Cys Arg Ile Ser Asp Ser Lys	Lys Met Thr Gln Lys	Arg Glu Ser
1025	1030	1035
Thr Leu Gly Asn Phe Trp Met	Lys Leu Leu Gln Leu	Pro Asp Lys
1040	1045	1050
Lys Lys Lys Ser Thr Glu Lys	Thr Lys Ile Ile Lys	Lys Met Lys
1055	1060	1065
Lys Arg Ile Met Val His Met	Cys Ser Ser Leu Ala	Leu Pro Thr
1070	1075	1080
Gly Leu Thr Ser Leu Ile Leu	Pro Ser Ser Asp Leu	Ala Val Leu
1085	1090	1095
Ile Ser Ser Ser Thr Ser His	Phe Leu Met Arg Ser	Pro Val Leu
1100	1105	1110
Pro Ser Ser Arg Leu Thr Cys	Ala Ser Pro Gln Leu	Pro Arg Met
1115	1120	1125
Trp Thr Trp Ser Ser Trp Leu	Lys Trp Leu Lys Asn	Trp Lys Arg
1130	1135	1140
Phe Lys Leu Lys Lys Lys Tyr	Ile Leu Ala Met Thr	Leu Thr Leu
1145	1150	1155
Asn Gly His Pro Arg Thr Ala	Ser Ile Thr Leu Pro	Thr Thr Ser
1160	1165	1170
Leu Lys Gly Ser Arg Thr Ser	Cys Cys Pro Arg Ser	His Pro Arg
1175	1180	1185
Leu Pro Arg Thr Lys Trp Pro	Leu Gln Cys Leu Leu	His Ser Leu
1190	1195	1200
Gly Thr Thr Gly Thr Leu Val	Trp Glu Arg Gly Val	Leu Gln Met
1205	1210	1215

Arg Ser	Leu Glu Ala His Cys	Pro Leu Gln Thr Phe	His Leu His
1220	1225	1230	
His Cys	Arg Thr Gln Pro Ser	Ser Cys Pro Pro Ala	Trp Ile Leu
1235	1240	1245	
Tyr Gln	Gly Gln Trp Ser Gly	Ala Val Val Gly Leu	Arg Pro Val
1250	1255	1260	
Ala His	His Leu Pro Arg Pro	Ile Gln Gly Leu His	Cys Pro Gln
1265	1270	1275	
Ala Pro	His Gln Pro Ala Leu	Ser Trp Gly Lys Trp	Pro Val Gly
1280	1285	1290	
Met Thr	Gly Pro Ala Arg Cys	Cys Arg Trp Pro Arg	Arg Glu Leu
1295	1300	1305	
Lys Lys	Asn Leu Leu Leu Pro	Cys Arg Cys Arg Arg	Glu Tyr Arg
1310	1315	1320	
Val Thr	Met Gly Gln Ala Phe	Gly Ser Phe Ser Ala	Asp Phe Ser
1325	1330	1335	
Ala Pro	Gln Val Leu Lys Lys	Asn Arg Lys Gln Asn	Lys Ile Ile
1340	1345	1350	
Cys Lys	Gly His Arg Ile Thr	Ser Leu Ile Leu Ser	Phe Gln Arg
1355	1360	1365	
Val Lys	Leu Lys Lys Lys Val	Asn Ala Cys Ser Pro	Ala Cys Thr
1370	1375	1380	
Ser Lys	Ala Trp Thr Pro Arg	Lys Leu Val Gly Arg	Ala Val Arg
1385	1390	1395	
Arg Lys	Gly Ile Ile Cys Ile	Lys Asn Met Phe Leu	Gln Arg Lys
1400	1405	1410	
Gly Phe	Leu Asn Leu Ser His	Val Glu Lys Phe Val	Pro Pro Ser
1415	1420	1425	
Pro Pro	Leu Ala Leu Gly Pro	Arg Met Gln Leu Cys	Thr Gln Leu
1430	1435	1440	
Ala Arg	Phe Phe Pro Ile Thr	Pro Pro Val Trp His	Ile Leu Gly

1445	1450	1455	
Pro Gln Arg His Thr Pro Cys Gln Lys Lys Val Pro Ser Ala Ser			
1460	1465	1470	
Pro Trp Gly Leu Arg Pro Ser Pro Cys Leu Ser Trp Ser Ser Arg			
1475	1480	1485	
Ile Val Ala Pro Gly His Ala Leu Ser Cys Arg Thr Arg Arg Arg			
1490	1495	1500	
Trp Ser Ser Lys			
1505			
<210> 1096			
<211> 4521			
<212> DNA			
<213> Artificial Sequence			
<220><223> polynucleotide 1A			
<400> 1096			
accgagatcc agctgacat gaacgacagc aagcacaagc tggaaagccc cgctctgaaa	60		
caggtgtcac cagcctctcc acctactcag cagcctcaga cacctcagga ttctagacag	120		
gtgctggccc tggccaagaa aacctgaca aatgcctcca gagccggaca gtttctgtg	180		
tggcggagaa caagcagagg catgagcctg cagtgggaagt ccggaatgc ctgcacacct	240		
ctgagatgcc ctacgagaag ccctgccaca ttctgacag ccctgaatgg ctggcacaga	300		
tctggcctga gagcccagat gcctagctct tggcttagca gcggcagaac actgaagctg	360		
gccccctgc aagtgaccac cactctgaag ctgatcctgg tcatgctgga aatcgtgacc	420		
gagcgtccc tgctgtactc cagaatgtgt ctggtgcaga tccccacaca cacctgggag	480		
cccgattact tcgtgtccct gcctatgatg ttcagctggg ccacacagtc ttttcccgtg	540		
ggcgccgtgt ttctgaccag acctgccatt ccttgctgca gctgtaccag ccacagcaac	600		
ccttgaggcc agagcaatca gcagctgaag tggaccctc acatcctgaa gtccgccagc	660		
ttcgacaaga aaggcttctg gatcctgagc cggcggagca agattgaggc ctctcctatc	720		
ggctctatcg ccagctctcc tggacatcct ctgggacct cactggccat cagattcatc	780		
agcggccctc agcctagcag ctctacagt acagctgccc ctagcggcca gtactttatc	840		
gccaagaagc ggatcaagct gcggcggaac aatatgggcg gcaacagatc catctgcctg	900		
accagaaagc gcaagagaga gaagcggagc cagaagtcca ggcaaacca tctgcagctg	960		

aaaagctgca gacggaagat cagcaactgg tccaagctga gaagcccctg gatcttcacc 1020
 aagtgcgaga tctgcgtgaa gaacaccgcc atcctggcta tcaccctgat caccctcag 1080
 gaccctcatc tggaccctgt gtgtcaccct catagaagge ctggatggaa gggccaccat 1140
 agagtgggtgt tctctacca tcttagcggc agcacaaaga gccactggca gcaaagagaa 1200
 cgcggaggcg gcagacgcga gaagaaggga ttagagaaac agcggaaagt ggtcaagaac 1260
 cctctcagc ccgtgcctct gagaaacgat ggcatcacca acggcaacga ctccaccaga 1320
 agctgctcca tcagcctgaa gaaaagcctg gaaaagatgc cctgatgcg gagagccaga 1380

 cctaccagct gtagcacctg tagaatgtgg tggaagggca agaaacggcg gaaagaaatc 1440
 gtgcctatga gcctggcctg cagcatcacc gtgtcttttg tgggacagat cagcacctg 1500
 gtgtggatg tgtctagcat cagccattgg cgctgcct gtaaagtac cgagagcagc 1560
 tccagcttct tctaccagc gcagaggacc cctctgagca tcagcagacc aaccagcaga 1620
 gctagacaga gctgttgtct gcccggactg acacaccctg ctaccaacc tctgggcagc 1680
 atgagacta gaagagagat gccaagccag gccacacctt ctccacctgg accttgaga 1740
 gccgctctgg gcaaagaagt gaagagatcc cagagcaagc tgcgctgag aaacacaagc 1800

 cctggggaga agaacgatct ccagctgttc gtgatgagcg acaccaccta caagatctac 1860
 tggacagtga tctgtctgaa cccctgcggc aacctgcacc tgaacaac atcactgcag 1920
 cgccacctc ggagcatcct gtctctgaat ggaatctggg aagtatgcc ccggacactg 1980
 gaaggctgca tcagcgtgaa ggatcacaga accagccaga accacagcaa gtgcatcacc 2040
 gaatgtgtgc ggactgccct gaactgttcc aagaagagac tgcctaagct gatgaagaag 2100
 aaggacagca ccatcttcat caacaaagtg cgccagaact tcaagcgcaa cttcaagaag 2160
 aagaaacccc tactttcag cccagcaga cggatgactc ggagaaccat gacaaccacc 2220

 aaaatgatga tgatgcggcg gaccaagcgg agaaggcgca aaaggcggag aatgaccatg 2280
 atgaccagac ggacctgtct gacaagaaa acctgtctga cccctagaac cagcgccgcc 2340
 acaaaagctc tgcctagaca gaccatcagc cagcggaggc ctattcagac cccacctgga 2400
 acatctctgg ccatctgggg cagaacaaga ctgacctga caggcaccag atccagcgga 2460
 acaagagcct ctcttccgc cgtgtgcctg tgtgttgga cctgtccaag cagaagcttc 2520
 ccagccgtt ctctagtgg actgagagca cctgttgag cccaggtcc tctgaagtg 2580
 acactgagag cctctgtgc ctctagcgc tctaaagcct gtgtggact ttggccttg 2640

 ggagcccaag ttcgagttgg agctggaaca ggcggaggac ctgcttgtgt tctgtggct 2700
 gaagcttcta caggcgcatg gacagctgaa ggcgccgtg gaacaagatg tagagcctct 2760
 agagccctt gccccaact tctgctagc tcccctacca agtgtgaaat ttgtgtgaag 2820

cgcagacggc ggagaaagag aagcagccag tctagaagcc ccgtgcctaa aaagcgcgag 2880
 aggatgatgc tgctgtgagc ggccagaaca gctagatctg cacttcctca gggcagagca 2940
 cctctggaag ggatgctgct tcttagagca ctgcctagcc tgctgagcag aatgcctgcc 3000
 agaagagagt cccggttttg gctggctctg caggcacttg gactcagacc tccacatctg 3060

 cctagctgtc atcctctgcc tcaactgttg ggccctccac ctctctatca ggccccaatg 3120
 aactgaagg ccttggttaa gacctggaca cagttccgca actaccccag agccgacaag 3180
 aagaatgtcc ggctaccgc cttcttctg ctggacatca tcctgggcga ttgccaaga 3240
 acaatggcgc gaccttctg ctctctgcat cctgcatctg gcagagcctc cagaaagacc 3300
 tggcagagaa ggctgagagc ttgtagagca ggcggacctg ctggatgggc tagacaggcc 3360
 tatcctagac tgaaacctt cggcgtgccc ctgggctcta ttctgtgtct ggccggcagc 3420
 ctgtccacaa tgatgatcat tagcaccacc agacaagagt gcggcaggcg ggcttctgtg 3480

 cctttagac ctatgatcgg aagcgcaga ccaggacctt ggccgacatc tgctatgcct 3540
 agtgccatgg gattcgccct gcctacctct tgtgaaagcg gaagatctcc tctgccacc 3600
 ggccgaagaa tgccaggatc tcatctatc atgatgagct ggatgcctcc actggctcca 3660
 tgtgccgtt gtccatgtc tccgctcct aactgtgcc cagcacatcc tgctagagca 3720
 ccaacagccg tgctgcctt tacacctctg tctgtctatc ctgtgccagt gctgtctgga 3780
 tgtcacctgg ccgtcagaac ctccatgtg aactgtctgc ccatggaagc caaaaagagc 3840
 atgaagcgtt ccaacgctaa gaaaatggaa gatatgatct gggagagccg gctgccactg 3900

 aggccacaaa gaggacctag acctctgcac agatggctgc agcagacaac cggctgtagc 3960
 cagaggcgga tcgtgttctt tctggcccca tacttccctc ggccacctca cagatctcca 4020
 ccaacatctt gccacctct gctggaagct ttccactgc caagagcttc tctgagggcc 4080
 acagtccaa gacatagctc tgttctgcc accggtctgc acctccacag acagatttct 4140
 ctgccccga gaggattcct cctgcacaa cactgccag gacagcatct gtggctgtct 4200
 cacagactga ggctgagact gccaggaca cagccatctt tgctggacc atgtgcaagc 4260
 ctgtgtcca cactgtctca gccaccact caggctccat ctcaagtgtg gactgccgt 4320

 aactgagat gtctgtctg tctgcagct gcctgtctc ctgtctgag atccatgcct 4380
 aagagccgga accaggtgct gttcagacgg aatctgacc caagccagct gagaacactg 4440
 gccccacctt atatgtctg gcccagtct ctgtccaga gcctgagtag aaagcagatc 4500
 cctagccagt ccatgtctg g 4521

<210> 1097

<211> 4503

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 2A

<400> 1097

agaaagatgc agagcctgaa tcacccacgc agactgacca atggctctcc tccactgcac	60
ctgtgccagc ctctgagaat gagcagaacc cctcctagaa gagtgtgcgc cgctcctcca	120
catagactgc tgggcccttc cagatggaac cctcggagaa agacctggaa gatgcggaag	180
aagtacgcc agaagcctag ccagaagaac cacctgtacg gcgcaagaa gcgctctaag	240
ttcagcagaa gccacctgga cttcagcccc tactggatga agaaagtga ggtgctgttc	300
aaggccgacc agagcgagtc tagcctgagc agcgggaagat gcagcctgat ggaacagatc	360
cctcacctga agtctcggcg gaagtggcag atcagacacg tgcgaagaa cctgtggctg	420
cccatgagaa gcctgggaga accttggaga gccggctttc agtggggaga gtctccttgg	480
caagtgatgg cctctctgac cggcagagcc acatttctgc tggccctttg ggaatgtagc	540
ctgcctcagg caagactgtg cctgatcgtg tctagaaccc tgctgctggt gcagagccgg	600
aacaagaaaa caaagctgtg gttcagcctg atcaacatcc accaccgga gaacccactg	660
ctgcctatga gatggtggtg taccagagcg gccggaaagc ggaaaaagaa aatgtgcaag	720
gtgtccggcg gctgcaccgc ctgtgttag agatgtcctt ggaaggcat ctgctggaag	780
tggcctgtga cagtggccgc cattagaatg tgtgccctgt ctaccctag cttctacatc	840
agcagcaccg tgtgtttct gagcaagcac tgcattgacc cctgcaccag aaagagaatg	900
aagaccggcg ccatccaaga gaaggcgct attcaagaga aaggggcat gaccaagcgg	960
atctgcgtgg tcaatttga gccctgcaga gagatgaaa gcctgagcgc ccctgagaag	1020
atcacctgt ttgaagccca catggcccgg tgcacctcca tcaatgtgct gtgtgtcgg	1080
gccagcctga ttgagaagct gatgaaagaa aagcgcaaga tgaagcggaa ccaggtggcc	1140
tctccacaga tcatgcagcg gctgttcac aagggtacc agaacaacca cttcaccttc	1200
catctgcaaa acttcgctt cttcagctcc ttggcaaca acaagtacat caatatcctg	1260
accatcctgt tccacgtgcg gaacatcgtg tacggcatcc aagtatgct gtgcgctagc	1320
cctcagatta tgcagagaac cagcggcgac cggttccgga tgaagagaag aatgcagaat	1380
ctggacaacc tggcggtgcc atggcctctg ttgcctggaa tccatctct gaacgccag	1440
tggatgttcc tgagaatcgc atccccgaa atcatgcaga ggatgagcgc cgtgaacttc	1500
gagacaatcc gggccagaaa ccggaacatg aagaaaacca tgagccacct gatcgcccat	1560
caggccctga agatgagcgg cctgagactg tttcaccca gactgctgac acggaagaag	1620

cccggaaaac tgctgctcgc ccatatgtac ggcttcagca cctacggcac ccagaaaggc 1680
 gagtgcgttt gtctgcagtg tctgagcggc agcagcctgt tcattctgaa gcagcccctg 1740
 gacctgaaga tcagcaagac cttcatgggc cacagagagg gcagcgagtc tgataatctg 1800

 ggccctgctgt atagcttccc tccaccttat cctatcagcg agggcctgac catgaccacc 1860
 ggacagaaaca tcaacagcaa ctccctgatg accaactgcc tgttcagccc catcttcctg 1920
 tgccaccacg ccatcatgca cagaaagatg acaagccctc acttcaggct gttcagcagc 1980
 aagatcccac atcctcaggt gccatctgtg gtggccctgt gcaagtccg ggcccttcac 2040
 cacacaccta gaagccctgg ctgcagcgtg tacgccaata tgtgctggcc caagtcttc 2100
 ctgaccttca gccagcagtg gtccagcgtg acatctctgg aatggacagc ccaagagaga 2160
 ggctgcagca gctggctgat gaagcagaca tggatgaagt cttggagcct gcgggacccc 2220

 agctacagat ccactctgga atacgtgtcc accagagtgc tgtggatgcc tacctctacc 2280
 gtgctgcagg ctcatccaca agttccagct ctggctcctc aagcctgggt gcctgctaga 2340
 agaggacctc tgacatctgc cccatccgtc cagcagtcctc tgaccagaga gaagattatc 2400
 aacccccacca tcagctgccc ctttcagagc cccaccaaga gactgatcta cctcctagc 2460
 acctgttctc tgcctgcag aggccttcctg cctagcagat ttccttgggg ccacctcct 2520
 ctgaacacgc tgatcgtgca caagatcgtg ctggtgttcc tgaagtcct gtccagctac 2580
 aactgcgagc ggagaatcag cggcatccag aagagagcca tcgagttcgc cgtgctgaaa 2640

 ctgctgaata tggacctgcc tctcgagaac acacagatcc ccagaacaag cccactgtgg 2700
 aagatcacia tgggtgtgac atacccaac tgcgtggtgc atgtgctgat gtttggcgcc 2760
 ctgagagcca cagctcctgc tacagctgca cctcaggctc agacccctca ttggagagct 2820
 gccacaacia gcagcatgag cagcagccct agagccgagc ctacatcttc tagctcttgg 2880
 gccacctgtt ggcccagatg ctgctccagc tcttgttact ggtcactgic tagctggcct 2940
 ccagctggcg ccgtgaagc tacaataacc agaaccagaa gccgcgagag ccagaggggt 3000
 agaatgctga cttggagaag ctccctgtgg ttgcagggca ccagatgttt tacaggcgtg 3060

 cggaccagct ccagatacaa gaaaagaggc gtgatcgctt ggccggagaca gatcaataga 3120
 cggaagctgc agagaaagaa gcactggaac agcgctacc tgggcagaa actgctggtc 3180
 acctgtatcc tgtatcccg gtggatcgtg acctccatgt gtcagtccea gagatggctg 3240
 accagacca caagtagatc tagcgccctg atgtggaccg agctgagcct ggaacctagg 3300
 attcctacc tgcacagca gaaaaccag cggacactgg aatccgccgg actgtttcct 3360
 ttgctgcaca cccagtgcga agagaagaaa agcagaaagc tgatgtccag ctgcacacac 3420

ccctgcacaa tgctgctgcc acagggatgt catcctgcct ggctgagccc tatctctgcc 3480

tgccaagac tgctgccata tccttttcac gtgctggctc tggaagtga ctttctctct 3540

ggaaccgcca tgcctcagat gcagttgcag gctctggcta tgtgggagaa aggctgggat 3600

aagcctggca ccagcctgca gtgctacctg aacagaagaa gaaacagccg gaagcagagc 3660

caggtgcaac tggccattca ggtgctgctc gtggacaagc acaagtactt tctgttcggc 3720

caaaagaaag gccacatgat ctttagcctg gccaacggcc tgtggtttaa cctgattttc 3780

aactcccga agaaactgct cgaggacatg aagcaaatg gcttcaccgg caaaggcctg 3840

acacaccccg tgcctctgaa gcggactctg cagaacaaaa gaaacaagaa tatcaaacgc 3900

gtcaaccaga agaagggcaa catcaagcgg aagtccatcc tgctgcacct gattgtgctg 3960

aatagccccg agagcaacct gatcctgatc cagcatggcg gcatcttcac ctttcggttc 4020

tgggtcgaga agctgtcctg gaacatctgc aagaacctga gcctgtacct ggacaagtgc 4080

gtgcagagac tgctgtacct gtacatcatc gagacaaacg tggtcgtgct gaacctgttt 4140

catgtgcccc tgaaccagat cttcatgatg gccttctacc tgaagtacac cgagaaggcc 4200

tgggtcatgg aactggaatg gctgatccaa cagcagtgtc atcagggcag ctgcggcaga 4260

gcttgttctt gtggaagagg ctgtggcacc cctagaggcg attggaagag acatcctcct 4320

cggagagcct tctggaagcc tcctagccag ggcatctcta gctgtctgat gaccggctgt 4380

tggctcgaga agaaagctac ctggatgcgg cggaccgcc ggaagaagag ggaagatcat 4440

tcgagactga gacacccag ctggccttgg acaagatgtc tgaggatgag gcctccaaga 4500

agc 4503

<210> 1098

<211> 4518

<212> PRT

<213> Artificial Sequence

<220><223> polynucleotide 3A

<400> 1098

Gly Gly Ala Gly Cys Thr Gly Cys Thr Gly Cys Thr Gly Cys Cys Thr

1 5 10 15

Cys Thr Thr Gly Thr Cys Ala Gly Thr Cys Thr Cys Cys Thr Cys Cys

20 25 30

Thr Thr Cys Thr Cys Cys Thr Cys Gly Gly Gly Ala Ala Ala Cys Cys

35 40 45

Ala Cys Ala Cys Cys Thr Ala Gly Cys Thr Cys Cys Gly Ala Cys Gly
 50 55 60
 Cys Cys Ala Cys Cys Ala Gly Ala Cys Gly Gly Ala Cys Ala Ala Gly
 65 70 75 80

Ala Cys Cys Thr Ala Thr Thr Gly Cys Cys Gly Cys Thr Cys Ala Gly
 85 90 95
 Ala Gly Cys Ala Ala Gly Ala Ala Ala Cys Cys Ala Thr Gly Ala
 100 105 110
 Cys Ala Gly Cys Cys Gly Cys Cys Gly Gly Ala Cys Thr Gly Ala Cys
 115 120 125
 Cys Cys Cys Thr Ala Thr Gly Ala Thr Cys Cys Gly Gly Ala Ala Gly
 130 135 140

Ala Thr Cys Cys Ala Gly Ala Ala Gly Cys Gly Gly Cys Gly Gly Ala
 145 150 155 160
 Gly Ala Ala Cys Cys Gly Cys Cys Ala Ala Cys Cys Gly Gly Thr Gly
 165 170 175
 Thr Cys Thr Gly Ala Gly Ala Gly Thr Thr Ala Gly Ala Thr Gly Thr
 180 185 190
 Gly Gly Cys Gly Gly Cys Thr Gly Gly Cys Thr Gly Thr Gly Thr Gly
 195 200 205

Gly Cys Thr Gly Gly Ala Cys Ala Cys Cys Thr Ala Gly Ala Gly Gly
 210 215 220
 Ala Cys Ala Gly Ala Ala Cys Ala Cys Cys Ala Gly Ala Ala Gly Cys
 225 230 235 240
 Ala Cys Cys Ala Ala Cys Cys Thr Gly Gly Ala Ala Ala Ala Gly Ala
 245 250 255
 Ala Cys Cys Cys Cys Ala Gly Cys Cys Thr Gly Ala Ala Gly Ala Ala
 260 265 270

Gly Cys Ala Gly Ala Gly Cys Cys Ala Gly Cys Gly Gly Ala Gly Ala
 275 280 285
 Gly Gly Ala Ala Ala Gly Cys Thr Gly Ala Gly Cys Ala Gly Cys Cys

290	295	300	
Thr Gly Thr Thr Cys Thr Thr Cys Ala Gly Cys Cys Ala Cys Thr Gly			
305	310	315	320
Cys Cys Thr Gly Thr Gly Cys Cys Gly Gly Ala Ala Cys Ala Gly Cys			
	325	330	335
Ala Gly Ala Ala Gly Gly Gly Cys Cys Ala Cys Ala Cys Cys Thr Ala			
	340	345	350
Cys Ala Thr Cys Thr Ala Ala Gly Gly Gly Cys Ala Gly Cys Cys Thr			
	355	360	365
Gly Cys Gly Gly Cys Gly Gly Ala Ala Gly Thr Ala Cys Cys Thr Gly			
	370	375	380
Ala Gly Ala Gly Thr Gly Cys Cys Thr Ala Thr Thr Cys Cys Thr Cys			
385	390	395	400
Cys Ala Cys Ala Cys Cys Thr Gly Ala Gly Ala Cys Ala Cys Cys Cys			
	405	410	415
Thr Cys Thr Gly Cys Thr Gly Cys Thr Gly Ala Thr Gly Gly Ala Cys			
	420	425	430
Cys Thr Gly Gly Ala Cys Gly Gly Ala Ala Thr Gly Cys Thr Gly Ala			
	435	440	445
Cys Cys Gly Thr Gly Ala Thr Cys Gly Gly Ala Cys Ala Gly Gly Gly			
	450	455	460
Ala Cys Thr Cys Gly Thr Gly Gly Gly Cys Ala Thr Gly Ala Cys Cys			
465	470	475	480
Cys Cys Thr Ala Gly Ala Gly Ala Thr Cys Thr Gly Gly Gly Ala Ala			
	485	490	495
Cys Ala Gly Thr Gly Gly Cys Thr Gly Gly Cys Gly Cys Cys Ala Cys			
	500	505	510
Cys Gly Cys Thr Cys Ala Gly Ala Thr Thr Cys Ala Gly Ala Gly Gly			
	515	520	525
Cys Cys Thr Ala Thr Thr Cys Ala Gly Gly Thr Gly Cys Ala Gly Ala			
	530	535	540

Cys Cys Gly Gly Cys Gly Gly Cys Ala Gly Ala Cys Thr Thr Ala Cys
 545 550 555 560
 Ala Cys Cys Thr Cys Cys Thr Cys Cys Thr Cys Thr Gly Ala Thr Thr
 565 570 575
 Cys Thr Gly Thr Gly Gly Cys Cys Thr Cys Ala Gly Gly Cys Cys Gly
 580 585 590

 Cys Thr Cys Cys Thr Gly Thr Thr Gly Ala Thr Cys Cys Thr Cys Cys
 595 600 605
 Thr Gly Gly Cys Thr Cys Thr Gly Thr Gly Thr Gly Gly Ala Thr Thr
 610 615 620
 Cys Thr Gly Cys Cys Cys Thr Gly Cys Ala Ala Gly Ala Ala Cys Ala
 625 630 635 640
 Ala Gly Ala Ala Gly Cys Gly Gly Ala Gly Ala Ala Ala Gly Cys Thr
 645 650 655

 Gly Cys Gly Gly Cys Cys Cys Ala Ala Gly Cys Gly Gly Cys Thr Gly
 660 665 670
 Gly Ala Cys Thr Thr Thr Cys Ala Cys Cys Cys Thr Ala Gly Ala Thr
 675 680 685
 Cys Thr Thr Cys Thr Ala Gly Cys Gly Gly Cys Gly Thr Gly Thr Cys
 690 695 700
 Cys Gly Thr Gly Ala Thr Cys Ala Cys Cys Ala Thr Gly Ala Ala Gly
 705 710 715 720

 Cys Thr Gly Thr Gly Gly Gly Ala Gly Ala Ala Gly Cys Ala Cys Thr
 725 730 735
 Thr Cys Ala Ala Gly Gly Gly Cys Cys Thr Gly Ala Ala Cys Thr Gly
 740 745 750
 Gly Ala Ala Cys Cys Thr Gly Gly Thr Cys Gly Thr Cys Thr Gly Gly
 755 760 765
 Ala Thr Thr Cys Thr Gly Ala Ala Cys Cys Thr Gly Ala Ala Gly Ala
 770 775 780

 Thr Gly Ala Thr Gly Ala Ala Cys Ala Thr Cys Gly Ala Gly Ala Thr

785 790 795 800
 Cys Ala Cys Cys Cys Cys Thr Cys Ala Gly Cys Gly Gly Ala Gly Cys
 805 810 815
 Ala Ala Gly Gly Cys Cys Ala Gly Ala Ala Ala Gly Thr Cys Cys Gly
 820 825 830
 Gly Cys Gly Thr Gly Ala Thr Gly Ala Ala Gly Thr Gly Cys Thr Gly
 835 840 845

 Gly Gly Ala Thr Cys Thr Gly Thr Gly Cys Cys Cys Cys Ala Gly Cys
 850 855 860
 Gly Ala Gly Ala Ala Gly Ala Ala Gly Ala Gly Gly Ala Ala Gly Cys
 865 870 875 880
 Thr Gly Cys Cys Thr Cys Thr Gly Cys Cys Thr Cys Thr Gly Ala Cys
 885 890 895
 Cys Thr Thr Cys Ala Gly Cys Ala Cys Cys Cys Thr Gly Cys Thr Gly
 900 905 910

 Thr Gly Gly Gly Ala Cys Thr Cys Thr Ala Gly Ala Cys Ala Thr Ala
 915 920 925
 Gly Ala Gly Gly Cys Gly Cys Cys Ala Gly Cys Thr Cys Cys Ala Gly
 930 935 940
 Cys Ala Cys Cys Ala Gly Cys Ala Gly Ala Gly Ala Cys Thr Cys Cys
 945 950 955 960
 Ala Gly Ala Ala Gly Cys Thr Thr Thr Thr Thr Cys Ala Cys Cys Ala
 965 970 975

 Gly Cys Gly Cys Thr Cys Ala Cys Cys Cys Cys Ala Gly Cys Ala Gly
 980 985 990
 Ala Cys Cys Cys Thr Gly Cys Ala Gly Ala Ala Thr Gly Ala Gly Ala
 995 1000 1005
 Cys Thr Gly Thr Ala Cys Cys Ala Gly Thr Thr Cys Cys Thr Gly
 1010 1015 1020
 Ala Thr Cys Cys Ala Cys Cys Thr Gly Ala Gly Ala Ala Ala Gly
 1025 1030 1035

Gly Thr	Gly Gly Ala Cys Ala	Cys Cys Cys Ala Cys	Cys Ala Thr
1040	1045	1050	
Cys Thr	Gly Cys Ala Gly Gly	Thr Cys Gly Thr Gly	Ala Cys Cys
1055	1060	1065	
Ala Ala	Gly Ala Cys Cys Gly	Thr Gly Ala Cys Ala	Gly Cys Cys
1070	1075	1080	
Ala Cys	Ala Ala Cys Ala Gly	Cys Thr Gly Ala Cys	Gly Gly Cys
1085	1090	1095	
Cys Ala	Gly Ala Gly Ala Ala	Thr Gly Cys Gly Gly	Ala Gly Ala
1100	1105	1110	
Cys Thr	Gly Ala Ala Gly Thr	Gly Cys Ala Ala Gly	Gly Cys Cys
1115	1120	1125	
Thr Gly	Cys Cys Gly Gly Cys	Thr Gly Ala Gly Ala	Thr Gly Gly
1130	1135	1140	
Gly Cys	Thr Ala Gly Ala Cys	Cys Thr Gly Ala Ala	Cys Cys Thr
1145	1150	1155	
Gly Cys	Thr Gly Cys Thr Cys	Ala Gly Gly Cys Cys	Cys Cys Thr
1160	1165	1170	
Cys Cys	Ala Ala Ala Gly Ala	Gly Cys Cys Ala Cys	Thr Thr Thr
1175	1180	1185	
Cys Cys	Ala Cys Cys Thr Cys	Ala Thr Cys Cys Thr	Ala Gly Cys
1190	1195	1200	
Gly Gly	Cys Cys Cys Thr Ala	Gly Cys Ala Gly Ala	Ala Cys Cys
1205	1210	1215	
Ala Gly	Thr Thr Cys Thr Cys	Thr Gly Cys Ala Gly	Cys Thr Gly
1220	1225	1230	
Cys Gly	Gly Ala Gly Cys Ala	Thr Cys Cys Cys Thr	Cys Ala Cys
1235	1240	1245	
Gly Thr	Gly Cys Cys Ala Ala	Ala Ala Gly Cys Cys	Ala Cys Ala
1250	1255	1260	
Gly Cys	Cys Gly Cys Thr Cys	Ala Cys Ala Gly Cys	Gly Thr Gly

1265	1270	1275
Ala Cys Ala Gly Thr Gly Ala	Ala Gly Cys Thr Gly	Cys Ala Gly
1280	1285	1290
Ala Ala Gly Gly Gly Ala Ala	Ala Gly Ala Ala Cys	Ala Gly Cys
1295	1300	1305
Cys Cys Cys Thr Gly Cys Thr	Gly Cys Cys Ala Ala	Ala Ala Gly
1310	1315	1320
Ala Ala Ala Cys Thr Gly Cys	Gly Gly Gly Thr Gly	Cys Ala Gly
1325	1330	1335
Ala Ala Thr Cys Ala Gly Gly	Gly Cys Cys Ala Thr	Cys Thr Gly
1340	1345	1350
Cys Thr Gly Ala Thr Gly Ala	Thr Cys Cys Thr Gly	Cys Thr Gly
1355	1360	1365
Cys Ala Cys Ala Ala Thr Ala	Cys Cys Thr Ala Cys	Ala Thr Gly
1370	1375	1380
Gly Ala Ala Ala Thr Gly Cys	Ala Cys Thr Ala Cys	Gly Gly Cys
1385	1390	1395
Cys Ala Thr Cys Ala Gly Gly	Cys Cys Cys Cys Ala	Cys Ala Gly
1400	1405	1410
Gly Thr Gly Gly Cys Cys Ala	Thr Gly Cys Thr Gly	Cys Cys Thr
1415	1420	1425
Ala Ala Gly Cys Thr Gly Cys	Thr Gly Thr Gly Cys	Ala Gly Ala
1430	1435	1440
Cys Ala Gly Ala Thr Gly Cys	Thr Gly Cys Cys Cys	Ala Cys Thr
1445	1450	1455
Cys Thr Gly Ala Gly Cys Ala	Cys Ala Cys Thr Gly	Cys Ala Gly
1460	1465	1470
Cys Ala Ala Ala Gly Ala Cys	Ala Cys Cys Cys Ala	Cys Ala Gly
1475	1480	1485
Gly Gly Cys Cys Cys Thr Thr	Gly Thr Cys Cys Thr	Cys Cys Ala
1490	1495	1500

Cys Cys Thr Gly Thr Gly Ala Cys Ala Cys Cys Ala Cys Thr Gly
 1505 1510 1515

Ala Gly Ala Gly Thr Cys Cys Ala Gly Thr Cys Thr Gly Thr Cys
 1520 1525 1530

Cys Thr Gly Cys Thr Gly Cys Thr Gly Gly Gly Ala Gly Thr Gly
 1535 1540 1545

Cys Cys Thr Cys Ala Gly Ala Cys Ala Gly Cys Thr Gly Cys Thr
 1550 1555 1560

Ala Gly Ala Cys Ala Gly Cys Cys Thr Ala Gly Cys Ala Gly Ala
 1565 1570 1575

Cys Cys Cys Ala Cys Cys Gly Gly Cys Ala Gly Ala Ala Cys Cys
 1580 1585 1590

Cys Cys Thr Ala Cys Cys Ala Cys Ala Ala Gly Ala Cys Thr Gly
 1595 1600 1605

Ala Thr Gly Gly Cys Cys Cys Cys Thr Gly Thr Cys Gly Gly Cys
 1610 1615 1620

Ala Gly Cys Gly Thr Gly Ala Thr Gly Ala Gly Cys Thr Gly Thr
 1625 1630 1635

Thr Cys Thr Cys Thr Gly Cys Thr Gly Ala Cys Cys Cys Ala Gly
 1640 1645 1650

Cys Cys Thr Thr Cys Thr Cys Cys Ala Gly Cys Cys Ala Gly Cys
 1655 1660 1665

Gly Cys Cys Thr Gly Thr Ala Cys Ala Ala Thr Gly Cys Cys Thr
 1670 1675 1680

Cys Cys Ala Cys Thr Gly Cys Thr Gly Cys Ala Thr Cys Cys Thr
 1685 1690 1695

Cys Ala Gly Thr Gly Gly Gly Cys Cys Cys Cys Ala Cys Ala Thr
 1700 1705 1710

Thr Cys Thr Gly Cys Thr Gly Gly Ala Thr Thr Gly Thr Cys Thr
 1715 1720 1725

Cys Cys Cys Gly Gly Cys Gly Cys Thr Thr Gly Cys Ala Gly Ala

1730	1735	1740
Cys Cys Thr Gly Cys Cys Thr Gly Thr Ala Cys Cys Thr Gly Thr		
1745	1750	1755
Ala Thr Cys Ala Gly Cys Ala Thr Gly Ala Cys Cys Ala Cys Cys		
1760	1765	1770
Ala Thr Cys Thr Cys Cys Ala Gly Ala Gly Cys Cys Ala Cys Cys		
1775	1780	1785
Thr Gly Gly Cys Ala Gly Gly Thr Thr Thr Cys Cys Gly Thr Gly		
1790	1795	1800
Thr Ala Cys Ala Gly Cys Gly Gly Cys Ala Ala Thr Cys Thr Gly		
1805	1810	1815
Cys Thr Gly Ala Gly Cys Thr Thr Cys Thr Cys Cys Ala Gly Ala		
1820	1825	1830
Cys Gly Gly Gly Gly Cys Ala Thr Gly Ala Ala Gly Ala Gly Thr		
1835	1840	1845
Ala Gly Cys Gly Thr Gly Cys Gly Gly Cys Thr Gly Ala Ala Ala		
1850	1855	1860
Ala Ala Cys Ala Gly Cys Cys Gly Gly Cys Gly Gly Ala Ala Cys		
1865	1870	1875
Ala Gly Ala Cys Gly Gly Thr Ala Cys Ala Gly Ala Ala Ala Gly		
1880	1885	1890
Ala Thr Cys Thr Ala Cys Gly Gly Cys Gly Ala Gly Cys Thr Gly		
1895	1900	1905
Ala Ala Gly Ala Thr Gly Thr Cys Cys Cys Thr Gly Cys Ala Gly		
1910	1915	1920
Gly Cys Cys Gly Thr Gly Gly Cys Thr Cys Cys Thr Ala Gly Ala		
1925	1930	1935
Thr Gly Thr Cys Cys Thr Ala Gly Ala Thr Cys Thr Gly Cys Cys		
1940	1945	1950
Gly Thr Gly Gly Ala Cys Ala Thr Cys Ala Gly Cys Cys Cys Cys		
1955	1960	1965

Gly Gly	Ala Cys Cys Thr	Ala Cys Cys Thr	Cys Thr	Cys Cys Thr
1970		1975		1980
Ala Gly	Cys Cys Thr Gly	Gly Gly	Cys Cys Thr	Cys Thr Thr Gly Thr
1985		1990		1995
Gly Cys	Cys Thr Cys Thr	Gly Thr	Gly Gly Cys Cys	Ala Thr Thr
2000		2005		2010
Gly Gly	Ala Ala Ala Ala	Cys Thr	Gly Gly Cys Cys	Cys Thr Gly
2015		2020		2025
Cys Thr	Thr Gly Gly Cys	Gly Cys Thr	Thr Cys Thr	Gly Cys Cys
2030		2035		2040
Cys Cys	Thr Thr Gly Thr	Gly Gly Thr	Gly Cys Thr	Gly Cys Thr
2045		2050		2055
Gly Gly	Cys Gly Cys Thr	Ala Gly Ala Gly	Gly Cys Thr	
2060		2065		2070
Gly Gly	Ala Ala Gly Ala	Thr Thr Thr	Gly Cys Cys	Gly Thr Gly
2075		2080		2085
Cys Thr	Gly Gly Gly Cys	Ala Cys Cys Ala	Thr Gly	Gly Thr Cys
2090		2095		2100
Ala Thr	Gly Ala Ala Gly	Cys Ala Cys Cys	Thr Gly	Ala Ala Cys
2105		2110		2115
Cys Gly	Cys Ala Ala Gly	Cys Thr	Gly Cys Ala	Thr Cys Thr Gly
2120		2125		2130
Ala Cys	Cys Cys Gly Gly	Thr Cys Cys Thr	Gly Cys	Cys Thr Gly
2135		2140		2145
Ala Thr	Cys Gly Ala Thr	Cys Thr	Gly Ala Cys Cys	Ala Thr Gly
2150		2155		2160
Ala Thr	Gly Ala Thr Gly	Ala Gly Cys Cys	Ala Gly	Ala Ala Gly
2165		2170		2175
Cys Thr	Cys Thr Gly Gly	Ala Ala Gly Ala	Ala Cys	Cys Ala Gly
2180		2185		2190
Cys Gly	Gly Ala Ala Gly	Ala Gly Ala	Ala Thr	Cys Cys Thr

2195	2200	2205
Cys Thr Gly Cys Cys Ala Thr	Cys Thr Cys Cys Thr	Ala Gly Ala
2210	2215	2220
Cys Ala Gly Cys Ala Thr Cys	Thr Gly Cys Thr Cys	Cys Cys Thr
2225	2230	2235
Cys Ala Gly Thr Ala Cys Cys	Cys Thr Cys Thr Gly	Cys Ala Cys
2240	2245	2250
Cys Cys Thr Cys Cys Thr Cys	Cys Ala Cys Cys Thr	Thr Gly Thr
2255	2260	2265
Cys Thr Gly Cys Thr Gly Cys	Thr Gly Cys Thr Cys	Cys Ala Cys
2270	2275	2280
Cys Ala Cys Ala Gly Ala Cys	Ala Cys Cys Ala Cys	Cys Thr Gly
2285	2290	2295
Gly Cys Cys Thr Thr Thr Cys	Thr Gly Gly Ala Ala	Ala Thr Gly
2300	2305	2310
Gly Cys Cys Thr Gly Cys Ala	Gly Cys Ala Gly Cys	Cys Ala Gly
2315	2320	2325
Cys Ala Cys Ala Cys Cys Cys	Ala Cys Thr Cys Cys	Ala Thr Cys
2330	2335	2340
Ala Ala Gly Ala Thr Cys Thr	Gly Gly Ala Thr Cys	Ala Gly Cys
2345	2350	2355
Thr Thr Thr Ala Gly Cys Cys	Ala Cys Gly Ala Gly	Cys Ala Gly
2360	2365	2370
Ala Gly Cys Ala Gly Cys Cys	Cys Ala Thr Thr Cys	Cys Thr Gly
2375	2380	2385
Gly Cys Cys Ala Gly Ala Thr	Cys Cys Thr Gly Gly	Ala Ala Cys
2390	2395	2400
Ala Cys Cys Ala Thr Gly Cys	Ala Gly Thr Gly Gly	Ala Ala Cys
2405	2410	2415
Ala Ala Cys Ala Ala Gly Ala	Ala Ala Ala Thr Gly	Gly Cys Cys
2420	2425	2430

Ala Thr Gly Ala Cys Ala Gly Thr Gly Ala Thr Cys Gly Cys Thr		
2435	2440	2445
Gly Gly Cys Gly Cys Cys Cys Ala Cys Cys Ala Cys Thr Gly Thr		
2450	2455	2460
Cys Ala Gly Thr Ala Cys Ala Ala Gly Cys Thr Gly Ala Cys Cys		
2465	2470	2475
Thr Ala Cys Ala Cys Cys Ala Ala Ala Gly Thr Gly Thr Gly Gly		
2480	2485	2490
Ala Ala Gly Ala Thr Gly Ala Ala Thr Thr Gly Gly Ala Ala Gly		
2495	2500	2505
Ala Ala Ala Ala Thr Gly Ala Thr Gly Ala Thr Cys Gly Gly Cys		
2510	2515	2520
Thr Cys Cys Cys Ala Gly Cys Ala Cys Cys Thr Cys Cys Thr Gly		
2525	2530	2535
Thr Thr Cys Ala Gly Cys Cys Cys Thr Cys Thr Gly Gly Ala Thr		
2540	2545	2550
Ala Gly Cys Thr Cys Thr Cys Cys Ala Cys Thr Gly Cys Ala Ala		
2555	2560	2565
Cys Thr Gly Cys Thr Gly Cys Thr Thr Cys Ala Cys Cys Cys Thr		
2570	2575	2580
Cys Ala Cys Gly Gly Cys Ala Ala Gly Ala Gly Ala Thr Gly Cys		
2585	2590	2595
Ala Ala Cys Cys Cys Thr Thr Gly Cys Thr Gly Cys Ala Gly Ala		
2600	2605	2610
Cys Thr Gly Ala Cys Ala Thr Gly Gly Ala Thr Gly Thr Cys Cys		
2615	2620	2625
Ala Thr Gly Cys Thr Gly Cys Ala Gly Ala Ala Ala Cys Ala Gly		
2630	2635	2640
Thr Gly Cys Thr Gly Cys Thr Ala Cys Ala Ala Cys Cys Thr Cys		
2645	2650	2655
Gly Thr Gly Ala Thr Cys Ala Ala Gly Cys Ala Cys Cys Cys Ala		

2660	2665	2670
Cys Thr Gly Ala Thr Cys Thr Thr Cys Ala Gly Ala Ala Thr Cys		
2675	2680	2685
Ala Ala Cys Cys Thr Gly Cys Gly Gly Ala Gly Ala Cys Ala Gly		
2690	2695	2700
Gly Gly Cys Ala Ala Gly Ala Cys Cys Ala Ala Gly Gly Ala Thr		
2705	2710	2715
Gly Gly Cys Gly Thr Thr Gly Thr Gly Cys Ala Gly Ala Gly Cys		
2720	2725	2730
Cys Thr Gly Gly Gly Cys Thr Thr Cys Cys Thr Gly Ala Ala Cys		
2735	2740	2745
Cys Ala Gly Cys Ala Gly Ala Thr Cys Ala Thr Cys Cys Thr Gly		
2750	2755	2760
Cys Ala Gly Ala Ala Ala Gly Ala Gly Thr Thr Cys Thr Thr Cys		
2765	2770	2775
Ala Thr Cys Thr Gly Cys Cys Thr Gly Cys Thr Cys Ala Thr Gly		
2780	2785	2790
Thr Thr Thr Ala Thr Cys Ala Ala Gly Cys Gly Gly Thr Gly Gly		
2795	2800	2805
Ala Ala Gly Cys Cys Thr Gly Cys Cys Gly Cys Cys Ala Cys Cys		
2810	2815	2820
Ala Ala Gly Ala Gly Ala Gly Ala Gly Thr Gly Gly Gly Ala Gly		
2825	2830	2835
Ala Ala Ala Cys Gly Cys Ala Ala Gly Cys Ala Gly Ala Thr Cys		
2840	2845	2850
Cys Thr Cys Gly Gly Cys Gly Gly Ala Gly Gly Cys Gly Gly Cys		
2855	2860	2865
Ala Ala Gly Thr Ala Cys Ala Ala Ala Gly Ala Gly Thr Ala Cys		
2870	2875	2880
Thr Thr Cys Cys Thr Gly Ala Ala Gly Cys Gly Cys Ala Thr Cys		
2885	2890	2895

Cys Thr Gly Ala Thr Thr Cys Gly Gly Ala Ala Gly Gly Cys Cys		
2900	2905	2910
Ala Thr Gly Ala Cys Thr Gly Thr Gly Cys Thr Gly Gly Cys Cys		
2915	2920	2925
Gly Gly Cys Gly Ala Cys Ala Ala Gly Ala Ala Ala Gly Gly Cys		
2930	2935	2940
Cys Thr Gly Gly Gly Cys Ala Gly Ala Thr Thr Cys Ala Thr Gly		
2945	2950	2955
Ala Gly Ala Thr Gly Cys Gly Thr Gly Cys Ala Gly Ala Gly Cys		
2960	2965	2970
Gly Ala Gly Ala Cys Ala Ala Ala Gly Gly Cys Cys Gly Thr Thr		
2975	2980	2985
Ala Gly Cys Cys Thr Gly Cys Ala Gly Cys Thr Cys Cys Cys Ala		
2990	2995	3000
Cys Thr Cys Gly Gly Ala Ala Gly Ala Gly Gly Cys Cys Cys Thr		
3005	3010	3015
Gly Thr Gly Thr Ala Cys Thr Ala Cys Gly Thr Gly Thr Gly Cys		
3020	3025	3030
Ala Ala Cys Cys Gly Gly Ala Thr Gly Ala Ala Cys Gly Thr Gly		
3035	3040	3045
Thr Cys Cys Ala Gly Cys Gly Thr Gly Cys Thr Gly Ala Ala Gly		
3050	3055	3060
Cys Cys Cys Thr Thr Cys Cys Thr Gly Thr Thr Cys Ala Cys Cys		
3065	3070	3075
Gly Thr Gly Cys Cys Thr Ala Thr Cys Gly Ala Gly Gly Ala Cys		
3080	3085	3090
Ala Thr Gly Ala Gly Ala Gly Ala Gly Thr Gly Cys Ala Cys Ala		
3095	3100	3105
Cys Thr Gly Gly Gly Cys Cys Gly Cys Ala Ala Cys Ala Gly Ala		
3110	3115	3120
Ala Thr Gly Ala Ala Thr Gly Thr Gly Thr Cys Cys Thr Cys Thr		

3125	3130	3135
Gly Thr Gly Cys Thr Gly Ala Ala Ala Cys Cys Cys Thr Gly Thr		
3140	3145	3150
Cys Thr Gly Ala Thr Cys Cys Cys Thr Gly Thr Gly Cys Cys Ala		
3155	3160	3165
Ala Thr Cys Gly Ala Cys Cys Thr Gly Cys Cys Thr Cys Gly Gly		
3170	3175	3180
Ala Thr Gly Cys Thr Gly Cys Cys Ala Ala Thr Cys Ala Gly Cys		
3185	3190	3195
Ala Gly Cys Cys Cys Ala Cys Thr Gly Cys Ala Cys Ala Gly Ala		
3200	3205	3210
Cys Cys Cys Cys Ala Gly Ala Thr Gly Cys Cys Ala Thr Thr Cys		
3215	3220	3225
Thr Gly Gly Ala Cys Cys Thr Gly Cys Ala Cys Cys Thr Thr Thr		
3230	3235	3240
Cys Cys Thr Gly Cys Cys Ala Cys Ala Ala Cys Ala Thr Gly Gly		
3245	3250	3255
Gly Gly Cys Ala Cys Cys Thr Gly Gly Gly Ala Gly Ala Cys Ala		
3260	3265	3270
Cys Cys Thr Thr Cys Thr Ala Cys Ala Thr Gly Gly Gly Gly Cys		
3275	3280	3285
Thr Gly Gly Cys Gly Gly Ala Cys Cys Thr Thr Thr Cys Gly Gly		
3290	3295	3300
Gly Gly Cys Cys Cys Thr Ala Gly Ala Ala Gly Ala Ala Ala Ala		
3305	3310	3315
Gly Thr Gly Cys Thr Gly Ala Thr Gly Gly Thr Gly Cys Thr Gly		
3320	3325	3330
Thr Gly Gly Cys Thr Gly Cys Cys Cys Gly Cys Cys Ala Ala Cys		
3335	3340	3345
Cys Ala Gly Ala Gly Thr Cys Thr Gly Cys Ala Gly Ala Ala Ala		
3350	3355	3360

Ala Gly Cys Cys Ala Ala Gly Thr Gly Thr Thr Cys Cys Ala Gly
3365 3370 3375

Thr Gly Gly Gly Thr Cys Cys Thr Gly Cys Gly Gly Ala Cys Cys
3380 3385 3390

Gly Ala Gly Ala Ala Cys Ala Thr Cys Cys Gly Gly Ala Ala Gly
3395 3400 3405

Cys Thr Gly Ala Thr Cys Thr Gly Gly Ala Cys Cys Ala Ala Gly
3410 3415 3420

Cys Ala Gly Cys Gly Gly Ala Gly Cys Thr Thr Cys Cys Thr Gly
3425 3430 3435

Thr Cys Thr Cys Thr Gly Thr Thr Cys Cys Cys Cys Ala Ala Gly
3440 3445 3450

Cys Thr Gly Ala Gly Ala Gly Cys Cys Ala Cys Cys Gly Ala Ala
3455 3460 3465

Cys Ala Gly Ala Thr Gly Ala Cys Cys Ala Ala Thr Gly Thr Gly
3470 3475 3480

Gly Gly Cys Thr Gly Cys Gly Cys Cys Thr Thr Cys Ala Gly Cys
3485 3490 3495

Gly Gly Cys Cys Gly Gly Ala Thr Thr Cys Thr Gly Cys Ala Thr
3500 3505 3510

Cys Ala Ala Cys Cys Thr Gly Ala Ala Ala Thr Gly Gly Cys Cys
3515 3520 3525

Gly Cys Cys Ala Thr Gly Cys Gly Gly Cys Thr Gly Ala Thr Gly
3530 3535 3540

Cys Cys Cys Ala Ala Gly Thr Thr Cys Cys Thr Gly Ala Ala Thr
3545 3550 3555

Ala Gly Cys Ala Cys Cys Ala Ala Cys Ala Gly Cys Thr Gly Gly
3560 3565 3570

Thr Gly Gly Ala Cys Cys Thr Gly Thr Ala Cys Cys Ala Ala Cys
3575 3580 3585

Cys Thr Gly Ala Gly Cys Gly Thr Gly Cys Cys Cys Ala Thr Gly

3590	3595	3600
Ala Thr Gly Cys Thr Gly Ala Cys Cys Ala Thr Thr Cys Thr Gly		
3605	3610	3615
Ala Thr Thr Thr Gly Gly Ala Ala Gly Cys Gly Gly Gly Thr Gly		
3620	3625	3630
Thr Thr Cys Ala Thr Thr Cys Thr Cys Cys Thr Gly Cys Thr Gly		
3635	3640	3645
Thr Cys Cys Gly Ala Cys Ala Ala Gly Ala Ala Gly Cys Thr Gly		
3650	3655	3660
Cys Thr Gly Ala Ala Gly Ala Ala Gly Thr Cys Thr Ala Gly Cys		
3665	3670	3675
Cys Ala Gly Cys Thr Gly Ala Gly Gly Cys Gly Gly Thr Cys Thr		
3680	3685	3690
Thr Gly Gly Ala Gly Ala Ala Ala Cys Gly Thr Gly Thr Cys Cys		
3695	3700	3705
Cys Gly Gly Ala Thr Cys Ala Gly Cys Cys Ala Cys Cys Ala Gly		
3710	3715	3720
Ala Thr Gly Ala Ala Gly Thr Gly Thr Cys Thr Gly Ala Cys Cys		
3725	3730	3735
Gly Cys Cys Gly Thr Gly Gly Ala Cys Thr Gly Thr Cys Thr Gly		
3740	3745	3750
Cys Ala Gly Gly Cys Cys Thr Thr Cys Thr Gly Gly Gly Ala Cys		
3755	3760	3765
Ala Thr Gly Ala Ala Cys Ala Thr Gly Gly Ala Ala Cys Ala Cys		
3770	3775	3780
Cys Gly Gly Cys Thr Gly Ala Cys Cys Ala Thr Gly Gly Ala Cys		
3785	3790	3795
Ala Gly Cys Gly Cys Cys Cys Thr Gly Ala Gly Cys Cys Thr Gly		
3800	3805	3810
Ala Cys Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Gly Gly Ala		
3815	3820	3825

Cys Cys Cys Gly Ala Gly Ala Cys Thr Thr Gly Cys Ala Ala Gly			
3830	3835	3840	
Ala Ala Gly Ala Ala Gly Cys Thr Cys Cys Thr Gly Cys Thr Gly			
3845	3850	3855	
Ala Ala Ala Cys Thr Gly Cys Thr Gly Ala Cys Ala Ala Thr Gly			
3860	3865	3870	
Ala Gly Cys Cys Thr Gly Ala Gly Cys Ala Ala Cys Ala Thr Cys			
3875	3880	3885	
Cys Thr Gly Ala Thr Gly Ala Ala Gly Thr Thr Cys Cys Gly Gly			
3890	3895	3900	
Cys Thr Gly Cys Gly Gly Cys Thr Gly Ala Gly Ala Ala Thr Cys			
3905	3910	3915	
Cys Cys Ala Ala Gly Cys Cys Thr Gly Ala Gly Gly Ala Ala Gly			
3920	3925	3930	
Thr Ala Thr Cys Gly Cys Cys Ala Gly Cys Ala Thr Cys Thr Gly			
3935	3940	3945	
Ala Ala Ala Ala Ala Gly Ala Cys Cys Ala Gly Cys Gly Cys Cys			
3950	3955	3960	
Ala Ala Gly Gly Gly Cys Gly Ala Gly Ala Ala Gly Cys Thr Gly			
3965	3970	3975	
Ala Ala Gly Cys Ala Cys Thr Gly Cys Thr Thr Thr Ala Ala Gly			
3980	3985	3990	
Gly Cys Thr Thr Gly Gly Gly Gly Cys Ala Gly Ala Gly Gly Cys			
3995	4000	4005	
Cys Cys Ala Cys Cys Thr Cys Thr Gly Cys Ala Cys Ala Cys Ala			
4010	4015	4020	
Ala Gly Ala Ala Gly Cys Cys Ala Gly Ala Ala Gly Ala Ala Ala			
4025	4030	4035	
Gly Ala Cys Cys Cys Thr Gly Cys Cys Gly Gly Cys Ala Ala Gly			
4040	4045	4050	
Cys Thr Gly Ala Ala Ala Ala Ala Ala Cys Thr Gly Ala Cys Cys			

4055	4060	4065
Ala Cys Ala Cys Thr Gly Ala Gly Cys Thr Thr Cys Gly Thr Gly		
4070	4075	4080
Cys Thr Gly Ala Thr Cys Gly Ala Gly Gly Ala Ala Cys Gly Gly		
4085	4090	4095
Cys Gly Gly Ala Ala Cys Cys Thr Gly Cys Ala Gly Cys Gly Gly		
4100	4105	4110
Ala Ala Thr Cys Thr Gly Ala Ala Ala Gly Thr Cys Cys Thr Gly		
4115	4120	4125
Thr Gly Gly Cys Thr Cys Ala Ala Gly Ala Ala Ala Ala Gly Cys		
4130	4135	4140
Ala Cys Cys Ala Ala Gly Ala Gly Cys Cys Gly Gly Thr Ala Thr		
4145	4150	4155
Cys Thr Gly Thr Thr Cys Thr Thr Cys Cys Thr Gly Ala Cys Cys		
4160	4165	4170
Gly Thr Gly Thr Gly Cys Gly Gly Cys Thr Thr Cys Thr Thr Cys		
4175	4180	4185
Gly Ala Gly Ala Ala Gly Ala Ala Ala Cys Gly Gly Cys Cys Thr		
4190	4195	4200
Gly Ala Gly Thr Gly Gly Cys Thr Gly Thr Cys Cys Thr Cys Cys		
4205	4210	4215
Ala Gly Ala Ala Ala Gly Ala Ala Gly Gly Gly Ala Cys Ala Cys		
4220	4225	4230
Ala Cys Ala Ala Ala Gly Ala Ala Thr Cys Gly Gly Ala Gly Gly		
4235	4240	4245
Ala Ala Gly Gly Cys Cys Ala Ala Gly Cys Gly Gly Ala Ala Gly		
4250	4255	4260
Cys Cys Cys Cys Ala Gly Ala Thr Cys Gly Thr Gly Cys Ala Cys		
4265	4270	4275
Ala Ala Gly Ala Ala Gly Ala Gly Ala Gly Gly Cys Cys Thr Gly		
4280	4285	4290

Thr Thr Cys Cys Thr Cys Ala Ala Ala Ala Ala Gly Ala Ala Ala		
4295	4300	4305
Thr Ala Cys Cys Thr Gly Gly Thr Gly Cys Ala Gly Gly Gly Cys		
4310	4315	4320
Gly Cys Cys Ala Ala Gly Ala Ala Gly Ala Thr Cys Ala Cys Cys		
4325	4330	4335
Thr Thr Cys Cys Thr Gly Thr Cys Cys Ala Ala Cys Gly Gly Cys		
4340	4345	4350
Ala Thr Gly Gly Ala Ala Gly Cys Thr Thr Gly Cys Gly Gly Cys		
4355	4360	4365
Ala Cys Ala Cys Ala Cys Cys Cys Cys Ala Cys Ala Cys Cys Ala		
4370	4375	4380
Ala Gly Ala Cys Thr Gly Ala Gly Cys Gly Ala Cys Ala Gly Ala		
4385	4390	4395
Gly Thr Gly Thr Thr Cys Cys Thr Gly Gly Thr Cys Ala Ala Gly		
4400	4405	4410
Ala Thr Cys Ala Cys Cys Ala Cys Cys Ala Cys Cys Ala Cys Ala		
4415	4420	4425
Ala Gly Cys Ala Gly Cys Cys Cys Cys Ala Gly Ala Ala Gly Ala		
4430	4435	4440
Ala Gly Cys Cys Cys Ala Gly Cys Ala Cys Thr Gly Ala Gly Ala		
4445	4450	4455
Gly Cys Thr Ala Gly Ala Gly Gly Cys Gly Gly Cys Ala Cys Cys		
4460	4465	4470
Ala Cys Ala Ala Thr Thr Gly Gly Cys Gly Ala Ala Gly Thr Gly		
4475	4480	4485
Ala Cys Cys Ala Gly Cys Cys Thr Gly Thr Gly Cys Thr Thr Cys		
4490	4495	4500
Thr Thr Cys Thr Ala Cys Cys Thr Gly Cys Thr Gly Thr Ala Cys		
4505	4510	4515

<210> 1099

<211> 4521

<212> PRT

<213> Artificial Sequence

<220><223> polynucleotide 4A

<400> 1099

Ala Thr Cys Cys Ala Gly Ala Ala Gly Ala Ala Gly Ala Ala Ala Cys

1 5 10 15

Ala Gly Ala Ala Ala Thr Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala

20 25 30

Gly Ala Ala Gly Thr Cys Cys Cys Ala Gly Cys Ala Gly Cys Cys Thr

35 40 45

Cys Thr Gly Gly Thr Gly Cys Thr Gly Ala Ala Gly Ala Ala Gly Ala

50 55 60

Ala Cys Cys Gly Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Gly

65 70 75 80

Gly Gly Gly Ala Gly Gly Ala Cys Ala Gly Gly Cys Cys Cys Ala Cys

85 90 95

Ala Gly Ala Cys Ala Gly Ala Gly Ala Ala Ala Cys Ala Ala Cys Gly

100 105 110

Cys Cys Ala Ala Gly Ala Ala Gly Ala Thr Gly Cys Cys Cys Thr Thr

115 120 125

Cys Cys Ala Ala Gly Ala Gly Gly Ala Ala Ala Ala Gly Ala Ala Gly

130 135 140

Ala Ala Cys Gly Gly Cys Cys Gly Gly Ala Thr Cys Ala Gly Cys Ala

145 150 155 160

Gly Cys Ala Gly Cys Cys Thr Gly Ala Thr Cys Cys Thr Gly Ala Gly

165 170 175

Cys Thr Thr Cys Cys Ala Gly Ala Gly Ala Gly Thr Gly Ala Ala Gly

180 185 190

Gly Ala Cys Ala Gly Cys Ala Ala Gly Ala Ala Ala Ala Thr Gly Ala

195 200 205

Cys Cys Cys Ala Gly Ala Ala Gly Ala Thr Gly Thr Gly Cys Ala Gly

210 215 220
 Cys Thr Cys Thr Cys Thr Gly Gly Cys Cys Cys Thr Gly Cys Cys Thr
 225 230 235 240

 Ala Cys Ala Gly Gly Cys Cys Thr Gly Ala Cys Ala Thr Cys Thr Cys
 245 250 255
 Thr Gly Ala Thr Cys Cys Thr Gly Cys Cys Thr Ala Gly Cys Ala Gly
 260 265 270
 Cys Gly Ala Thr Cys Thr Gly Gly Cys Cys Gly Thr Gly Cys Thr Gly
 275 280 285
 Ala Thr Cys Thr Cys Thr Ala Gly Cys Ala Gly Cys Ala Cys Cys Ala
 290 295 300

 Gly Cys Cys Ala Cys Thr Thr Thr Cys Thr Gly Ala Thr Gly Cys Gly
 305 310 315 320
 Gly Ala Gly Cys Cys Cys Thr Gly Thr Gly Cys Thr Gly Cys Cys Ala
 325 330 335
 Ala Gly Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Ala Cys Ala Thr
 340 345 350
 Gly Thr Gly Cys Cys Thr Cys Thr Cys Cys Ala Cys Ala Gly Cys Thr
 355 360 365

 Gly Cys Cys Cys Cys Gly Gly Ala Thr Gly Thr Gly Gly Ala Cys Ala
 370 375 380
 Thr Gly Gly Thr Cys Thr Ala Gly Cys Thr Gly Gly Cys Thr Gly Ala
 385 390 395 400
 Ala Gly Cys Ala Cys Cys Cys Cys Ala Gly Ala Ala Cys Cys Gly Cys
 405 410 415
 Thr Ala Gly Cys Ala Thr Cys Ala Cys Ala Cys Thr Gly Cys Cys Thr
 420 425 430

 Ala Cys Cys Ala Cys Ala Ala Gly Cys Cys Thr Gly Ala Ala Gly Gly
 435 440 445
 Gly Cys Ala Gly Cys Ala Gly Ala Ala Cys Cys Ala Gly Cys Thr Gly
 450 455 460

Cys Thr Gly Cys Cys Cys Ala Ala Gly Ala Thr Cys Thr Cys Ala Cys
 465 470 475 480
 Cys Cys Cys Ala Gly Ala Cys Thr Gly Cys Cys Thr Ala Gly Gly Ala
 485 490 495

 Cys Cys Ala Ala Gly Thr Gly Gly Cys Cys Thr Cys Thr Gly Cys Ala
 500 505 510
 Gly Thr Gly Thr Cys Thr Gly Cys Thr Gly Cys Ala Cys Ala Gly Cys
 515 520 525
 Cys Thr Gly Gly Gly Ala Ala Cys Ala Ala Cys Ala Gly Gly Cys Ala
 530 535 540
 Cys Ala Cys Thr Cys Gly Thr Thr Thr Gly Gly Gly Ala Ala Ala Gly
 545 550 555 560

 Gly Gly Gly Cys Gly Thr Gly Cys Thr Gly Cys Ala Gly Ala Thr Gly
 565 570 575
 Ala Gly Ala Ala Gly Cys Cys Thr Cys Gly Ala Ala Gly Cys Cys Cys
 580 585 590
 Ala Thr Thr Gly Thr Cys Cys Thr Cys Thr Gly Cys Ala Gly Ala Cys
 595 600 605
 Cys Thr Thr Cys Cys Ala Thr Cys Thr Gly Cys Ala Cys Cys Ala Cys
 610 615 620

 Thr Gly Cys Ala Gly Ala Ala Cys Cys Cys Ala Gly Cys Cys Ala Ala
 625 630 635 640
 Gly Cys Thr Cys Thr Thr Gly Thr Cys Cys Thr Cys Cys Thr Gly Cys
 645 650 655
 Cys Thr Gly Gly Ala Thr Thr Cys Thr Gly Thr Ala Cys Cys Ala Ala
 660 665 670
 Gly Gly Cys Cys Ala Gly Thr Gly Gly Ala Gly Cys Gly Gly Ala Gly
 675 680 685

 Cys Cys Gly Thr Cys Gly Thr Thr Gly Gly Ala Cys Thr Thr Ala Gly
 690 695 700
 Ala Cys Cys Cys Gly Thr Gly Gly Cys Thr Cys Ala Cys Cys Ala Thr

705	710	715	720
Cys Thr Gly Cys Cys Thr Ala Gly Ala Cys Cys Thr Ala Thr Cys Cys			
	725	730	735
Ala Gly Gly Gly Cys Cys Thr Gly Cys Ala Cys Thr Gly Thr Cys Cys			
	740	745	750
Thr Cys Ala Gly Gly Cys Thr Cys Cys Thr Cys Ala Thr Cys Ala Ala			
	755	760	765
Cys Cys Thr Gly Cys Thr Cys Thr Gly Ala Gly Cys Thr Gly Gly Gly			
	770	775	780
Gly Ala Ala Ala Gly Thr Gly Gly Cys Cys Cys Gly Thr Gly Gly Gly			
785	790	795	800
Ala Ala Thr Gly Ala Cys Ala Gly Gly Ala Cys Cys Thr Gly Cys Cys			
	805	810	815
Ala Gly Ala Thr Gly Cys Thr Gly Thr Cys Gly Gly Thr Gly Gly Cys			
	820	825	830
Cys Cys Cys Gly Cys Ala Gly Ala Thr Cys Thr Cys Ala Gly Ala Ala			
	835	840	845
Gly Thr Cys Thr Cys Ala Gly Cys Ala Thr Cys Ala Cys Thr Gly Cys			
	850	855	860
Gly Cys Cys Cys Thr Gly Cys Gly Gly Ala Ala Gly Ala Thr Cys Gly			
865	870	875	880
Ala Gly Thr Gly Gly Gly Cys Cys Ala Cys Ala Ala Ala Ala Cys Thr			
	885	890	895
Gly Thr Cys Thr Cys Thr Cys Gly Gly Cys Gly Gly Ala Ala Ala Ala			
	900	905	910
Gly Cys Cys Gly Gly Ala Cys Cys Ala Cys Ala Gly Gly Cys Thr Cys			
	915	920	925
Ala Ala Gly Ala Gly Ala Ala Gly Gly Cys Cys Ala Gly Ala Cys Cys			
	930	935	940
Thr Thr Cys Thr Cys Cys Thr Thr Gly Cys Cys Thr Gly Thr Cys Cys			
945	950	955	960

Thr	Gly	Gly	Thr	Cys	Cys	Ala	Gly	Cys	Ala	Gly	Ala	Ala	Thr	Thr	Gly		
				965						970						975	
Thr	Gly	Gly	Cys	Cys	Cys	Cys	Thr	Gly	Gly	Ala	Cys	Ala	Cys	Gly	Cys		
				980						985						990	
Cys	Cys	Thr	Gly	Ala	Gly	Cys	Thr	Gly	Thr	Cys	Gly	Gly	Ala	Cys	Thr		
				995						1000						1005	
Cys	Gly	Thr	Ala	Gly	Ala	Ala	Gly	Ala	Thr	Gly	Gly	Thr	Cys	Cys			
				1010						1015						1020	
Thr	Cys	Cys	Ala	Ala	Gly	Thr	Gly	Cys	Ala	Gly	Ala	Gly	Gly	Cys			
				1025						1030						1035	
Gly	Gly	Cys	Cys	Cys	Thr	Ala	Gly	Cys	Gly	Cys	Cys	Ala	Gly	Cys			
				1040						1045						1050	
Gly	Ala	Thr	Ala	Gly	Ala	Thr	Gly	Thr	Thr	Gly	Thr	Ala	Gly	Cys			
				1055						1060						1065	
Thr	Gly	Thr	Ala	Gly	Cys	Cys	Cys	Cys	Ala	Gly	Cys	Gly	Gly	Cys			
				1070						1075						1080	
Thr	Thr	Cys	Ala	Gly	Cys	Gly	Cys	Cys	Gly	Gly	Ala	Ala	Gly	Ala			
				1085						1090						1095	
Gly	Gly	Cys	Ala	Gly	Ala	Thr	Gly	Thr	Cys	Cys	Thr	Gly	Thr	Gly			
				1100						1105						1110	
Cys	Ala	Gly	Gly	Gly	Ala	Thr	Gly	Thr	Cys	Thr	Gly	Ala	Gly	Gly			
				1115						1120						1125	
Cys	Cys	Ala	Cys	Ala	Cys	Ala	Gly	Ala	Gly	Thr	Thr	Cys	Ala	Gly			
				1130						1135						1140	
Cys	Thr	Gly	Cys	Thr	Gly	Ala	Gly	Ala	Ala	Gly	Ala	Thr	Gly	Gly			
				1145						1150						1155	
Gly	Gly	Cys	Cys	Cys	Ala	Gly	Gly	Ala	Thr	Cys	Thr	Cys	Cys	Thr			
				1160						1165						1170	
Gly	Cys	Thr	Gly	Gly	Cys	Cys	Ala	Gly	Ala	Gly	Ala	Cys	Thr	Gly			
				1175						1180						1185	
Thr	Cys	Thr	Ala	Ala	Gly	Gly	Gly	Cys	Thr	Thr	Cys	Cys	Ala	Ala			

1190	1195	1200
Cys Thr Gly Cys Thr Gly Cys Gly Thr Thr Gly Gly Thr Gly Gly		
1205	1210	1215
Gly Gly Ala Cys Cys Thr Gly Gly Ala Thr Cys Thr Cys Cys Ala		
1220	1225	1230
Gly Cys Thr Cys Cys Thr Gly Ala Gly Cys Cys Thr Ala Gly Ala		
1235	1240	1245
Ala Ala Gly Gly Gly Cys Cys Cys Ala Thr Thr Thr Cys Cys Thr		
1250	1255	1260
Cys Cys Ala Cys Cys Thr Gly Ala Thr Cys Cys Thr Cys Cys Ala		
1265	1270	1275
Thr Gly Gly Cys Cys Thr Gly Thr Gly Ala Cys Cys Gly Cys Thr		
1280	1285	1290
Gly Thr Gly Ala Cys Ala Gly Thr Gly Ala Thr Gly Gly Cys Thr		
1295	1300	1305
Gly Gly Cys Thr Cys Thr Gly Thr Gly Cys Cys Thr Ala Gly Cys		
1310	1315	1320
Gly Cys Ala Cys Ala Gly Thr Cys Thr Gly Thr Gly Gly Ala Thr		
1325	1330	1335
Gly Cys Cys Cys Thr Gly Gly Ala Ala Thr Cys Thr Cys Cys Thr		
1340	1345	1350
Gly Gly Ala Cys Cys Thr Cys Thr Gly Gly Cys Thr Cys Thr Gly		
1355	1360	1365
Gly Ala Ala Gly Gly Cys Cys Cys Thr Ala Gly Cys Ala Gly Cys		
1370	1375	1380
Cys Cys Thr Ala Gly Ala Ala Ala Cys Cys Thr Gly Cys Thr Gly		
1385	1390	1395
Thr Gly Gly Cys Gly Gly Gly Ala Ala Ala Thr Gly Ala Gly Cys		
1400	1405	1410
Ala Thr Cys Thr Thr Thr Cys Thr Gly Cys Cys Cys Gly Gly Cys		
1415	1420	1425

Ala Thr Cys Thr Thr Cys Thr Gly Cys Cys Ala Ala Ala Ala Gly		
1430	1435	1440
Ala Ala Gly Gly Thr Gly Cys Cys Ala Thr Cys Thr Gly Cys Cys		
1445	1450	1455
Ala Gly Cys Cys Cys Cys Thr Gly Gly Gly Gly Ala Cys Thr Thr		
1460	1465	1470
Gly Thr Thr Cys Cys Thr Cys Cys Thr Thr Cys Thr Cys Cys Ala		
1475	1480	1485
Cys Cys Ala Cys Thr Cys Gly Cys Thr Cys Thr Gly Gly Gly Cys		
1490	1495	1500
Cys Cys Thr Ala Gly Ala Ala Thr Gly Cys Ala Gly Cys Thr Gly		
1505	1510	1515
Thr Gly Thr Ala Cys Cys Cys Ala Gly Cys Thr Cys Gly Cys Cys		
1520	1525	1530
Ala Gly Ala Thr Thr Cys Thr Thr Cys Cys Cys Cys Ala Thr Cys		
1535	1540	1545
Ala Cys Ala Cys Cys Thr Cys Cys Ala Gly Thr Gly Thr Gly Gly		
1550	1555	1560
Cys Ala Cys Ala Thr Cys Cys Thr Gly Gly Gly Ala Cys Cys Thr		
1565	1570	1575
Cys Ala Gly Ala Gly Ala Cys Ala Cys Ala Cys Ala Cys Cys Thr		
1580	1585	1590
Cys Ala Gly Gly Thr Gly Gly Thr Cys Cys Thr Gly Ala Gly Ala		
1595	1600	1605
Cys Thr Gly Gly Gly Cys Ala Ala Cys Cys Thr Gly Cys Cys Thr		
1610	1615	1620
Cys Cys Ala Thr Thr Cys Thr Thr Cys Ala Gly Ala Gly Gly Cys		
1625	1630	1635
Ala Gly Cys Gly Ala Gly Gly Thr Gly Cys Cys Cys Thr Thr Thr		
1640	1645	1650
Cys Cys Thr Ala Gly Ala Cys Cys Thr Thr Gly Cys Cys Gly Gly		

1655	1660	1665
Ala Cys Cys Ala Ala Gly Ala	Ala Cys Gly Ala Gly	Gly Gly Cys
1670	1675	1680
Ala Ala Cys Ala Ala Thr Cys	Ala Cys Thr Gly Gly	Cys Cys Cys
1685	1690	1695
Ala Gly Ala Gly Thr Gly Gly	Ala Ala Ala Thr Gly	Cys Cys Thr
1700	1705	1710
Ala Cys Cys Gly Gly Cys Thr	Gly Gly Cys Thr Gly	Cys Thr Cys
1715	1720	1725
Gly Thr Gly Gly Gly Cys Thr	Ala Cys Ala Ala Cys	Ala Cys Cys
1730	1735	1740
Ala Gly Ala Ala Ala Cys Ala	Cys Ala Gly Cys Cys	Cys Ala Gly
1745	1750	1755
Ala Ala Thr Cys Cys Thr Cys	Gly Gly Cys Thr Gly	Cys Ala Gly
1760	1765	1770
Cys Ala Gly Cys Ala Thr Cys	Thr Gly Ala Ala Ala	Cys Ala Cys
1775	1780	1785
Thr Gly Gly Cys Ala Gly Cys	Ala Gly Thr Gly Cys	Ala Cys Ala
1790	1795	1800
Cys Gly Gly Gly Cys Cys Ala	Gly Ala Thr Gly Gly	Thr Gly Thr
1805	1810	1815
Cys Ala Ala Gly Ala Gly Cys	Cys Thr Thr Gly Thr	Cys Ala Gly
1820	1825	1830
Ala Cys Cys Cys Thr Gly Ala	Cys Cys Thr Thr Cys	Thr Thr Cys
1835	1840	1845
Cys Ala Cys Thr Thr Cys Thr	Thr Cys Thr Thr Cys	Thr Thr Thr
1850	1855	1860
Thr Thr Cys Ala Ala Ala Ala	Cys Gly Gly Thr Gly	Thr Cys Cys
1865	1870	1875
Cys Thr Gly Thr Gly Thr Thr	Gly Thr Cys Cys Cys	Gly Gly Cys
1880	1885	1890

Thr	Gly	Gly	Thr	Cys	Cys	Ala	Ala	Ala	Gly	Gly	Ala	Cys	Ala	Ala
1895						1900						1905		

Cys	Cys	Thr	Cys	Cys	Ala	Cys	Cys	Thr	Cys	Cys	Thr	Gly	Gly	Cys
1910						1915						1920		

Cys	Thr	Gly	Ala	Ala	Gly	Cys	Cys	Thr	Thr	Cys	Thr	Ala	Gly	Cys
1925						1930						1935		

Cys	Thr	Gly	Gly	Cys	Thr	Thr	Cys	Thr	Cys	Ala	Gly	Gly	Thr	Gly
1940						1945						1950		

Gly	Cys	Cys	Ala	Gly	Ala	Ala	Cys	Cys	Ala	Cys	Ala	Gly	Gly	Cys
1955						1960						1965		

Gly	Thr	Gly	Thr	Ala	Cys	Cys	Ala	Gly	Cys	Ala	Cys	Gly	Thr	Gly
1970						1975						1980		

Thr	Gly	Gly	Cys	Thr	Gly	Ala	Thr	Cys	Thr	Gly	Cys	Thr	Thr	Cys
1985						1990						1995		

Gly	Thr	Gly	Thr	Thr	Cys	Thr	Thr	Cys	Gly	Thr	Gly	Thr	Gly	Cys
2000						2005						2010		

Gly	Thr	Gly	Gly	Ala	Ala	Ala	Cys	Cys	Gly	Gly	Cys	Thr	Thr	Cys
2015						2020						2025		

Thr	Gly	Thr	Cys	Ala	Cys	Gly	Thr	Gly	Gly	Cys	Ala	Cys	Ala	Ala
2030						2035						2040		

Gly	Thr	Gly	Gly	Gly	Cys	Cys	Thr	Cys	Gly	Ala	Gly	Ala	Gly	Ala
2045						2050						2055		

Cys	Thr	Gly	Gly	Thr	Thr	Thr	Cys	Thr	Cys	Thr	Gly	Ala	Gly	Cys
2060						2065						2070		

Gly	Gly	Cys	Ala	Thr	Cys	Ala	Cys	Cys	Gly	Ala	Cys	Gly	Thr	Gly
2075						2080						2085		

Ala	Ala	Cys	Cys	Ala	Thr	Thr	Gly	Gly	Gly	Cys	Cys	Cys	Ala	Gly
2090						2095						2100		

Cys	Cys	Thr	Ala	Ala	Gly	Cys	Cys	Ala	Thr	Cys	Thr	Cys	Cys	Thr
2105						2110						2115		

Ala	Gly	Cys	Ala	Ala	Ala	Gly	Gly	Cys	Ala	Cys	Cys	Gly	Gly	Cys

2120	2125	2130
Ala Thr Gly Ala Ala Cys Ala Gly Ala Cys Cys Cys Ala Thr Cys		
2135	2140	2145
Gly Gly Cys Cys Thr Gly Ala Gly Ala Gly Thr Thr Gly Gly Cys		
2150	2155	2160
Ala Ala Ala Gly Gly Cys Gly Thr Gly Thr Gly Gly Gly Cys Cys		
2165	2170	2175
Ala Gly Ala Cys Thr Gly Cys Thr Cys Ala Ala Gly Ala Ala Gly		
2180	2185	2190
Ala Ala Gly Cys Cys Thr Ala Gly Ala Gly Ala Cys Ala Thr Cys		
2195	2200	2205
Thr Gly Thr Cys Gly Gly Ala Thr Cys Thr Cys Cys Ala Ala Cys		
2210	2215	2220
Ala Gly Ala Ala Ala Gly Ala Cys Cys Cys Gly Gly Ala Ala Gly		
2225	2230	2235
Gly Cys Cys Gly Cys Cys Ala Gly Ala Gly Ala Gly Ala Ala Gly		
2240	2245	2250
Cys Ala Cys Cys Gly Cys Ala Ala Ala Ala Cys Ala Gly Ala Thr		
2255	2260	2265
Ala Gly Ala Gly Cys Cys Ala Gly Cys Gly Thr Gly Thr Cys Cys		
2270	2275	2280
Thr Thr Cys Thr Gly Gly Ala Cys Thr Cys Thr Gly Cys Thr Gly		
2285	2290	2295
Cys Cys Thr Ala Cys Ala Ala Cys Ala Gly Gly Cys Gly Thr Gly		
2300	2305	2310
Cys Gly Gly Ala Cys Ala Ala Gly Ala Gly Gly Ala Ala Gly Cys		
2315	2320	2325
Cys Cys Thr Cys Thr Gly Ala Gly Ala Cys Thr Gly Ala Cys Thr		
2330	2335	2340
Cys Thr Gly Thr Gly Gly Cys Cys Thr Cys Cys Thr Ala Gly Ala		
2345	2350	2355

Thr Gly Cys Ala Gly Ala Thr Gly Cys Ala Gly Ala Cys Gly Cys		
2360	2365	2370
Gly Ala Gly Thr Ala Cys Ala Gly Ala Gly Thr Gly Ala Cys Cys		
2375	2380	2385
Ala Thr Gly Ala Ala Cys Ala Thr Cys Cys Thr Gly Ala Ala Cys		
2390	2395	2400
Ala Gly Cys Cys Thr Gly Cys Cys Ala Ala Gly Cys Ala Gly Cys		
2405	2410	2415
Ala Thr Gly Gly Ala Ala Ala Thr Cys Gly Cys Cys Gly Thr Gly		
2420	2425	2430
Cys Thr Gly Cys Ala Ala Gly Ala Ala Ala Cys Cys Gly Cys Cys		
2435	2440	2445
Ala Ala Gly Ala Ala Ala Ala Gly Cys Cys Cys Thr Ala Cys Cys		
2450	2455	2460
Ala Gly Cys Thr Thr Cys Thr Gly Cys Thr Gly Cys Ala Ala Cys		
2465	2470	2475
Cys Thr Gly Gly Ala Cys Cys Thr Gly Cys Ala Gly Cys Ala Thr		
2480	2485	2490
Cys Ala Gly Cys Gly Cys Ala Gly Ala Cys Gly Cys Ala Ala Ala		
2495	2500	2505
Ala Ala Gly Ala Ala Gly Ala Ala Ala Gly Ala Cys Ala Ala Gly		
2510	2515	2520
Gly Thr Cys Gly Ala Gly Ala Thr Cys Cys Gly Gly Ala Ala Thr		
2525	2530	2535
Cys Gly Gly Ala Gly Cys Cys Cys Cys Ala Ala Gly Gly Cys Cys		
2540	2545	2550
Ala Ala Thr Ala Gly Cys Ala Cys Ala Gly Ala Gly Thr Gly Thr		
2555	2560	2565
Cys Ala Gly Gly Gly Cys Gly Ala Gly Cys Ala Cys Ala Gly Cys		
2570	2575	2580
Ala Gly Ala Gly Ala Gly Cys Ala Gly Ala Ala Thr Cys Thr Gly		

2585	2590	2595
Cys Thr Gly Ala Ala Thr	Cys Thr Gly Gly Thr	Gly Cys Ala Gly
2600	2605	2610
Cys Thr Gly Ala Ala Thr	Cys Cys Thr Cys Ala Cys	Ala Gly Cys
2615	2620	2625
Cys Cys Thr Cys Ala Cys Cys	Ala Cys Cys Gly Gly	Ala Ala Gly
2630	2635	2640
Gly Ala Cys Gly Ala Ala Gly	Ala Gly Gly Ala Cys	Cys Ala Cys
2645	2650	2655
Cys Ala Gly Ala Ala Gly Ala	Gly Ala Cys Ala Cys	Cys Ala Cys
2660	2665	2670
Cys Ala Cys Cys Ala Cys Ala	Ala Thr Cys Ala Ala	Ala Ala Gly
2675	2680	2685
Ala Ala Gly Ala Thr Gly Ala	Gly Cys Gly Thr Cys	Cys Cys Ala
2690	2695	2700
Cys Thr Gly Thr Thr Cys Thr	Thr Cys Cys Ala Cys	Gly Gly Cys
2705	2710	2715
Gly Ala Cys Cys Thr Gly Thr	Gly Thr Ala Gly Ala	Gly Ala Gly
2720	2725	2730
Ala Gly Cys Ala Cys Cys Cys	Thr Gly Gly Gly Cys	Ala Ala Thr
2735	2740	2745
Thr Thr Cys Thr Gly Gly Ala	Thr Gly Ala Ala Gly	Cys Thr Gly
2750	2755	2760
Cys Thr Cys Cys Ala Gly Cys	Thr Gly Cys Cys Thr	Cys Ala Gly
2765	2770	2775
Ala Gly Gly Cys Cys Thr Cys	Cys Ala Cys Thr Gly	Cys Ala Ala
2780	2785	2790
Cys Cys Ala Gly Thr Gly Ala	Cys Cys Gly Gly Ala	Ala Thr Gly
2795	2800	2805
Gly Ala Ala Ala Thr Cys Cys	Thr Gly Cys Thr Thr	Thr Gly Gly
2810	2815	2820

Ala Thr Thr Cys Thr Gly Cys Thr Gly Ala Ala Gly Ala Thr Gly		
2825	2830	2835
Gly Ala Ala Ala Thr Thr Cys Ala Gly Ala Thr Cys Thr Thr Cys		
2840	2845	2850
Ala Ala Gly Ala Thr Thr Thr Gly Cys Cys Thr Gly Gly Gly Cys		
2855	2860	2865
Gly Ala Gly Ala Thr Gly Cys Ala Gly Cys Thr Cys Thr Gly Cys		
2870	2875	2880
Ala Cys Cys Thr Cys Thr Cys Gly Gly Ala Thr Thr Cys Thr Gly		
2885	2890	2895
Ala Ala Cys Cys Thr Gly Cys Ala Ala Gly Thr Gly Cys Thr Gly		
2900	2905	2910
Ala Ala Ala Ala Ala Gly Ala Thr Cys Cys Thr Gly Cys Gly Gly		
2915	2920	2925
Ala Gly Cys Thr Thr Thr Ala Thr Gly Ala Ala Gly Cys Thr Gly		
2930	2935	2940
Thr Ala Cys Cys Ala Cys Ala Gly Cys Cys Thr Cys Gly Thr Gly		
2945	2950	2955
Ala Thr Gly Thr Gly Cys Cys Thr Gly Cys Gly Gly Cys Thr Gly		
2960	2965	2970
Ala Gly Gly Ala Cys Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala		
2975	2980	2985
Ala Ala Gly Gly Cys Thr Cys Thr Gly Ala Gly Cys Gly Cys Cys		
2990	2995	3000
Cys Thr Gly Thr Thr Cys Ala Thr Cys Thr Gly Gly Cys Cys Thr		
3005	3010	3015
Cys Ala Gly Cys Ala Cys Thr Cys Cys Thr Ala Cys Ala Ala Gly		
3020	3025	3030
Ala Thr Cys Ala Cys Ala Cys Ala Cys Cys Cys Ala Thr Thr Cys		
3035	3040	3045
Gly Cys Cys Ala Gly Cys Cys Ala Gly Cys Cys Ala Cys Thr Gly		

3050	3055	3060
Gly Gly Ala Cys Ala Ala Gly	Ala Gly Ala Thr Gly	Cys Cys Cys
3065	3070	3075
Ala Ala Cys Ala Ala Cys Ala	Cys Cys Cys Ala Gly	Ala Thr Cys
3080	3085	3090
Cys Gly Gly Cys Thr Gly Cys	Thr Gly Ala Ala Gly	Cys Cys Cys
3095	3100	3105
Gly Ala Cys Ala Ala Gly Ala	Ala Gly Ala Ala Gly	Ala Ala Ala
3110	3115	3120
Ala Gly Cys Ala Cys Cys Gly	Ala Ala Ala Ala Gly	Ala Cys Cys
3125	3130	3135
Ala Ala Ala Gly Gly Cys Cys	Ala Gly Gly Cys Thr	Thr Thr Cys
3140	3145	3150
Gly Gly Cys Ala Gly Cys Thr	Thr Cys Thr Cys Cys	Gly Cys Cys
3155	3160	3165
Gly Ala Thr Thr Thr Thr Thr	Cys Ala Gly Cys Cys	Cys Cys Thr
3170	3175	3180
Cys Ala Ala Gly Gly Ala Cys	Ala Gly Gly Cys Thr	Thr Thr Thr
3185	3190	3195
Gly Gly Cys Thr Cys Cys Cys	Thr Gly Thr Gly Thr	Cys Ala Gly
3200	3205	3210
Cys Thr Gly Gly Thr Gly Thr	Cys Cys Gly Cys Cys	Gly Ala Cys
3215	3220	3225
Thr Thr Thr Ala Gly Cys Gly	Cys Cys Cys Cys Ala	Cys Ala Ala
3230	3235	3240
Gly Thr Gly Ala Cys Cys Ala	Gly Ala Cys Thr Gly	Cys Gly Gly
3245	3250	3255
Ala Gly Cys Cys Thr Gly Ala	Ala Cys Cys Ala Thr	Cys Thr Gly
3260	3265	3270
Cys Thr Gly Ala Thr Thr Thr	Gly Gly Cys Thr Gly	Ala Ala Gly
3275	3280	3285

Ala Ala Thr Thr Gly Gly Ala Ala Gly Cys Gly Gly Thr Thr Cys		
3290	3295	3300
Ala Ala Gly Cys Thr Cys Ala Ala Ala Ala Gly Ala Ala Ala		
3305	3310	3315
Thr Ala Thr Cys Ala Gly Gly Cys Cys Cys Cys Thr Cys Thr Gly		
3320	3325	3330
Cys Gly Gly Cys Thr Gly Thr Gly Gly Thr Cys Thr Thr Gly Gly		
3335	3340	3345
Thr Gly Cys Gly Gly Ala Ala Cys Ala Ala Gly Cys Cys Ala Gly		
3350	3355	3360
Ala Cys Cys Thr Ala Cys Thr Thr Cys Gly Gly Cys Ala Gly Cys		
3365	3370	3375
Ala Thr Cys Ala Thr Cys Thr Gly Thr Ala Thr Cys Ala Ala Gly		
3380	3385	3390
Ala Ala Thr Ala Thr Gly Thr Thr Cys Cys Thr Gly Cys Ala Gly		
3395	3400	3405
Cys Gly Gly Ala Ala Gly Gly Gly Thr Thr Thr Cys Cys Thr Gly		
3410	3415	3420
Ala Ala Cys Cys Thr Gly Ala Gly Cys Cys Ala Cys Gly Thr Gly		
3425	3430	3435
Gly Ala Ala Ala Ala Gly Thr Thr Cys Gly Ala Gly Cys Thr Thr		
3440	3445	3450
Ala Ala Gly Ala Ala Gly Ala Ala Thr Cys Thr Thr Cys Thr Gly		
3455	3460	3465
Cys Thr Cys Cys Cys Cys Gly Thr Cys Gly Thr Gly Ala Thr Cys		
3470	3475	3480
Ala Ala Cys Cys Thr Gly Ala Ala Gly Ala Gly Ala Cys Thr Gly		
3485	3490	3495
Cys Ala Gly Ala Ala Ala Thr Thr Cys Ala Thr Gly Cys Thr Gly		
3500	3505	3510
Ala Ala Cys Cys Ala Gly Ala Ala Gly Thr Gly Cys Cys Thr Gly		

3515	3520	3525
Gly Cys Thr Cys Cys Ala Thr Thr Thr Cys Cys Thr Gly Cys Cys		
3530	3535	3540
Thr Gly Cys Ala Cys Cys Ala Gly Cys Ala Ala Ala Gly Cys Cys		
3545	3550	3555
Thr Gly Gly Ala Cys Ala Cys Cys Cys Ala Gly Ala Ala Ala Ala		
3560	3565	3570
Cys Thr Cys Gly Thr Gly Gly Gly Cys Ala Gly Ala Gly Cys Cys		
3575	3580	3585
Gly Thr Gly Cys Gly Gly Ala Gly Ala Ala Ala Gly Gly Gly Cys		
3590	3595	3600
Ala Thr Thr Cys Thr Gly Gly Cys Cys Ala Thr Gly Ala Cys Ala		
3605	3610	3615
Cys Thr Gly Ala Cys Cys Cys Thr Gly Ala Ala Cys Gly Gly Ala		
3620	3625	3630
Ala Thr Cys Gly Ala Gly Gly Cys Cys Cys Thr Gly Ala Cys Ala		
3635	3640	3645
Gly Cys Cys Cys Thr Gly Thr Thr Thr Ala Cys Cys Thr Gly Thr		
3650	3655	3660
Ala Gly Ala Ala Cys Cys Gly Cys Cys Thr Cys Cys Ala Thr Cys		
3665	3670	3675
Ala Gly Cys Gly Thr Gly Ala Ala Cys Ala Thr Cys Ala Gly Cys		
3680	3685	3690
Ala Cys Cys Cys Thr Gly Ala Thr Gly Ala Gly Cys Ala Thr Cys		
3695	3700	3705
Cys Thr Gly Gly Ala Ala Gly Cys Cys Ala Thr Cys Ala Thr Cys		
3710	3715	3720
Ala Ala Gly Ala Ala Gly Ala Thr Gly Ala Ala Gly Ala Ala Ala		
3725	3730	3735
Cys Gly Gly Ala Thr Cys Ala Thr Gly Gly Thr Gly Cys Ala Cys		
3740	3745	3750

Cys Gly Gly Thr Gly Gly Ala Thr Cys Thr Thr Cys Thr Cys Cys	3755	3760	3765
Ala Ala Thr Cys Ala Gly Cys Thr Gly Ala Cys Cys Gly Thr Gly	3770	3775	3780
Cys Ala Gly Ala Thr Gly Cys Thr Cys Thr Gly Cys Cys Thr Gly	3785	3790	3795
Cys Cys Thr Cys Thr Gly Cys Thr Gly Ala Cys Cys Cys Cys Thr	3800	3805	3810
Gly Ala Cys Ala Cys Cys Ala Gly Ala Thr Gly Gly Ala Thr Cys	3815	3820	3825
Thr Thr Thr Ala Gly Thr Ala Ala Thr Cys Ala Gly Cys Thr Gly	3830	3835	3840
Cys Ala Gly Ala Cys Ala Gly Thr Gly Cys Ala Ala Ala Thr Gly	3845	3850	3855
Cys Thr Gly Thr Gly Thr Cys Thr Gly Cys Cys Ala Cys Cys Thr	3860	3865	3870
Cys Thr Gly Ala Ala Gly Cys Ala Gly Gly Gly Cys Gly Ala Gly	3875	3880	3885
Ala Gly Ala Ala Thr Cys Ala Thr Thr Thr Gly Gly Cys Cys Ala	3890	3895	3900
Cys Thr Cys Gly Gly Cys Gly Gly Cys Thr Thr Thr Cys Ala Gly	3905	3910	3915
Ala Thr Cys Cys Cys Cys Ala Ala Thr Thr Thr Cys Thr Thr Cys	3920	3925	3930
Thr Gly Gly Thr Cys Cys Cys Thr Cys Gly Gly Cys Ala Thr Cys	3935	3940	3945
Gly Gly Ala Cys Ala Cys Ala Cys Thr Gly Gly Cys Gly Cys Ala	3950	3955	3960
Thr Gly Gly Thr Gly Gly Cys Ala Thr Ala Cys Thr Gly Gly Thr	3965	3970	3975
Ala Gly Ala Ala Gly Gly Cys Gly Gly Ala Gly Ala Gly Ala Gly			

3980	3985	3990
Thr Gly Gly Gly Gly Cys Gly Gly Cys Thr Cys Thr Ala Cys Cys		
3995	4000	4005
Gly Thr Gly Thr Cys Thr Ala Gly Ala Ala Gly Cys Cys Cys Ala		
4010	4015	4020
Cys Thr Gly Thr Gly Gly Ala Thr Cys Ala Gly Cys Thr Cys Cys		
4025	4030	4035
Ala Thr Gly Ala Thr Cys Thr Ala Cys Cys Thr Gly Ala Gly Ala		
4040	4045	4050
Gly Gly Cys Ala Thr Gly Gly Cys Cys Thr Thr Cys Gly Cys Cys		
4055	4060	4065
Ala Gly Cys Gly Ala Cys Ala Gly Cys Thr Cys Cys Ala Thr Cys		
4070	4075	4080
Ala Gly Ala Ala Cys Cys Ala Cys Cys Ala Gly Ala Gly Thr Gly		
4085	4090	4095
Thr Cys Cys Thr Gly Gly Thr Gly Thr Cys Gly Gly Ala Gly Ala		
4100	4105	4110
Thr Gly Thr Gly Gly Cys Gly Cys Cys Ala Ala Gly Thr Cys Thr		
4115	4120	4125
Gly Cys Cys Gly Cys Ala Gly Cys Cys Thr Cys Thr Thr Cys Thr		
4130	4135	4140
Thr Cys Thr Cys Cys Ala Cys Thr Gly Thr Gly Gly Gly Ala Thr		
4145	4150	4155
Thr Gly Cys Ala Gly Cys Ala Cys Cys Ala Cys Ala Ala Cys Cys		
4160	4165	4170
Gly Gly Cys Ala Cys Ala Cys Ala Cys Cys Ala Cys Gly Gly Ala		
4175	4180	4185
Thr Gly Cys Cys Thr Gly Thr Gly Gly Gly Ala Gly Ala Thr Cys		
4190	4195	4200
Cys Cys Thr Ala Gly Cys Gly Thr Thr Ala Cys Cys Cys Thr Gly		
4205	4210	4215

Cys Thr Gly Gly Cys Thr Ala Ala Cys Cys Thr Gly Cys Ala Cys		
4220	4225	4230
Cys Thr Gly Thr Gly Cys Thr Ala Cys Thr Ala Cys Cys Ala Cys		
4235	4240	4245
Thr Cys Thr Cys Ala Gly Ala Gly Cys Ala Ala Cys Ala Gly Ala		
4250	4255	4260
Ala Ala Cys Ala Ala Gly Ala Gly Cys Cys Gly Cys Cys Ala Gly		
4265	4270	4275
Ala Thr Gly Gly Ala Ala Thr Cys Cys Cys Thr Gly Gly Gly Cys		
4280	4285	4290
Ala Thr Gly Ala Ala Gly Cys Thr Cys Cys Ala Ala Cys Thr Thr		
4295	4300	4305
Ala Ala Ala Ala Ala Gly Ala Ala Ala Gly Thr Gly Ala Ala Cys		
4310	4315	4320
Gly Cys Cys Thr Gly Cys Ala Gly Cys Ala Cys Cys Thr Ala Cys		
4325	4330	4335
Ala Cys Ala Cys Cys Cys Cys Ala Cys Ala Thr Cys Thr Gly Cys		
4340	4345	4350
Ala Gly Ala Cys Ala Cys Ala Cys Cys Thr Gly Thr Cys Gly Cys		
4355	4360	4365
Gly Thr Gly Ala Ala Cys Gly Cys Cys Gly Thr Cys Gly Ala Gly		
4370	4375	4380
Gly Ala Ala Cys Thr Gly Cys Ala Cys Thr Cys Thr Ala Gly Ala		
4385	4390	4395
Ala Gly Gly Ala Thr Gly Thr Cys Cys Gly Thr Gly Cys Gly Gly		
4400	4405	4410
Ala Thr Cys Gly Thr Gly Ala Ala Ala Ala Thr Thr Gly Gly		
4415	4420	4425
Gly Thr Gly Thr Cys Cys Thr Gly Cys Thr Gly Cys Thr Ala Cys		
4430	4435	4440
Gly Thr Gly Cys Gly Gly Cys Thr Gly Thr Cys Ala Gly Cys Thr		

4445	4450	4455	
Gly Thr Gly Gly Gly Ala Cys Thr Gly Thr Cys Thr Ala Cys Thr			
4460	4465	4470	
Thr Gly Gly Ala Gly Cys Gly Cys Thr Cys Thr Gly Gly Ala Cys			
4475	4480	4485	
Ala Ala Cys Ala Ala Gly Ala Thr Cys Ala Thr Cys Thr Gly Cys			
4490	4495	4500	
Ala Ala Gly Gly Gly Cys Cys Ala Cys Ala Gly Ala Ala Thr Cys			
4505	4510	4515	
Ala Cys Cys			
4520			
<210> 1100			
<211> 4521			
<212> DNA			
<213> Artificial Sequence			
<220><223> polynucleotide 1B			
<400> 1100			
accgagatcc aattgacat gaacgacagc aagcacaagc tggaaagccc cgctctgaaa	60		
caggtgtcac cagcctctcc acctactcag cagcctcaga cacctcagga tagcagacag	120		
gtgctggcca tgcctagcag ctggcttagc tctggcagaa cccagcggaa ggtggtcaag	180		
aatcctagcc agcctgtgcc tctgagaaac gacggcatca ccaacggcaa cgactccacc	240		
agaagctgca gcatcagcct gaagaaaagc ctggaaaaga tgccctcat gatgaagaag	300		
aaggacagca ccatttcat cgtgcccatg agcctggcct gtagcatcac cgtgtctttc	360		
gtgggcccaga tcagcacact ggtgtgtgat gtgtccagca tctccactg gaacaaagt	420		
cggcagaact tcaagcggaa cgccgacaag aagaacgttc ggagcggcga gaagaacgac	480		
ctgcagctgt ttgtgatgag cgacaccacc tacaagatct actggaccgt gatcctgctg	540		
aaccctgcg gcaatctgca cctgaaaacc accagcctgg gcgactgtcc tagaacaatg	600		
gccggacctt ctgcctctct gcacctgca tctggcagag cctctagaaa gacctggcag	660		
agaaggctga gagcctgtag agctggtgga cctgtgtgat gggccagaca ggccttcgat	720		
aagaaaggct ttgtgatcct gagcgtcgga gccggaacag gcggaggacc tgcttgtgtt	780		
cctgtggctg aagctttctac aggcgcttgg acagctgaag gcgccgtgg aacaagatgt	840		
agagcttcta gagccccttg cagacagctg cctgccagct ctcctacaa gtgcgagatc	900		

tgctgaagc gcagacggcg gagaaagaga agcagccagt ctagaagccc cgtgcctaag	960
aaacgcgaga gaatgatgct gcccgtgcgg gccagaacag ctatatctgc acttcctcag	1020
gggagagccc ctcttgaggg aatgctgctt cctagagcac tgcccagcct gctgtctaga	1080
atgccagcca gaagagagag ccggttttgg ctggctctgc aggcacttgg actcagacct	1140
ccacatctgc ctatctgtca tctctgcct caactgcttg gccctccacc tctcatcag	1200
gcccctacag ctttcttctt gctggacatc attctgcggc tgcctgcaa agtgaccgag	1260
tctagcaata tgggcgga cagatccatc tgctgacca acgccaagaa aatggaagat	1320
atgatctggg agagcacgcc cctgagcatc agcagaccta catctagagc caggcagagc	1380
tgttgtctgc ccgactgac acatcctgct caccagccac tgggatctat gaccctggcc	1440
atcagattca tcagcgtcc tcagcctagc tccagcacag tgacagctgc tcttagcggc	1500
cagtacttca agggcaagaa gcggcgga gagatcttca agaagaagaa acccctgaca	1560
ttcagcccca gcctggccaa aaagaccctg accaatagca gcttcttcta caccagcgac	1620
cgcgaggcca agaaatctat gaagcggagc atgaccctga aggccttgg caagacctgg	1680
acacagtcca gaaactacc cagagcctcc tctctggac accctctggg acctaattggc	1740
atctgggaag tgatgccag aacactggaa ggctgcatct ccgtgaagga ccacagaaca	1800
agccagaacc acagcaagtg catcaccgag tgtgtgcgga cagccctgaa cagaagaagc	1860
aagatcgagg cctctctat cggtctatc gccctgagat ccatgcctaa gagcagaaac	1920
caggtgctgt tcagacgaa tctgaccca agccagctga gaactctggc cctctctat	1980
atgtgctgc ccagttctt gagccagagc ctgagcagaa agcagatccc tagccagtec	2040
atgtggtgg cctctagagc aggacagttt cctgtgtggc ggagaaccag cagaggaatg	2100
agcctgcagt ggaagtccg caatgcctgc acacctctga gatgccctag cagaagccct	2160
gccacattcc tgacagctct gaacggctgg cacagatctg gactgagagc ccagagaaag	2220
cgcaagcgcg agaagagaag ccagaagtcc aggcagaacc atctgcagct gaagtctgc	2280
cggcgcaaga tctccaactg gtccaagtgc agaagccct ggatcttctg gtccaagaag	2340
agactgcccc agctgaccaa gtgtgaaatc tgtgtcaaga acaccgcat cctggctatc	2400
accctgatca cccctcagga cctcatctg gaccctgtgt gtcacctca tagaaggcct	2460
ggatggaagg gccaccacag agtggtgttt tctcatcacc ctagcggcag caccaagagc	2520
cactggcagc aaagagaacg cggaggcggc agacgggaaa agaagggtg tagagagaga	2580
tccctgctgt actccagaat gtgcctggtg cagatcccca cacacacctg ggagcccgat	2640

tacttcgtgt ctctgccat gatgttcagc tgggccacac agtcattccc cgtgggagcc	2700
gtgtttctga ccagacctgc cattccttgc ttagctgca caagccacag caacccttgg	2760
agtcagagca gacaccaca cagaagccca cctacctctt gtctctcgct gctggaagcc	2820
tttccactgc ctagagcatc cctgagagcc accgtgccaa gacatagctc tgtgctggca	2880
accggactgc atctgcacag acagatttct ctgccctga gaggattcct gctgcatcaa	2940
ccactgccag gccagcatct gtggctgtct catagactgc ggctgagact gccaagaact	3000
cagcggcctc ctagatccat cctgagcctt agactgccac tgaggccaca gagaggaccc	3060
agacctctgc atagatggct gcagcagacc acaggctgta gccagagaag ataccccaga	3120
ctgaaaacct tcggcgtgcc actgggctcc attctgtgtc tggctggatc tctgagcacc	3180
atgatgatca ttagcaccac cagacaagag tgtggcaggc gggcatctgt gccctgtaga	3240
cctatgatcg gaagcgccag accaggacct tggagaacat ctgctatgcc tagcgccatg	3300
ggcgtcgcac tgcctacaag ctgtgaatcc ggaagatctc ctctgccac cggcgggaaga	3360
atgcctggaa gccagagcat tatgatgagc tggatgcctc ctctggctcc ttgtgccgt	3420
tgtcttgttt ctcccgctcc tacactgtgt cccgctcacc ctgctagagc acctacagcc	3480
gtgcctgcct ttacacctct gtctgcacat cctgtgcctg tgctgtctgg atgtcacctg	3540
gccgtcagaa cctccatgct gacactgtct cctatgtga agctggcccc actgcaagtg	3600
accaccacac tgaagctgat cctggctcatg ctggaaatcg tgaccgagag cactcggaga	3660
gagatgcctt ctcaggccac accttctcca cctggacctt ggcgagccgc tctgggcaaa	3720
gaagtgaaga gatcccagag caagctgcgc ctgagaaaca caagcccat cgtgttcttt	3780
ctggcccat acctccccag acggatgacc agacggacca tgacaaccac caaatgatg	3840
atgatcgggc ggaccaagcg gagaaggcgc aaaaggcgga gaatgacaat gatgacaagg	3900
cggacctgc tgacaaagaa aacctgtctg acccctagaa ccagcgccgc taccaaagct	3960
ctgccaaggc agacaatctc ccagcggagg cctattcaga cccctcctgg aacatctctg	4020
gccatctggg gcaaccagca gctgaaatgg acccctcaca tctgaagtc cgccagcaga	4080
agggccagac ctaccagctg tagcacctgt agaatgtggt ggatcgccaa aaagcggatc	4140
aagctcgggc ggaacagaac cagactgaca ctgacaggca caagaagcag cggcaccaga	4200
gcttctccat ccgccgtttg cctgtgttgc tggacctgtc cttccagaag cttccagcc	4260
gcttctccaa gcggattgag agcacctgtt ggagcacagg cccctccaga agttacactg	4320
agagctagct gtgcctccag gcctctaaag gcttgtgtg gactttggcc ttggggagca	4380
caagttcggc aaccatcttt gcctggacca tgcgcttctc tctgagcac actgtctcag	4440
ccacctccac aggtctccac tcaagtgtgg acagccgcaa cactgagatg tctgtctgtt	4500

ccagctgctg cctgtctctcc t 4521

<210> 1101

<211> 4053

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 2B

<400> 1101

agaaagatgc agagcctgaa tcaccccagc agactgacca acatgagcag aacacctcca 60

agacgcgtgt gcaaccctcg gagaaagacc tggaagatgc ggaagaagta cgcccagaag 120

cctagccaga agaaccacct gtacaacagc cggaagaaac tgctcgagga catgaagcag 180

aatggcttca caggccacag agagggcagc gagtctgata atctgggcct gctgtactcc 240

tttctccta tccggatgtg cgccctgtct caccctagct tctacatcag cagcaccgtg 300

tgctttctga gcaagcactg catgaccgcc tgcacacaaa agaaaggcca catgatcttc 360

agccgcgaga agatcatcaa cccaccatc agctgcccct ttcagagccc cacaaagcgg 420

ctggaactga gcctggaacc ttggattccc tacctgcacc agcagaaaac ccaaggcggc 480

aagaagagaa gcaagttccc tggcaccagc ctgcagtgt acctgaacag atgcagcctg 540

atggaacaga tcctcacct gaagtccgcc tctccacaga tcatgcagag aaccagcgcc 600

gaccggttcc ggatgaagcg gagaatgcag aacctggaca atctgggcgt tccatggcca 660

ctgctgcctg gacctctgga aaacacacag atccccagaa caagccctct gtggaagatc 720

acaatggtgc tgacataccc caactgcgtg gtgcacgtgc tgatgttctg gctgcctatg 780

agatctctgg gcgagcctg gagagctggc ttccagtggg gagagtcccc ttggcaagtg 840

atggctagcc tgacaggccc ctatcctatc agcgagggcc tgaccatgac caccggcaga 900

aacatcaaca gcaactccct gatgaccaac tgcctgttca gccccatctt cctgtgccac 960

cacgccatca tgcaccggaa gatgacaagc ccacacttca gactgttcag cagcaagatc 1020

ccacatcctc aggtgccatc tgtggtggcc ctgtgcaagt tcagagccac atttctgctc 1080

gccctgtggg agtgtagtct gcctcaagcc agactgtgcc tgatcgtgtc tagaacctg 1140

ctgctggttc agtctgccgc tctccacat agactgtctg gcccttctag atggtccaga 1200

agccacctgg acttcagccc ctactggatg aagaaagtga agctggccaa cggcctgtgg 1260

ttcaacctga tcttcgtgct gttcaaggcc gaccagagcg agtctagcct gtctagcggc 1320

cggaacaaga aaacaaagct gtggttctcc ctcatcaaca tccaccaccg caagaatcct 1380

ctgctgcccc tgagaatccc cagcctgaat gccagtgga tgttctgag aatcctgctt 1440

ctggcccata tgiacggctt cagcacctac ggcacccaga aaggcgagtg cgtttgtctg	1500
cagtgtctga gggcagcag cctgttcatt ctgaagcagc ccctggacct gaagatctcc	1560
aagaccttca tgcctgaagc tccccacag gtgccagctc ttgctctca agcttggtgg	1620
ccctgctaga gaggccctct gacatctgct ccatccgctc agcagtctct gacagctagc	1680
cctcagatta tgcagcggtg gagcgccgtg aacttcgaga caatcatcta ccctccaagc	1740
acctgtagcc tgcctttag aggcagaaca ctggaaagcg ccggactgtt tccttggtg	1800
cacaccaggt gtacacacc ctgtaccatg ctgctgccac aaggctggtg gtgtacaaga	1860
ggcggcgga agcggaaaaa gaaaatgtgc aaggtgtccg gcggtgcac cgcctgtgtt	1920
gagagatgtc ctiggaaggg catctgctgg aagtggccag tgacagtggc tgctcagtgg	1980
tctagcgtga cctctctgga atggacagcc caagagagag gctgcagcag ctggctgatg	2040
aagcaaacat ggatgaagtc ttggtccctg cgggacccca gctacagatc catcctggaa	2100
tacgtgtcca ccagagtgt gtggatgcc acaagcaccg tgcggagaag aaacagcaga	2160
aagcagtctc aggtgcagct ggccattcag gtgctgctcg tggacaagca caagtacttt	2220
ctgttcggca gagccccga cgggaacatg aagaaaacca tgagccacct gatcgcccat	2280
caggccctga agatgagcgg cctgaggctg ttcatcctc ggctgctgac aagaaagaag	2340
cccggcaagt tctgcttag cagatttct tggggccctc ctctctgtg tcatcctgt	2400
tggttagacc ctatctccg ctgtccaaga ctgctgccat atccttttca cgtgctggcc	2460
ctggaagtga ctttccacc tggaaacagc atgcctcaga tgcaactgca ggccctggcc	2520
atgtgggaga aaggctggga taagcggaag agaataaga ccggcgccat ccaagagaag	2580
ggcgctattc aagagaaagg ggccatgacc aagcggatct gcgtggtcaa ttctgaggcc	2640
tgcagagaga tgaaagcct gagcgccctt gagaagatta ccctgtttga agcccatatg	2700
gcccgtgca cctccatcaa tgtgtgtgt gtcagagcct ctctgatcga gaagctgatg	2760
aaagaaaagc gcaagatgaa gcgcaaccag gtggcatccc cacaattat gcagaggctg	2820
ttcattaagg gctaccagaa caaccattc accttccatc tgcaaaactt cgccttcttc	2880
agcagcttcg gcaacaacaa gtacatcaat atcctgacgc ggcgcaagaa aagagaggac	2940
cactgcggac tgcctgacct gatccagcac ggcggcatct tcacctttcg gttctgggtc	3000
gaaaagctga gctggaacat ctgcaagaac ctgagcctgt acctggataa gttcgtgcag	3060
cggctgctgt acgtgtacat catcgagaca aacgtgttcg tgctgaacct gttccacgtg	3120
ccagtgaacc agatcttcat gatggccttc tacctgaagt acaccgagaa ggcctgggtc	3180
atggaactgg aatggctgat ccaacagcag tgttaccagc aagagaagaa aagccggaaa	3240
ctgatgagca gctgccgggc cttcatccac acacctagaa gccctggctg cagcgtgtac	3300

gccaatatgt gctgggcctt ttggaagcct cctagccagg gcatcagctc ttgtctgatg 3360
acaggctgtt ggggcagccc tcctctgcac ctgtgtcagc ctctgaggcg gtataagaaa 3420
aggggcgtga tcgcctggcg gcggagaaaag tggcagatcc ggcatgtgct gaaaaacctg 3480

atcctgtttc atgtgcggaa catcgtgtac ggcatccaag tgatgctgtg cggcaaggga 3540
ctgacacacc ctgtgcctct gaaacggacc ctgcagaaca agaggaacaa gaacatcaag 3600
cgggtcaacc agaagaagg caacatcaag aggaagtcca tcctgctgca cctcattgtg 3660
ctgaatagcc ccgagagcaa cccaagtgc ttctgacct ttagccagct cgagaagaaa 3720
gctacctgga tgagaagaac aggcgccctg agagccacag ctctgctac agcagctcct 3780
caggctcaga ctctcattg gagagccgcc acaacaagca gcatgagcag cagccctaga 3840
gccgagccta catcttctag ctcttgggcc acctgttggc ccagatgctg tagctccagc 3900

tgttactggt cctgagttc ttggcctcct gctggcgccg ctgaggctac aaacaccaga 3960
actagaagca gagagtccca gcggggcaga atgctgactt ggagaagtag tctgtggctg 4020
cagggcacca gatgttttac aggcgtgcgg aca 4053

<210> 1102
<211> 4518
<212> DNA
<213> Artificial Sequence
<220><223> polynucleotide 3B
<400> 1102

ggagctgctg ctgcctcttg tcagttcct ctttctctc gggaaaccac acctagctcc 60
gacgccacca gacggacaag accaattgcc gctcagagca agaaaaccat gacagccgcc 120
ggactgacct ctaagaacaa gaagcggaga aagctgcggc ccaagatgat ccggaagatc 180

cagaagagaa ggcggaccgc caaccggcgg aatagcagaa gggctacccc tacaagcaag 240
ggcagcctga gaagaaagta cctgagagtg cggggacctc ctctgcacac ccggaacatc 300
agaaagctga tctggaccaa gcagcggagc ttctgtctc tgttcccaa getgagagcc 360
accgagcaga tgaccaatgt gggctgctct atccctcacg tgcccaaagc cacagccgt 420
cactctgtga cagtgaact gcagctgccc ctgacctca gcacctgct gtgggtagc 480
agacacacca tgagcctgag caacatcctg atgaagtcc ggctgcagtc tagccattc 540
ctggccagat cctggaacac catgcagtgg aacaacaaga aaatggccat gaccgtgatc 600

gctggcgccc accactgtca gtacaagctg acctacacca aagtgtggaa gatgaactgg 660
aagaaaatga tgatcggcag ccagcatctg ctgttcagcc ctctggatag cagtcacctg 720

cagctcctgc tgcacctca cggcaagaga tgcaaccctt gctgcagact gacctggatg 780
 agccagaaca ccagaagcac caacctggaa aagaacccca gcctgaagaa gcagagccag 840
 cggagaggaa agctgagcgc ctttagcggc agaatcctgc accagccaga aatggccgcc 900
 atgagactga tgcccaagtt cctgaactcc accaacagct ggtggaccct gaccacactg 960
 agcttcctgc tgatcgagga agccagacag cccagcagac ctaccggcag aacacctacc 1020

 accagactga tggccctgt gggcagcgtg atgagctgtt ctctgctgac ccagccttct 1080
 ccagccagcg cctgtacaat gcctccactg ctgcatccac agtgggcccc tcatagtgt 1140
 ggactttctc caggcgttg cagacctgcc tgcacctgta tcagcatgac caccatcagc 1200
 agggccacat ggggcccagt gtactacgtg tgcaaccgga tgaacgtgtc cagcgtgctg 1260
 aagcccttcc tgttcaccgt gcctatcgag gacatgagag agtgcaccct gggcagaaac 1320
 agaatgaatg tgtcctctgt gctgaaaccc tgtctgatcc ctgtgccaat cagcgagaag 1380
 aagaggaagc tgcccaacat cgagatcacc cctcagcggg ctaaggccat gctgcagaag 1440

 cagtgtgtgt acaacctcgt gatcaagcac cctctgatct tcagaatcaa cctgcggcgg 1500
 cagggaaga ccaaagatgg cgttgtgcag agcctgggct tcctcaacca gcagatcatc 1560
 ctgcagaaag agttcttcat ctgcctgtct atgttcatca agcgggtggaa gcctgccgcc 1620
 accaagagca gaaagaaggg ccacaccaag aacagacgga aggccaagag aaagccccag 1680
 atctacctgt tcttctgac cgtgtgcggc ttccacctga aaaagaccag cgccaagtgg 1740
 ctgaagaagt ccaccaagtc cagatccaac ggcatggaag cttgcggcac acacccact 1800
 cctagactga gctgcctgag agttagatgc ggcggctggc tgtgtggctg gacacctaga 1860

 ggtagaaagt ccggcgtgat gaagtgtgg gatctgtgcc ccgtgcacaa gaagagaggc 1920
 ctgttcagac tggattttca cccagaagc agctccggca agggaaagaa cagcccctgc 1980
 tgccaaaaga aactgcgggt gcagaaccag ggccatctgc tgatgattct getgcacaat 2040
 gaccgggtgt tcctcgtgaa gatcggcgag aagctgaagc actgtttcaa ggcctggggc 2100
 tccagacgga accggcggtg cagaaagatc tacggcgagc tgaagatgtc cctgcaggcc 2160
 ttctgatcc acctgagaaa ggtggacacc caccacctcc aggtggtcac caaacagtg 2220
 accgccacaa cagccgacgg ccagagaatg cggagactga agtgcaaggc ctgccggctg 2280

 agatgggcca gacctgaacc tgetgtcag gcccctccta agagccactt tccacctcat 2340
 cctagcggcc ccagcagaac aagtagcctg cagctgagaa gcctgttctt tagccactgc 2400
 ctgtgcagcc agaagaagga ccctgccggc aagctgaaaa agctgctgaa gaaaagcagc 2460
 cagctgcgga gaagctggcg caatgtgtcc agaatacga cccctctcc actgatcctg 2520
 tggcctcaag ctgctcctgt gtccgtgatc accatgaagc tgtgggagaa gcacttcaag 2580

ggcctgaatt ggaacctggt cgtgtggatt ctgaacctga agatgatgac ctacatggaa	2640
atgcactacg gccatcaggc cccacagggtg gcaatgctgc ctaagctgct gtgcagacag	2700
atgtgcccc ctctgagcac actgcagcag agacatcctc agggcccttg tctctctct	2760
gtgacacctc tgagagtcca gtctgtcctg ctgctgggag tgcctcagac agccagagga	2820
cctagaagaa aggtcctgat ggtgctgtgg ctcccccca atcagtctct gcagaaaagc	2880
caggttttcc agtgggtgct gcggacagag gtggcccta gatgtcctag atctgccgtg	2940
gacatcagcc ccggacctac atctcctagc ctggcctctt gtgcctctgt ggccattgga	3000
aagctggcac tgcctggcgc ctctgctcct tgtggtgctg ctggcgctag agaggccgga	3060
agatttgctg tgctgggcac catggtcatg aagctttgtt tcttctacct gctgtaccgg	3120
ctgcgcattc caagcctgag gaagtacaga cagcacctga accggaagct gcacctgaca	3180
agatcctgcc tgatcgatct gaccatgatg atgtcccaga agctctggaa gaaccagcgg	3240
aagagaatcc ctctgccatc tccacggcaa catctgctgc cacagtacc tctgcaccca	3300
cctccacctt gtctgtctgt gctgcacat agacaccacc tggcctttct cgagatggcc	3360
tgtagctctc agcacaccca cagcatcaag atctggatca gcttcagcca tgaagtggac	3420
cctccaggca gcgtgtggat actgccttgc gatctgcctc ggatgctgcc aatctcttca	3480
ccctgcaca gaccccagat gcctttctgg acctgcacct ttcctgccac aacctggggc	3540
acatgggaga caccttctac atggggctgg cggactttca gaggcgctag cagcagcaca	3600
tcccgaggaca gcagatcctt cttcacctct gctcaccta gcaggccctg cagaatgaga	3660
ctgtaccagt gcaagaagaa gctctctctg aaactgctga ccaccaccac aagcagcccc	3720
agaagatccc ctgctctgag agcaagaggc ggaccacaa tcggcgaagt gaccagctgt	3780
accaacctga gcgtgcccat gatctgacc atcctgattt ggaagcgggt gttcatctc	3840
ctgctgagcg ataagaagg cgccaagaag atcaccttcc tgctattcc tccacacctg	3900
agacaccctc tgctgtctgt cgagaagaaa cggcctgagt ggctgagcat ggacctggac	3960
ggaatgctga cagtgatcgg ccagggactc gtgggcatga cccctagaga tctgggaaca	4020
gtggcaggcg ccaccgtca gattcagcga cctatccagg tgcagactgg cggcagactc	4080
agaagaaacc tgcagagaaa cctgaagggt ctccagggtt ccgtgtacag cggcaacctg	4140
ctgtccttta gcagacgggg catgaagtct agcgtgcggc tgaanaaccg cgagtgggag	4200
aaacggaagc agattctcgg aggcggcgga aagtacaaag agtacttct gaagcgcac	4260
ctcatccgga aggctatgac agtctgtggc ggcgacaaga aaggactggg cagattcatg	4320

agatgcgtgc agagcgagac aaaggccgtg tctctgcaac tgcctctggg aagaaacatg 4380

gaacaccggt tgacatgga cagcgcctg agcctgacaa agagagagg acccgagaca 4440

ctcaaaaaga aatacctggt ccagcaccag atgaagtgtc tgaccgccgt ggattgtctg 4500

caggcttttt gggacatg 4518

<210> 1103

<211> 4521

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 4B

<400> 1103

atccagaaga agaagcagaa gtccaacctg gacctgcagc accagcgcag acgcaaaaag 60

aagaaggaca aggtcgagat ccggaatcgg agccccaagg ccaatagcac agagtgtcag 120

ggcgagcaca gcagagagca gaacctgctg aatctggtgc agctgaaccc tcacagccct 180

caccacagaa aggacgaaga ggaccaccag aagcggcacc accaccacaa tcaaaagaaa 240

atgagcgtga tggccaagaa gtcccagcag cctctcggac aggccttttg cttctgtgt 300

cagctggtgt ccgccattt cagcgcctt caagtacca gactgcggag cctgaacct 360

ctgctgatca acgagggcaa caaccactgg cctagagtgg aaatgcctac cggttggctg 420

ctcgtgggct acaacaccag aaacacagcc cagaatctc ggctgcagca gcactgaaa 480

cactggcagc agtgcaccag agccagatgg tgccaagagc cttgtcagac cctgaccttc 540

ttccatttct tcttcttttt caaaacggtg tcctgtgtct gccccggctg gtctaaagga 600

caacctctc cactggcct gaagccttct agcctggctt ctcaggtggc cagaaccaca 660

ggcgtgtacc agcacgtgtg gctgatctgc ttcgtgttct tcgtgtgctt ggaaaccggc 720

ttctgtcacg tggccaagt gggactcgag agactggtgt cttgagcgg catcacgcac 780

gtgaaccatt gggcccagcc taagccatct cctagcaaag gcaccggcat gaacagacct 840

atcggcctga gagtggcaa aggcgtgtgg gccagactga gagcctccgt gtctttctgg 900

accctgctgc ctacaacagg cgtgcggaca agaggaagcc cttgagact gacactgtgg 960

cctccacgga acatctgaa cagcctgcct agcagcatgg aaatcgccgt gctgcaagag 1020

aaccgcaaga ccagaaaggc cgccagagag aagcacagaa agaccgacaa cctgcacctg 1080

tgctactacc acagccagag caaccggaac aagagccggc agatggaaag cctgggcatg 1140

aagctgcaga gccctctgtg ggattgtctc accacaacag gcacacacca cggctgtctg 1200

tgggagatcc ctacggttac actgctggcc tgcagagtga acgccgtgga agaactgcac 1260

agcaggcgga tgictgtgcg gatcgtgaag aactgggtgt cctgctgtta cgtgcgcctg 1320
 tctgctgtgg gcctgtctac ttggagcgcc ctggacgtgg tcatcaacct gaagcggtg 1380
 cagaagtcca gccagaagtc tcagcaccac tgcgcctga gaaagatcga gtgggccaca 1440

 aagctgagcc tcggcggaag agctggaccc caggctcaag agaaggccaa cgccaagaag 1500
 atgcccttcc agcgggtggat cttcagcaat cagctgaccg tgcagatgct gtgcctgcct 1560
 attgaagccc tgactgccct gttcacctgt cggacagcca gcatcagcgt gaacatcagc 1620
 accctgatga gcatcctgga agccctctg ttttttcacg gcgacctgtg cgaggaaaag 1680
 aagaacggcc ggatcagcag ccaggtctct ctgagacttt ggtcttgggt cggcacaagc 1740
 cagacctact ttggcagcac cgccaagaaa agccccacca gcttttgctg cgagtgggga 1800
 ggacaggctc accggcagag aaataccgga atggaaatcc tgctgtggat tctgctcaag 1860

 atggaaattc agatcttcaa gatttgcctg ggcgagatgc agctgtgcac ctacacaccc 1920
 cacatctgca gacacacctg tagaggcgga cctagcgcca gcgatagatg ctgtagctgt 1980
 agccctagcg gcttcagcgc cggaagaggc agatgtccag ttcagggatg tctgcgcct 2040
 cacagagtgc agctgctgag aagatggggc cctggatctc ctgctggcca gagactgtct 2100
 aagggctttc agctgctccg ttggtgggga ccaggatctc cagctcctga gcctagaaag 2160
 ggcccatctc caccacctga tcttccatgg cctgtgaccg ctgtgacagt gatggctggc 2220
 tctgtgccta gcgtcagtc tgtggatgct ctggaaagcc ctggacctct ggcaactggaa 2280

 ggacctagca gccccagaaa cctgctctgg cgggaaatga gcatcttctt gcctggcatc 2340
 ttcacctctc ggattctgaa cctgcaagtg ctgaagaaga tctgcggag ctttatgaag 2400
 ctgtaccact ctctggtcat gtgcctgcgg ctgcggacca agctggaaaa agctctgagc 2460
 gctctgttca tctggcccca gcacagctac aagcagaggc ctctctgca gcctgtgcag 2520
 gtctgtctca gactgggaaa cctgcctcca ttcttcagag gcagcgaggt gccctttct 2580
 agaccttgcc ggaccaagat gctgaaccag aagtgtctgg cccctttcat cacacacca 2640
 ttcgcctctc agccctggg acaagagatg cccaacaaca ccagatcag actgctgaag 2700

 cccctgctga cccctgacac cagatggatc ttctccaacc agctgcagac agtccagatg 2760
 ctctgtctgc cacctctgaa gcaggcgag agaatcattt ggccctcgg cggtttcag 2820
 atccccaact tcttttggag cctcggaatc ggccacactg gcgcctgggt gcatactgga 2880
 aggcgagaaa gagaatgggg cggtccacc gtgtctagaa gccactgtg gatcagctcc 2940
 atgatctacc tgagaggcat ggccttcgcc agcgacagct ccatcagaac caccagagtg 3000
 tcttggtgca gaagatcggg cgccaaatct gccgtgcct ccagcctcaa gaagaaaccc 3060

cgggacatct gtcggatcag cgactctaag aagatgaccc agaagcgca gagcacctg 3120

ggcaatttct ggatgaagct cctccagctg ccagacaaga agaagaagtc taccgaaaag 3180

accaagatca tcaagaagat gaagaaacgg atcatggtcc acatgtgcag ctccctggt 3240

ctgccaacag gcctgacatc tctgatcctg ccaagcagcg atctggccgt gctgatctct 3300

agctccacca gccactttct gatgcggagc ccagtgtgc ctagtccag actgacttgt 3360

gcctctccac agctgccag aatgtggacc tggccagct ggctgaagtg gctgaaaaac 3420

tggaagcgtt tcaagcttaa aaagaagtac atcctggcca tgacgtgac cctgaacggg 3480

catcaagaa ccgcctctat caccctgcct accaccagcc tgaagggtc tagaaccagc 3540

tggtgcccc gaatcaccc cagactgcct aggacaaagt ggcctctgca gtgcctgctg 3600

cacagcctgg gaacaactgg aacactcgtg tgggaaagg gcgtgctgca gatgagaagt 3660

ctggaagctc actgccctct cgagaccttc caccctcacc actgtagaac tcagcccagc 3720

tcttgccctc ctgcatggat tctgtacaa ggacagtgga gcggagccgt cgtgggactt 3780

agacctgtgg ctccatctt gccaaacct attcagggcc tgcactgccc acaggctcca 3840

catcaaccag ctctgtcttg gggcaagtgg ccggtgggaa tgacaggacc tgccagatgt 3900

tgccggtggc ctgacggga actcaaaaag aatctgtgc tcccctgccg gtgcagacgc 3960

gagtatagag tgacaatggg ccaagccttc ggcagcttta gcgccgactt tagcgtccc 4020

caggtgttga agaagaatcg gaagcagaac aagattatct gcaagggccca ccgcatcaca 4080

agcctgatcc tgagctttca gcgcgtgaaa cttaagaaga aagtcaacgc ctgctctccc 4140

gcctgcacct ctaaagcctg gactcccaga aagctcgtgg ggagagccgt cagaagaaag 4200

ggcatcatct gtatcaagaa tatgttcctg cagcgggaagg gtttcctgaa cctgagccac 4260

gtggaaaagt tcgtgcctcc ttctctcct ctggctctcg gccctagaat gcagctctgt 4320

accagctgg ccggttctt ccctatcaca cctctgtgt ggcacatct gggacctcag 4380

aggcacacc ctgtcaaaa gaagtgccc tccgtagcc catggggcct tagaccatct 4440

ccttgctga gctggctcct cagaattgtg gccctggac acgccctgag ctgtcggact 4500

agaagaagat ggtccagca g 4521

<210> 1104

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> hTPA amino acid sequence

<400> 1104

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg

20 25

<210> 1105

<211> 232

<212> PRT

<213> Artificial Sequence

<220><223> Human Invariant chain (hINV) amino acid sequence

<400> 1105

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175
 Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu
 180 185 190
 Met Ser Arg His Ser Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys
 195 200 205
 Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys
 210 215 220
 Gln Asp Leu Gly Pro Val Pro Met
 225 230

<210> 1106

<211> 11

<212> PRT

<213> Artificial Sequence

<220><223> HA tag amino acid sequence

<400> 1106

Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser

1 5 10

<210> 1107

<211> 1547

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 1A

<400> 1107

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Thr Glu Ile

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

Ala Ser Arg Ala Gly Gln Phe Pro Val Trp Arg Arg Thr Ser Arg Gly

85 90 95

Met Ser Leu Gln Trp Lys Ser Gly Asn Ala Cys Thr Pro Leu Arg Cys

100 105 110

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

115 120 125

Arg Ser Gly Leu Arg Ala Gln Met Pro Ser Ser Trp Ser Ser Ser Gly

130 135 140

Arg Thr Leu Lys Leu Ala Pro Leu Gln Val Thr Thr Thr Leu Lys Leu

145 150 155 160

Ile Leu Val Met Leu Glu Ile Val Thr Glu Arg Ser Leu Leu Tyr Ser

165 170 175

Arg Met Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro Asp Tyr

180 185 190

Phe Val Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser Phe Pro

195 200 205

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

210 215 220

Thr Ser His Ser Asn Pro Trp Ser Gln Ser Asn Gln Gln Leu Lys Trp

225 230 235 240

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

245 250 255

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

260 265 270

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

275 280 285

Ile Ser Ala Pro Gln Pro Ser Ser Ser Thr Val Thr Ala Ala Pro Ser

290 295 300

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

305 310 315 320

Met Gly Gly Asn Arg Ser Ile Cys Leu Thr Arg Lys Arg Lys Arg Glu

325 330 335
 Lys Arg Ser Gln Lys Ser Arg Gln Asn His Leu Gln Leu Lys Ser Cys

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

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

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

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

Pro Gly Leu Thr His Pro Ala His Gln Pro Leu Gly Ser Met Ser Thr
580 585 590

Arg Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro Gly Pro Trp
595 600 605

Arg Ala Ala Leu Gly Lys Glu Val Lys Arg Ser Gln Ser Lys Leu Arg
610 615 620

Leu Arg Asn Thr Ser Pro Gly Glu Lys Asn Asp Leu Gln Leu Phe Val
625 630 635 640

Met Ser Asp Thr Thr Tyr Lys Ile Tyr Trp Thr Val Ile Leu Leu Asn
645 650 655

Pro Cys Gly Asn Leu His Leu Lys Thr Thr Ser Leu Gln Arg Pro Pro
660 665 670

Arg Ser Ile Leu Ser Leu Asn Gly Ile Trp Glu Val Met Pro Arg Thr
675 680 685

Leu Glu Gly Cys Ile Ser Val Lys Asp His Arg Thr Ser Gln Asn His
690 695 700

Ser Lys Cys Ile Thr Glu Cys Val Arg Thr Ala Leu Asn Val Ser Lys
705 710 715 720

Lys Arg Leu Pro Lys Leu Met Lys Lys Lys Asp Ser Thr Ile Phe Ile
725 730 735

Asn Lys Val Arg Gln Asn Phe Lys Arg Asn Phe Lys Lys Lys Lys Pro
740 745 750

Leu Thr Phe Ser Pro Ser Arg Arg Met Thr Arg Arg Thr Met Thr Thr
755 760 765

Thr Lys Met Met Met Met Arg Arg Thr Lys Arg Arg Arg Arg Lys Arg
770 775 780

Arg Arg Met Thr Met Met Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr
785 790 795 800

Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln
805 810 815

Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro Gly Thr Ser Leu

820 825 830
 Ala Ile Trp Gly Arg Thr Arg Leu Thr Leu Thr Gly Thr Arg Ser Ser
 835 840 845
 Gly Thr Arg Ala Ser Pro Ser Ala Val Cys Leu Cys Cys Trp Thr Cys

 850 855 860
 Pro Ser Arg Ser Phe Pro Ala Ala Ser Pro Ser Gly Leu Arg Ala Pro
 865 870 875 880
 Val Gly Ala Gln Ala Pro Pro Glu Val Thr Leu Arg Ala Ser Cys Ala
 885 890 895
 Ser Ser Ala Ser Lys Ala Cys Ala Gly Leu Trp Pro Trp Gly Ala Gln
 900 905 910
 Val Arg Val Gly Ala Gly Thr Gly Gly Gly Pro Ala Cys Val Pro Val

 915 920 925
 Ala Glu Ala Ser Thr Gly Ala Trp Thr Ala Glu Gly Ala Ala Gly Thr
 930 935 940
 Arg Cys Arg Ala Ser Arg Ala Pro Cys Arg Gln Leu Pro Ala Ser Ser
 945 950 955 960
 Pro Thr Lys Cys Glu Ile Cys Val Lys Arg Arg Arg Arg Arg Lys Arg
 965 970 975
 Ser Ser Gln Ser Arg Ser Pro Val Pro Lys Lys Arg Glu Arg Met Met

 980 985 990
 Leu Pro Val Arg Ala Arg Thr Ala Arg Ser Ala Leu Pro Gln Gly Arg
 995 1000 1005
 Ala Pro Leu Glu Gly Met Leu Leu Pro Arg Ala Leu Pro Ser Leu
 1010 1015 1020
 Leu Ser Arg Met Pro Ala Arg Arg Glu Ser Arg Phe Trp Leu Ala
 1025 1030 1035
 Leu Gln Ala Leu Gly Leu Arg Pro Pro His Leu Pro Ser Cys His

 1040 1045 1050
 Pro Leu Pro Gln Leu Leu Gly Pro Pro Pro Pro His Gln Ala Pro
 1055 1060 1065

Met Thr	Leu Lys Ala Leu Val	Lys Thr Trp Thr Gln	Phe Arg Asn
1070	1075	1080	
Tyr Pro	Arg Ala Asp Lys Lys	Asn Val Arg Ser Thr	Ala Phe Phe
1085	1090	1095	
Leu Leu	Asp Ile Ile Leu Gly	Asp Cys Pro Arg Thr	Met Ala Gly
1100	1105	1110	
Pro Ser	Ala Ser Leu His Pro	Ala Ser Gly Arg Ala	Ser Arg Lys
1115	1120	1125	
Thr Trp	Gln Arg Arg Leu Arg	Ala Cys Arg Ala Gly	Gly Pro Ala
1130	1135	1140	
Gly Trp	Ala Arg Gln Ala Tyr	Pro Arg Leu Lys Thr	Phe Gly Val
1145	1150	1155	
Pro Leu	Gly Ser Ile Leu Cys	Leu Ala Gly Ser Leu	Ser Thr Met
1160	1165	1170	
Met Ile	Ile Ser Thr Thr Arg	Gln Glu Cys Gly Arg	Arg Ala Ser
1175	1180	1185	
Val Pro	Cys Arg Pro Met Ile	Gly Ser Ala Arg Pro	Gly Pro Trp
1190	1195	1200	
Arg Thr	Ser Ala Met Pro Ser	Ala Met Gly Val Ala	Leu Pro Thr
1205	1210	1215	
Ser Cys	Glu Ser Gly Arg Ser	Pro Pro Ala Thr Gly	Gly Arg Met
1220	1225	1230	
Pro Gly	Ser Gln Ser Ile Met	Met Ser Trp Met Pro	Pro Leu Ala
1235	1240	1245	
Pro Cys	Ala Ala Cys Pro Cys	Ser Pro Ala Pro Thr	Leu Cys Pro
1250	1255	1260	
Ala His	Pro Ala Arg Ala Pro	Thr Ala Val Pro Ala	Phe Thr Pro
1265	1270	1275	
Leu Ser	Ala His Pro Val Pro	Val Leu Ser Gly Cys	His Leu Ala
1280	1285	1290	
Val Arg	Thr Ser Met Leu Thr	Leu Leu Pro Met Glu	Ala Lys Lys

1295	1300	1305
Ser Met Lys Arg Ser Asn Ala	Lys Lys Met Glu Asp	Met Ile Trp
1310	1315	1320
Glu Ser Arg Leu Pro Leu Arg	Pro Gln Arg Gly Pro	Arg Pro Leu
1325	1330	1335
His Arg Trp Leu Gln Gln Thr	Thr Gly Cys Ser Gln	Arg Arg Ile

1340	1345	1350
Val Phe Phe Leu Ala Pro Tyr	Phe Pro Arg His Pro	His Arg Ser
1355	1360	1365
Pro Pro Thr Ser Cys Pro Pro	Leu Leu Glu Ala Phe	Pro Leu Pro
1370	1375	1380
Arg Ala Ser Leu Arg Ala Thr	Val Pro Arg His Ser	Ser Val Leu
1385	1390	1395
Ala Thr Gly Leu His Leu His	Arg Gln Ile Ser Leu	Pro Leu Arg

1400	1405	1410
Gly Phe Leu Leu His Gln Pro	Leu Pro Gly Gln His	Leu Trp Leu
1415	1420	1425
Ser His Arg Leu Arg Leu Arg	Leu Pro Arg Thr Gln	Pro Ser Leu
1430	1435	1440
Pro Gly Pro Cys Ala Ser Leu	Leu Ser Thr Leu Ser	Gln Pro Pro
1445	1450	1455
Pro Gln Ala Pro Ser Gln Val	Trp Thr Ala Ala Thr	Leu Arg Cys

1460	1465	1470
Pro Ala Val Pro Ala Ala Ala	Cys Pro Pro Ala Leu	Arg Ser Met
1475	1480	1485
Pro Lys Ser Arg Asn Gln Val	Leu Phe Arg Arg Asn	Leu Thr Pro
1490	1495	1500
Ser Gln Leu Arg Thr Leu Ala	Pro Pro Tyr Met Leu	Leu Pro Gln
1505	1510	1515
Ser Leu Ser Gln Ser Leu Ser	Arg Lys Gln Ile Pro	Ser Gln Ser

1520	1525	1530

Met Leu Val Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser

1535

1540

1545

<210> 1108

<211> 1541

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 2A

<400> 1108

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1

5

10

15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Arg Lys Met

20

25

30

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

35

40

45

His Leu Cys Gln Pro Leu Arg Met Ser Arg Thr Pro Pro Arg Arg Val

50

55

60

Cys Ala Ala Pro Pro His Arg Leu Leu Gly Pro Ser Arg Trp Asn Pro

65

70

75

80

Arg Arg Lys Thr Trp Lys Met Arg Lys Lys Tyr Ala Gln Lys Pro Ser

85

90

95

Gln Lys Asn His Leu Tyr Gly Gly Lys Lys Arg Ser Lys Phe Ser Arg

100

105

110

Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys Val Lys Val Leu

115

120

125

Phe Lys Ala Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly Arg Cys Ser

130

135

140

Leu Met Glu Gln Ile Pro His Leu Lys Ser Arg Arg Lys Trp Gln Ile

145

150

155

160

Arg His Val Leu Lys Asn Leu Trp Leu Pro Met Arg Ser Leu Gly Glu

165

170

175

Pro Trp Arg Ala Gly Phe Gln Trp Gly Glu Ser Pro Trp Gln Val Met

180

185

190

Ala Ser Leu Thr Gly Arg Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys
195 200 205

Ser Leu Pro Gln Ala Arg Leu Cys Leu Ile Val Ser Arg Thr Leu Leu
210 215 220

Leu Val Gln Ser Arg Asn Lys Lys Thr Lys Leu Trp Phe Ser Leu Ile
225 230 235 240

Asn Ile His His Arg Lys Asn Pro Leu Leu Pro Met Arg Trp Trp Cys
245 250 255

Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys Met Cys Lys Val Ser Gly
260 265 270

Gly Cys Thr Ala Cys Val Glu Arg Cys Pro Trp Lys Gly Ile Cys Trp
275 280 285

Lys Trp Pro Val Thr Val Ala Ala Ile Arg Met Cys Ala Leu Ser His
290 295 300

Pro Ser Phe Tyr Ile Ser Ser Thr Val Cys Phe Leu Ser Lys His Cys
305 310 315 320

Met Thr Ala Cys Thr Arg Lys Arg Met Lys Thr Gly Ala Ile Gln Glu
325 330 335

Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys Val
340 345 350

Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro Glu
355 360 365

Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile Asn
370 375 380

Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu Lys
385 390 395 400

Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln Arg
405 410 415

Leu Phe Ile Lys Gly Tyr Gln Asn Asn His Phe Thr Phe His Leu Gln
420 425 430

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

435 440 445
 Leu Thr Ile Leu Phe His Val Arg Asn Ile Val Tyr Gly Ile Gln Val
 450 455 460
 Met Leu Cys Ala Ser Pro Gln Ile Met Gln Arg Thr Ser Ala Asp Arg

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

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

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

 660 665 670
 Ala Ile Met His Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe Ser
 675 680 685

Ser Lys Ile Pro His Pro Gln Val Pro Ser Val Val Ala Leu Cys Lys
690 695 700

Phe Arg Ala Phe Ile His Thr Pro Arg Ser Pro Gly Cys Ser Val Tyr
705 710 715 720

Ala Asn Met Cys Trp Pro Lys Phe Phe Leu Thr Phe Ser Gln Gln Trp
725 730 735

Ser Ser Val Thr Ser Leu Glu Trp Thr Ala Gln Glu Arg Gly Cys Ser
740 745 750

Ser Trp Leu Met Lys Gln Thr Trp Met Lys Ser Trp Ser Leu Arg Asp
755 760 765

Pro Ser Tyr Arg Ser Ile Leu Glu Tyr Val Ser Thr Arg Val Leu Trp
770 775 780

Met Pro Thr Ser Thr Val Leu Gln Ala His Pro Gln Val Pro Ala Leu
785 790 795 800

Ala Pro Gln Ala Trp Trp Pro Ala Arg Arg Gly Pro Leu Thr Ser Ala
805 810 815

Pro Ser Ala Gln Gln Ser Leu Thr Arg Glu Lys Ile Ile Asn Pro Thr
820 825 830

Ile Ser Cys Pro Phe Gln Ser Pro Thr Lys Arg Leu Ile Tyr Pro Pro
835 840 845

Ser Thr Cys Ser Leu Pro Cys Arg Gly Phe Leu Pro Ser Arg Phe Pro
850 855 860

Trp Gly Pro Pro Pro Leu Asn Ser Val Ile Val His Lys Ile Val Leu
865 870 875 880

Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn Cys Glu Arg Arg Ile Ser
885 890 895

Gly Ile Gln Lys Arg Ala Ile Glu Phe Ala Val Leu Lys Leu Leu Asn
900 905 910

Met Asp Leu Pro Leu Glu Asn Thr Gln Ile Pro Arg Thr Ser Pro Leu
915 920 925

Trp Lys Ile Thr Met Val Leu Thr Tyr Pro Asn Cys Val Val His Val

930 935 940
 Leu Met Phe Gly Ala Leu Arg Ala Thr Ala Pro Ala Thr Ala Ala Pro
 945 950 955 960
 Gln Ala Gln Thr Pro His Trp Arg Ala Ala Thr Thr Ser Ser Met Ser
 965 970 975
 Ser Ser Pro Arg Ala Glu Pro Thr Ser Ser Ser Ser Trp Ala Thr Cys

980 985 990
 Trp Pro Arg Cys Cys Ser Ser Ser Cys Tyr Trp Ser Leu Ser Ser Trp
 995 1000 1005
 Pro Pro Ala Gly Ala Ala Glu Ala Thr Asn Thr Arg Thr Arg Ser
 1010 1015 1020
 Arg Glu Ser Gln Arg Gly Arg Met Leu Thr Trp Arg Ser Ser Leu
 1025 1030 1035
 Trp Leu Gln Gly Thr Arg Cys Phe Thr Gly Val Arg Thr Ser Ser

1040 1045 1050
 Arg Tyr Lys Lys Arg Gly Val Ile Ala Trp Arg Arg Gln Ile Asn
 1055 1060 1065
 Arg Arg Lys Leu Gln Arg Lys Lys His Trp Asn Ser Ala Tyr Leu
 1070 1075 1080
 Gly Arg Thr Leu Leu Val Thr Cys Ile Leu Tyr His Arg Trp Ile
 1085 1090 1095
 Val Thr Ser Met Cys Gln Ser Gln Arg Trp Leu Thr Ser Thr Thr

1100 1105 1110
 Ser Arg Ser Ser Ala Leu Met Trp Thr Glu Leu Ser Leu Glu Pro
 1115 1120 1125
 Trp Ile Pro Tyr Leu His Gln Gln Lys Thr Gln Arg Thr Leu Glu
 1130 1135 1140
 Ser Ala Gly Leu Phe Pro Trp Leu His Thr Gln Cys Gln Glu Lys
 1145 1150 1155
 Lys Ser Arg Lys Leu Met Ser Ser Cys Thr His Pro Cys Thr Met

1160 1165 1170

Leu Leu	Pro Gln Gly Cys His	Pro Ala Trp Leu Ser	Pro Ile Ser
1175	1180	1185	
Ala Cys	Pro Arg Leu Leu Pro	Tyr Pro Phe His Val	Leu Ala Leu
1190	1195	1200	
Glu Val	Thr Phe Pro Pro Gly	Thr Ala Met Pro Gln	Met Gln Leu
1205	1210	1215	
Gln Ala	Leu Ala Met Trp Glu	Lys Gly Trp Asp Lys	Pro Gly Thr
1220	1225	1230	
Ser Leu	Gln Cys Tyr Leu Asn	Arg Arg Arg Asn Ser	Arg Lys Gln
1235	1240	1245	
Ser Gln	Val Gln Leu Ala Ile	Gln Val Leu Leu Val	Asp Lys His
1250	1255	1260	
Lys Tyr	Phe Leu Phe Gly Gln	Lys Lys Gly His Met	Ile Phe Ser
1265	1270	1275	
Leu Ala	Asn Gly Leu Trp Phe	Asn Leu Ile Phe Asn	Ser Arg Lys
1280	1285	1290	
Lys Leu	Leu Glu Asp Met Lys	Gln Asn Gly Phe Thr	Gly Lys Gly
1295	1300	1305	
Leu Thr	His Pro Val Pro Leu	Lys Arg Thr Leu Gln	Asn Lys Arg
1310	1315	1320	
Asn Lys	Asn Ile Lys Arg Val	Asn Gln Lys Lys Gly	Asn Ile Lys
1325	1330	1335	
Arg Lys	Ser Ile Leu Leu His	Leu Ile Val Leu Asn	Ser Pro Glu
1340	1345	1350	
Ser Asn	Leu Ile Leu Ile Gln	His Gly Gly Ile Phe	Thr Phe Arg
1355	1360	1365	
Phe Trp	Val Glu Lys Leu Ser	Trp Asn Ile Cys Lys	Asn Leu Ser
1370	1375	1380	
Leu Tyr	Leu Asp Lys Phe Val	Gln Arg Leu Leu Tyr	Val Tyr Ile
1385	1390	1395	
Ile Glu	Thr Asn Val Phe Val	Leu Asn Leu Phe His	Val Pro Val

1400 1405 1410
 Asn Gln Ile Phe Met Met Ala Phe Tyr Leu Lys Tyr Thr Glu Lys
 1415 1420 1425
 Ala Trp Val Met Glu Leu Glu Trp Leu Ile Gln Gln Gln Cys Tyr
 1430 1435 1440
 Gln Gly Ser Cys Gly Arg Ala Cys Ser Cys Gly Arg Gly Cys Gly
 1445 1450 1455
 Thr Pro Arg Gly Asp Trp Lys Arg His Pro Pro Arg Arg Ala Phe

1460 1465 1470
 Trp Lys Pro Pro Ser Gln Gly Ile Ser Ser Cys Leu Met Thr Gly
 1475 1480 1485
 Cys Trp Leu Glu Lys Lys Ala Thr Trp Met Arg Arg Thr Arg Arg
 1490 1495 1500
 Lys Lys Arg Glu Asp His Cys Gly Leu Arg His Pro Ser Trp Pro
 1505 1510 1515
 Trp Thr Arg Cys Leu Arg Met Arg Pro Pro Arg Ser Gly Tyr Pro

1520 1525 1530
 Tyr Asp Val Pro Asp Tyr Ala Ser
 1535 1540

<210> 1109

<211> 1546

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 3A

<400> 1109

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Gly Ala Ala
 20 25 30

Ala Ala Ser Cys Gln Ser Pro Pro Ser Pro Arg Glu Thr Thr Pro Ser
 35 40 45
 Ser Asp Ala Thr Arg Arg Thr Arg Pro Ile Ala Ala Gln Ser Lys Lys

50	55	60	
Thr Met Thr Ala Ala Gly Leu Thr Pro Met Ile Arg Lys Ile Gln Lys			
65	70	75	80
Arg Arg Arg Thr Ala Asn Arg Cys Leu Arg Val Arg Cys Gly Gly Trp			
	85	90	95
Leu Cys Gly Trp Thr Pro Arg Gly Gln Asn Thr Arg Ser Thr Asn Leu			
	100	105	110
Glu Lys Asn Pro Ser Leu Lys Lys Gln Ser Gln Arg Arg Gly Lys Leu			
	115	120	125
Ser Ser Leu Phe Phe Ser His Cys Leu Cys Arg Asn Ser Arg Arg Ala			
	130	135	140
Thr Pro Thr Ser Lys Gly Ser Leu Arg Arg Lys Tyr Leu Arg Val Pro			
145	150	155	160
Ile Pro Pro His Leu Arg His Pro Leu Leu Leu Met Asp Leu Asp Gly			
	165	170	175
Met Leu Thr Val Ile Gly Gln Gly Leu Val Gly Met Thr Pro Arg Asp			
	180	185	190
Leu Gly Thr Val Ala Gly Ala Thr Ala Gln Ile Gln Arg Pro Ile Gln			
	195	200	205
Val Gln Thr Gly Gly Arg Leu Thr Pro Pro Pro Leu Ile Leu Trp Pro			
	210	215	220
Gln Ala Ala Pro Val Asp Pro Pro Gly Ser Val Trp Ile Leu Pro Cys			
225	230	235	240
Lys Asn Lys Lys Arg Arg Lys Leu Arg Pro Lys Arg Leu Asp Phe His			
	245	250	255
Pro Arg Ser Ser Ser Gly Val Ser Val Ile Thr Met Lys Leu Trp Glu			
	260	265	270
Lys His Phe Lys Gly Leu Asn Trp Asn Leu Val Val Trp Ile Leu Asn			
	275	280	285
Leu Lys Met Met Asn Ile Glu Ile Thr Pro Gln Arg Ser Lys Ala Arg			
	290	295	300

Lys Ser Gly Val Met Lys Cys Trp Asp Leu Cys Pro Ser Glu Lys Lys
 305 310 315 320
 Arg Lys Leu Pro Leu Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser
 325 330 335
 Arg His Arg Gly Ala Ser Ser Ser Thr Ser Arg Asp Ser Arg Ser Phe
 340 345 350

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

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

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

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

545 550 555 560
 Pro Thr Thr Arg Leu Met Ala Pro Val Gly Ser Val Met Ser Cys Ser
 565 570 575
 Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr Met Pro Pro Leu
 580 585 590
 Leu His Pro Gln Trp Ala Pro His Ser Ala Gly Leu Ser Pro Gly Ala
 595 600 605

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

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

 Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu Thr Met Met Met
 740 745 750
 Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile Pro Leu Pro Ser
 755 760 765
 Pro Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His Pro Pro Pro Pro
 770 775 780
 Cys Leu Leu Leu Leu His His Arg His His Leu Ala Phe Leu Glu Met
 785 790 795 800

Ala Cys Ser Ser Gln His Thr His Ser Ile Lys Ile Trp Ile Ser Phe
805 810 815

Ser His Glu Gln Ser Ser Pro Phe Leu Ala Arg Ser Trp Asn Thr Met
820 825 830

Gln Trp Asn Asn Lys Lys Met Ala Met Thr Val Ile Ala Gly Ala His
835 840 845

His Cys Gln Tyr Lys Leu Thr Tyr Thr Lys Val Trp Lys Met Asn Trp
850 855 860

Lys Lys Met Met Ile Gly Ser Gln His Leu Leu Phe Ser Pro Leu Asp
865 870 875 880

Ser Ser Pro Leu Gln Leu Leu Leu His Pro His Gly Lys Arg Cys Asn
885 890 895

Pro Cys Cys Arg Leu Thr Trp Met Ser Met Leu Gln Lys Gln Cys Cys
900 905 910

Tyr Asn Leu Val Ile Lys His Pro Leu Ile Phe Arg Ile Asn Leu Arg
915 920 925

Arg Gln Gly Lys Thr Lys Asp Gly Val Val Gln Ser Leu Gly Phe Leu
930 935 940

Asn Gln Gln Ile Ile Leu Gln Lys Glu Phe Phe Ile Cys Leu Leu Met
945 950 955 960

Phe Ile Lys Arg Trp Lys Pro Ala Ala Thr Lys Arg Glu Trp Glu Lys
965 970 975

Arg Lys Gln Ile Leu Gly Gly Gly Gly Lys Tyr Lys Glu Tyr Phe Leu
980 985 990

Lys Arg Ile Leu Ile Arg Lys Ala Met Thr Val Leu Ala Gly Asp Lys
995 1000 1005

Lys Gly Leu Gly Arg Phe Met Arg Cys Val Gln Ser Glu Thr Lys
1010 1015 1020

Ala Val Ser Leu Gln Leu Pro Leu Gly Arg Gly Pro Val Tyr Tyr
1025 1030 1035

Val Cys Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Phe Leu

1040	1045	1050
Phe Thr Val Pro Ile Glu Asp Met Arg Glu Cys Thr Leu Gly Arg		
1055	1060	1065
Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Cys Leu Ile Pro		
1070	1075	1080
Val Pro Ile Asp Leu Pro Arg Met Leu Pro Ile Ser Ser Pro Leu		
1085	1090	1095
His Arg Pro Gln Met Pro Phe Trp Thr Cys Thr Phe Pro Ala Thr		
1100	1105	1110
Thr Trp Gly Thr Trp Glu Thr Pro Ser Thr Trp Gly Trp Arg Thr		
1115	1120	1125
Phe Arg Gly Pro Arg Arg Lys Val Leu Met Val Leu Trp Leu Pro		
1130	1135	1140
Ala Asn Gln Ser Leu Gln Lys Ser Gln Val Phe Gln Trp Val Leu		
1145	1150	1155
Arg Thr Glu Asn Ile Arg Lys Leu Ile Trp Thr Lys Gln Arg Ser		
1160	1165	1170
Phe Leu Ser Leu Phe Pro Lys Leu Arg Ala Thr Glu Gln Met Thr		
1175	1180	1185
Asn Val Gly Cys Ala Phe Ser Gly Arg Ile Leu His Gln Pro Glu		
1190	1195	1200
Met Ala Ala Met Arg Leu Met Pro Lys Phe Leu Asn Ser Thr Asn		
1205	1210	1215
Ser Trp Trp Thr Cys Thr Asn Leu Ser Val Pro Met Met Leu Thr		
1220	1225	1230
Ile Leu Ile Trp Lys Arg Val Phe Ile Leu Leu Leu Ser Asp Lys		
1235	1240	1245
Lys Leu Leu Lys Lys Ser Ser Gln Leu Arg Arg Ser Trp Arg Asn		
1250	1255	1260
Val Ser Arg Ile Ser His Gln Met Lys Cys Leu Thr Ala Val Asp		
1265	1270	1275

Cys Leu Gln Ala Phe Trp Asp Met Asn Met Glu His Arg Leu Thr
1280 1285 1290

Met Asp Ser Ala Leu Ser Leu Thr Lys Arg Glu Gly Pro Glu Thr
1295 1300 1305

Cys Lys Lys Lys Leu Leu Leu Lys Leu Leu Thr Met Ser Leu Ser
1310 1315 1320

Asn Ile Leu Met Lys Phe Arg Leu Arg Leu Arg Ile Pro Ser Leu
1325 1330 1335

Arg Lys Tyr Arg Gln His Leu Lys Lys Thr Ser Ala Lys Gly Glu
1340 1345 1350

Lys Leu Lys His Cys Phe Lys Ala Trp Gly Arg Gly Pro Pro Leu
1355 1360 1365

His Thr Arg Ser Gln Lys Lys Asp Pro Ala Gly Lys Leu Lys Lys
1370 1375 1380

Leu Thr Thr Leu Ser Phe Val Leu Ile Glu Glu Arg Arg Asn Leu
1385 1390 1395

Gln Arg Asn Leu Lys Val Leu Trp Leu Lys Lys Ser Thr Lys Ser
1400 1405 1410

Arg Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe Phe Glu Lys Lys
1415 1420 1425

Arg Pro Glu Trp Leu Ser Ser Arg Lys Lys Gly His Thr Lys Asn
1430 1435 1440

Arg Arg Lys Ala Lys Arg Lys Pro Gln Ile Val His Lys Lys Arg
1445 1450 1455

Gly Leu Phe Leu Lys Lys Lys Tyr Leu Val Gln Gly Ala Lys Lys
1460 1465 1470

Ile Thr Phe Leu Ser Asn Gly Met Glu Ala Cys Gly Thr His Pro
1475 1480 1485

Thr Pro Arg Leu Ser Asp Arg Val Phe Leu Val Lys Ile Thr Thr
1490 1495 1500

Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg Ala Arg Gly

1505 1510 1515
 Gly Thr Thr Ile Gly Glu Val Thr Ser Leu Cys Phe Phe Tyr Leu
 1520 1525 1530

 Leu Tyr Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1535 1540 1545
 <210> 1110
 <211> 1547
 <212> PRT
 <213> Artificial Sequence
 <220><223> HTPA- AND HA-EXTENDED POLY-FSP POLYPEPTIDE 4A
 <400> 1110
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Ile Gln Lys
 20 25 30

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

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

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

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

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

 Arg Ile Val Ala Pro Gly His Ala Leu Ser Cys Arg Thr Arg Arg Arg
 355 360 365
 Trp Ser Ser Lys Cys Arg Gly Gly Pro Ser Ala Ser Asp Arg Cys Cys
 370 375 380
 Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly Arg Cys Pro Val
 385 390 395 400
 Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu Arg Arg Trp Gly

405	410	415
Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly Phe Gln Leu Leu		
420	425	430
Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro Arg Lys Gly Pro		
435	440	445
Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Ala Val Thr Val Met		
450	455	460
Ala Gly Ser Val Pro Ser Ala Gln Ser Val Asp Ala Leu Glu Ser Pro		
465	470	475
		480
Gly Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro Arg Asn Leu Leu Trp		
485	490	495
Arg Glu Met Ser Ile Phe Leu Pro Gly Ile Phe Cys Gln Lys Lys Val		
500	505	510
Pro Ser Ala Ser Pro Trp Gly Leu Val Pro Pro Ser Pro Pro Leu Ala		
515	520	525
Leu Gly Pro Arg Met Gln Leu Cys Thr Gln Leu Ala Arg Phe Phe Pro		
530	535	540
Ile Thr Pro Pro Val Trp His Ile Leu Gly Pro Gln Arg His Thr Pro		
545	550	555
		560
Gln Val Val Leu Arg Leu Gly Asn Leu Pro Pro Phe Phe Arg Gly Ser		
565	570	575
Glu Val Pro Phe Pro Arg Pro Cys Arg Thr Lys Asn Glu Gly Asn Asn		
580	585	590
His Trp Pro Arg Val Glu Met Pro Thr Gly Trp Leu Leu Val Gly Tyr		
595	600	605
Asn Thr Arg Asn Thr Ala Gln Asn Pro Arg Leu Gln Gln His Leu Lys		
610	615	620
His Trp Gln Gln Cys Thr Arg Ala Arg Trp Cys Gln Glu Pro Cys Gln		
625	630	635
		640
Thr Leu Thr Phe Phe His Phe Phe Phe Phe Phe Lys Thr Val Ser Leu		
645	650	655

Cys Cys Pro Gly Trp Ser Lys Gly Gln Pro Pro Pro Pro Gly Leu Lys
 660 665 670

Pro Ser Ser Leu Ala Ser Gln Val Ala Arg Thr Thr Gly Val Tyr Gln
 675 680 685

His Val Trp Leu Ile Cys Phe Val Phe Phe Val Cys Val Glu Thr Gly
 690 695 700

Phe Cys His Val Ala Gln Val Gly Leu Glu Arg Leu Val Ser Leu Ser
 705 710 715 720

Gly Ile Thr Asp Val Asn His Trp Ala Gln Pro Lys Pro Ser Pro Ser
 725 730 735

Lys Gly Thr Gly Met Asn Arg Pro Ile Gly Leu Arg Val Gly Lys Gly
 740 745 750

Val Trp Ala Arg Leu Leu Lys Lys Lys Pro Arg Asp Ile Cys Arg Ile
 755 760 765

Ser Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr
 770 775 780

Asp Arg Ala Ser Val Ser Phe Trp Thr Leu Leu Pro Thr Thr Gly Val
 785 790 795 800

Arg Thr Arg Gly Ser Pro Leu Arg Leu Thr Leu Trp Pro Pro Arg Cys
 805 810 815

Arg Cys Arg Arg Glu Tyr Arg Val Thr Met Asn Ile Leu Asn Ser Leu
 820 825 830

Pro Ser Ser Met Glu Ile Ala Val Leu Gln Glu Thr Ala Lys Lys Ser
 835 840 845

Pro Thr Ser Phe Cys Cys Asn Leu Asp Leu Gln His Gln Arg Arg Arg
 850 855 860

Lys Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro Lys Ala
 865 870 875 880

Asn Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln Asn Leu Leu
 885 890 895

Asn Leu Val Gln Leu Asn Pro His Ser Pro His His Arg Lys Asp Glu

900	905	910
Glu Asp His Gln Lys Arg His His His His Asn Gln Lys Lys Met Ser		
915	920	925
Val Pro Leu Phe Phe His Gly Asp Leu Cys Arg Glu Ser Thr Leu Gly		
930	935	940
Asn Phe Trp Met Lys Leu Leu Gln Leu Pro Gln Arg Pro Pro Leu Gln		
945	950	955
Pro Val Thr Gly Met Glu Ile Leu Leu Trp Ile Leu Leu Lys Met Glu		
965	970	975
Ile Gln Ile Phe Lys Ile Cys Leu Gly Glu Met Gln Leu Cys Thr Ser		
980	985	990
Arg Ile Leu Asn Leu Gln Val Leu Lys Lys Ile Leu Arg Ser Phe Met		
995	1000	1005
Lys Leu Tyr His Ser Leu Val Met Cys Leu Arg Leu Arg Thr Lys		
1010	1015	1020
Leu Glu Lys Ala Leu Ser Ala Leu Phe Ile Trp Pro Gln His Ser		
1025	1030	1035
Tyr Lys Ile Thr His Pro Phe Ala Ser Gln Pro Leu Gly Gln Glu		
1040	1045	1050
Met Pro Asn Asn Thr Gln Ile Arg Leu Leu Lys Pro Asp Lys Lys		
1055	1060	1065
Lys Lys Ser Thr Glu Lys Thr Lys Gly Gln Ala Phe Gly Ser Phe		
1070	1075	1080
Ser Ala Asp Phe Ser Ala Pro Gln Gly Gln Ala Phe Gly Ser Leu		
1085	1090	1095
Cys Gln Leu Val Ser Ala Asp Phe Ser Ala Pro Gln Val Thr Arg		
1100	1105	1110
Leu Arg Ser Leu Asn His Leu Leu Ile Trp Leu Lys Asn Trp Lys		
1115	1120	1125
Arg Phe Lys Leu Lys Lys Lys Tyr Gln Ala Pro Leu Arg Leu Trp		
1130	1135	1140

Ser Trp Cys Gly Thr Ser Gln Thr Tyr Phe Gly Ser Ile Ile Cys		
1145	1150	1155
Ile Lys Asn Met Phe Leu Gln Arg Lys Gly Phe Leu Asn Leu Ser		
1160	1165	1170
His Val Glu Lys Phe Glu Leu Lys Lys Asn Leu Leu Leu Pro Val		
1175	1180	1185
Val Ile Asn Leu Lys Arg Leu Gln Lys Phe Met Leu Asn Gln Lys		
1190	1195	1200
Cys Leu Ala Pro Phe Pro Ala Cys Thr Ser Lys Ala Trp Thr Pro		
1205	1210	1215
Arg Lys Leu Val Gly Arg Ala Val Arg Arg Lys Gly Ile Leu Ala		
1220	1225	1230
Met Thr Leu Thr Leu Asn Gly Ile Glu Ala Leu Thr Ala Leu Phe		
1235	1240	1245
Thr Cys Arg Thr Ala Ser Ile Ser Val Asn Ile Ser Thr Leu Met		
1250	1255	1260
Ser Ile Leu Glu Ala Ile Ile Lys Lys Met Lys Lys Arg Ile Met		
1265	1270	1275
Val His Arg Trp Ile Phe Ser Asn Gln Leu Thr Val Gln Met Leu		
1280	1285	1290
Cys Leu Pro Leu Leu Thr Pro Asp Thr Arg Trp Ile Phe Ser Asn		
1295	1300	1305
Gln Leu Gln Thr Val Gln Met Leu Cys Leu Pro Pro Leu Lys Gln		
1310	1315	1320
Gly Glu Arg Ile Ile Trp Pro Leu Gly Gly Phe Gln Ile Pro Asn		
1325	1330	1335
Phe Phe Trp Ser Leu Gly Ile Gly His Thr Gly Ala Trp Trp His		
1340	1345	1350
Thr Gly Arg Arg Arg Arg Glu Trp Gly Gly Ser Thr Val Ser Arg		
1355	1360	1365
Ser Pro Leu Trp Ile Ser Ser Met Ile Tyr Leu Arg Gly Met Ala		

1370 1375 1380
Phe Ala Ser Asp Ser Ser Ile Arg Thr Thr Arg Val Ser Trp Cys

1385 1390 1395
Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala Ser Ser Ser Pro Leu

1400 1405 1410

Trp Asp Cys Ser Thr Thr Thr Gly Thr His His Gly Cys Leu Trp
1415 1420 1425

Glu Ile Pro Ser Val Thr Leu Leu Ala Asn Leu His Leu Cys Tyr
1430 1435 1440

Tyr His Ser Gln Ser Asn Arg Asn Lys Ser Arg Gln Met Glu Ser
1445 1450 1455

Leu Gly Met Lys Leu Gln Leu Lys Lys Lys Val Asn Ala Cys Ser
1460 1465 1470

Thr Tyr Thr Pro His Ile Cys Arg His Thr Cys Arg Val Asn Ala
1475 1480 1485

Val Glu Glu Leu His Ser Arg Arg Met Ser Val Arg Ile Val Lys
1490 1495 1500

Asn Trp Val Ser Cys Cys Tyr Val Arg Leu Ser Ala Val Gly Leu
1505 1510 1515

Ser Thr Trp Ser Ala Leu Asp Asn Lys Ile Ile Cys Lys Gly His
1520 1525 1530

Arg Ile Thr Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1535 1540 1545

<210> 1111

<211> 1547

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 1B

<400> 1111

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Thr Glu Ile

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

Phe Val Ile Leu Ser Val Gly Ala Gly Thr Gly Gly Gly Pro Ala Cys
 275 280 285

Val Pro Val Ala Glu Ala Ser Thr Gly Ala Trp Thr Ala Glu Gly Ala
 290 295 300

Ala Gly Thr Arg Cys Arg Ala Ser Arg Ala Pro Cys Arg Gln Leu Pro
 305 310 315 320

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

Arg Lys Arg Ser Ser Gln Ser Arg Ser Pro Val Pro Lys Lys Arg Glu
 340 345 350

Arg Met Met Leu Pro Val Arg Ala Arg Thr Ala Arg Ser Ala Leu Pro
 355 360 365

Gln Gly Arg Ala Pro Leu Glu Gly Met Leu Leu Pro Arg Ala Leu Pro
 370 375 380

Ser Leu Leu Ser Arg Met Pro Ala Arg Arg Glu Ser Arg Phe Trp Leu
 385 390 395 400

Ala Leu Gln Ala Leu Gly Leu Arg Pro Pro His Leu Pro Ser Cys His
 405 410 415

Pro Leu Pro Gln Leu Leu Gly Pro Pro Pro Pro His Gln Ala Pro Thr
 420 425 430

Ala Phe Phe Leu Leu Asp Ile Ile Leu Arg Leu Pro Cys Lys Val Thr
 435 440 445

Glu Ser Ser Asn Met Gly Gly Asn Arg Ser Ile Cys Leu Thr Asn Ala
 450 455 460

Lys Lys Met Glu Asp Met Ile Trp Glu Ser Thr Pro Leu Ser Ile Ser
 465 470 475 480

Arg Pro Thr Ser Arg Ala Arg Gln Ser Cys Cys Leu Pro Gly Leu Thr
 485 490 495

His Pro Ala His Gln Pro Leu Gly Ser Met Thr Leu Ala Ile Arg Phe
 500 505 510

Ile Ser Ala Pro Gln Pro Ser Ser Ser Thr Val Thr Ala Ala Pro Ser

515 520 525
 Gly Gln Tyr Phe Lys Gly Lys Lys Arg Arg Lys Glu Ile Phe Lys Lys
 530 535 540

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

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

 Phe Arg Arg Asn Leu Thr Pro Ser Gln Leu Arg Thr Leu Ala Pro Pro
 675 680 685
 Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser Arg Lys Gln
 690 695 700
 Ile Pro Ser Gln Ser Met Leu Val Ala Ser Arg Ala Gly Gln Phe Pro
 705 710 715 720
 Val Trp Arg Arg Thr Ser Arg Gly Met Ser Leu Gln Trp Lys Ser Gly
 725 730 735

 Asn Ala Cys Thr Pro Leu Arg Cys Pro Ser Arg Ser Pro Ala Thr Phe
 740 745 750
 Leu Thr Ala Leu Asn Gly Trp His Arg Ser Gly Leu Arg Ala Gln Arg
 755 760 765

Lys Arg Lys Arg Glu Lys Arg Ser Gln Lys Ser Arg Gln Asn His Leu
 770 775 780
 Gln Leu Lys Ser Cys Arg Arg Lys Ile Ser Asn Trp Ser Lys Leu Arg
 785 790 795 800

Ser Pro Trp Ile Phe Val Ser Lys Lys Arg Leu Pro Lys Leu Thr Lys
 805 810 815
 Cys Glu Ile Cys Val Lys Asn Thr Ala Ile Leu Ala Ile Thr Leu Ile
 820 825 830
 Thr Pro Gln Asp Pro His Leu Asp Pro Val Cys His Pro His Arg Arg
 835 840 845
 Pro Gly Trp Lys Gly His His Arg Val Val Phe Ser His His Pro Ser
 850 855 860

Gly Ser Thr Lys Ser His Trp Gln Gln Arg Glu Arg Gly Gly Gly Arg
 865 870 875 880
 Arg Glu Lys Lys Gly Cys Arg Glu Arg Ser Leu Leu Tyr Ser Arg Met
 885 890 895
 Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro Asp Tyr Phe Val
 900 905 910
 Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser Phe Pro Val Gly
 915 920 925

Ala Val Phe Leu Thr Arg Pro Ala Ile Pro Cys Cys Ser Cys Thr Ser
 930 935 940
 His Ser Asn Pro Trp Ser Gln Ser Arg His Pro His Arg Ser Pro Pro
 945 950 955 960
 Thr Ser Cys Pro Pro Leu Leu Glu Ala Phe Pro Leu Pro Arg Ala Ser
 965 970 975
 Leu Arg Ala Thr Val Pro Arg His Ser Ser Val Leu Ala Thr Gly Leu
 980 985 990

His Leu His Arg Gln Ile Ser Leu Pro Leu Arg Gly Phe Leu Leu His
 995 1000 1005
 Gln Pro Leu Pro Gly Gln His Leu Trp Leu Ser His Arg Leu Arg

1010	1015	1020
Leu Arg Leu Pro Arg Thr Gln Arg Pro Pro Arg Ser Ile Leu Ser		
1025	1030	1035
Leu Arg Leu Pro Leu Arg Pro Gln Arg Gly Pro Arg Pro Leu His		
1040	1045	1050
Arg Trp Leu Gln Gln Thr Thr Gly Cys Ser Gln Arg Arg Tyr Pro		
1055	1060	1065
Arg Leu Lys Thr Phe Gly Val Pro Leu Gly Ser Ile Leu Cys Leu		
1070	1075	1080
Ala Gly Ser Leu Ser Thr Met Met Ile Ile Ser Thr Thr Arg Gln		
1085	1090	1095
Glu Cys Gly Arg Arg Ala Ser Val Pro Cys Arg Pro Met Ile Gly		
1100	1105	1110
Ser Ala Arg Pro Gly Pro Trp Arg Thr Ser Ala Met Pro Ser Ala		
1115	1120	1125
Met Gly Val Ala Leu Pro Thr Ser Cys Glu Ser Gly Arg Ser Pro		
1130	1135	1140
Pro Ala Thr Gly Gly Arg Met Pro Gly Ser Gln Ser Ile Met Met		
1145	1150	1155
Ser Trp Met Pro Pro Leu Ala Pro Cys Ala Ala Cys Pro Cys Ser		
1160	1165	1170
Pro Ala Pro Thr Leu Cys Pro Ala His Pro Ala Arg Ala Pro Thr		
1175	1180	1185
Ala Val Pro Ala Phe Thr Pro Leu Ser Ala His Pro Val Pro Val		
1190	1195	1200
Leu Ser Gly Cys His Leu Ala Val Arg Thr Ser Met Leu Thr Leu		
1205	1210	1215
Leu Pro Met Leu Lys Leu Ala Pro Leu Gln Val Thr Thr Thr Leu		
1220	1225	1230
Lys Leu Ile Leu Val Met Leu Glu Ile Val Thr Glu Ser Thr Arg		
1235	1240	1245

Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro Gly Pro Trp		
1250	1255	1260
Arg Ala Ala Leu Gly Lys Glu Val Lys Arg Ser Gln Ser Lys Leu		
1265	1270	1275
Arg Leu Arg Asn Thr Ser Pro Ile Val Phe Phe Leu Ala Pro Tyr		
1280	1285	1290
Phe Pro Arg Arg Met Thr Arg Arg Thr Met Thr Thr Thr Lys Met		
1295	1300	1305
Met Met Met Arg Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg Arg		
1310	1315	1320
Met Thr Met Met Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr Cys		
1325	1330	1335
Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln		
1340	1345	1350
Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro Gly Thr Ser		
1355	1360	1365
Leu Ala Ile Trp Gly Asn Gln Gln Leu Lys Trp Thr Pro His Ile		
1370	1375	1380
Leu Lys Ser Ala Ser Arg Arg Ala Arg Pro Thr Ser Cys Ser Thr		
1385	1390	1395
Cys Arg Met Trp Trp Ile Ala Lys Lys Arg Ile Lys Leu Arg Arg		
1400	1405	1410
Asn Arg Thr Arg Leu Thr Leu Thr Gly Thr Arg Ser Ser Gly Thr		
1415	1420	1425
Arg Ala Ser Pro Ser Ala Val Cys Leu Cys Cys Trp Thr Cys Pro		
1430	1435	1440
Ser Arg Ser Phe Pro Ala Ala Ser Pro Ser Gly Leu Arg Ala Pro		
1445	1450	1455
Val Gly Ala Gln Ala Pro Pro Glu Val Thr Leu Arg Ala Ser Cys		
1460	1465	1470
Ala Ser Ser Ala Ser Lys Ala Cys Ala Gly Leu Trp Pro Trp Gly		

1475 1480 1485
 Ala Gln Val Arg Gln Pro Ser Leu Pro Gly Pro Cys Ala Ser Leu
 1490 1495 1500
 Leu Ser Thr Leu Ser Gln Pro Pro Pro Gln Ala Pro Ser Gln Val
 1505 1510 1515
 Trp Thr Ala Ala Thr Leu Arg Cys Pro Ala Val Pro Ala Ala Ala
 1520 1525 1530

 Cys Pro Pro Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1535 1540 1545
 <210> 1112
 <211> 1541
 <212> PRT
 <213> Artificial Sequence
 <220><223> hTPA- and HA-extended poly-FSP polypeptide 2B
 <400> 1112
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Arg Lys Met
 20 25 30

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

 Glu Gly Ser Glu Ser Asp Asn Leu Gly Leu Leu Tyr Ser Phe Pro Pro
 100 105 110
 Ile Arg Met Cys Ala Leu Ser His Pro Ser Phe Tyr Ile Ser Ser Thr
 115 120 125
 Val Cys Phe Leu Ser Lys His Cys Met Thr Ala Cys Thr Gln Lys Lys

130 135 140
 Gly His Met Ile Phe Ser Arg Glu Lys Ile Ile Asn Pro Thr Ile Ser
 145 150 155 160

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

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

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

 Met His Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe Ser Ser Lys
 355 360 365
 Ile Pro His Pro Gln Val Pro Ser Val Val Ala Leu Cys Lys Phe Arg
 370 375 380

Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro Gln Ala Arg
385 390 395 400
Leu Cys Leu Ile Val Ser Arg Thr Leu Leu Leu Val Gln Ser Ala Ala
405 410 415

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

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

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

Ser Thr Cys Ser Leu Pro Cys Arg Gly Arg Thr Leu Glu Ser Ala Gly
610 615 620
Leu Phe Pro Trp Leu His Thr Gln Cys Thr His Pro Cys Thr Met Leu

625	630	635	640
Leu Pro Gln Gly Trp Trp Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys			
	645	650	655
Lys Met Cys Lys Val Ser Gly Gly Cys Thr Ala Cys Val Glu Arg Cys			
	660	665	670
Pro Trp Lys Gly Ile Cys Trp Lys Trp Pro Val Thr Val Ala Ala Gln			
	675	680	685
Trp Ser Ser Val Thr Ser Leu Glu Trp Thr Ala Gln Glu Arg Gly Cys			
	690	695	700
Ser Ser Trp Leu Met Lys Gln Thr Trp Met Lys Ser Trp Ser Leu Arg			
705	710	715	720
Asp Pro Ser Tyr Arg Ser Ile Leu Glu Tyr Val Ser Thr Arg Val Leu			
	725	730	735
Trp Met Pro Thr Ser Thr Val Arg Arg Arg Asn Ser Arg Lys Gln Ser			
	740	745	750
Gln Val Gln Leu Ala Ile Gln Val Leu Leu Val Asp Lys His Lys Tyr			
	755	760	765
Phe Leu Phe Gly Arg Ala Arg Asn Arg Asn Met Lys Lys Thr Met Ser			
	770	775	780
His Leu Ile Ala His Gln Ala Leu Lys Met Ser Gly Leu Arg Leu Phe			
785	790	795	800
His Pro Arg Leu Leu Thr Arg Lys Lys Pro Gly Lys Phe Leu Pro Ser			
	805	810	815
Arg Phe Pro Trp Gly Pro Pro Pro Leu Cys His Pro Ala Trp Leu Ser			
	820	825	830
Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe His Val Leu			
	835	840	845
Ala Leu Glu Val Thr Phe Pro Pro Gly Thr Ala Met Pro Gln Met Gln			
	850	855	860
Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp Lys Arg Lys Arg			
865	870	875	880

Met Lys Thr Gly Ala Ile Gln Glu Lys Gly Ala Ile Gln Glu Lys Gly
885 890 895

Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe Glu Ala Cys Arg Glu
900 905 910

Met Glu Ser Leu Ser Ala Pro Glu Lys Ile Thr Leu Phe Glu Ala His
915 920 925

Met Ala Arg Cys Thr Ser Ile Asn Val Leu Cys Val Arg Ala Ser Leu
930 935 940

Ile Glu Lys Leu Met Lys Glu Lys Arg Lys Met Lys Arg Asn Gln Val
945 950 955 960

Ala Ser Pro Gln Ile Met Gln Arg Leu Phe Ile Lys Gly Tyr Gln Asn
965 970 975

Asn His Phe Thr Phe His Leu Gln Asn Phe Ala Phe Phe Ser Ser Phe
980 985 990

Gly Asn Asn Lys Tyr Ile Asn Ile Leu Thr Arg Arg Lys Lys Arg Glu
995 1000 1005

Asp His Cys Gly Leu Leu Ile Leu Ile Gln His Gly Gly Ile Phe
1010 1015 1020

Thr Phe Arg Phe Trp Val Glu Lys Leu Ser Trp Asn Ile Cys Lys
1025 1030 1035

Asn Leu Ser Leu Tyr Leu Asp Lys Phe Val Gln Arg Leu Leu Tyr
1040 1045 1050

Val Tyr Ile Ile Glu Thr Asn Val Phe Val Leu Asn Leu Phe His
1055 1060 1065

Val Pro Val Asn Gln Ile Phe Met Met Ala Phe Tyr Leu Lys Tyr
1070 1075 1080

Thr Glu Lys Ala Trp Val Met Glu Leu Glu Trp Leu Ile Gln Gln
1085 1090 1095

Gln Cys Tyr Gln Gln Glu Lys Lys Ser Arg Lys Leu Met Ser Ser
1100 1105 1110

Cys Arg Ala Phe Ile His Thr Pro Arg Ser Pro Gly Cys Ser Val

1115	1120	1125
Tyr Ala Asn Met Cys Trp	Ala Phe Trp Lys Pro Pro	Ser Gln Gly
1130	1135	1140
Ile Ser Ser Cys Leu Met Thr	Gly Cys Trp Gly Ser	Pro Pro Leu
1145	1150	1155
His Leu Cys Gln Pro Leu Arg	Arg Tyr Lys Lys Arg	Gly Val Ile
1160	1165	1170
Ala Trp Arg Arg Arg Lys Trp	Gln Ile Arg His Val	Leu Lys Asn
1175	1180	1185
Leu Ile Leu Phe His Val Arg	Asn Ile Val Tyr Gly	Ile Gln Val
1190	1195	1200
Met Leu Cys Gly Lys Gly Leu	Thr His Pro Val Pro	Leu Lys Arg
1205	1210	1215
Thr Leu Gln Asn Lys Arg Asn	Lys Asn Ile Lys Arg	Val Asn Gln
1220	1225	1230
Lys Lys Gly Asn Ile Lys Arg	Lys Ser Ile Leu Leu	His Leu Ile
1235	1240	1245
Val Leu Asn Ser Pro Glu Ser	Asn Pro Lys Phe Phe	Leu Thr Phe
1250	1255	1260
Ser Gln Leu Glu Lys Lys Ala	Thr Trp Met Arg Arg	Thr Gly Ala
1265	1270	1275
Leu Arg Ala Thr Ala Pro Ala	Thr Ala Ala Pro Gln	Ala Gln Thr
1280	1285	1290
Pro His Trp Arg Ala Ala Thr	Thr Ser Ser Met Ser	Ser Ser Pro
1295	1300	1305
Arg Ala Glu Pro Thr Ser Ser	Ser Ser Trp Ala Thr	Cys Trp Pro
1310	1315	1320
Arg Cys Cys Ser Ser Ser Cys	Tyr Trp Ser Leu Ser	Ser Trp Pro
1325	1330	1335
Pro Ala Gly Ala Ala Glu Ala	Thr Asn Thr Arg Thr	Arg Ser Arg
1340	1345	1350

Glu Ser	Gln Arg Gly Arg Met	Leu Thr Trp Arg Ser	Ser Leu Trp
1355	1360	1365	
Leu Gln	Gly Thr Arg Cys Phe	Thr Gly Val Arg Thr	Ser Ser Gly
1370	1375	1380	
Ser Cys	Gly Arg Ala Cys Ser	Cys Gly Arg Gly Cys	Gly Thr Pro
1385	1390	1395	
Arg Gly	Asp Trp Lys Arg His	Pro Pro Arg Arg Asn	Ser Val Ile
1400	1405	1410	
Val His	Lys Ile Val Leu Val	Phe Leu Lys Ser Leu	Ser Ser Tyr
1415	1420	1425	
Asn Cys	Glu Arg Arg Ile Ser	Gly Ile Gln Lys Arg	Ala Ile Glu
1430	1435	1440	
Phe Ala	Val Leu Lys Leu Leu	Asn Met Asp Leu His	Trp Asn Ser
1445	1450	1455	
Ala Tyr	Leu Gly Arg Thr Leu	Leu Val Thr Cys Ile	Leu Tyr His
1460	1465	1470	
Arg Trp	Ile Val Thr Ser Met	Cys Gln Ser Gln Arg	Trp Leu Thr
1475	1480	1485	
Ser Thr	Thr Ser Arg Ser Ser	Ala Leu Met Trp Thr	Arg Gln Ile
1490	1495	1500	
Asn Arg	Arg Lys Leu Gln Arg	Lys Lys Arg His Pro	Ser Trp Pro
1505	1510	1515	
Trp Thr	Arg Cys Leu Arg Met	Arg Pro Pro Arg Ser	Gly Tyr Pro
1520	1525	1530	
Tyr Asp	Val Pro Asp Tyr Ala	Ser	
1535	1540		
<210>	1113		
<211>	1546		
<212>	PRT		
<213>	Artificial Sequence		
<220><223>	hTPA- and HA-extended poly-FSP polypeptide 3B		
<400>	1113		

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Gly Ala Ala
20 25 30
Ala Ala Ser Cys Gln Ser Pro Pro Ser Pro Arg Glu Thr Thr Pro Ser
35 40 45
Ser Asp Ala Thr Arg Arg Thr Arg Pro Ile Ala Ala Gln Ser Lys Lys
50 55 60
Thr Met Thr Ala Ala Gly Leu Thr Pro Lys Asn Lys Lys Arg Arg Lys
65 70 75 80
Leu Arg Pro Lys Met Ile Arg Lys Ile Gln Lys Arg Arg Arg Thr Ala
85 90 95
Asn Arg Arg Asn Ser Arg Arg Ala Thr Pro Thr Ser Lys Gly Ser Leu
100 105 110
Arg Arg Lys Tyr Leu Arg Val Arg Gly Pro Pro Leu His Thr Arg Asn
115 120 125
Ile Arg Lys Leu Ile Trp Thr Lys Gln Arg Ser Phe Leu Ser Leu Phe
130 135 140
Pro Lys Leu Arg Ala Thr Glu Gln Met Thr Asn Val Gly Cys Ser Ile
145 150 155 160
Pro His Val Pro Lys Ala Thr Ala Ala His Ser Val Thr Val Lys Leu
165 170 175
Gln Leu Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser Arg His Thr
180 185 190
Met Ser Leu Ser Asn Ile Leu Met Lys Phe Arg Leu Gln Ser Ser Pro
195 200 205
Phe Leu Ala Arg Ser Trp Asn Thr Met Gln Trp Asn Asn Lys Lys Met
210 215 220
Ala Met Thr Val Ile Ala Gly Ala His His Cys Gln Tyr Lys Leu Thr
225 230 235 240
Tyr Thr Lys Val Trp Lys Met Asn Trp Lys Lys Met Met Ile Gly Ser

245 250 255
 Gln His Leu Leu Phe Ser Pro Leu Asp Ser Ser Pro Leu Gln Leu Leu
 260 265 270
 Leu His Pro His Gly Lys Arg Cys Asn Pro Cys Cys Arg Leu Thr Trp
 275 280 285
 Met Ser Gln Asn Thr Arg Ser Thr Asn Leu Glu Lys Asn Pro Ser Leu

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

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

 420 425 430
 Trp Gly Pro Val Tyr Tyr Val Cys Asn Arg Met Asn Val Ser Ser Val
 435 440 445
 Leu Lys Pro Phe Leu Phe Thr Val Pro Ile Glu Asp Met Arg Glu Cys
 450 455 460
 Thr Leu Gly Arg Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Cys
 465 470 475 480
 Leu Ile Pro Val Pro Ile Ser Glu Lys Lys Arg Lys Leu Pro Asn Ile

 485 490 495

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

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

 610 615 620
 Gly Thr His Pro Thr Pro Arg Leu Ser Cys Leu Arg Val Arg Cys Gly
 625 630 635 640
 Gly Trp Leu Cys Gly Trp Thr Pro Arg Gly Arg Lys Ser Gly Val Met
 645 650 655
 Lys Cys Trp Asp Leu Cys Pro Val His Lys Lys Arg Gly Leu Phe Arg
 660 665 670
 Leu Asp Phe His Pro Arg Ser Ser Ser Gly Lys Gly Lys Asn Ser Pro

 675 680 685
 Cys Cys Gln Lys Lys Leu Arg Val Gln Asn Gln Gly His Leu Leu Met
 690 695 700
 Ile Leu Leu His Asn Asp Arg Val Phe Leu Val Lys Ile Gly Glu Lys
 705 710 715 720
 Leu Lys His Cys Phe Lys Ala Trp Gly Ser Arg Arg Asn Arg Arg Tyr
 725 730 735
 Arg Lys Ile Tyr Gly Glu Leu Lys Met Ser Leu Gln Ala Phe Leu Ile

740 745 750
 His Leu Arg Lys Val Asp Thr His His Leu Gln Val Val Thr Lys Thr
 755 760 765
 Val Thr Ala Thr Thr Ala Asp Gly Gln Arg Met Arg Arg Leu Lys Cys
 770 775 780
 Lys Ala Cys Arg Leu Arg Trp Ala Arg Pro Glu Pro Ala Ala Gln Ala
 785 790 795 800
 Pro Pro Lys Ser His Phe Pro Pro His Pro Ser Gly Pro Ser Arg Thr

 805 810 815
 Ser Ser Leu Gln Leu Arg Ser Leu Phe Phe Ser His Cys Leu Cys Ser
 820 825 830
 Gln Lys Lys Asp Pro Ala Gly Lys Leu Lys Lys Leu Leu Lys Lys Ser
 835 840 845
 Ser Gln Leu Arg Arg Ser Trp Arg Asn Val Ser Arg Ile Ser Thr Pro
 850 855 860
 Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala Pro Val Ser Val Ile Thr

 865 870 875 880
 Met Lys Leu Trp Glu Lys His Phe Lys Gly Leu Asn Trp Asn Leu Val
 885 890 895
 Val Trp Ile Leu Asn Leu Lys Met Met Thr Tyr Met Glu Met His Tyr
 900 905 910
 Gly His Gln Ala Pro Gln Val Ala Met Leu Pro Lys Leu Leu Cys Arg
 915 920 925
 Gln Met Leu Pro Thr Leu Ser Thr Leu Gln Gln Arg His Pro Gln Gly

 930 935 940
 Pro Cys Pro Pro Pro Val Thr Pro Leu Arg Val Gln Ser Val Leu Leu
 945 950 955 960
 Leu Gly Val Pro Gln Thr Ala Arg Gly Pro Arg Arg Lys Val Leu Met
 965 970 975
 Val Leu Trp Leu Pro Ala Asn Gln Ser Leu Gln Lys Ser Gln Val Phe
 980 985 990

Gln Trp Val Leu Arg Thr Glu Val Ala Pro Arg Cys Pro Arg Ser Ala

995	1000	1005
Val Asp Ile Ser Pro Gly Pro Thr Ser Pro Ser Leu Ala Ser Cys		
1010	1015	1020
Ala Ser Val Ala Ile Gly Lys Leu Ala Leu Leu Gly Ala Ser Ala		
1025	1030	1035
Pro Cys Gly Ala Ala Gly Ala Arg Glu Ala Gly Arg Phe Ala Val		
1040	1045	1050
Leu Gly Thr Met Val Met Lys Leu Cys Phe Phe Tyr Leu Leu Tyr		

1055	1060	1065
Arg Leu Arg Ile Pro Ser Leu Arg Lys Tyr Arg Gln His Leu Asn		
1070	1075	1080
Arg Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu Thr Met		
1085	1090	1095
Met Met Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile Pro		
1100	1105	1110
Leu Pro Ser Pro Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His		

1115	1120	1125
Pro Pro Pro Pro Cys Leu Leu Leu Leu His His Arg His His Leu		
1130	1135	1140
Ala Phe Leu Glu Met Ala Cys Ser Ser Gln His Thr His Ser Ile		
1145	1150	1155
Lys Ile Trp Ile Ser Phe Ser His Glu Val Asp Pro Pro Gly Ser		
1160	1165	1170
Val Trp Ile Leu Pro Cys Asp Leu Pro Arg Met Leu Pro Ile Ser		

1175	1180	1185
Ser Pro Leu His Arg Pro Gln Met Pro Phe Trp Thr Cys Thr Phe		
1190	1195	1200
Pro Ala Thr Thr Trp Gly Thr Trp Glu Thr Pro Ser Thr Trp Gly		
1205	1210	1215
Trp Arg Thr Phe Arg Gly Ala Ser Ser Ser Thr Ser Arg Asp Ser		

1220 1225 1230
Arg Ser Phe Phe Thr Ser Ala His Pro Ser Arg Pro Cys Arg Met

1235 1240 1245
Arg Leu Tyr Gln Cys Lys Lys Lys Leu Leu Leu Lys Leu Leu Thr

1250 1255 1260
Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg Ala Arg

1265 1270 1275
Gly Gly Thr Thr Ile Gly Glu Val Thr Ser Cys Thr Asn Leu Ser

1280 1285 1290
Val Pro Met Met Leu Thr Ile Leu Ile Trp Lys Arg Val Phe Ile

1295 1300 1305
Leu Leu Leu Ser Asp Lys Lys Gly Ala Lys Lys Ile Thr Phe Leu

1310 1315 1320
Pro Ile Pro Pro His Leu Arg His Pro Leu Leu Leu Phe Glu Lys

1325 1330 1335
Lys Arg Pro Glu Trp Leu Ser Met Asp Leu Asp Gly Met Leu Thr

1340 1345 1350
Val Ile Gly Gln Gly Leu Val Gly Met Thr Pro Arg Asp Leu Gly

1355 1360 1365
Thr Val Ala Gly Ala Thr Ala Gln Ile Gln Arg Pro Ile Gln Val

1370 1375 1380
Gln Thr Gly Gly Arg Leu Arg Arg Asn Leu Gln Arg Asn Leu Lys

1385 1390 1395
Val Leu Gln Val Ser Val Tyr Ser Gly Asn Leu Leu Ser Phe Ser

1400 1405 1410
Arg Arg Gly Met Lys Ser Ser Val Arg Leu Lys Asn Arg Glu Trp

1415 1420 1425
Glu Lys Arg Lys Gln Ile Leu Gly Gly Gly Gly Lys Tyr Lys Glu

1430 1435 1440
Tyr Phe Leu Lys Arg Ile Leu Ile Arg Lys Ala Met Thr Val Leu

1445 1450 1455

Ala Gly Asp Lys Lys Gly Leu Gly Arg Phe Met Arg Cys Val Gln
1460 1465 1470
Ser Glu Thr Lys Ala Val Ser Leu Gln Leu Pro Leu Gly Arg Asn
1475 1480 1485
Met Glu His Arg Leu Thr Met Asp Ser Ala Leu Ser Leu Thr Lys
1490 1495 1500
Arg Glu Gly Pro Glu Thr Leu Lys Lys Lys Tyr Leu Val Gln His
1505 1510 1515
Gln Met Lys Cys Leu Thr Ala Val Asp Cys Leu Gln Ala Phe Trp
1520 1525 1530
Asp Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1535 1540 1545
<210> 1114
<211> 1547
<212> PRT
<213> Artificial Sequence
<220><223> hTPA- and HA-extended poly-FSP polypeptide 4B
<400> 1114
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Ile Gln Lys
20 25 30
Lys Lys Gln Lys Ser Asn Leu Asp Leu Gln His Gln Arg Arg Arg Lys
35 40 45
Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro Lys Ala Asn
50 55 60
Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln Asn Leu Leu Asn
65 70 75 80
Leu Val Gln Leu Asn Pro His Ser Pro His His Arg Lys Asp Glu Glu
85 90 95
Asp His Gln Lys Arg His His His His Asn Gln Lys Lys Met Ser Val

100	105	110	
Met Ala Lys Lys Ser Gln Gln Pro Leu Gly Gln Ala Phe Gly Ser Leu			
115	120	125	
Cys Gln Leu Val Ser Ala Asp Phe Ser Ala Pro Gln Val Thr Arg Leu			
130	135	140	
Arg Ser Leu Asn His Leu Leu Ile Asn Glu Gly Asn Asn His Trp Pro			
145	150	155	160
Arg Val Glu Met Pro Thr Gly Trp Leu Leu Val Gly Tyr Asn Thr Arg			
165	170	175	
Asn Thr Ala Gln Asn Pro Arg Leu Gln Gln His Leu Lys His Trp Gln			
180	185	190	
Gln Cys Thr Arg Ala Arg Trp Cys Gln Glu Pro Cys Gln Thr Leu Thr			
195	200	205	
Phe Phe His Phe Phe Phe Phe Phe Lys Thr Val Ser Leu Cys Cys Pro			
210	215	220	
Gly Trp Ser Lys Gly Gln Pro Pro Pro Pro Gly Leu Lys Pro Ser Ser			
225	230	235	240
Leu Ala Ser Gln Val Ala Arg Thr Thr Gly Val Tyr Gln His Val Trp			
245	250	255	
Leu Ile Cys Phe Val Phe Phe Val Cys Val Glu Thr Gly Phe Cys His			
260	265	270	
Val Ala Gln Val Gly Leu Glu Arg Leu Val Ser Leu Ser Gly Ile Thr			
275	280	285	
Asp Val Asn His Trp Ala Gln Pro Lys Pro Ser Pro Ser Lys Gly Thr			
290	295	300	
Gly Met Asn Arg Pro Ile Gly Leu Arg Val Gly Lys Gly Val Trp Ala			
305	310	315	320
Arg Leu Arg Ala Ser Val Ser Phe Trp Thr Leu Leu Pro Thr Thr Gly			
325	330	335	
Val Arg Thr Arg Gly Ser Pro Leu Arg Leu Thr Leu Trp Pro Pro Arg			
340	345	350	

Asn Ile Leu Asn Ser Leu Pro Ser Ser Met Glu Ile Ala Val Leu Gln

355 360 365
Glu Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr

370 375 380
Asp Asn Leu His Leu Cys Tyr Tyr His Ser Gln Ser Asn Arg Asn Lys

385 390 395 400
Ser Arg Gln Met Glu Ser Leu Gly Met Lys Leu Gln Ser Pro Leu Trp

405 410 415
Asp Cys Ser Thr Thr Thr Gly Thr His His Gly Cys Leu Trp Glu Ile

420 425 430
Pro Ser Val Thr Leu Leu Ala Cys Arg Val Asn Ala Val Glu Glu Leu

435 440 445
His Ser Arg Arg Met Ser Val Arg Ile Val Lys Asn Trp Val Ser Cys

450 455 460
Cys Tyr Val Arg Leu Ser Ala Val Gly Leu Ser Thr Trp Ser Ala Leu

465 470 475 480
Asp Val Val Ile Asn Leu Lys Arg Leu Gln Lys Phe Ser Gln Lys Ser

485 490 495
Gln His His Cys Ala Leu Arg Lys Ile Glu Trp Ala Thr Lys Leu Ser

500 505 510
Leu Gly Gly Lys Ala Gly Pro Gln Ala Gln Glu Lys Ala Asn Ala Lys

515 520 525
Lys Met Pro Phe Gln Arg Trp Ile Phe Ser Asn Gln Leu Thr Val Gln

530 535 540
Met Leu Cys Leu Pro Ile Glu Ala Leu Thr Ala Leu Phe Thr Cys Arg

545 550 555 560
Thr Ala Ser Ile Ser Val Asn Ile Ser Thr Leu Met Ser Ile Leu Glu

565 570 575
Ala Pro Leu Phe Phe His Gly Asp Leu Cys Glu Glu Lys Lys Asn Gly

580 585 590
Arg Ile Ser Ser Gln Ala Pro Leu Arg Leu Trp Ser Trp Cys Gly Thr

595 600 605
Ser Gln Thr Tyr Phe Gly Ser Thr Ala Lys Lys Ser Pro Thr Ser Phe

610 615 620
Cys Cys Glu Trp Gly Gly Gln Ala His Arg Gln Arg Asn Thr Gly Met
625 630 635 640

Glu Ile Leu Leu Trp Ile Leu Leu Lys Met Glu Ile Gln Ile Phe Lys
645 650 655

Ile Cys Leu Gly Glu Met Gln Leu Cys Thr Tyr Thr Pro His Ile Cys
660 665 670

Arg His Thr Cys Arg Gly Gly Pro Ser Ala Ser Asp Arg Cys Cys Ser

675 680 685
Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly Arg Cys Pro Val Gln
690 695 700

Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu Arg Arg Trp Gly Pro
705 710 715 720

Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly Phe Gln Leu Leu Arg
725 730 735

Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro Arg Lys Gly Pro Phe

740 745 750
Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Ala Val Thr Val Met Ala
755 760 765

Gly Ser Val Pro Ser Ala Gln Ser Val Asp Ala Leu Glu Ser Pro Gly
770 775 780

Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro Arg Asn Leu Leu Trp Arg
785 790 795 800

Glu Met Ser Ile Phe Leu Pro Gly Ile Phe Thr Ser Arg Ile Leu Asn

805 810 815
Leu Gln Val Leu Lys Lys Ile Leu Arg Ser Phe Met Lys Leu Tyr His
820 825 830

Ser Leu Val Met Cys Leu Arg Leu Arg Thr Lys Leu Glu Lys Ala Leu
835 840 845

Ser Ala Leu Phe Ile Trp Pro Gln His Ser Tyr Lys Gln Arg Pro Pro
850 855 860
Leu Gln Pro Val Gln Val Val Leu Arg Leu Gly Asn Leu Pro Pro Phe
865 870 875 880
Phe Arg Gly Ser Glu Val Pro Phe Pro Arg Pro Cys Arg Thr Lys Met
885 890 895
Leu Asn Gln Lys Cys Leu Ala Pro Phe Ile Thr His Pro Phe Ala Ser
900 905 910
Gln Pro Leu Gly Gln Glu Met Pro Asn Asn Thr Gln Ile Arg Leu Leu
915 920 925
Lys Pro Leu Leu Thr Pro Asp Thr Arg Trp Ile Phe Ser Asn Gln Leu
930 935 940
Gln Thr Val Gln Met Leu Cys Leu Pro Pro Leu Lys Gln Gly Glu Arg
945 950 955 960
Ile Ile Trp Pro Leu Gly Gly Phe Gln Ile Pro Asn Phe Phe Trp Ser
965 970 975
Leu Gly Ile Gly His Thr Gly Ala Trp Trp His Thr Gly Arg Arg Arg
980 985 990
Arg Glu Trp Gly Gly Ser Thr Val Ser Arg Ser Pro Leu Trp Ile Ser
995 1000 1005
Ser Met Ile Tyr Leu Arg Gly Met Ala Phe Ala Ser Asp Ser Ser
1010 1015 1020
Ile Arg Thr Thr Arg Val Ser Trp Cys Arg Arg Cys Gly Ala Lys
1025 1030 1035
Ser Ala Ala Ala Ser Ser Leu Lys Lys Lys Pro Arg Asp Ile Cys
1040 1045 1050
Arg Ile Ser Asp Ser Lys Lys Met Thr Gln Lys Arg Glu Ser Thr
1055 1060 1065
Leu Gly Asn Phe Trp Met Lys Leu Leu Gln Leu Pro Asp Lys Lys
1070 1075 1080
Lys Lys Ser Thr Glu Lys Thr Lys Ile Ile Lys Lys Met Lys Lys

1085	1090	1095
Arg Ile Met Val His Met Cys Ser Ser Leu Ala Leu Pro Thr Gly		
1100	1105	1110
Leu Thr Ser Leu Ile Leu Pro Ser Ser Asp Leu Ala Val Leu Ile		
1115	1120	1125
Ser Ser Ser Thr Ser His Phe Leu Met Arg Ser Pro Val Leu Pro		
1130	1135	1140
Ser Ser Arg Leu Thr Cys Ala Ser Pro Gln Leu Pro Arg Met Trp		
1145	1150	1155
Thr Trp Ser Ser Trp Leu Lys Trp Leu Lys Asn Trp Lys Arg Phe		
1160	1165	1170
Lys Leu Lys Lys Lys Tyr Ile Leu Ala Met Thr Leu Thr Leu Asn		
1175	1180	1185
Gly His Pro Arg Thr Ala Ser Ile Thr Leu Pro Thr Thr Ser Leu		
1190	1195	1200
Lys Gly Ser Arg Thr Ser Cys Cys Pro Arg Ser His Pro Arg Leu		
1205	1210	1215
Pro Arg Thr Lys Trp Pro Leu Gln Cys Leu Leu His Ser Leu Gly		
1220	1225	1230
Thr Thr Gly Thr Leu Val Trp Glu Arg Gly Val Leu Gln Met Arg		
1235	1240	1245
Ser Leu Glu Ala His Cys Pro Leu Gln Thr Phe His Leu His His		
1250	1255	1260
Cys Arg Thr Gln Pro Ser Ser Cys Pro Pro Ala Trp Ile Leu Tyr		
1265	1270	1275
Gln Gly Gln Trp Ser Gly Ala Val Val Gly Leu Arg Pro Val Ala		
1280	1285	1290
His His Leu Pro Arg Pro Ile Gln Gly Leu His Cys Pro Gln Ala		
1295	1300	1305
Pro His Gln Pro Ala Leu Ser Trp Gly Lys Trp Pro Val Gly Met		
1310	1315	1320

Thr Gly	Pro Ala Arg Cys Cys	Arg Trp Pro Arg Arg	Glu Leu Lys
1325	1330	1335	
Lys Asn	Leu Leu Leu Pro Cys	Arg Cys Arg Arg Glu	Tyr Arg Val
1340	1345	1350	
Thr Met	Gly Gln Ala Phe Gly	Ser Phe Ser Ala Asp	Phe Ser Ala
1355	1360	1365	
Pro Gln	Val Leu Lys Lys Asn	Arg Lys Gln Asn Lys	Ile Ile Cys
1370	1375	1380	
Lys Gly	His Arg Ile Thr Ser	Leu Ile Leu Ser Phe	Gln Arg Val
1385	1390	1395	
Lys Leu	Lys Lys Lys Val Asn	Ala Cys Ser Pro Ala	Cys Thr Ser
1400	1405	1410	
Lys Ala	Trp Thr Pro Arg Lys	Leu Val Gly Arg Ala	Val Arg Arg
1415	1420	1425	
Lys Gly	Ile Ile Cys Ile Lys	Asn Met Phe Leu Gln	Arg Lys Gly
1430	1435	1440	
Phe Leu	Asn Leu Ser His Val	Glu Lys Phe Val Pro	Pro Ser Pro
1445	1450	1455	
Pro Leu	Ala Leu Gly Pro Arg	Met Gln Leu Cys Thr	Gln Leu Ala
1460	1465	1470	
Arg Phe	Phe Pro Ile Thr Pro	Pro Val Trp His Ile	Leu Gly Pro
1475	1480	1485	
Gln Arg	His Thr Pro Cys Gln	Lys Lys Val Pro Ser	Ala Ser Pro
1490	1495	1500	
Trp Gly	Leu Arg Pro Ser Pro	Cys Leu Ser Trp Ser	Ser Arg Ile
1505	1510	1515	
Val Ala	Pro Gly His Ala Leu	Ser Cys Arg Thr Arg	Arg Arg Trp
1520	1525	1530	
Ser Ser	Lys Gly Tyr Pro Tyr	Asp Val Pro Asp Tyr	Ala Ser
1535	1540	1545	

<210> 1115

<211> 1750

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 1A

<400> 1115

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu

180 185 190

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

195 200 205

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys

210 215 220
 Gln Asp Leu Gly Pro Val Pro Met Thr Glu Ile Gln Leu Thr Met Asn

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

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

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

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

Ser Lys Ile Glu Ala Ser Pro Ile Gly Ser Ile Ala Ser Ser Pro Gly
 465 470 475 480
 His Pro Leu Gly Pro Thr Leu Ala Ile Arg Phe Ile Ser Ala Pro Gln

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

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

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

 675 680 685
 Arg Arg Ala Arg Pro Thr Ser Cys Ser Thr Cys Arg Met Trp Trp Lys
 690 695 700
 Gly Lys Lys Arg Arg Lys Glu Ile Val Pro Met Ser Leu Ala Cys Ser

705 710 715 720
 Ile Thr Val Ser Phe Val Gly Gln Ile Ser Thr Leu Val Leu Asp Val
 725 730 735
 Ser Ser Ile Ser His Trp Arg Leu Pro Cys Lys Val Thr Glu Ser Ser

 740 745 750
 Ser Ser Phe Phe Tyr Thr Ser Asp Arg Thr Pro Leu Ser Ile Ser Arg
 755 760 765
 Pro Thr Ser Arg Ala Arg Gln Ser Cys Cys Leu Pro Gly Leu Thr His
 770 775 780
 Pro Ala His Gln Pro Leu Gly Ser Met Ser Thr Arg Arg Glu Met Pro
 785 790 795 800
 Ser Gln Ala Thr Pro Ser Pro Pro Gly Pro Trp Arg Ala Ala Leu Gly

 805 810 815
 Lys Glu Val Lys Arg Ser Gln Ser Lys Leu Arg Leu Arg Asn Thr Ser
 820 825 830
 Pro Gly Glu Lys Asn Asp Leu Gln Leu Phe Val Met Ser Asp Thr Thr
 835 840 845
 Tyr Lys Ile Tyr Trp Thr Val Ile Leu Leu Asn Pro Cys Gly Asn Leu
 850 855 860
 His Leu Lys Thr Thr Ser Leu Gln Arg Pro Pro Arg Ser Ile Leu Ser

 865 870 875 880
 Leu Asn Gly Ile Trp Glu Val Met Pro Arg Thr Leu Glu Gly Cys Ile
 885 890 895
 Ser Val Lys Asp His Arg Thr Ser Gln Asn His Ser Lys Cys Ile Thr
 900 905 910
 Glu Cys Val Arg Thr Ala Leu Asn Val Ser Lys Lys Arg Leu Pro Lys
 915 920 925
 Leu Met Lys Lys Lys Asp Ser Thr Ile Phe Ile Asn Lys Val Arg Gln

 930 935 940
 Asn Phe Lys Arg Asn Phe Lys Lys Lys Lys Pro Leu Thr Phe Ser Pro
 945 950 955 960

Ser	Arg	Arg	Met	Thr	Arg	Arg	Thr	Met	Thr	Thr	Thr	Lys	Met	Met	Met		
				965					970					975			
Met	Arg	Arg	Thr	Lys	Arg	Arg	Arg	Arg	Lys	Arg	Arg	Arg	Met	Thr	Met		
				980					985					990			
Met	Thr	Arg	Arg	Thr	Leu	Leu	Thr	Lys	Lys	Thr	Cys	Leu	Thr	Pro	Arg		
				995					1000					1005			
Thr	Ser	Ala	Ala	Thr	Lys	Ala	Leu	Pro	Arg	Gln	Thr	Ile	Ser	Gln			
				1010					1015					1020			
Arg	Arg	Pro	Ile	Gln	Thr	Pro	Pro	Gly	Thr	Ser	Leu	Ala	Ile	Trp			
				1025					1030					1035			
Gly	Arg	Thr	Arg	Leu	Thr	Leu	Thr	Gly	Thr	Arg	Ser	Ser	Gly	Thr			
				1040					1045					1050			
Arg	Ala	Ser	Pro	Ser	Ala	Val	Cys	Leu	Cys	Cys	Trp	Thr	Cys	Pro			
				1055					1060					1065			
Ser	Arg	Ser	Phe	Pro	Ala	Ala	Ser	Pro	Ser	Gly	Leu	Arg	Ala	Pro			
				1070					1075					1080			
Val	Gly	Ala	Gln	Ala	Pro	Pro	Glu	Val	Thr	Leu	Arg	Ala	Ser	Cys			
				1085					1090					1095			
Ala	Ser	Ser	Ala	Ser	Lys	Ala	Cys	Ala	Gly	Leu	Trp	Pro	Trp	Gly			
				1100					1105					1110			
Ala	Gln	Val	Arg	Val	Gly	Ala	Gly	Thr	Gly	Gly	Gly	Pro	Ala	Cys			
				1115					1120					1125			
Val	Pro	Val	Ala	Glu	Ala	Ser	Thr	Gly	Ala	Trp	Thr	Ala	Glu	Gly			
				1130					1135					1140			
Ala	Ala	Gly	Thr	Arg	Cys	Arg	Ala	Ser	Arg	Ala	Pro	Cys	Arg	Gln			
				1145					1150					1155			
Leu	Pro	Ala	Ser	Ser	Pro	Thr	Lys	Cys	Glu	Ile	Cys	Val	Lys	Arg			
				1160					1165					1170			
Arg	Arg	Arg	Arg	Lys	Arg	Ser	Ser	Gln	Ser	Arg	Ser	Pro	Val	Pro			
				1175					1180					1185			
Lys	Lys	Arg	Glu	Arg	Met	Met	Leu	Pro	Val	Arg	Ala	Arg	Thr	Ala			

1190	1195	1200
Arg Ser Ala Leu Pro Gln Gly	Arg Ala Pro Leu Glu	Gly Met Leu
1205	1210	1215
Leu Pro Arg Ala Leu Pro Ser	Leu Leu Ser Arg Met	Pro Ala Arg
1220	1225	1230
Arg Glu Ser Arg Phe Trp Leu	Ala Leu Gln Ala Leu	Gly Leu Arg

1235	1240	1245
Pro Pro His Leu Pro Ser Cys	His Pro Leu Pro Gln	Leu Leu Gly
1250	1255	1260
Pro Pro Pro Pro His Gln Ala	Pro Met Thr Leu Lys	Ala Leu Val
1265	1270	1275
Lys Thr Trp Thr Gln Phe Arg	Asn Tyr Pro Arg Ala	Asp Lys Lys
1280	1285	1290
Asn Val Arg Ser Thr Ala Phe	Phe Leu Leu Asp Ile	Ile Leu Gly

1295	1300	1305
Asp Cys Pro Arg Thr Met Ala	Gly Pro Ser Ala Ser	Leu His Pro
1310	1315	1320
Ala Ser Gly Arg Ala Ser Arg	Lys Thr Trp Gln Arg	Arg Leu Arg
1325	1330	1335
Ala Cys Arg Ala Gly Gly Pro	Ala Gly Trp Ala Arg	Gln Ala Tyr
1340	1345	1350
Pro Arg Leu Lys Thr Phe Gly	Val Pro Leu Gly Ser	Ile Leu Cys

1355	1360	1365
Leu Ala Gly Ser Leu Ser Thr	Met Met Ile Ile Ser	Thr Thr Arg
1370	1375	1380
Gln Glu Cys Gly Arg Arg Ala	Ser Val Pro Cys Arg	Pro Met Ile
1385	1390	1395
Gly Ser Ala Arg Pro Gly Pro	Trp Arg Thr Ser Ala	Met Pro Ser
1400	1405	1410
Ala Met Gly Val Ala Leu Pro	Thr Ser Cys Glu Ser	Gly Arg Ser

1415	1420	1425

Pro	Pro	Ala	Thr	Gly	Gly	Arg	Met	Pro	Gly	Ser	Gln	Ser	Ile	Met
1430							1435					1440		
Met	Ser	Trp	Met	Pro	Pro	Leu	Ala	Pro	Cys	Ala	Ala	Cys	Pro	Cys
1445							1450					1455		
Ser	Pro	Ala	Pro	Thr	Leu	Cys	Pro	Ala	His	Pro	Ala	Arg	Ala	Pro
1460							1465					1470		
Thr	Ala	Val	Pro	Ala	Phe	Thr	Pro	Leu	Ser	Ala	His	Pro	Val	Pro
1475							1480					1485		
Val	Leu	Ser	Gly	Cys	His	Leu	Ala	Val	Arg	Thr	Ser	Met	Leu	Thr
1490							1495					1500		
Leu	Leu	Pro	Met	Glu	Ala	Lys	Lys	Ser	Met	Lys	Arg	Ser	Asn	Ala
1505							1510					1515		
Lys	Lys	Met	Glu	Asp	Met	Ile	Trp	Glu	Ser	Arg	Leu	Pro	Leu	Arg
1520							1525					1530		
Pro	Gln	Arg	Gly	Pro	Arg	Pro	Leu	His	Arg	Trp	Leu	Gln	Gln	Thr
1535							1540					1545		
Thr	Gly	Cys	Ser	Gln	Arg	Arg	Ile	Val	Phe	Phe	Leu	Ala	Pro	Tyr
1550							1555					1560		
Phe	Pro	Arg	His	Pro	His	Arg	Ser	Pro	Pro	Thr	Ser	Cys	Pro	Pro
1565							1570					1575		
Leu	Leu	Glu	Ala	Phe	Pro	Leu	Pro	Arg	Ala	Ser	Leu	Arg	Ala	Thr
1580							1585					1590		
Val	Pro	Arg	His	Ser	Ser	Val	Leu	Ala	Thr	Gly	Leu	His	Leu	His
1595							1600					1605		
Arg	Gln	Ile	Ser	Leu	Pro	Leu	Arg	Gly	Phe	Leu	Leu	His	Gln	Pro
1610							1615					1620		
Leu	Pro	Gly	Gln	His	Leu	Trp	Leu	Ser	His	Arg	Leu	Arg	Leu	Arg
1625							1630					1635		
Leu	Pro	Arg	Thr	Gln	Pro	Ser	Leu	Pro	Gly	Pro	Cys	Ala	Ser	Leu
1640							1645					1650		
Leu	Ser	Thr	Leu	Ser	Gln	Pro	Pro	Pro	Gln	Ala	Pro	Ser	Gln	Val

1655 1660 1665
 Trp Thr Ala Ala Thr Leu Arg Cys Pro Ala Val Pro Ala Ala Ala
 1670 1675 1680
 Cys Pro Pro Ala Leu Arg Ser Met Pro Lys Ser Arg Asn Gln Val
 1685 1690 1695
 Leu Phe Arg Arg Asn Leu Thr Pro Ser Gln Leu Arg Thr Leu Ala
 1700 1705 1710
 Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser

1715 1720 1725
 Arg Lys Gln Ile Pro Ser Gln Ser Met Leu Val Gly Tyr Pro Tyr
 1730 1735 1740

Asp Val Pro Asp Tyr Ala Ser

1745 1750

<210> 1116

<211> 1744

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 2A

<400> 1116

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
 1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met
 20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala
 35 40 45

Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Leu Ala Gly Gln
 50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys
 65 70 75 80

Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg Met Lys
 85 90 95

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

100	105	110	
Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met			
115	120	125	
Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His			
130	135	140	
Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly			
145	150	155	160
Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile			
165	170	175	
Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu			
180	185	190	
Met Ser Arg His Ser Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys			
195	200	205	
Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys			
210	215	220	
Gln Asp Leu Gly Pro Val Pro Met Arg Lys Met Gln Ser Leu Asn His			
225	230	235	240
Pro Ser Arg Leu Thr Asn Gly Ser Pro Pro Leu His Leu Cys Gln Pro			
245	250	255	
Leu Arg Met Ser Arg Thr Pro Pro Arg Arg Val Cys Ala Ala Pro Pro			
260	265	270	
His Arg Leu Leu Gly Pro Ser Arg Trp Asn Pro Arg Arg Lys Thr Trp			
275	280	285	
Lys Met Arg Lys Lys Tyr Ala Gln Lys Pro Ser Gln Lys Asn His Leu			
290	295	300	
Tyr Gly Gly Lys Lys Arg Ser Lys Phe Ser Arg Ser His Leu Asp Phe			
305	310	315	320
Ser Pro Tyr Trp Met Lys Lys Val Lys Val Leu Phe Lys Ala Asp Gln			
325	330	335	
Ser Glu Ser Ser Leu Ser Ser Gly Arg Cys Ser Leu Met Glu Gln Ile			
340	345	350	

Pro His Leu Lys Ser Arg Arg Lys Trp Gln Ile Arg His Val Leu Lys
355 360 365

Asn Leu Trp Leu Pro Met Arg Ser Leu Gly Glu Pro Trp Arg Ala Gly
370 375 380

Phe Gln Trp Gly Glu Ser Pro Trp Gln Val Met Ala Ser Leu Thr Gly
385 390 395 400

Arg Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro Gln Ala
405 410 415

Arg Leu Cys Leu Ile Val Ser Arg Thr Leu Leu Leu Val Gln Ser Arg
420 425 430

Asn Lys Lys Thr Lys Leu Trp Phe Ser Leu Ile Asn Ile His His Arg
435 440 445

Lys Asn Pro Leu Leu Pro Met Arg Trp Trp Cys Thr Arg Gly Gly Gly
450 455 460

Lys Arg Lys Lys Lys Met Cys Lys Val Ser Gly Gly Cys Thr Ala Cys
465 470 475 480

Val Glu Arg Cys Pro Trp Lys Gly Ile Cys Trp Lys Trp Pro Val Thr
485 490 495

Val Ala Ala Ile Arg Met Cys Ala Leu Ser His Pro Ser Phe Tyr Ile
500 505 510

Ser Ser Thr Val Cys Phe Leu Ser Lys His Cys Met Thr Ala Cys Thr
515 520 525

Arg Lys Arg Met Lys Thr Gly Ala Ile Gln Glu Lys Gly Ala Ile Gln
530 535 540

Glu Lys Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe Glu Ala
545 550 555 560

Cys Arg Glu Met Glu Ser Leu Ser Ala Pro Glu Lys Ile Thr Leu Phe
565 570 575

Glu Ala His Met Ala Arg Cys Thr Ser Ile Asn Val Leu Cys Val Arg
580 585 590

Ala Ser Leu Ile Glu Lys Leu Met Lys Glu Lys Arg Lys Met Lys Arg

595	600	605	
Asn Gln Val Ala Ser Pro Gln Ile Met Gln Arg Leu Phe Ile Lys Gly			
610	615	620	
Tyr Gln Asn Asn His Phe Thr Phe His Leu Gln Asn Phe Ala Phe Phe			
625	630	635	640
Ser Ser Phe Gly Asn Asn Lys Tyr Ile Asn Ile Leu Thr Ile Leu Phe			
645	650	655	
His Val Arg Asn Ile Val Tyr Gly Ile Gln Val Met Leu Cys Ala Ser			
660	665	670	
Pro Gln Ile Met Gln Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg			
675	680	685	
Arg Met Gln Asn Leu Asp Asn Leu Gly Val Pro Trp Pro Leu Leu Pro			
690	695	700	
Gly Ile Pro Ser Leu Asn Ala Gln Trp Met Phe Leu Arg Ile Ala Ser			
705	710	715	720
Pro Gln Ile Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr Ile Arg			
725	730	735	
Ala Arg Asn Arg Asn Met Lys Lys Thr Met Ser His Leu Ile Ala His			
740	745	750	
Gln Ala Leu Lys Met Ser Gly Leu Arg Leu Phe His Pro Arg Leu Leu			
755	760	765	
Thr Arg Lys Lys Pro Gly Lys Leu Leu Leu Ala His Met Tyr Gly Phe			
770	775	780	
Ser Thr Tyr Gly Thr Gln Lys Gly Glu Cys Val Cys Leu Gln Cys Leu			
785	790	795	800
Ser Gly Ser Ser Leu Phe Ile Leu Lys Gln Pro Leu Asp Leu Lys Ile			
805	810	815	
Ser Lys Thr Phe Met Gly His Arg Glu Gly Ser Glu Ser Asp Asn Leu			
820	825	830	
Gly Leu Leu Tyr Ser Phe Pro Pro Pro Tyr Pro Ile Ser Glu Gly Leu			
835	840	845	

Thr Met Thr Thr Gly Arg Asn Ile Asn Ser Asn Ser Leu Met Thr Asn
 850 855 860
 Cys Leu Phe Ser Pro Ile Phe Leu Cys His His Ala Ile Met His Arg
 865 870 875 880
 Lys Met Thr Ser Pro His Phe Arg Leu Phe Ser Ser Lys Ile Pro His
 885 890 895
 Pro Gln Val Pro Ser Val Val Ala Leu Cys Lys Phe Arg Ala Phe Ile
 900 905 910

 His Thr Pro Arg Ser Pro Gly Cys Ser Val Tyr Ala Asn Met Cys Trp
 915 920 925
 Pro Lys Phe Phe Leu Thr Phe Ser Gln Gln Trp Ser Ser Val Thr Ser
 930 935 940
 Leu Glu Trp Thr Ala Gln Glu Arg Gly Cys Ser Ser Trp Leu Met Lys
 945 950 955 960
 Gln Thr Trp Met Lys Ser Trp Ser Leu Arg Asp Pro Ser Tyr Arg Ser
 965 970 975

 Ile Leu Glu Tyr Val Ser Thr Arg Val Leu Trp Met Pro Thr Ser Thr
 980 985 990
 Val Leu Gln Ala His Pro Gln Val Pro Ala Leu Ala Pro Gln Ala Trp
 995 1000 1005
 Trp Pro Ala Arg Arg Gly Pro Leu Thr Ser Ala Pro Ser Ala Gln
 1010 1015 1020
 Gln Ser Leu Thr Arg Glu Lys Ile Ile Asn Pro Thr Ile Ser Cys
 1025 1030 1035

 Pro Phe Gln Ser Pro Thr Lys Arg Leu Ile Tyr Pro Pro Ser Thr
 1040 1045 1050
 Cys Ser Leu Pro Cys Arg Gly Phe Leu Pro Ser Arg Phe Pro Trp
 1055 1060 1065
 Gly Pro Pro Pro Leu Asn Ser Val Ile Val His Lys Ile Val Leu
 1070 1075 1080
 Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn Cys Glu Arg Arg Ile

1085	1090	1095
Ser Gly Ile Gln Lys Arg Ala	Ile Glu Phe Ala Val	Leu Lys Leu
1100	1105	1110
Leu Asn Met Asp Leu Pro Leu	Glu Asn Thr Gln Ile	Pro Arg Thr
1115	1120	1125
Ser Pro Leu Trp Lys Ile Thr	Met Val Leu Thr Tyr	Pro Asn Cys
1130	1135	1140
Val Val His Val Leu Met Phe	Gly Ala Leu Arg Ala	Thr Ala Pro
1145	1150	1155
Ala Thr Ala Ala Pro Gln Ala	Gln Thr Pro His Trp	Arg Ala Ala
1160	1165	1170
Thr Thr Ser Ser Met Ser Ser	Ser Pro Arg Ala Glu	Pro Thr Ser
1175	1180	1185
Ser Ser Ser Trp Ala Thr Cys	Trp Pro Arg Cys Cys	Ser Ser Ser
1190	1195	1200
Cys Tyr Trp Ser Leu Ser Ser	Trp Pro Pro Ala Gly	Ala Ala Glu
1205	1210	1215
Ala Thr Asn Thr Arg Thr Arg	Ser Arg Glu Ser Gln	Arg Gly Arg
1220	1225	1230
Met Leu Thr Trp Arg Ser Ser	Leu Trp Leu Gln Gly	Thr Arg Cys
1235	1240	1245
Phe Thr Gly Val Arg Thr Ser	Ser Arg Tyr Lys Lys	Arg Gly Val
1250	1255	1260
Ile Ala Trp Arg Arg Gln Ile	Asn Arg Arg Lys Leu	Gln Arg Lys
1265	1270	1275
Lys His Trp Asn Ser Ala Tyr	Leu Gly Arg Thr Leu	Leu Val Thr
1280	1285	1290
Cys Ile Leu Tyr His Arg Trp	Ile Val Thr Ser Met	Cys Gln Ser
1295	1300	1305
Gln Arg Trp Leu Thr Ser Thr	Thr Ser Arg Ser Ser	Ala Leu Met
1310	1315	1320

Trp Thr Glu Leu Ser Leu Glu Pro Trp Ile Pro Tyr Leu His Gln
1325 1330 1335

Gln Lys Thr Gln Arg Thr Leu Glu Ser Ala Gly Leu Phe Pro Trp
1340 1345 1350

Leu His Thr Gln Cys Gln Glu Lys Lys Ser Arg Lys Leu Met Ser
1355 1360 1365

Ser Cys Thr His Pro Cys Thr Met Leu Leu Pro Gln Gly Cys His
1370 1375 1380

Pro Ala Trp Leu Ser Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro
1385 1390 1395

Tyr Pro Phe His Val Leu Ala Leu Glu Val Thr Phe Pro Pro Gly
1400 1405 1410

Thr Ala Met Pro Gln Met Gln Leu Gln Ala Leu Ala Met Trp Glu
1415 1420 1425

Lys Gly Trp Asp Lys Pro Gly Thr Ser Leu Gln Cys Tyr Leu Asn
1430 1435 1440

Arg Arg Arg Asn Ser Arg Lys Gln Ser Gln Val Gln Leu Ala Ile
1445 1450 1455

Gln Val Leu Leu Val Asp Lys His Lys Tyr Phe Leu Phe Gly Gln
1460 1465 1470

Lys Lys Gly His Met Ile Phe Ser Leu Ala Asn Gly Leu Trp Phe
1475 1480 1485

Asn Leu Ile Phe Asn Ser Arg Lys Lys Leu Leu Glu Asp Met Lys
1490 1495 1500

Gln Asn Gly Phe Thr Gly Lys Gly Leu Thr His Pro Val Pro Leu
1505 1510 1515

Lys Arg Thr Leu Gln Asn Lys Arg Asn Lys Asn Ile Lys Arg Val
1520 1525 1530

Asn Gln Lys Lys Gly Asn Ile Lys Arg Lys Ser Ile Leu Leu His
1535 1540 1545

Leu Ile Val Leu Asn Ser Pro Glu Ser Asn Leu Ile Leu Ile Gln

1550	1555	1560
His Gly Gly Ile Phe Thr Phe	Arg Phe Trp Val Glu	Lys Leu Ser
1565	1570	1575
Trp Asn Ile Cys Lys Asn Leu	Ser Leu Tyr Leu Asp	Lys Phe Val
1580	1585	1590
Gln Arg Leu Leu Tyr Val Tyr	Ile Ile Glu Thr Asn	Val Phe Val
1595	1600	1605
Leu Asn Leu Phe His Val Pro	Val Asn Gln Ile Phe	Met Met Ala
1610	1615	1620
Phe Tyr Leu Lys Tyr Thr Glu	Lys Ala Trp Val Met	Glu Leu Glu
1625	1630	1635
Trp Leu Ile Gln Gln Gln Cys	Tyr Gln Gly Ser Cys	Gly Arg Ala
1640	1645	1650
Cys Ser Cys Gly Arg Gly Cys	Gly Thr Pro Arg Gly	Asp Trp Lys
1655	1660	1665
Arg His Pro Pro Arg Arg Ala	Phe Trp Lys Pro Pro	Ser Gln Gly
1670	1675	1680
Ile Ser Ser Cys Leu Met Thr	Gly Cys Trp Leu Glu	Lys Lys Ala
1685	1690	1695
Thr Trp Met Arg Arg Thr Arg	Arg Lys Lys Arg Glu	Asp His Cys
1700	1705	1710
Gly Leu Arg His Pro Ser Trp	Pro Trp Thr Arg Cys	Leu Arg Met
1715	1720	1725
Arg Pro Pro Arg Ser Gly Tyr	Pro Tyr Asp Val Pro	Asp Tyr Ala
1730	1735	1740
Ser		

<210> 1117

<211> 1749

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 3A

<400> 1117

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu

180 185 190

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

195 200 205

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys

210 215 220

Gln Asp Leu Gly Pro Val Pro Met Gly Ala Ala Ala Ala Ser Cys Gln

225 230 235 240
 Ser Pro Pro Ser Pro Arg Glu Thr Thr Pro Ser Ser Asp Ala Thr Arg
 245 250 255

 Arg Thr Arg Pro Ile Ala Ala Gln Ser Lys Lys Thr Met Thr Ala Ala
 260 265 270
 Gly Leu Thr Pro Met Ile Arg Lys Ile Gln Lys Arg Arg Arg Thr Ala
 275 280 285
 Asn Arg Cys Leu Arg Val Arg Cys Gly Gly Trp Leu Cys Gly Trp Thr
 290 295 300
 Pro Arg Gly Gln Asn Thr Arg Ser Thr Asn Leu Glu Lys Asn Pro Ser
 305 310 315 320

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

 Gly Gln Gly Leu Val Gly Met Thr Pro Arg Asp Leu Gly Thr Val Ala
 385 390 395 400
 Gly Ala Thr Ala Gln Ile Gln Arg Pro Ile Gln Val Gln Thr Gly Gly
 405 410 415
 Arg Leu Thr Pro Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala Pro Val
 420 425 430
 Asp Pro Pro Gly Ser Val Trp Ile Leu Pro Cys Lys Asn Lys Lys Arg
 435 440 445

 Arg Lys Leu Arg Pro Lys Arg Leu Asp Phe His Pro Arg Ser Ser Ser
 450 455 460
 Gly Val Ser Val Ile Thr Met Lys Leu Trp Glu Lys His Phe Lys Gly
 465 470 475 480

Leu Asn Trp Asn Leu Val Val Trp Ile Leu Asn Leu Lys Met Met Asn
 485 490 495
 Ile Glu Ile Thr Pro Gln Arg Ser Lys Ala Arg Lys Ser Gly Val Met
 500 505 510

 Lys Cys Trp Asp Leu Cys Pro Ser Glu Lys Lys Arg Lys Leu Pro Leu
 515 520 525
 Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser Arg His Arg Gly Ala
 530 535 540
 Ser Ser Ser Thr Ser Arg Asp Ser Arg Ser Phe Phe Thr Ser Ala His
 545 550 555 560
 Pro Ser Arg Pro Cys Arg Met Arg Leu Tyr Gln Phe Leu Ile His Leu
 565 570 575

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

 Leu Gln Leu Arg Ser Ile Pro His Val Pro Lys Ala Thr Ala Ala His
 645 650 655
 Ser Val Thr Val Lys Leu Gln Lys Gly Lys Asn Ser Pro Cys Cys Gln
 660 665 670
 Lys Lys Leu Arg Val Gln Asn Gln Gly His Leu Leu Met Ile Leu Leu
 675 680 685
 His Asn Thr Tyr Met Glu Met His Tyr Gly His Gln Ala Pro Gln Val
 690 695 700

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

725	730	735	
Pro Leu Arg Val Gln Ser Val Leu Leu Leu Gly Val Pro Gln Thr Ala			
740	745	750	
Ala Arg Gln Pro Ser Arg Pro Thr Gly Arg Thr Pro Thr Thr Arg Leu			
755	760	765	
Met Ala Pro Val Gly Ser Val Met Ser Cys Ser Leu Leu Thr Gln Pro			
770	775	780	
Ser Pro Ala Ser Ala Cys Thr Met Pro Pro Leu Leu His Pro Gln Trp			
785	790	795	800
Ala Pro His Ser Ala Gly Leu Ser Pro Gly Ala Cys Arg Pro Ala Cys			
805	810	815	
Thr Cys Ile Ser Met Thr Thr Ile Ser Arg Ala Thr Trp Gln Val Ser			
820	825	830	
Val Tyr Ser Gly Asn Leu Leu Ser Phe Ser Arg Arg Gly Met Lys Ser			
835	840	845	
Ser Val Arg Leu Lys Asn Ser Arg Arg Asn Arg Arg Tyr Arg Lys Ile			
850	855	860	
Tyr Gly Glu Leu Lys Met Ser Leu Gln Ala Val Ala Pro Arg Cys Pro			
865	870	875	880
Arg Ser Ala Val Asp Ile Ser Pro Gly Pro Thr Ser Pro Ser Leu Ala			
885	890	895	
Ser Cys Ala Ser Val Ala Ile Gly Lys Leu Ala Leu Leu Gly Ala Ser			
900	905	910	
Ala Pro Cys Gly Ala Ala Gly Ala Arg Glu Ala Gly Arg Phe Ala Val			
915	920	925	
Leu Gly Thr Met Val Met Lys His Leu Asn Arg Lys Leu His Leu Thr			
930	935	940	
Arg Ser Cys Leu Ile Asp Leu Thr Met Met Met Ser Gln Lys Leu Trp			
945	950	955	960
Lys Asn Gln Arg Lys Arg Ile Pro Leu Pro Ser Pro Arg Gln His Leu			
965	970	975	

Leu	Pro	Gln	Tyr	Pro	Leu	His	Pro	Pro	Pro	Pro	Cys	Leu	Leu	Leu	Leu
980				985				990							
His	His	Arg	His	His	Leu	Ala	Phe	Leu	Glu	Met	Ala	Cys	Ser	Ser	Gln
995				1000				1005							
His	Thr	His	Ser	Ile	Lys	Ile	Trp	Ile	Ser	Phe	Ser	His	Glu	Gln	
1010				1015				1020							
Ser	Ser	Pro	Phe	Leu	Ala	Arg	Ser	Trp	Asn	Thr	Met	Gln	Trp	Asn	
1025				1030				1035							
Asn	Lys	Lys	Met	Ala	Met	Thr	Val	Ile	Ala	Gly	Ala	His	His	Cys	
1040				1045				1050							
Gln	Tyr	Lys	Leu	Thr	Tyr	Thr	Lys	Val	Trp	Lys	Met	Asn	Trp	Lys	
1055				1060				1065							
Lys	Met	Met	Ile	Gly	Ser	Gln	His	Leu	Leu	Phe	Ser	Pro	Leu	Asp	
1070				1075				1080							
Ser	Ser	Pro	Leu	Gln	Leu	Leu	Leu	His	Pro	His	Gly	Lys	Arg	Cys	
1085				1090				1095							
Asn	Pro	Cys	Cys	Arg	Leu	Thr	Trp	Met	Ser	Met	Leu	Gln	Lys	Gln	
1100				1105				1110							
Cys	Cys	Tyr	Asn	Leu	Val	Ile	Lys	His	Pro	Leu	Ile	Phe	Arg	Ile	
1115				1120				1125							
Asn	Leu	Arg	Arg	Gln	Gly	Lys	Thr	Lys	Asp	Gly	Val	Val	Gln	Ser	
1130				1135				1140							
Leu	Gly	Phe	Leu	Asn	Gln	Gln	Ile	Ile	Leu	Gln	Lys	Glu	Phe	Phe	
1145				1150				1155							
Ile	Cys	Leu	Leu	Met	Phe	Ile	Lys	Arg	Trp	Lys	Pro	Ala	Ala	Thr	
1160				1165				1170							
Lys	Arg	Glu	Trp	Glu	Lys	Arg	Lys	Gln	Ile	Leu	Gly	Gly	Gly	Gly	
1175				1180				1185							
Lys	Tyr	Lys	Glu	Tyr	Phe	Leu	Lys	Arg	Ile	Leu	Ile	Arg	Lys	Ala	
1190				1195				1200							
Met	Thr	Val	Leu	Ala	Gly	Asp	Lys	Lys	Gly	Leu	Gly	Arg	Phe	Met	

1205	1210	1215
Arg Cys Val Gln Ser Glu Thr	Lys Ala Val Ser Leu	Gln Leu Pro
1220	1225	1230
Leu Gly Arg Gly Pro Val Tyr	Tyr Val Cys Asn Arg	Met Asn Val
1235	1240	1245
Ser Ser Val Leu Lys Pro Phe	Leu Phe Thr Val Pro	Ile Glu Asp
1250	1255	1260
Met Arg Glu Cys Thr Leu Gly	Arg Asn Arg Met Asn	Val Ser Ser
1265	1270	1275
Val Leu Lys Pro Cys Leu Ile	Pro Val Pro Ile Asp	Leu Pro Arg
1280	1285	1290
Met Leu Pro Ile Ser Ser Pro	Leu His Arg Pro Gln	Met Pro Phe
1295	1300	1305
Trp Thr Cys Thr Phe Pro Ala	Thr Thr Trp Gly Thr	Trp Glu Thr
1310	1315	1320
Pro Ser Thr Trp Gly Trp Arg	Thr Phe Arg Gly Pro	Arg Arg Lys
1325	1330	1335
Val Leu Met Val Leu Trp Leu	Pro Ala Asn Gln Ser	Leu Gln Lys
1340	1345	1350
Ser Gln Val Phe Gln Trp Val	Leu Arg Thr Glu Asn	Ile Arg Lys
1355	1360	1365
Leu Ile Trp Thr Lys Gln Arg	Ser Phe Leu Ser Leu	Phe Pro Lys
1370	1375	1380
Leu Arg Ala Thr Glu Gln Met	Thr Asn Val Gly Cys	Ala Phe Ser
1385	1390	1395
Gly Arg Ile Leu His Gln Pro	Glu Met Ala Ala Met	Arg Leu Met
1400	1405	1410
Pro Lys Phe Leu Asn Ser Thr	Asn Ser Trp Trp Thr	Cys Thr Asn
1415	1420	1425
Leu Ser Val Pro Met Met Leu	Thr Ile Leu Ile Trp	Lys Arg Val
1430	1435	1440

Phe Ile	Leu Leu Leu Ser Asp	Lys Lys Leu Leu Lys	Lys Ser Ser
1445	1450	1455	
Gln Leu	Arg Arg Ser Trp Arg	Asn Val Ser Arg Ile	Ser His Gln
1460	1465	1470	
Met Lys	Cys Leu Thr Ala Val	Asp Cys Leu Gln Ala	Phe Trp Asp
1475	1480	1485	
Met Asn	Met Glu His Arg Leu	Thr Met Asp Ser Ala	Leu Ser Leu
1490	1495	1500	
Thr Lys	Arg Glu Gly Pro Glu	Thr Cys Lys Lys Lys	Leu Leu Leu
1505	1510	1515	
Lys Leu	Leu Thr Met Ser Leu	Ser Asn Ile Leu Met	Lys Phe Arg
1520	1525	1530	
Leu Arg	Leu Arg Ile Pro Ser	Leu Arg Lys Tyr Arg	Gln His Leu
1535	1540	1545	
Lys Lys	Thr Ser Ala Lys Gly	Glu Lys Leu Lys His	Cys Phe Lys
1550	1555	1560	
Ala Trp	Gly Arg Gly Pro Pro	Leu His Thr Arg Ser	Gln Lys Lys
1565	1570	1575	
Asp Pro	Ala Gly Lys Leu Lys	Lys Leu Thr Thr Leu	Ser Phe Val
1580	1585	1590	
Leu Ile	Glu Glu Arg Arg Asn	Leu Gln Arg Asn Leu	Lys Val Leu
1595	1600	1605	
Trp Leu	Lys Lys Ser Thr Lys	Ser Arg Tyr Leu Phe	Phe Leu Thr
1610	1615	1620	
Val Cys	Gly Phe Phe Glu Lys	Lys Arg Pro Glu Trp	Leu Ser Ser
1625	1630	1635	
Arg Lys	Lys Gly His Thr Lys	Asn Arg Arg Lys Ala	Lys Arg Lys
1640	1645	1650	
Pro Gln	Ile Val His Lys Lys	Arg Gly Leu Phe Leu	Lys Lys Lys
1655	1660	1665	
Tyr Leu	Val Gln Gly Ala Lys	Lys Ile Thr Phe Leu	Ser Asn Gly

1670 1675 1680

Met Glu Ala Cys Gly Thr His Pro Thr Pro Arg Leu Ser Asp Arg

1685 1690 1695

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

1700 1705 1710

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

1715 1720 1725

Thr Ser Leu Cys Phe Phe Tyr Leu Leu Tyr Gly Tyr Pro Tyr Asp

1730 1735 1740

Val Pro Asp Tyr Ala Ser

1745

<210> 1118

<211> 1750

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 4A

<400> 1118

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

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

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

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

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

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

Pro His Arg Val Gln Leu Leu Arg Arg Trp Gly Pro Gly Ser Pro Ala

610

615

620

Gly Gln Arg Leu Ser Lys Gly Phe Gln Leu Leu Arg Trp Trp Gly Pro

625

630

635

640

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

645

650

655

Pro Pro Trp Pro Val Thr Ala Val Thr Val Met Ala Gly Ser Val Pro

660

665

670

Ser Ala Gln Ser Val Asp Ala Leu Glu Ser Pro Gly Pro Leu Ala Leu

675

680

685

Glu Gly Pro Ser Ser Pro Arg Asn Leu Leu Trp Arg Glu Met Ser Ile

690

695

700

Phe Leu Pro Gly Ile Phe Cys Gln Lys Lys Val Pro Ser Ala Ser Pro

705

710

715

720

Trp Gly Leu Val Pro Pro Ser Pro Pro Leu Ala Leu Gly Pro Arg Met

725

730

735

Gln Leu Cys Thr Gln Leu Ala Arg Phe Phe Pro Ile Thr Pro Pro Val

740

745

750

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

755

760

765

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

770

775

780

Arg Pro Cys Arg Thr Lys Asn Glu Gly Asn Asn His Trp Pro Arg Val

785

790

795

800

Glu Met Pro Thr Gly Trp Leu Leu Val Gly Tyr Asn Thr Arg Asn Thr

805

810

815

Ala Gln Asn Pro Arg Leu Gln Gln His Leu Lys His Trp Gln Gln Cys

820

825

830

Thr Arg Ala Arg Trp Cys Gln Glu Pro Cys Gln Thr Leu Thr Phe Phe

835

840

845

His Phe Phe Phe Phe Phe Lys Thr Val Ser Leu Cys Cys Pro Gly Trp

850 855 860
 Ser Lys Gly Gln Pro Pro Pro Pro Gly Leu Lys Pro Ser Ser Leu Ala

 865 870 875 880
 Ser Gln Val Ala Arg Thr Thr Gly Val Tyr Gln His Val Trp Leu Ile

 885 890 895
 Cys Phe Val Phe Phe Val Cys Val Glu Thr Gly Phe Cys His Val Ala

 900 905 910
 Gln Val Gly Leu Glu Arg Leu Val Ser Leu Ser Gly Ile Thr Asp Val

 915 920 925
 Asn His Trp Ala Gln Pro Lys Pro Ser Pro Ser Lys Gly Thr Gly Met

 930 935 940
 Asn Arg Pro Ile Gly Leu Arg Val Gly Lys Gly Val Trp Ala Arg Leu
 945 950 955 960
 Leu Lys Lys Lys Pro Arg Asp Ile Cys Arg Ile Ser Asn Arg Lys Thr

 965 970 975
 Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr Asp Arg Ala Ser Val

 980 985 990
 Ser Phe Trp Thr Leu Leu Pro Thr Thr Gly Val Arg Thr Arg Gly Ser

 995 1000 1005
 Pro Leu Arg Leu Thr Leu Trp Pro Pro Arg Cys Arg Cys Arg Arg
 1010 1015 1020
 Glu Tyr Arg Val Thr Met Asn Ile Leu Asn Ser Leu Pro Ser Ser

 1025 1030 1035
 Met Glu Ile Ala Val Leu Gln Glu Thr Ala Lys Lys Ser Pro Thr

 1040 1045 1050
 Ser Phe Cys Cys Asn Leu Asp Leu Gln His Gln Arg Arg Arg Lys

 1055 1060 1065
 Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro Lys Ala

 1070 1075 1080
 Asn Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln Asn Leu

 1085 1090 1095

Leu Asn	Leu Val	Gln Leu	Asn Pro	His Ser	Pro His	His Arg	Lys
1100			1105			1110	
Asp Glu	Glu Asp	His Gln	Lys Arg	His His	His His	Asn Gln	Lys
1115			1120			1125	
Lys Met	Ser Val	Pro Leu	Phe Phe	His Gly	Asp Leu	Cys Arg	Glu
1130			1135			1140	
Ser Thr	Leu Gly	Asn Phe	Trp Met	Lys Leu	Leu Gln	Leu Pro	Gln
1145			1150			1155	
Arg Pro	Pro Leu	Gln Pro	Val Thr	Gly Met	Glu Ile	Leu Leu	Trp
1160			1165			1170	
Ile Leu	Leu Lys	Met Glu	Ile Gln	Ile Phe	Lys Ile	Cys Leu	Gly
1175			1180			1185	
Glu Met	Gln Leu	Cys Thr	Ser Arg	Ile Leu	Asn Leu	Gln Val	Leu
1190			1195			1200	
Lys Lys	Ile Leu	Arg Ser	Phe Met	Lys Leu	Tyr His	Ser Leu	Val
1205			1210			1215	
Met Cys	Leu Arg	Leu Arg	Thr Lys	Leu Glu	Lys Ala	Leu Ser	Ala
1220			1225			1230	
Leu Phe	Ile Trp	Pro Gln	His Ser	Tyr Lys	Ile Thr	His Pro	Phe
1235			1240			1245	
Ala Ser	Gln Pro	Leu Gly	Gln Glu	Met Pro	Asn Asn	Thr Gln	Ile
1250			1255			1260	
Arg Leu	Leu Lys	Pro Asp	Lys Lys	Lys Lys	Ser Thr	Glu Lys	Thr
1265			1270			1275	
Lys Gly	Gln Ala	Phe Gly	Ser Phe	Ser Ala	Asp Phe	Ser Ala	Pro
1280			1285			1290	
Gln Gly	Gln Ala	Phe Gly	Ser Leu	Cys Gln	Leu Val	Ser Ala	Asp
1295			1300			1305	
Phe Ser	Ala Pro	Gln Val	Thr Arg	Leu Arg	Ser Leu	Asn His	Leu
1310			1315			1320	
Leu Ile	Trp Leu	Lys Asn	Trp Lys	Arg Phe	Lys Leu	Lys Lys	Lys

1325	1330	1335
Tyr Gln Ala Pro Leu Arg Leu	Trp Ser Trp Cys Gly	Thr Ser Gln
1340	1345	1350
Thr Tyr Phe Gly Ser Ile Ile	Cys Ile Lys Asn Met	Phe Leu Gln
1355	1360	1365
Arg Lys Gly Phe Leu Asn Leu	Ser His Val Glu Lys	Phe Glu Leu
1370	1375	1380
Lys Lys Asn Leu Leu Leu Pro	Val Val Ile Asn Leu	Lys Arg Leu
1385	1390	1395
Gln Lys Phe Met Leu Asn Gln	Lys Cys Leu Ala Pro	Phe Pro Ala
1400	1405	1410
Cys Thr Ser Lys Ala Trp Thr	Pro Arg Lys Leu Val	Gly Arg Ala
1415	1420	1425
Val Arg Arg Lys Gly Ile Leu	Ala Met Thr Leu Thr	Leu Asn Gly
1430	1435	1440
Ile Glu Ala Leu Thr Ala Leu	Phe Thr Cys Arg Thr	Ala Ser Ile
1445	1450	1455
Ser Val Asn Ile Ser Thr Leu	Met Ser Ile Leu Glu	Ala Ile Ile
1460	1465	1470
Lys Lys Met Lys Lys Arg Ile	Met Val His Arg Trp	Ile Phe Ser
1475	1480	1485
Asn Gln Leu Thr Val Gln Met	Leu Cys Leu Pro Leu	Leu Thr Pro
1490	1495	1500
Asp Thr Arg Trp Ile Phe Ser	Asn Gln Leu Gln Thr	Val Gln Met
1505	1510	1515
Leu Cys Leu Pro Pro Leu Lys	Gln Gly Glu Arg Ile	Ile Trp Pro
1520	1525	1530
Leu Gly Gly Phe Gln Ile Pro	Asn Phe Phe Trp Ser	Leu Gly Ile
1535	1540	1545
Gly His Thr Gly Ala Trp Trp	His Thr Gly Arg Arg	Arg Arg Glu
1550	1555	1560

Trp Gly	Gly Ser	Thr Val	Ser Arg	Ser Pro	Leu Trp	Ile Ser	Ser
1565			1570			1575	
Met Ile	Tyr Leu	Arg Gly	Met Ala	Phe Ala	Ser Asp	Ser Ser	Ile
1580			1585			1590	
Arg Thr	Thr Arg	Val Ser	Trp Cys	Arg Arg	Cys Gly	Ala Lys	Ser
1595			1600			1605	
Ala Ala	Ala Ser	Ser Ser	Pro Leu	Trp Asp	Cys Ser	Thr Thr	Thr
1610			1615			1620	
Gly Thr	His His	Gly Cys	Leu Trp	Glu Ile	Pro Ser	Val Thr	Leu
1625			1630			1635	
Leu Ala	Asn Leu	His Leu	Cys Tyr	Tyr His	Ser Gln	Ser Asn	Arg
1640			1645			1650	
Asn Lys	Ser Arg	Gln Met	Glu Ser	Leu Gly	Met Lys	Leu Gln	Leu
1655			1660			1665	
Lys Lys	Lys Val	Asn Ala	Cys Ser	Thr Tyr	Thr Pro	His Ile	Cys
1670			1675			1680	
Arg His	Thr Cys	Arg Val	Asn Ala	Val Glu	Glu Leu	His Ser	Arg
1685			1690			1695	
Arg Met	Ser Val	Arg Ile	Val Lys	Asn Trp	Val Ser	Cys Cys	Tyr
1700			1705			1710	
Val Arg	Leu Ser	Ala Val	Gly Leu	Ser Thr	Trp Ser	Ala Leu	Asp
1715			1720			1725	
Asn Lys	Ile Ile	Cys Lys	Gly His	Arg Ile	Thr Gly	Tyr Pro	Tyr
1730			1735			1740	
Asp Val	Pro Asp	Tyr Ala	Ser				
1745			1750				
<210>	1119						
<211>	1750						
<212>	PRT						
<213>	Artificial Sequence						
<220><223>	hINV- and HA-extended poly-FSP polypeptide 1B						
<400>	1119						

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met
20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala
35 40 45

Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Leu Ala Gly Gln
50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys
65 70 75 80

Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg Met Lys
85 90 95

Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala Thr Pro
100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met
115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His
130 135 140

Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly
145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile
165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu
180 185 190

Met Ser Arg His Ser Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys
195 200 205

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys
210 215 220

Gln Asp Leu Gly Pro Val Pro Met Thr Glu Ile Gln Leu Thr Met Asn
225 230 235 240

Asp Ser Lys His Lys Leu Glu Ser Pro Ala Leu Lys Gln Val Ser Pro

245 250 255
Ala Ser Pro Pro Thr Gln Gln Pro Gln Thr Pro Gln Asp Ser Arg Gln
260 265 270

Val Leu Ala Met Pro Ser Ser Trp Ser Ser Ser Gly Arg Thr Gln Arg
275 280 285

Lys Val Val Lys Asn Pro Ser Gln Pro Val Pro Leu Arg Asn Asp Gly
290 295 300

Ile Thr Asn Gly Asn Asp Ser Thr Arg Ser Cys Ser Ile Ser Leu Lys
305 310 315 320

Lys Ser Leu Glu Lys Met Pro Leu Met Met Lys Lys Lys Asp Ser Thr
325 330 335

Ile Phe Ile Val Pro Met Ser Leu Ala Cys Ser Ile Thr Val Ser Phe
340 345 350

Val Gly Gln Ile Ser Thr Leu Val Leu Asp Val Ser Ser Ile Ser His
355 360 365

Trp Asn Lys Val Arg Gln Asn Phe Lys Arg Asn Ala Asp Lys Lys Asn
370 375 380

Val Arg Ser Gly Glu Lys Asn Asp Leu Gln Leu Phe Val Met Ser Asp
385 390 395 400

Thr Thr Tyr Lys Ile Tyr Trp Thr Val Ile Leu Leu Asn Pro Cys Gly
405 410 415

Asn Leu His Leu Lys Thr Thr Ser Leu Gly Asp Cys Pro Arg Thr Met
420 425 430

Ala Gly Pro Ser Ala Ser Leu His Pro Ala Ser Gly Arg Ala Ser Arg
435 440 445

Lys Thr Trp Gln Arg Arg Leu Arg Ala Cys Arg Ala Gly Gly Pro Ala
450 455 460

Gly Trp Ala Arg Gln Ala Phe Asp Lys Lys Gly Phe Val Ile Leu Ser
465 470 475 480

Val Gly Ala Gly Thr Gly Gly Gly Pro Ala Cys Val Pro Val Ala Glu
485 490 495

Ala Ser Thr Gly Ala Trp Thr Ala Glu Gly Ala Ala Gly Thr Arg Cys
500 505 510

Arg Ala Ser Arg Ala Pro Cys Arg Gln Leu Pro Ala Ser Ser Pro Thr
515 520 525

Lys Cys Glu Ile Cys Val Lys Arg Arg Arg Arg Arg Lys Arg Ser Ser
530 535 540

Gln Ser Arg Ser Pro Val Pro Lys Lys Arg Glu Arg Met Met Leu Pro
545 550 555 560

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

Leu Glu Gly Met Leu Leu Pro Arg Ala Leu Pro Ser Leu Leu Ser Arg
580 585 590

Met Pro Ala Arg Arg Glu Ser Arg Phe Trp Leu Ala Leu Gln Ala Leu
595 600 605

Gly Leu Arg Pro Pro His Leu Pro Ser Cys His Pro Leu Pro Gln Leu
610 615 620

Leu Gly Pro Pro Pro Pro His Gln Ala Pro Thr Ala Phe Phe Leu Leu
625 630 635 640

Asp Ile Ile Leu Arg Leu Pro Cys Lys Val Thr Glu Ser Ser Asn Met
645 650 655

Gly Gly Asn Arg Ser Ile Cys Leu Thr Asn Ala Lys Lys Met Glu Asp
660 665 670

Met Ile Trp Glu Ser Thr Pro Leu Ser Ile Ser Arg Pro Thr Ser Arg
675 680 685

Ala Arg Gln Ser Cys Cys Leu Pro Gly Leu Thr His Pro Ala His Gln
690 695 700

Pro Leu Gly Ser Met Thr Leu Ala Ile Arg Phe Ile Ser Ala Pro Gln
705 710 715 720

Pro Ser Ser Ser Thr Val Thr Ala Ala Pro Ser Gly Gln Tyr Phe Lys
725 730 735

Gly Lys Lys Arg Arg Lys Glu Ile Phe Lys Lys Lys Lys Pro Leu Thr

740	745	750
Phe Ser Pro Ser Leu Ala Lys Lys Thr Leu Thr Asn Ser Ser Phe Phe		
755	760	765
Tyr Thr Ser Asp Arg Glu Ala Lys Lys Ser Met Lys Arg Ser Met Thr		
770	775	780
Leu Lys Ala Leu Val Lys Thr Trp Thr Gln Phe Arg Asn Tyr Pro Arg		
785	790	795
Ala Ser Ser Pro Gly His Pro Leu Gly Pro Asn Gly Ile Trp Glu Val		
805	810	815
Met Pro Arg Thr Leu Glu Gly Cys Ile Ser Val Lys Asp His Arg Thr		
820	825	830
Ser Gln Asn His Ser Lys Cys Ile Thr Glu Cys Val Arg Thr Ala Leu		
835	840	845
Asn Arg Arg Ser Lys Ile Glu Ala Ser Pro Ile Gly Ser Ile Ala Leu		
850	855	860
Arg Ser Met Pro Lys Ser Arg Asn Gln Val Leu Phe Arg Arg Asn Leu		
865	870	875
Thr Pro Ser Gln Leu Arg Thr Leu Ala Pro Pro Tyr Met Leu Leu Pro		
885	890	895
Gln Ser Leu Ser Gln Ser Leu Ser Arg Lys Gln Ile Pro Ser Gln Ser		
900	905	910
Met Leu Val Ala Ser Arg Ala Gly Gln Phe Pro Val Trp Arg Arg Thr		
915	920	925
Ser Arg Gly Met Ser Leu Gln Trp Lys Ser Gly Asn Ala Cys Thr Pro		
930	935	940
Leu Arg Cys Pro Ser Arg Ser Pro Ala Thr Phe Leu Thr Ala Leu Asn		
945	950	955
Gly Trp His Arg Ser Gly Leu Arg Ala Gln Arg Lys Arg Lys Arg Glu		
965	970	975
Lys Arg Ser Gln Lys Ser Arg Gln Asn His Leu Gln Leu Lys Ser Cys		
980	985	990

Arg	Arg	Lys	Ile	Ser	Asn	Trp	Ser	Lys	Leu	Arg	Ser	Pro	Trp	Ile	Phe
995				1000				1005							
Val	Ser	Lys	Lys	Arg	Leu	Pro	Lys	Leu	Thr	Lys	Cys	Glu	Ile	Cys	
1010				1015				1020							
Val	Lys	Asn	Thr	Ala	Ile	Leu	Ala	Ile	Thr	Leu	Ile	Thr	Pro	Gln	
1025				1030				1035							
Asp	Pro	His	Leu	Asp	Pro	Val	Cys	His	Pro	His	Arg	Arg	Pro	Gly	
1040				1045				1050							
Trp	Lys	Gly	His	His	Arg	Val	Val	Phe	Ser	His	His	Pro	Ser	Gly	
1055				1060				1065							
Ser	Thr	Lys	Ser	His	Trp	Gln	Gln	Arg	Glu	Arg	Gly	Gly	Gly	Arg	
1070				1075				1080							
Arg	Glu	Lys	Lys	Gly	Cys	Arg	Glu	Arg	Ser	Leu	Leu	Tyr	Ser	Arg	
1085				1090				1095							
Met	Cys	Leu	Val	Gln	Ile	Pro	Thr	His	Thr	Trp	Glu	Pro	Asp	Tyr	
1100				1105				1110							
Phe	Val	Ser	Leu	Pro	Met	Met	Phe	Ser	Trp	Ala	Thr	Gln	Ser	Phe	
1115				1120				1125							
Pro	Val	Gly	Ala	Val	Phe	Leu	Thr	Arg	Pro	Ala	Ile	Pro	Cys	Cys	
1130				1135				1140							
Ser	Cys	Thr	Ser	His	Ser	Asn	Pro	Trp	Ser	Gln	Ser	Arg	His	Pro	
1145				1150				1155							
His	Arg	Ser	Pro	Pro	Thr	Ser	Cys	Pro	Pro	Leu	Leu	Glu	Ala	Phe	
1160				1165				1170							
Pro	Leu	Pro	Arg	Ala	Ser	Leu	Arg	Ala	Thr	Val	Pro	Arg	His	Ser	
1175				1180				1185							
Ser	Val	Leu	Ala	Thr	Gly	Leu	His	Leu	His	Arg	Gln	Ile	Ser	Leu	
1190				1195				1200							
Pro	Leu	Arg	Gly	Phe	Leu	Leu	His	Gln	Pro	Leu	Pro	Gly	Gln	His	
1205				1210				1215							
Leu	Trp	Leu	Ser	His	Arg	Leu	Arg	Leu	Arg	Leu	Pro	Arg	Thr	Gln	

1220	1225	1230
Arg Pro Pro Arg Ser Ile Leu	Ser Leu Arg Leu Pro	Leu Arg Pro
1235	1240	1245
Gln Arg Gly Pro Arg Pro Leu	His Arg Trp Leu Gln	Gln Thr Thr
1250	1255	1260
Gly Cys Ser Gln Arg Arg Tyr	Pro Arg Leu Lys Thr	Phe Gly Val
1265	1270	1275
Pro Leu Gly Ser Ile Leu Cys	Leu Ala Gly Ser Leu	Ser Thr Met
1280	1285	1290
Met Ile Ile Ser Thr Thr Arg	Gln Glu Cys Gly Arg	Arg Ala Ser
1295	1300	1305
Val Pro Cys Arg Pro Met Ile	Gly Ser Ala Arg Pro	Gly Pro Trp
1310	1315	1320
Arg Thr Ser Ala Met Pro Ser	Ala Met Gly Val Ala	Leu Pro Thr
1325	1330	1335
Ser Cys Glu Ser Gly Arg Ser	Pro Pro Ala Thr Gly	Gly Arg Met
1340	1345	1350
Pro Gly Ser Gln Ser Ile Met	Met Ser Trp Met Pro	Pro Leu Ala
1355	1360	1365
Pro Cys Ala Ala Cys Pro Cys	Ser Pro Ala Pro Thr	Leu Cys Pro
1370	1375	1380
Ala His Pro Ala Arg Ala Pro	Thr Ala Val Pro Ala	Phe Thr Pro
1385	1390	1395
Leu Ser Ala His Pro Val Pro	Val Leu Ser Gly Cys	His Leu Ala
1400	1405	1410
Val Arg Thr Ser Met Leu Thr	Leu Leu Pro Met Leu	Lys Leu Ala
1415	1420	1425
Pro Leu Gln Val Thr Thr Thr	Leu Lys Leu Ile Leu	Val Met Leu
1430	1435	1440
Glu Ile Val Thr Glu Ser Thr	Arg Arg Glu Met Pro	Ser Gln Ala
1445	1450	1455

Thr	Pro	Ser	Pro	Pro	Gly	Pro	Trp	Arg	Ala	Ala	Leu	Gly	Lys	Glu
1460						1465						1470		
Val	Lys	Arg	Ser	Gln	Ser	Lys	Leu	Arg	Leu	Arg	Asn	Thr	Ser	Pro
1475						1480						1485		
Ile	Val	Phe	Phe	Leu	Ala	Pro	Tyr	Phe	Pro	Arg	Arg	Met	Thr	Arg
1490						1495						1500		
Arg	Thr	Met	Thr	Thr	Thr	Lys	Met	Met	Met	Met	Arg	Arg	Thr	Lys
1505						1510						1515		
Arg	Arg	Arg	Arg	Lys	Arg	Arg	Arg	Met	Thr	Met	Met	Thr	Arg	Arg
1520						1525						1530		
Thr	Leu	Leu	Thr	Lys	Lys	Thr	Cys	Leu	Thr	Pro	Arg	Thr	Ser	Ala
1535						1540						1545		
Ala	Thr	Lys	Ala	Leu	Pro	Arg	Gln	Thr	Ile	Ser	Gln	Arg	Arg	Pro
1550						1555						1560		
Ile	Gln	Thr	Pro	Pro	Gly	Thr	Ser	Leu	Ala	Ile	Trp	Gly	Asn	Gln
1565						1570						1575		
Gln	Leu	Lys	Trp	Thr	Pro	His	Ile	Leu	Lys	Ser	Ala	Ser	Arg	Arg
1580						1585						1590		
Ala	Arg	Pro	Thr	Ser	Cys	Ser	Thr	Cys	Arg	Met	Trp	Trp	Ile	Ala
1595						1600						1605		
Lys	Lys	Arg	Ile	Lys	Leu	Arg	Arg	Asn	Arg	Thr	Arg	Leu	Thr	Leu
1610						1615						1620		
Thr	Gly	Thr	Arg	Ser	Ser	Gly	Thr	Arg	Ala	Ser	Pro	Ser	Ala	Val
1625						1630						1635		
Cys	Leu	Cys	Cys	Trp	Thr	Cys	Pro	Ser	Arg	Ser	Phe	Pro	Ala	Ala
1640						1645						1650		
Ser	Pro	Ser	Gly	Leu	Arg	Ala	Pro	Val	Gly	Ala	Gln	Ala	Pro	Pro
1655						1660						1665		
Glu	Val	Thr	Leu	Arg	Ala	Ser	Cys	Ala	Ser	Ser	Ala	Ser	Lys	Ala
1670						1675						1680		
Cys	Ala	Gly	Leu	Trp	Pro	Trp	Gly	Ala	Gln	Val	Arg	Gln	Pro	Ser

1685 1690 1695
 Leu Pro Gly Pro Cys Ala Ser Leu Leu Ser Thr Leu Ser Gln Pro
 1700 1705 1710
 Pro Pro Gln Ala Pro Ser Gln Val Trp Thr Ala Ala Thr Leu Arg
 1715 1720 1725
 Cys Pro Ala Val Pro Ala Ala Ala Cys Pro Pro Gly Tyr Pro Tyr
 1730 1735 1740
 Asp Val Pro Asp Tyr Ala Ser
 1745 1750
 <210> 1120
 <211> 1744
 <212> PRT
 <213> Artificial Sequence

 <220><223> hINV- and HA-extended poly-FSP polypeptide 2B
 <400> 1120
 Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
 1 5 10 15
 Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met
 20 25 30
 Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala
 35 40 45
 Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Leu Ala Gly Gln

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

 115 120 125

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

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

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

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

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

Leu Gly Pro Ser Arg Trp Ser Arg Ser His Leu Asp Phe Ser Pro Tyr

625 630 635 640

Trp Met Lys Lys Val Lys Leu Ala Asn Gly Leu Trp Phe Asn Leu Ile

645 650 655

Phe Val Leu Phe Lys Ala Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly

660 665 670

Arg Asn Lys Lys Thr Lys Leu Trp Phe Ser Leu Ile Asn Ile His His

675 680 685

Arg Lys Asn Pro Leu Leu Pro Met Arg Ile Pro Ser Leu Asn Ala Gln

690 695 700

Trp Met Phe Leu Arg Ile Leu Leu Leu Ala His Met Tyr Gly Phe Ser

705 710 715 720

Thr Tyr Gly Thr Gln Lys Gly Glu Cys Val Cys Leu Gln Cys Leu Ser

725 730 735

Gly Ser Ser Leu Phe Ile Leu Lys Gln Pro Leu Asp Leu Lys Ile Ser

740 745 750

Lys Thr Phe Met Leu Gln Ala His Pro Gln Val Pro Ala Leu Ala Pro

755 760 765

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

770 775 780

Ala Gln Gln Ser Leu Thr Ala Ser Pro Gln Ile Met Gln Arg Met Ser

785 790 795 800

Ala Val Asn Phe Glu Thr Ile Ile Tyr Pro Pro Ser Thr Cys Ser Leu

805 810 815

Pro Cys Arg Gly Arg Thr Leu Glu Ser Ala Gly Leu Phe Pro Trp Leu

820 825 830

His Thr Gln Cys Thr His Pro Cys Thr Met Leu Leu Pro Gln Gly Trp

835 840 845

Trp Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys Met Cys Lys Val

850 855 860

Ser Gly Gly Cys Thr Ala Cys Val Glu Arg Cys Pro Trp Lys Gly Ile

865 870 875 880
 Cys Trp Lys Trp Pro Val Thr Val Ala Ala Gln Trp Ser Ser Val Thr

 885 890 895
 Ser Leu Glu Trp Thr Ala Gln Glu Arg Gly Cys Ser Ser Trp Leu Met
 900 905 910
 Lys Gln Thr Trp Met Lys Ser Trp Ser Leu Arg Asp Pro Ser Tyr Arg
 915 920 925
 Ser Ile Leu Glu Tyr Val Ser Thr Arg Val Leu Trp Met Pro Thr Ser
 930 935 940
 Thr Val Arg Arg Arg Asn Ser Arg Lys Gln Ser Gln Val Gln Leu Ala

 945 950 955 960
 Ile Gln Val Leu Leu Val Asp Lys His Lys Tyr Phe Leu Phe Gly Arg
 965 970 975
 Ala Arg Asn Arg Asn Met Lys Lys Thr Met Ser His Leu Ile Ala His
 980 985 990
 Gln Ala Leu Lys Met Ser Gly Leu Arg Leu Phe His Pro Arg Leu Leu
 995 1000 1005
 Thr Arg Lys Lys Pro Gly Lys Phe Leu Pro Ser Arg Phe Pro Trp

 1010 1015 1020
 Gly Pro Pro Pro Leu Cys His Pro Ala Trp Leu Ser Pro Ile Ser
 1025 1030 1035
 Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe His Val Leu Ala Leu
 1040 1045 1050
 Glu Val Thr Phe Pro Pro Gly Thr Ala Met Pro Gln Met Gln Leu
 1055 1060 1065
 Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp Lys Arg Lys Arg

 1070 1075 1080
 Met Lys Thr Gly Ala Ile Gln Glu Lys Gly Ala Ile Gln Glu Lys
 1085 1090 1095
 Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe Glu Ala Cys
 1100 1105 1110

Arg Glu Met Glu Ser Leu Ser	Ala Pro Glu Lys Ile Thr Leu Phe	
1115	1120	1125
Glu Ala His Met Ala Arg Cys	Thr Ser Ile Asn Val Leu Cys Val	
1130	1135	1140
Arg Ala Ser Leu Ile Glu Lys	Leu Met Lys Glu Lys Arg Lys Met	
1145	1150	1155
Lys Arg Asn Gln Val Ala Ser	Pro Gln Ile Met Gln Arg Leu Phe	
1160	1165	1170
Ile Lys Gly Tyr Gln Asn Asn	His Phe Thr Phe His Leu Gln Asn	
1175	1180	1185
Phe Ala Phe Phe Ser Ser Phe	Gly Asn Asn Lys Tyr Ile Asn Ile	
1190	1195	1200
Leu Thr Arg Arg Lys Lys Arg	Glu Asp His Cys Gly Leu Leu Ile	
1205	1210	1215
Leu Ile Gln His Gly Gly Ile	Phe Thr Phe Arg Phe Trp Val Glu	
1220	1225	1230
Lys Leu Ser Trp Asn Ile Cys	Lys Asn Leu Ser Leu Tyr Leu Asp	
1235	1240	1245
Lys Phe Val Gln Arg Leu Leu	Tyr Val Tyr Ile Ile Glu Thr Asn	
1250	1255	1260
Val Phe Val Leu Asn Leu Phe	His Val Pro Val Asn Gln Ile Phe	
1265	1270	1275
Met Met Ala Phe Tyr Leu Lys	Tyr Thr Glu Lys Ala Trp Val Met	
1280	1285	1290
Glu Leu Glu Trp Leu Ile Gln	Gln Gln Cys Tyr Gln Gln Glu Lys	
1295	1300	1305
Lys Ser Arg Lys Leu Met Ser	Ser Cys Arg Ala Phe Ile His Thr	
1310	1315	1320
Pro Arg Ser Pro Gly Cys Ser	Val Tyr Ala Asn Met Cys Trp Ala	
1325	1330	1335
Phe Trp Lys Pro Pro Ser Gln	Gly Ile Ser Ser Cys Leu Met Thr	

1340	1345	1350
Gly Cys Trp Gly Ser Pro Pro	Leu His Leu Cys Gln	Pro Leu Arg
1355	1360	1365
Arg Tyr Lys Lys Arg Gly Val	Ile Ala Trp Arg Arg	Arg Lys Trp
1370	1375	1380
Gln Ile Arg His Val Leu Lys	Asn Leu Ile Leu Phe	His Val Arg
1385	1390	1395
Asn Ile Val Tyr Gly Ile Gln	Val Met Leu Cys Gly	Lys Gly Leu
1400	1405	1410
Thr His Pro Val Pro Leu Lys	Arg Thr Leu Gln Asn	Lys Arg Asn
1415	1420	1425
Lys Asn Ile Lys Arg Val Asn	Gln Lys Lys Gly Asn	Ile Lys Arg
1430	1435	1440
Lys Ser Ile Leu Leu His Leu	Ile Val Leu Asn Ser	Pro Glu Ser
1445	1450	1455
Asn Pro Lys Phe Phe Leu Thr	Phe Ser Gln Leu Glu	Lys Lys Ala
1460	1465	1470
Thr Trp Met Arg Arg Thr Gly	Ala Leu Arg Ala Thr	Ala Pro Ala
1475	1480	1485
Thr Ala Ala Pro Gln Ala Gln	Thr Pro His Trp Arg	Ala Ala Thr
1490	1495	1500
Thr Ser Ser Met Ser Ser Ser	Pro Arg Ala Glu Pro	Thr Ser Ser
1505	1510	1515
Ser Ser Trp Ala Thr Cys Trp	Pro Arg Cys Cys Ser	Ser Ser Cys
1520	1525	1530
Tyr Trp Ser Leu Ser Ser Trp	Pro Pro Ala Gly Ala	Ala Glu Ala
1535	1540	1545
Thr Asn Thr Arg Thr Arg Ser	Arg Glu Ser Gln Arg	Gly Arg Met
1550	1555	1560
Leu Thr Trp Arg Ser Ser Leu	Trp Leu Gln Gly Thr	Arg Cys Phe
1565	1570	1575

Thr Gly Val Arg Thr Ser Ser Gly Ser Cys Gly Arg Ala Cys Ser
1580 1585 1590

Cys Gly Arg Gly Cys Gly Thr Pro Arg Gly Asp Trp Lys Arg His
1595 1600 1605

Pro Pro Arg Arg Asn Ser Val Ile Val His Lys Ile Val Leu Val

1610 1615 1620

Phe Leu Lys Ser Leu Ser Ser Tyr Asn Cys Glu Arg Arg Ile Ser
1625 1630 1635

Gly Ile Gln Lys Arg Ala Ile Glu Phe Ala Val Leu Lys Leu Leu
1640 1645 1650

Asn Met Asp Leu His Trp Asn Ser Ala Tyr Leu Gly Arg Thr Leu
1655 1660 1665

Leu Val Thr Cys Ile Leu Tyr His Arg Trp Ile Val Thr Ser Met

1670 1675 1680

Cys Gln Ser Gln Arg Trp Leu Thr Ser Thr Thr Ser Arg Ser Ser
1685 1690 1695

Ala Leu Met Trp Thr Arg Gln Ile Asn Arg Arg Lys Leu Gln Arg
1700 1705 1710

Lys Lys Arg His Pro Ser Trp Pro Trp Thr Arg Cys Leu Arg Met
1715 1720 1725

Arg Pro Pro Arg Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1730 1735 1740

Ser

<210> 1121

<211> 1749

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 3B

<400> 1121

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

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

260 265 270
 Gly Leu Thr Pro Lys Asn Lys Lys Arg Arg Lys Leu Arg Pro Lys Met
 275 280 285
 Ile Arg Lys Ile Gln Lys Arg Arg Arg Thr Ala Asn Arg Arg Asn Ser

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

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

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

 485 490 495
 Arg Ser Thr Asn Leu Glu Lys Asn Pro Ser Leu Lys Lys Gln Ser Gln
 500 505 510

Arg Arg Gly Lys Leu Ser Ala Phe Ser Gly Arg Ile Leu His Gln Pro
 515 520 525
 Glu Met Ala Ala Met Arg Leu Met Pro Lys Phe Leu Asn Ser Thr Asn
 530 535 540
 Ser Trp Trp Thr Leu Thr Thr Leu Ser Phe Val Leu Ile Glu Glu Ala

 545 550 555 560
 Arg Gln Pro Ser Arg Pro Thr Gly Arg Thr Pro Thr Thr Arg Leu Met
 565 570 575
 Ala Pro Val Gly Ser Val Met Ser Cys Ser Leu Leu Thr Gln Pro Ser
 580 585 590
 Pro Ala Ser Ala Cys Thr Met Pro Pro Leu Leu His Pro Gln Trp Ala
 595 600 605
 Pro His Ser Ala Gly Leu Ser Pro Gly Ala Cys Arg Pro Ala Cys Thr

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

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

 740 745 750
 Leu Gln Lys Glu Phe Phe Ile Cys Leu Leu Met Phe Ile Lys Arg Trp

755 760 765
 Lys Pro Ala Ala Thr Lys Ser Arg Lys Lys Gly His Thr Lys Asn Arg
 770 775 780
 Arg Lys Ala Lys Arg Lys Pro Gln Ile Tyr Leu Phe Phe Leu Thr Val
 785 790 795 800
 Cys Gly Phe His Leu Lys Lys Thr Ser Ala Lys Trp Leu Lys Lys Ser

 805 810 815
 Thr Lys Ser Arg Ser Asn Gly Met Glu Ala Cys Gly Thr His Pro Thr
 820 825 830
 Pro Arg Leu Ser Cys Leu Arg Val Arg Cys Gly Gly Trp Leu Cys Gly
 835 840 845
 Trp Thr Pro Arg Gly Arg Lys Ser Gly Val Met Lys Cys Trp Asp Leu
 850 855 860
 Cys Pro Val His Lys Lys Arg Gly Leu Phe Arg Leu Asp Phe His Pro

 865 870 875 880
 Arg Ser Ser Ser Gly Lys Gly Lys Asn Ser Pro Cys Cys Gln Lys Lys
 885 890 895
 Leu Arg Val Gln Asn Gln Gly His Leu Leu Met Ile Leu Leu His Asn
 900 905 910
 Asp Arg Val Phe Leu Val Lys Ile Gly Glu Lys Leu Lys His Cys Phe
 915 920 925
 Lys Ala Trp Gly Ser Arg Arg Asn Arg Arg Tyr Arg Lys Ile Tyr Gly

 930 935 940
 Glu Leu Lys Met Ser Leu Gln Ala Phe Leu Ile His Leu Arg Lys Val
 945 950 955 960
 Asp Thr His His Leu Gln Val Val Thr Lys Thr Val Thr Ala Thr Thr
 965 970 975
 Ala Asp Gly Gln Arg Met Arg Arg Leu Lys Cys Lys Ala Cys Arg Leu
 980 985 990
 Arg Trp Ala Arg Pro Glu Pro Ala Ala Gln Ala Pro Pro Lys Ser His

 995 1000 1005

Phe Pro	Pro His Pro Ser Gly	Pro Ser Arg Thr Ser	Ser Leu Gln
1010	1015	1020	
Leu Arg	Ser Leu Phe Phe Ser	His Cys Leu Cys Ser	Gln Lys Lys
1025	1030	1035	
Asp Pro	Ala Gly Lys Leu Lys	Lys Leu Leu Lys Lys	Ser Ser Gln
1040	1045	1050	
Leu Arg	Arg Ser Trp Arg Asn	Val Ser Arg Ile Ser	Thr Pro Pro
1055	1060	1065	
Pro Leu	Ile Leu Trp Pro Gln	Ala Ala Pro Val Ser	Val Ile Thr
1070	1075	1080	
Met Lys	Leu Trp Glu Lys His	Phe Lys Gly Leu Asn	Trp Asn Leu
1085	1090	1095	
Val Val	Trp Ile Leu Asn Leu	Lys Met Met Thr Tyr	Met Glu Met
1100	1105	1110	
His Tyr	Gly His Gln Ala Pro	Gln Val Ala Met Leu	Pro Lys Leu
1115	1120	1125	
Leu Cys	Arg Gln Met Leu Pro	Thr Leu Ser Thr Leu	Gln Gln Arg
1130	1135	1140	
His Pro	Gln Gly Pro Cys Pro	Pro Pro Val Thr Pro	Leu Arg Val
1145	1150	1155	
Gln Ser	Val Leu Leu Leu Gly	Val Pro Gln Thr Ala	Arg Gly Pro
1160	1165	1170	
Arg Arg	Lys Val Leu Met Val	Leu Trp Leu Pro Ala	Asn Gln Ser
1175	1180	1185	
Leu Gln	Lys Ser Gln Val Phe	Gln Trp Val Leu Arg	Thr Glu Val
1190	1195	1200	
Ala Pro	Arg Cys Pro Arg Ser	Ala Val Asp Ile Ser	Pro Gly Pro
1205	1210	1215	
Thr Ser	Pro Ser Leu Ala Ser	Cys Ala Ser Val Ala	Ile Gly Lys
1220	1225	1230	
Leu Ala	Leu Leu Gly Ala Ser	Ala Pro Cys Gly Ala	Ala Gly Ala

1235	1240	1245
Arg Glu Ala Gly Arg Phe Ala	Val Leu Gly Thr Met	Val Met Lys
1250	1255	1260
Leu Cys Phe Phe Tyr Leu Leu	Tyr Arg Leu Arg Ile	Pro Ser Leu
1265	1270	1275
Arg Lys Tyr Arg Gln His Leu	Asn Arg Lys Leu His	Leu Thr Arg
1280	1285	1290
Ser Cys Leu Ile Asp Leu Thr	Met Met Met Ser Gln	Lys Leu Trp

1295	1300	1305
Lys Asn Gln Arg Lys Arg Ile	Pro Leu Pro Ser Pro	Arg Gln His
1310	1315	1320
Leu Leu Pro Gln Tyr Pro Leu	His Pro Pro Pro Pro	Cys Leu Leu
1325	1330	1335
Leu Leu His His Arg His His	Leu Ala Phe Leu Glu	Met Ala Cys
1340	1345	1350
Ser Ser Gln His Thr His Ser	Ile Lys Ile Trp Ile	Ser Phe Ser

1355	1360	1365
His Glu Val Asp Pro Pro Gly	Ser Val Trp Ile Leu	Pro Cys Asp
1370	1375	1380
Leu Pro Arg Met Leu Pro Ile	Ser Ser Pro Leu His	Arg Pro Gln
1385	1390	1395
Met Pro Phe Trp Thr Cys Thr	Phe Pro Ala Thr Thr	Trp Gly Thr
1400	1405	1410
Trp Glu Thr Pro Ser Thr Trp	Gly Trp Arg Thr Phe	Arg Gly Ala

1415	1420	1425
Ser Ser Ser Thr Ser Arg Asp	Ser Arg Ser Phe Phe	Thr Ser Ala
1430	1435	1440
His Pro Ser Arg Pro Cys Arg	Met Arg Leu Tyr Gln	Cys Lys Lys
1445	1450	1455
Lys Leu Leu Leu Lys Leu Leu	Thr Thr Thr Thr Ser	Ser Pro Arg
1460	1465	1470

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

1475 1480 1485

Val Thr Ser Cys Thr Asn Leu Ser Val Pro Met Met Leu Thr Ile

1490 1495 1500

Leu Ile Trp Lys Arg Val Phe Ile Leu Leu Leu Ser Asp Lys Lys

1505 1510 1515

Gly Ala Lys Lys Ile Thr Phe Leu Pro Ile Pro Pro His Leu Arg

1520 1525 1530

His Pro Leu Leu Leu Phe Glu Lys Lys Arg Pro Glu Trp Leu Ser

1535 1540 1545

Met Asp Leu Asp Gly Met Leu Thr Val Ile Gly Gln Gly Leu Val

1550 1555 1560

Gly Met Thr Pro Arg Asp Leu Gly Thr Val Ala Gly Ala Thr Ala

1565 1570 1575

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

1580 1585 1590

Arg Asn Leu Gln Arg Asn Leu Lys Val Leu Gln Val Ser Val Tyr

1595 1600 1605

Ser Gly Asn Leu Leu Ser Phe Ser Arg Arg Gly Met Lys Ser Ser

1610 1615 1620

Val Arg Leu Lys Asn Arg Glu Trp Glu Lys Arg Lys Gln Ile Leu

1625 1630 1635

Gly Gly Gly Gly Lys Tyr Lys Glu Tyr Phe Leu Lys Arg Ile Leu

1640 1645 1650

Ile Arg Lys Ala Met Thr Val Leu Ala Gly Asp Lys Lys Gly Leu

1655 1660 1665

Gly Arg Phe Met Arg Cys Val Gln Ser Glu Thr Lys Ala Val Ser

1670 1675 1680

Leu Gln Leu Pro Leu Gly Arg Asn Met Glu His Arg Leu Thr Met

1685 1690 1695

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

1700 1705 1710
Lys Lys Lys Tyr Leu Val Gln His Gln Met Lys Cys Leu Thr Ala

1715 1720 1725
Val Asp Cys Leu Gln Ala Phe Trp Asp Met Gly Tyr Pro Tyr Asp

1730 1735 1740
Val Pro Asp Tyr Ala Ser

1745

<210> 1122

<211> 1750

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 4B

<400> 1122

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

 Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys
 210 215 220
 Gln Asp Leu Gly Pro Val Pro Met Ile Gln Lys Lys Lys Gln Lys Ser
 225 230 235 240
 Asn Leu Asp Leu Gln His Gln Arg Arg Arg Lys Lys Lys Lys Asp Lys
 245 250 255
 Val Glu Ile Arg Asn Arg Ser Pro Lys Ala Asn Ser Thr Glu Cys Gln
 260 265 270

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

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

385 390 395 400
 Arg Trp Cys Gln Glu Pro Cys Gln Thr Leu Thr Phe Phe His Phe Phe
 405 410 415
 Phe Phe Phe Lys Thr Val Ser Leu Cys Cys Pro Gly Trp Ser Lys Gly
 420 425 430
 Gln Pro Pro Pro Pro Gly Leu Lys Pro Ser Ser Leu Ala Ser Gln Val
 435 440 445
 Ala Arg Thr Thr Gly Val Tyr Gln His Val Trp Leu Ile Cys Phe Val
 450 455 460

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

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

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

Leu Ala Cys Arg Val Asn Ala Val Glu Glu Leu His Ser Arg Arg Met
645 650 655

Ser Val Arg Ile Val Lys Asn Trp Val Ser Cys Cys Tyr Val Arg Leu
660 665 670

Ser Ala Val Gly Leu Ser Thr Trp Ser Ala Leu Asp Val Val Ile Asn
675 680 685

Leu Lys Arg Leu Gln Lys Phe Ser Gln Lys Ser Gln His His Cys Ala
690 695 700

Leu Arg Lys Ile Glu Trp Ala Thr Lys Leu Ser Leu Gly Gly Lys Ala
705 710 715 720

Gly Pro Gln Ala Gln Glu Lys Ala Asn Ala Lys Lys Met Pro Phe Gln
725 730 735

Arg Trp Ile Phe Ser Asn Gln Leu Thr Val Gln Met Leu Cys Leu Pro
740 745 750

Ile Glu Ala Leu Thr Ala Leu Phe Thr Cys Arg Thr Ala Ser Ile Ser
755 760 765

Val Asn Ile Ser Thr Leu Met Ser Ile Leu Glu Ala Pro Leu Phe Phe
770 775 780

His Gly Asp Leu Cys Glu Glu Lys Lys Asn Gly Arg Ile Ser Ser Gln
785 790 795 800

Ala Pro Leu Arg Leu Trp Ser Trp Cys Gly Thr Ser Gln Thr Tyr Phe
805 810 815

Gly Ser Thr Ala Lys Lys Ser Pro Thr Ser Phe Cys Cys Glu Trp Gly
820 825 830

Gly Gln Ala His Arg Gln Arg Asn Thr Gly Met Glu Ile Leu Leu Trp
835 840 845

Ile Leu Leu Lys Met Glu Ile Gln Ile Phe Lys Ile Cys Leu Gly Glu
850 855 860

Met Gln Leu Cys Thr Tyr Thr Pro His Ile Cys Arg His Thr Cys Arg
865 870 875 880

Gly Gly Pro Ser Ala Ser Asp Arg Cys Cys Ser Cys Ser Pro Ser Gly

	885		890		895
Phe	Ser	Ala	Gly	Arg	Gly
		Arg	Cys	Pro	Val
			Gln	Gly	Cys
				Leu	Arg
					Pro
	900		905		910
His	Arg	Val	Gln	Leu	Leu
		Arg	Arg	Trp	Gly
			Pro	Gly	Ser
				Pro	Ala
					Gly
	915		920		925
Gln	Arg	Leu	Ser	Lys	Gly
		Phe	Gln	Leu	Leu
			Arg	Trp	Trp
				Gly	Pro
					Gly
	930		935		940
Ser	Pro	Ala	Pro	Glu	Pro
		Arg	Lys	Gly	Pro
			Phe	Pro	Pro
				Pro	Asp
					Pro
945		950		955	
960					
Pro	Trp	Pro	Val	Thr	Ala
		Val	Thr	Val	Met
				Ala	Gly
				Ser	Val
					Pro
					Ser
	965		970		975
Ala	Gln	Ser	Val	Asp	Ala
		Leu	Glu	Ser	Pro
			Gly	Pro	Leu
				Ala	Leu
					Glu
	980		985		990
Gly	Pro	Ser	Ser	Pro	Arg
		Asn	Leu	Leu	Trp
				Arg	Glu
				Met	Ser
					Ile
					Phe
	995		1000		1005
Leu	Pro	Gly	Ile	Phe	Thr
		Ser	Arg	Ile	Leu
			Asn	Leu	Gln
					Val
					Leu
	1010		1015		1020
Lys	Lys	Ile	Leu	Arg	Ser
		Phe	Met	Lys	Leu
				Tyr	His
					Ser
					Leu
					Val
	1025		1030		1035
Met	Cys	Leu	Arg	Leu	Arg
		Thr	Lys	Leu	Glu
			Lys	Ala	Leu
				Ser	Ala
	1040		1045		1050
Leu	Phe	Ile	Trp	Pro	Gln
		His	Ser	Tyr	Lys
			Gln	Arg	Pro
				Pro	Pro
					Leu
	1055		1060		1065
Gln	Pro	Val	Gln	Val	Val
		Leu	Arg	Leu	Gly
			Asn	Leu	Pro
				Pro	Pro
					Phe
	1070		1075		1080
Phe	Arg	Gly	Ser	Glu	Val
		Pro	Phe	Pro	Arg
			Pro	Cys	Arg
				Thr	Lys
	1085		1090		1095
Met	Leu	Asn	Gln	Lys	Cys
		Leu	Ala	Pro	Phe
			Ile	Thr	His
				Pro	Phe
	1100		1105		1110
Ala	Ser	Gln	Pro	Leu	Gly
		Gln	Glu	Met	Pro
			Asn	Asn	Thr
				Gln	Ile
	1115		1120		1125

Arg Leu	Leu Lys Pro Leu Leu	Thr Pro Asp Thr Arg	Trp Ile Phe
1130	1135	1140	
Ser Asn	Gln Leu Gln Thr Val	Gln Met Leu Cys Leu	Pro Pro Leu
1145	1150	1155	
Lys Gln	Gly Glu Arg Ile Ile	Trp Pro Leu Gly Gly	Phe Gln Ile
1160	1165	1170	
Pro Asn	Phe Phe Trp Ser Leu	Gly Ile Gly His Thr	Gly Ala Trp
1175	1180	1185	
Trp His	Thr Gly Arg Arg Arg	Arg Glu Trp Gly Gly	Ser Thr Val
1190	1195	1200	
Ser Arg	Ser Pro Leu Trp Ile	Ser Ser Met Ile Tyr	Leu Arg Gly
1205	1210	1215	
Met Ala	Phe Ala Ser Asp Ser	Ser Ile Arg Thr Thr	Arg Val Ser
1220	1225	1230	
Trp Cys	Arg Arg Cys Gly Ala	Lys Ser Ala Ala Ala	Ser Ser Leu
1235	1240	1245	
Lys Lys	Lys Pro Arg Asp Ile	Cys Arg Ile Ser Asp	Ser Lys Lys
1250	1255	1260	
Met Thr	Gln Lys Arg Glu Ser	Thr Leu Gly Asn Phe	Trp Met Lys
1265	1270	1275	
Leu Leu	Gln Leu Pro Asp Lys	Lys Lys Lys Ser Thr	Glu Lys Thr
1280	1285	1290	
Lys Ile	Ile Lys Lys Met Lys	Lys Arg Ile Met Val	His Met Cys
1295	1300	1305	
Ser Ser	Leu Ala Leu Pro Thr	Gly Leu Thr Ser Leu	Ile Leu Pro
1310	1315	1320	
Ser Ser	Asp Leu Ala Val Leu	Ile Ser Ser Ser Thr	Ser His Phe
1325	1330	1335	
Leu Met	Arg Ser Pro Val Leu	Pro Ser Ser Arg Leu	Thr Cys Ala
1340	1345	1350	
Ser Pro	Gln Leu Pro Arg Met	Trp Thr Trp Ser Ser	Trp Leu Lys

1355	1360	1365
Trp Leu Lys Asn Trp Lys Arg Phe Lys Leu Lys Lys Lys Tyr Ile		
1370	1375	1380
Leu Ala Met Thr Leu Thr Leu Asn Gly His Pro Arg Thr Ala Ser		
1385	1390	1395
Ile Thr Leu Pro Thr Thr Ser Leu Lys Gly Ser Arg Thr Ser Cys		
1400	1405	1410
Cys Pro Arg Ser His Pro Arg Leu Pro Arg Thr Lys Trp Pro Leu		
1415	1420	1425
Gln Cys Leu Leu His Ser Leu Gly Thr Thr Gly Thr Leu Val Trp		
1430	1435	1440
Glu Arg Gly Val Leu Gln Met Arg Ser Leu Glu Ala His Cys Pro		
1445	1450	1455
Leu Gln Thr Phe His Leu His His Cys Arg Thr Gln Pro Ser Ser		
1460	1465	1470
Cys Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln Trp Ser Gly Ala		
1475	1480	1485
Val Val Gly Leu Arg Pro Val Ala His His Leu Pro Arg Pro Ile		
1490	1495	1500
Gln Gly Leu His Cys Pro Gln Ala Pro His Gln Pro Ala Leu Ser		
1505	1510	1515
Trp Gly Lys Trp Pro Val Gly Met Thr Gly Pro Ala Arg Cys Cys		
1520	1525	1530
Arg Trp Pro Arg Arg Glu Leu Lys Lys Asn Leu Leu Leu Pro Cys		
1535	1540	1545
Arg Cys Arg Arg Glu Tyr Arg Val Thr Met Gly Gln Ala Phe Gly		
1550	1555	1560
Ser Phe Ser Ala Asp Phe Ser Ala Pro Gln Val Leu Lys Lys Asn		
1565	1570	1575
Arg Lys Gln Asn Lys Ile Ile Cys Lys Gly His Arg Ile Thr Ser		
1580	1585	1590

Leu Ile Leu Ser Phe Gln Arg Val Lys Leu Lys Lys Lys Val Asn
 1595 1600 1605
 Ala Cys Ser Pro Ala Cys Thr Ser Lys Ala Trp Thr Pro Arg Lys
 1610 1615 1620
 Leu Val Gly Arg Ala Val Arg Arg Lys Gly Ile Ile Cys Ile Lys
 1625 1630 1635

Asn Met Phe Leu Gln Arg Lys Gly Phe Leu Asn Leu Ser His Val
 1640 1645 1650
 Glu Lys Phe Val Pro Pro Ser Pro Pro Leu Ala Leu Gly Pro Arg
 1655 1660 1665
 Met Gln Leu Cys Thr Gln Leu Ala Arg Phe Phe Pro Ile Thr Pro
 1670 1675 1680
 Pro Val Trp His Ile Leu Gly Pro Gln Arg His Thr Pro Cys Gln
 1685 1690 1695

Lys Lys Val Pro Ser Ala Ser Pro Trp Gly Leu Arg Pro Ser Pro
 1700 1705 1710
 Cys Leu Ser Trp Ser Ser Arg Ile Val Ala Pro Gly His Ala Leu
 1715 1720 1725
 Ser Cys Arg Thr Arg Arg Arg Trp Ser Ser Lys Gly Tyr Pro Tyr
 1730 1735 1740
 Asp Val Pro Asp Tyr Ala Ser
 1745 1750

<210> 1123

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA⁻ and HA-extended poly-FSP
 polypeptide 1A

<400> 1123

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt	60
tcgccagacc aggaaatcca tgcccgaacc gagatccagc tgaccatgaa cgacagcaag	120
cacaagctgg aaagccccgc tctgaacag gtgtcaccag cctctccacc tactcagcag	180

cctcagacac ctcaggattc tagacagggtg ctggccctgg ccaagaaaac cctgacaaat 240
 gcctccagag ccggacagtt tctgtgtgg cggagaacaa gcagaggcat gaggctgcag 300
 tggaagtccg gcaatgcctg cacacctctg agatgcccta gcagaagccc tgccacattc 360

 ctgacagccc tgaatggctg gcacagatct ggctgagag cccagatgcc tagctcttgg 420
 tctagcagcg gcagaacact gaagctggcc cctctgcaag tgaccaccac tctgaagctg 480
 atcctgggtca tgettgaaat cgtgaccgag cgtccctgc tgtactccag aatgtgtctg 540
 gtgcagatcc ccacacacac ctgggagccc gattacttcg tgtccctgcc tatgatgttc 600
 agctgggcca cacagtcttt tcccgtaggc gccgtgttcc tgaccagacc tgccattcct 660
 tgctgcagct gtaccagcca cagcaaccct tggagccaga gcaatcagca gctgaagtgg 720
 acccctcaca tctgaagtc cgccagcttc gacaagaaag gcttcgtgat cctgagccgg 780

 cggagcaaga ttgaggctc tcctatcggc tctatcgcca gctctctgg acatcctctg 840
 ggacctacac tggccatcag attcatcagc gccctcagc ctgacagctc tacagtgaca 900
 gctgccccta gcggccagta ctttatcgcc aagaagcgga tcaagctgcg gcggaacaat 960
 atgggcggca acagatccat ctgctgacc agaaagcgca agagagagaa gcggagccag 1020
 aagtccaggc agaaccatct gcagctgaaa agctgcagac ggaagatcag caactggtcc 1080
 aagctgagaa gccctggat cttaccaag tgcgagatct gcgtgaagaa caccgcatc 1140
 ctggctatca cctgatcac ccctcaggac cctcatctgg accctgtgtg tcacctcat 1200

 agaaggcctg gatggaaggg ccaccataga gtggtgttct ctcacatcc tagcggcagc 1260
 acaaagagcc actggcagca aagagaacgc ggaggcggca gacgcgagaa gaagggatgt 1320
 agagaacagc ggaagggtgt caagaacccc tctcagcccg tgcctctgag aaacgatggc 1380
 atcaccaacg gcaacgactc caccagaagc tgctccatca gcctgaagaa aagcctgga 1440
 aagatgcccc tgatgcggag agccagacct accagctgta gcacctgtag aatgtggtgg 1500
 aagggaaga aacggcgga agaaatctg cctatgagcc tggcctgcag catcacctg 1560
 tcttttggg gacagatcag caccctggtg ctggatgtgt ctagcatcag ccattggcgg 1620

 ctgccctgta aagtaccga gagcagctcc agcttcttct acaccagcga caggaccct 1680
 ctgagcatca gcagaccaac cagcagagct agacagagct gttgtctgcc cggactgaca 1740
 caccctgctc accaacctct gggcagcatg agcactagaa gagagatgcc aagccaggcc 1800
 acaccttctc cacttgacc ttggagagcc gctctgggca aagaagtga gagatcccag 1860
 agcaagctgc gcctgagaaa cacaagccct ggggagaaga acgatctcca gctgttcgtg 1920
 atgagcgaca ccacctaaa gatctactgg acagtatcc tgetgaacct ctgcggcaac 1980

ctgcacctga aaacaacatc actgcagcgg ccacctcgga gcatcctgtc tctgaatgga 2040

atctgggaag tgatgccccg gacactggaa ggctgcatca gcgtgaagga tcacagaacc 2100

agccagaacc acagcaagtg catcaccgaa tgtgtgcgga ctgccctgaa cgtgtccaag 2160

aagagactgc ctaagctgat gaagaagaag gacagcacca tcttcatcaa caaagtgcgc 2220

cagaacttca agcgcaactt caagaagaag aaaccctca ctttcagccc cagcagacgg 2280

atgactcgga gaacatgac aaccacaaaa atgatgatga tgcggcggac caagcggaga 2340

aggcgcaaaa ggcgagagaat gaccatgatg accagacgga ccctgctgac aaagaaaacc 2400

tgtctgacct ctagaaccag cgccgccaca aaagctctgc ctagacagac catcagccag 2460

cggaggccta ttcagacccc acctggaaca tctctggcca tctggggcag aacaagactg 2520

acctgacag gcaccagatc cagcgggaaca agagcctctc cttccgccgt gtgcctgtgt 2580

tgttggacct gtccaagcag aagcttccca gccgcttctc ctagtggact gagagcacct 2640

gttggagccc aggtctctcc tgaagtgaca ctgagagcct cttgtgcctc tagcgctct 2700

aaagcctgtg ctggactttg gccttgggga gcccaagtgc gagttggagc tggaacaggc 2760

ggaggacctg cttgtgttcc tgtggctgaa gcttctacag gcgcatggac agctgaaggc 2820

gccgctggaa caagatglag agcctctaga gcccttgcc gccaaacttc tgctagctcc 2880

cctaccaagt gtgaaatttg tgtgaagcgc agacggcgga gaaagagaag cagccagtct 2940

agaagccccg tgcttaaaaa gcgcgagagg atgatgtgc ctgtgcgggc cagaacagct 3000

agatctgcac ttcctcaggg cagagcacct ctggaaggga tgcctcttcc tagagcactg 3060

cctagcctgc tgagcagaat gcctgccaga agagagtcgc ggttttggct ggctctgcag 3120

gcacttggac tcagacctcc acatctgcct agctgtcatc ctcctgcctca actgttgggc 3180

cctccacctc ctcatcagge cccaatgaca ctgaaggccc tggttaagac ctggacacag 3240

ttccgcaact accccagagc cgacaagaag aatgtccggt ctaccgctt cttcctgctg 3300

gacatcatcc tgggcgattg cccaagaaca atggccggac cttctgcctc tctgcatcct 3360

gcatctggca gagcctccag aaagacctgg cagagaaggc tgagagcttg tagagcaggc 3420

ggacctgctg gatgggctag acaggcctat cctagactga aaaccttcgg cgtgccctg 3480

ggctctattc tgtgtctggc cggcagcctg tccacaatga tgatcattag caccaccaga 3540

caagagtgcg gcaggcgggc ttctgtgcct ttagaccta tgatcggaag cgccagacca 3600

ggaccttggc ggacatctgc tatgcctagt gccatgggag tcgcctgcc tacctcttgt 3660

gaaagcgga gatctctcc tgccaccggc ggaagaatgc caggatctca gtctatcatg 3720

atgagctgga tgcctccact ggctccatgt gccgcttgtc catgttctcc cgctcctaca 3780
ctgtgcccag cacatcttgc tagagcacca acagccgtgc ctgcctttac acctctgtct 3840
gctcatcctg tgccagtgtg gtctggatgt cacctggccg tcagaacctc catgctgaca 3900
ctgctgcccc tggaagccaa aaagagcatg aagcgggtcca acgctaagaa aatggaagat 3960
atgatctggg agagccggct gccactgagg ccacaaagag gacctagacc tctgcacaga 4020
tggctgcagc agacaaccgg ctgtagccag aggcggatcg tgttctttct ggccccatac 4080
ttccctcggc accctcacag atctccacca acatcttgcc cacctctgct ggaagctttc 4140

ccactgccaa gagcttctct gagggccaca gtccaagac atagctctgt tctcgccacc 4200
ggctctgacc tccacagaca gatttctctg cccctgagag gattcctcct gcaccaacca 4260
ctgccaggac agcatctgtg gctgtctcac agactgaggc tgagactgcc caggacacag 4320
ccatctttgc ctggaccatg tgcaagcctg ctgtccacac tgtctcagcc accacctcag 4380
gtccatctc aagtgtggac tgccgctaca ctgagatgtc ctgctgttcc tgcagctgcc 4440
tgtcctctg ctctgagatc catgcctaag agccggaacc aggtgctgtt cagacggaat 4500
ctgaccccaa gccagctgag aacactggcc ccaccttata tgctgctgcc ccagtctctg 4560

tcccagagcc tgagtagaaa gcagatccct agccagtcca tgctcgtggg ctaccctac 4620
gatgtccctg actatgcgtc c 4641

<210> 1124

<211> 4623

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 2A

<400> 1124

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60
tcgccagcc aggaaatcca tgcccgaaga aagatgcaga gcctgaatca cccagcaga 120
ctgaccaatg gctctctcc actgcacctg tgccagcctc tgagaatgag cagaaccct 180

cctagaagag tgtgcgccgc tctccacat agactgctgg gcccttcag atggaacct 240
cggagaaaga cctggaagat gcggaagaag tacgccaga agcctagcca gaagaaccac 300
ctgtacggcg gcaagaagcg ctctaagttc agcagaagcc acctggactt cagcccctac 360
tggatgaaga aagtgaaggt gctgttcaag gccgaccaga gcgagtctag cctgagcagc 420
ggaagatgca gcctgatgga acagatccct cacctgaagt ctcgcgga gtggcagatc 480
agacacgtgc tgaagaacct gtggctgccc atgagaagcc tgggagaacc ttggagagcc 540

ggctttcagt ggggagagtc tccttggcaa gtgatggcct ctctgaccgg cagagccaca 600

 tttctgctgg ccctttggga atgtagcctg cctcaggcaa gactgtgcct gatcgtgtct 660
 agaaccctgc tgctggtgca gagccggaac aagaaaacaa agctgtggtt cagcctgac 720
 aacatccacc accggaagaa cccactgctg cctatgagat ggtggtgtac cagaggcggc 780
 ggaaagcgga aaaagaaaat gtgcaagggtg tccggcggct gcaccgcctg tgttagaga 840
 tgtccttggg agggcatctg ctggaagtgg cctgtgacag tggccgcat tagaatgtgt 900
 gccctgtctc accctagctt ctacatcagc agcaccgtgt gctttctgag caagcactgc 960
 atgaccgcct gcaccagaaa gagaatgaag accggcgcca tccaagagaa gggcgctatt 1020

 caagagaaag gggccatgac caagcggatc tgcgtggtca atttcgaggc ctgcagagag 1080
 atggaaagcc tgagcgcccc tgagaagatc accctgtttg aagcccatat gggccggtgc 1140
 acctccatca atgtgctgtg tgtgcgggcc agcctgattg agaagctgat gaaagaaaag 1200
 cgcaagatga agcggaacca ggtggcctct ccacagatca tgcagcggct gttcatcaag 1260
 ggctaccaga acaaccactt caccttccat ctgcaaaact tcgccttctt cagctccttc 1320
 ggcaacaaca agtatcatca tatctgacc atcctgttcc acgtgcggaa catcgtgtac 1380
 ggcatccaag tgatgctgtg cgctagccct cagattatgc agagaaccag cgccgaccgg 1440

 ttccggatga agagaagaat gcagaatctg gacaacctgg gcgtgccatg gcctctgttg 1500
 cctggaatcc catctctgaa cgcccagtgg atgttctga gaatcgatc cccgcaaate 1560
 atgcagagga tgagcgccgt gaacttcgag acaatccggg ccagaaaccg gaacatgaag 1620
 aaaaccatga gccacctgat cgcccatcag gccctgaaga tgagcggcct gagactgttt 1680
 caccacagac tgctgacacg gaagaagccc ggaaaactgc tgctcgcca tatgtacggc 1740
 ttcagacct acggcaccca gaaaggcgag tgcgtttgtc tgcagtgtct gagcggcagc 1800
 agcctgttca ttctgaagca gccctggac ctgaagatca gcaagacctt catgggccac 1860

 agagagggca gcgagtctga taatctgggc ctgctgtata gcttccctcc acctatcct 1920
 atcagcgagg gcctgaccat gaccaccggc agaaacatca acagcaactc cctgatgacc 1980
 aactgcctgt tcagcccat ctctctgtgc caccacgcca tcatgcacag aaagatgaca 2040
 agccctcact tcaggctgtt cagcagcaag atcccacatc ctgaggtgcc atctgtggtg 2100
 gccctgtgca agttccgggc ctccatccac acacctagaa gccctggctg cagcgtgtac 2160
 gccaatatgt gctggcccaa gttcttcttg accttcagcc agcagtggct cagcgtgaca 2220
 tctctggaat ggacagccca agagagaggc tgcagcagct ggctgatgaa gcagacatgg 2280

atgaagtctt ggagcctgcg ggaccccagc tacagatcca tcctggaata cgtgtccacc	2340
agagtgtctg ggatgcctac ctctaccgtg ctgcaggctc atccacaagt tccagctctg	2400
gctcctcaag cctggtggcc tgctagaaga ggacctctga catctgcccc atccgctcag	2460
cagtccctga ccagagagaa gattatcaac cccaccatca gctgcccc ttccagagcccc	2520
accaagagac tgatctaccc tcttagcacc tgttctctgc cctgcagagg ctctctgcct	2580
agcagatttc ctggggcccc acctcctctg aacagcgtga tcgtgcacaa gatcgtgctg	2640
gtgttctga agtccctgtc cagctacaac tgcgagcgga gaatcagcgg catccagaag	2700
agagccatcg agttcgccgt gctgaaactg ctgaatatgg acctgcctct cgagaacaca	2760
cagatcccca gaacaagccc actgtggaag atcacaatgg tgctgacata ccccaactgc	2820
gtggtgcatg tgctgatgtt tggcgccctg agagccacag ctctgtctac agctgcacct	2880
caggctcaga cccctcattg gagagctgcc acaacaagca gcatgagcag cagccctaga	2940
gccgagccta catcttctag ctcttgggcc acctgttggc ccagatgctg ctccagctct	3000
tgttactggt cactgtctag ctggcctcca gctggcgccg ctgaagctac aaataccaga	3060
accagaagcc gcgagagcca gaggggtaga atgctgactt ggagaagctc cctgtggttg	3120
cagggcacca gatgttttac aggcgtgcgg accagctcca gatacaagaa aagaggcgtg	3180
atgcctggc ggagacagat caatagacgg aagctgcaga gaaagaagca ctggaacagc	3240
gcctacctgg gcagaacact gctggtcacc tgtatctgt atcaccggtg gatcgtgacc	3300
tccatgtgtc agtcccagag atggctgacc agcaccacaa gtagatctag cgccctgatg	3360
tggaccgagc tgagcctgga accatggatt ccctacctgc atcagcagaa aaccagcgg	3420
acactggaat ccgcccgaact gtttccttgg ctgcacaccc agtgccaaga gaagaaaagc	3480
agaaagctga tgtccagctg cacacacccc tgcacaatgc tgctgccaca gggatgtcat	3540
cctgcctggc tgagccctat ctctgcctgt ccaagactgc tgccatatcc ttttcacgtg	3600
ctggctctgg aagtgcctt tctcctgga accgcatgc ctccagatgca gttgcaggct	3660
ctggctatgt gggagaaagg ctgggataag cctggcacca gcctgcagtg ctacctgaac	3720
agaagaagaa acagccggaa gcagagccag gtgcaactgg ccattcaggt gctgctcgtg	3780
gacaagcaca agtactttct gttcgcccaa aagaaaggcc acatgatctt tagcctggcc	3840
aacggcctgt ggtttaacct gatcttcaac tcccgaaga aactgctcga ggacatgaag	3900
caaaatggct tcaccggcaa aggcctgaca cccccgtgc ctctgaagcg gactctgcag	3960
aacaaaagaa acaagaatat caaacgcgtc aaccagaaga agggcaacat caagcgggaag	4020
tccatctgc tgcacctgat tgtgtgaat agccccgaga gcaacctgat cctgatccag	4080
catggcggca tcttcacctt tcggttctgg gtcgagaagc tgtcctggaa catctgcaag	4140

aacctgagcc tgiacctgga caagtctgtg cagagactgc tgtacgtgta catcatcgag 4200
 acaaactgtg tctgtctgaa cctgtttcat gtgcccgtga accagatctt catgatggcc 4260
 ttctacctga agtacaccga gaaggcctgg gtcattggaac tggaatggct gatccaacag 4320
 cagtgtctatc agggcagctg cggcagagct tgttcttgtg gaagaggctg tggcacccct 4380

agaggcgatt ggaagagaca tctctctcgg agagccttct ggaagcctcc tagccagggc 4440
 atctctagct gtctgatgac cggctgttgg ctcgagaaga aagctacctg gatgcggcgg 4500
 acccgccgga agaagaggga agatcattgc ggactgagac accccagctg gccttggaca 4560
 agatgtctga ggatgaggcc tccaagaagc ggctaccctc acgatgtccc tgactatgcg 4620
 tcc 4623

<210> 1125

<211> 4638

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP

polypeptide 3A

<400> 1125

atggatgcaa tgaagagagg gctctgctgt gtgctgtgct tgtgtggagc agtcttcgtt 60
 tcgcccagcc aggaaatcca tgcccagga gctgtgctgt cctcttgtca gtctctctct 120
 tctctctggg aaaccacacc tagctccgac gccaccagac ggacaagacc tattgccgct 180
 cagagcaaga aaaccatgac agccgccgga ctgaccctta tgatccggaa gatccagaag 240
 cggcggagaa ccgccaaccg gtgtctgaga gtttagatgtg gcggctggct gtgtggctgg 300
 acacctagag gacagaacac cagaagcacc aacctggaaa agaaccaccag cctgaagaag 360
 cagagccagc ggagaggaaa gctgagcagc ctgttcttca gccactgcct gtgccggaac 420

agcagaaggg ccacacctac atctaagggc agcctgcggc ggaagtacct gagagtgcct 480
 attctctcac acctgagaca ccctctgctg ctgatggacc tggacggaat getgaccgtg 540
 atcggacagg gactcgtggg catgaccctc agagatctgg gaacagtggc tggcgccacc 600
 gctcagattc agaggcctat tcaggtgcag accggcggca gacttacacc tctctctctg 660
 attctgtggc ctcaggccgc tctgttgat cctctggct ctgtgtggat tctgcctctg 720
 aagaacaaga agcggagaaa gctgcggccc aagcggctgg actttcacc tagatcttct 780
 agcggcgtgt ccgtgatcac catgaagctg tgggagaagc acttcaagg cctgaactgg 840

aacctggtcg tctggattct gaacctgaag atgatgaaca tcgagatcac ccctcagcgg 900

agcaaggcca gaaagtccgg cgtgatgaag tgcctgggac tgtgccccag cgagaagaag 960

aggaagctgc ctctgcctct gaccttcagc accctgctgt gggactctag acatagaggc 1020

gccagctcca gcaccagcag agactccaga agctttttca ccagcgtca ccccagcaga 1080

ccctgcagaa tgagactgta ccagttcctg atccacctga gaaagggtga caccacccat 1140

ctgcaggtcg tgaccaagac cgtgacagcc acaacagctg acggccagag aatgcggaga 1200

ctgaagtga aggcctgccg gctgagatgg gctagacctg aacctgctgc tcaggccct 1260

ccaaagagcc actttccacc tcactctagc ggccctagca gaaccagttc tctgcagctg 1320

cggagcatcc ctacagtgc aaaagccaca gccgtcaca gcgtgacagt gaagctgcag 1380

aagggaaaga acagccctg ctgccaaaag aaactgcggg tgcagaatca gggccatctg 1440

ctgatgatcc tgcctcaca tacctacatg gaaatgcact acggccatca ggccccacag 1500

gtggccatgc tgcctaagct gctgtgcaga cagatgctgc ccactctgag cacactgcag 1560

caaagacacc cacagggccc ttgtcctcca cctgtgacac cactgagagt ccagtctgtc 1620

ctgctgctgg gagtgcctca gacagctgct agacagccta gcagaccac cggcagaacc 1680

cctaccacaa gactgatggc ccctgtcggc agcgtgatga gctgttctct gctgaccag 1740

ccttctccag ccagcgcctg tacaatgcct ccactgctgc atcctcagtg ggccccacat 1800

tctgtggat tgtctccgg cgttgcaga cctgcctgta cctgtatcag catgaccacc 1860

atctccagag ccacctggca ggtttccgtg tacagcggca atctgctgag cttctccaga 1920

cggggcatga agagtagcgt gcggctgaaa aacagccggc ggaacagacg gtacagaaag 1980

atctacggcg agctgaagat gtccctgcag gccgtggctc ctatagatcc tagatctgcc 2040

gtggacatca gccccggacc tacctctcct agcctggcct cttgtgcctc tgtggccatt 2100

ggaaaactgg ccctgcttgg cgcttctgcc ccttgtgtg ctgctggcgc tagagaggct 2160

ggaagatttg ccgtgctggg caccatggtc atgaagcacc tgaaccgcaa gctgcatctg 2220

acccggtcct gcctgatcga tctgacctg atgatgagcc agaagctctg gaagaaccag 2280

cggagagaaa tccctctgcc atctctaga cagcatctgc tccctcagta ccctctgcac 2340

cctctctcac cttgtctgct gctgtctcac cacagacacc acctggcctt tctggaaatg 2400

gcctgcagca gccagcacac ccactccatc aagatctgga tcagctttag ccacagcag 2460

agcagcccat tctggccag atcctggaac accatgcagt ggaacaacaa gaaaatggcc 2520

atgacagtga tcgtggcgc ccaccactgt cagtacaagc tgacctacac caaagtgtgg 2580

aagatgaatt ggaagaaaat gatgatcggc tcccagcacc tctgttcag ccctctggat 2640

agctctccac tgcaactgct gcttcacctc cagggcaaga gatgcaacct ttgctgcaga 2700

ctgacatgga tgtccatgct gcagaaacag tgctgttaca acctcgtgat caagcaccca 2760

ctgatcttca gaatcaacct gcggagacag ggcaagacca aggatggcgt tgtgcagagc	2820
ctgggcttcc tgaaccagca gatcatcctg cagaaagagt tcttcatctg cctgctcatg	2880
tttatcaagc ggtggaagcc tgccgccacc aagagagagt gggagaaaacg caagcagatc	2940
ctcggcggag gcggcaagta caaagagtac ttctgaagc gcatcctgat tcggaaggcc	3000
atgactgtgc tggccggcga caagaaaggc ctgggcagat tcatgagatg cgtgcagagc	3060
gagacaaagg ccgttagcct gcagctccca ctcggaagag gccctgtgta ctacgtgtgc	3120
aaccggatga acgtgtccag cgtgtgtgaag cccttctgtg tcaccgtgcc tatcgaggac	3180
atgagagagt gcacactggg ccgcaacaga atgaatgtgt cctctgtgct gaaacctgtg	3240
ctgatccctg tgccaatcga cctgcctcgg atgctgcca tcagcagccc actgcacaga	3300
ccccagatgc cattctggac ctgcaccttt cctgccacaa catggggcac ctgggagaca	3360
cctttctacat ggggctggcg gacctttcgg ggccctagaa gaaaagtgt gatggtgctg	3420
tggctgcccc ccaaccagag tctgcagaaa agccaagtgt tcagtggtt cctgcggacc	3480
gagaacatcc ggaagctgat ctggaccaag cagcggagct tcctgtctct gtccccaaag	3540
ctgagagcca ccgaacagat gaccaatgtg ggctgcccct tcagcggcgg gattctgcat	3600
caacctgaaa tggccgccat gcggctgatg cccaagtcc tgaatagcac caacagctgg	3660
tggacctgta ccaacctgag cgtgcccatt atgctgacca ttctgatttg gaagcgggtg	3720
ttcattctcc tgctgtccga caagaagctg ctgaagaagt ctagccagct gaggcggctt	3780
tggagaaacg tgtcccggat cagccaccag atgaagtgtc tgaccgccgt ggactgtctg	3840
caggccttct gggacatgaa catggaacac cggctgacca tggacagcgc cctgagcctg	3900
acaaagagag agggaccgga gacttgcaag aagaagctcc tgctgaaact gctgacaatg	3960
agcctgagca acatcctgat gaagttccgg ctgcggctga gaatcccaag cctgaggaag	4020
tatcgccagc atctgaaaaa gaccagcgcc aaggcgagga agctgaagca ctgctttaag	4080
gcttggggca gagggccacc tctgcacaca agaagccaga agaaagacc tgccggcaag	4140
ctgaaaaaac tgaccacact gagcttcgtg ctgatcgagg aacggcggaa cctgcagcgg	4200
aatctgaaag tctgtggct caagaaaagc accaagagcc ggtatctgtt cttcctgacc	4260
gltgtcggct tcttcgagaa gaaacggcct gactggctgt cctccagaaa gaaggacac	4320
acaaagaatc ggaggaaggc caagcggaag cccagatcg tgcacaagaa gagaggcctg	4380
ttctcaaaa agaaatacct ggtgcagggc gccaaagaaga tcaccttct gtccaacggc	4440
atggaagctt gcggcacaca cccacacca agactgagcg acagagtgtt cctggtcaag	4500
atcaccacca ccacaagcag cccagaaga agcccagcac tgagagctag aggcggcacc	4560

acaattggcg aagtgaccag cctgtgcttc ttctacctgc tgtacggcta cccctacgat 4620

gtccctgact atgcgtcc 4638

<210> 1126

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 4A

<400> 1126

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgccagcc aggaaatcca tgcccgaatc cagaagaaga aacagaaatc catggccaag 120

aagtccagc agcctctggt gctgaagaag aaccggaagc aagagtgggg aggacaggcc 180

cacagacaga gaaacaacgc caagaagatg cccttccaag aggaaaagaa gaacggccgg 240

atcagcagca gcctgacct gagcttccag agagtgaagg acagcaagaa aatgaccag 300

aagatgtgca gctctctggc cctgcctaca ggctgacat ctctgacct gcctagcagc 360

gatctggccg tgctgatctc tagcagcacc agccactttc tgatgcggag ccctgtgctg 420

ccaagctcca gactgacatg tgccctccca cagctgcccc ggatgtggac atggtctagc 480

tggctgaagc accccagaac cgctagcatc acactgccta ccacaagcct gaagggcagc 540

agaaccagct gctgccaag atctcaccac agactgccta ggaccaagtg gcctctgcag 600

tgtctgctgc acagcctggg aacaacaggc acactcgttt gggaaagggg cgtgctgcag 660

atgagaagcc tcgaagccca ttgtcctctg cagaccttcc atctgcacca ctgcagaacc 720

cagccaagct cttgtctcc tgccctggatt ctgtaccaag gccagtggag cggagccgtc 780

gttggactta gaccctggc tcaccatctg cctagaccta tccagggcct gcactgtcct 840

caggctctc atcaacctgc tctgagctgg ggaaagtggc ccgtgggaat gacaggacct 900

gccagatgct gtcggtggcc ccgcagatct cagaagtctc agcatcactg cgccctgcgg 960

aagatcgagt gggccacaaa actgtctctc ggcggaaaag ccggaccaca ggctcaagag 1020

aaggccagac cttctccttg cctgtcctgg tccagcagaa ttgtggcccc tggacacgcc 1080

ctgagctgtc ggactcgtag aagatgggtc tccaagtga gaggcggccc tagcgccagc 1140

gatagatgtt gtagctgtag cccagcggc ttcagcgccg gaagaggcag atgtcctgtg 1200

cagggatgtc tgaggccaca cagagttag ctgctgagaa gatggggccc aggatctcct 1260

gctggccaga gactgtctaa gggcttccaa ctgctgcgtt ggtggggacc tggatctcca 1320

gctcctgagc ctagaaaggg ccattttcct ccacctgac ctcctatggcc tgtgaccgct 1380
gtgacagtga tggctggctc tgtgcctagc gcacagtctg tggatgccct ggaatctcct 1440
ggacctctgg ctctggaagg ccctagcagc cctagaaacc tgctgtggcg ggaaatgagc 1500

atctttctgc ccggcatctt ctgcaaaaag aaggtgccat ctgccagccc ctggggactt 1560
gttctctctt ctccaccact cgctctgggc cctagaatgc agctgtgtac ccagctcgcc 1620
agattcttcc ccatcacacc tccagtgtgg cacatcctgg gacctcagag acacacacct 1680
caggtggtcc tgagactggg caacctgcct ccattcttca gaggcagcga ggtgcccttt 1740
cctagacctt gccggacca gaacgagggc aacaatcact ggcccagagt ggaaatgcct 1800
accggctggc tgctctggg ctacaacacc agaaacacag ccagaaatcc tcggctgcag 1860
cagcatctga aacctggca gcagtgcaca cgggccagat ggtgtcaaga gccttgtcag 1920

acctgacct tcttccactt cttcttcttt ttcaaaacgg tgtccctgtg ttgtcccggc 1980
tggtccaaag gacaacctcc acctcctggc ctgaagcctt ctagcctggc ttctcaggtg 2040
gccagaacca caggcgtgta ccagcacgtg tggtgatct gcttcgtgtt cttcgtgtgc 2100
gtggaaacgg gcttctgtca cgtggcacia gtgggcctcg agagactggt ttctctgagc 2160
ggcatcacgg acgtgaacca ttgggcccag cctaagccat ctccctagca aggcaccggc 2220
atgaacagac ccatcggcct gagagttggc aaaggcgtgt gggccagact gctcaagaag 2280
aagcctagag acatctgtcg gatctccaac agaaagaccc ggaaggccgc cagagagaag 2340

caccgaaaa cagatagagc cagcgtgtcc ttctggactc tgctgcctac aacaggcgtg 2400
cggacaagag gaagccctct gagactgact ctgtggcctc ctatagtcag atgcagacgc 2460
gagtacagag tgacctgaa catcctgaac agcctgcaa gcagcatgga aatcgccgtg 2520
ctgcaagaaa ccgccaagaa aagccctacc agcttctgct gcaacctgga cctgcagcat 2580
cagcgagac gcaaaaagaa gaaagacaag gtcgagatcc ggaatcgag ccccaaggcc 2640
aatagcacag agtgtcaggg cgagcacagc agagagcaga atctgctgaa tctggtgcag 2700
ctgaatctc acagccctca ccaccggaag gacgaagagg accaccagaa gagacaccac 2760

caccacaatc aaaagaagat gagcgtccca ctgttcttcc acggcgacct gtgtagagag 2820
agcaccctgg gcaatttctg gatgaagctg ctccagctgc ctgagaggcc tccactgcaa 2880
ccagtaccg gaatggaaat cctgctttgg attctgtga agatggaaat tcagatcttc 2940
aagatttgcc tgggcgagat gcagctctgc acctctcgga ttctgaacct gcaagtgtg 3000
aaaaagatcc tgcggagctt tatgaagctg taccacagcc tcgtgatgtg cctgcggctg 3060
aggaccaagc tggaaaaggc tctgagcgcc ctgttcatct ggctcagca ctctacaag 3120

atcacacacc cattcgccag ccagccactg ggacaagaga tgcccaacaa cacccagatc 3180

cggtgtctga agcccgacaa gaagaagaaa agcaccgaaa agaccaaagg ccaggctttc 3240

ggcagcttct ccgccgattt ttcagccctt caaggacagg cttttggctc cctgtgtcag 3300

ctggtgtccg ccgactttag cgccccacaa gtgaccagac tgcggagcct gaaccatctg 3360

ctgatttggc tgaagaattg gaagcgggtt aagctcaaaa agaaatatca ggcccctctg 3420

cggctgtggt cttggtgcgg aacaagccag acctacttcg gcagcatcat ctgtatcaag 3480

aatatgttcc tgcagcgga gggtttctt aacctgagcc acgtggaaaa gttcgagctt 3540

aagaagaatc ttctgtccc cgtcgtgatc aacctgaaga gactgcagaa attcatgtg 3600

aaccagaagt gcctggctcc atttctgcc tgcaccagca aagcctggac acccagaaaa 3660

ctcgtgggca gagccgtgcg gagaaagggc attctggcca tgacactgac cctgaacgga 3720

atcgaggccc tgacagccct gtttacctgt agaaccgcct ccatcagcgt gaacatcagc 3780

acctgatga gcatcctgga agccatcatc aagaagatga agaaacggat catggtgcac 3840

cgggtgatct tctccaatca gctgaccgtg cagatgtctt gcctgcctct gctgaccctt 3900

gacaccagat ggatctttag taatcagctg cagacagtgc aaatgctgtg tetgccacct 3960

ctgaagcagg gcgagagaat catttggcca ctggcggtt ttcagatccc caatttctt 4020

tggtccctcg gcatcggaca cactggcgca tgggtggcata ctggtagaag gcggagagag 4080

tggggcggct ctaccgtgtc tagaagccca ctgtggatca gctccatgat ctacctgaga 4140

ggcatggcct tcgccagcga cagctccatc agaaccacca gagtgtcctg gtgtcggaga 4200

tgtggcgcca agtctgccgc agcctcttct tctccactgt gggattgcag caccacaacc 4260

ggcacacacc acggatgcct gtgggagatc cctagcgtta ccttgcctggc taacctgcac 4320

ctgtgtact accacttca gagcaacaga aacaagagcc gccagatgga atccctgggc 4380

atgaagctcc aacttaaaaa gaaagtgaac gctgcagca cctacacacc ccacatctgc 4440

agacacacct gtgcgtgaa cgccgtcgag gaactgcact ctagaaggat gtccgtgcgg 4500

atcgtgaaaa attgggtgtc ctgctgttac gtgcggctgt cagctgtggg actgtctact 4560

tggagcgctc tggacaacaa gatcatctgc aagggccaca gaatcaccgg ctaccctac 4620

gatgtccctg actatgcgtc c 4641

<210> 1127

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP

polypeptide 1B

<400> 1127

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt	60
tcgcccagcc aggaaatcca tgcccgaacc gagatccaat tgaccatgaa cgacagcaag	120
cacaagctgg aaagccccgc tctgaaacag gtgtcaccag cctctccacc tactcagcag	180
cctcagacac ctcaggatag cagacagggtg ctggccatgc ctagcagctg gtctagctct	240
ggcagaaccc agcggaaggt ggtcaagaat cctagccagc ctgtgcctct gaaaaacgac	300
ggcatcacca acggcaacga ctccaccaga agctgcagca tcagcctgaa gaaaagcctg	360
gaaaagatgc cctcatgat gaagaagaag gacagcacca tcttcacgtg gcccatgagc	420
ctggcctgta gcatcacctg gtctttcgtg ggccagatca gcacactggt gctggatgtg	480
tccagcatct ccactggaa caaagtgcgg cagaacttca agcggaacgc cgacaagaag	540
aacgttcgga gcggcgagaa gaacgacctg cagctgtttg tgatgagcga caccacctac	600
aagatctact ggacctgat cctgtgaac cctgcggca atctgcacct gaaaaccacc	660
agcctgggcg actgtcctag aacaatggcc ggaccttctg cctctctgca cctgcatct	720
ggcagagcct ctagaaagac ctggcagaga aggctgagag cctglagagc tgggtggacct	780
gctggatggg ccagacaggc cttcgataag aaaggctttg tgatcctgag cgtcggagcc	840
ggaacaggcg gaggacctgc ttgtgttct gtggctgaag cttctacagg cgcttggaca	900
gctgaaggcg ccgttgaac aagatgtaga gcttctagag ccccttgagc acagctgcct	960
gccagctctc ctaccaagtg cgagatctgc gtgaagcgca gacggcggag aaagagaagc	1020
agccagtcta gaagccccgt gcctaagaaa cgcgagagaa tgatgctgcc cgtgcgggcc	1080
agaacagcta gatctgact tctcagggg agagccccctc ttgaggaat gctgttctct	1140
agagcactgc ccagcctgct gtctagaatg ccagccagaa gagagagcgg gttttggctg	1200
gctctgcagg cacttggact cagacctcca catctgccta gctgtcatcc tctgcctcaa	1260
ctgcttggcc ctccacctcc tcatcaggcc cctacagctt tcttcctgct ggacatcatt	1320
ctgcggctgc cctgcaaagt gaccgagtct agcaatatgg gcggcaacag atccatctgc	1380
ctgaccaacg ccaagaaaat ggaagatatg atctgggaga gcacgccct gagcatcagc	1440
agacctacat ctagagccag cgagagctgt tgtctgccg gactgacaca tctgtctcac	1500
cagccactgg gatctatgac cctggccatc agattcatca gcgtcctca gcctagctcc	1560
agcacagtga cagctgtctc tagcggccag tacttcaagg gcaagaagcg gcggaaaagag	1620
atcttcaaga agaagaaacc cctgacattc agccccagcc tggccaaaaa gaccctgacc	1680

aatagcagct tcttctacac cagcgaccgc gaggccaaga aatctatgaa gcggagcatg	1740
accctgaagg ccttgggtcaa gacctggaca cagttcagaa actaccccag agcctcctct	1800
cctggacacc ctctgggacc taatggcatc tgggaagtga tgcccagaac actggaaggc	1860
tgcattctccg tgaaggacca cagaacaagc cagaaccaca gcaagtgcac caccgagtgt	1920
gtgcggcagc ccttgaacag aagaagcaag atcgaggcct ctctatcgg ctctatcgc	1980
ctgagatcca tgcctaagag cagaaaccag gtgctgttca gacggaatct gacccaagc	2040
cagctgagaa ctctggcccc tctttatatg ctgctgcccc agtctctgag ccagagcctg	2100
agcagaaagc agatccctag ccagtccatg ctggtggcct ctagagcagg acagtttct	2160
gtgtggcgga gaaccagcag aggaatgagc ctgcagtgga agtccggcaa tgcctgcaca	2220
cctctgagat gccctagcag aagccctgcc acattcctga cagctctgaa cggctggcac	2280
agatctggac tgagagccca gagaagcgc aagcgcgaga agagaagcca gaagtccagg	2340
cagaaccatc tgcagctgaa gtcttgcgg cgcaagatct ccaactggtc caagctgaga	2400
agcccttggg tcttctgttc caagaagaga ctgccaagc tgaccaagtg tgaatctgt	2460
gtcaagaaca ccgccatctt ggctatcacc ctgatcacc ctcaggacce tcatctggac	2520
cctgtgtgtc accctcatag aaggcctgga tggaagggcc accacagagt ggtgttttct	2580
catcaccta gcggcagcac caagagccac tggcagcaaa gagaacgcgg aggcggcaga	2640
cgggaaaaga agggctgtag agagagatcc ctgctgtact ccagaatgtg cctggtgcag	2700
atccccacac acacctggga gcccattac ttcgtgtctc tgcccatgat gttcagctgg	2760
gccacacagt cattccccgt gggagccgtg tttctgacca gacctgcat tcttctgtgt	2820
agctgcacaa gccacagcaa ccttggagt cagagcagac acccacacag aagcccacct	2880
acctctgtgc ctccgtgtct ggaagccttt cactgccta gagcatcct gagagccacc	2940
gtgccaagac atagctctgt gctggcaacc ggactgcac tgcacagaca gatttctctg	3000
cccctgagag gattcctgt gcatcaacca ctgccaggcc agcatctgtg gctgtctcat	3060
agactcgggc tgagactgcc aagaactcag cgccctccta gatccatcct gagccttaga	3120
ctgccactga ggccacagag aggaccaga cctctgcata gatggctgca gcagaccaca	3180
ggctgtagcc agagaagata cccagactg aaaaccttcg gcgtgccact gggtccatt	3240
ctgtgtctgg ctggatctct gagcaccatg atgacatta gcaccaccag acaagagtgt	3300
ggcaggcggg catctgtgcc ctgtagacct atgatcgaa gcgccagacc aggaccttgg	3360
agaacatctg ctatgcctag cgccatgggc gtcgactgc ctacaagctg tgaatccgga	3420

agatctcctc ctgccaccgg cggaagaatg cctggaagcc agagcattat gatgagctgg 3480
 atgcctcctc tggtccttg tgccgcttgi ccttggtctc ccgtcctac actgtgtccc 3540
 gtcatactcg ctagagcacc tacagccgtg cctgccttta cacctctgtc tgcacatcct 3600
 gtgcctgtgc tgictggatg tcacctggcc gtcagaacct ccatgctgac actgctgcct 3660
 atgctgaagc tggccccact gcaagtgacc accacactga agctgaccc ggcatgctg 3720
 gaaatcgtga ccgagagcac tcggagagag atgccttctc aggccacacc ttctccacct 3780
 ggaccttggc gagccgctct gggcaaagaa gtgaagagat cccagagcaa gctgcgcctg 3840

 agaaacacaa gccccatcgt gttctttctg gccccatact tccccagacg gatgaccaga 3900
 cggaccatga caaccaccaa aatgatgatg atgcggcgga ccaagcggag aaggcgcaaa 3960
 aggcggagaa tgacaatgat gacaaggcgg accctgtga caaagaaaac ctgtctgacc 4020
 cctagaacca gcgccctac caaagctctg ccaaggcaga caatctccca gcggaggcct 4080
 attcagacc ctcttggaac atctctggcc atctggggca accagcagct gaaatggacc 4140
 cctcacatcc tgaagtccg cagcagaagg gccagaccta ccagctgtag cacctgtaga 4200
 atgtggtgga tcgcaaaaa gcggatcaag ctgcggcgga acagaaccag actgacactg 4260

 acaggcacia gaagcagcgg caccagagct tctccatccg ccgtttgcct gtgttgctgg 4320
 acctgtcctt ccagaagctt cccagccgt tctccaagcg gattgagagc acctgttgga 4380
 gcacaggccc ctccagaagt tactctgaga gctagctgtg cctccagcgc ctctaaggct 4440
 tgtgtggac ttggccttg gggagcacia gtccgcaac catctttgcc tggaccatgc 4500
 gcttctctgc tgagcacact gtctcagcca cctccacagg ctccatctca agtgtggaca 4560
 gccgcaacac tgagatgtcc tgctgttcca gctgtgcct gtctcctgg ctaccctac 4620
 gatgtccctg actatgcgtc c 4641

<210> 1128

<211> 4623

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
 polypeptide 2B

<400> 1128

atggatgcaa tgaagagagg gctctgctgt gtgctgtgc tgtgtggagc agtcttcgtt 60
 tcgccagcc aggaatcca tgccgaaga aagatgcaga gcctgaatca cccagcaga 120
 ctgaccaaca tgagcagaac acctccaaga cgcgtgtgca accctcgag aaagacctgg 180
 aagatgcgga agaagtacgc ccagaagcct agccagaaga accacctgta caacagccgg 240

aagaaactgc tcgaggacat gaagcagaat ggcttcacag gccacagaga gggcagcgag 300

tctgataatc tgggcctgct gtactccttt cctcctatcc ggatgtgcgc cctgtctcac 360

cctagcttct acatcagcag caccgtgtgc tttctgagca agcactgcat gaccgcctgc 420

acacaaaaga aaggccacat gatcttcagc cgcgagaaga tcatcaaccc caccatcagc 480

tgcccttttc agagccccac aaagcggtcg gaactgagcc tggaaccttg gattccctac 540

ctgcaccagc agaaaaccca aggcggcaag aagagaagca agttccctgg caccagcctg 600

cagtgtctacc tgaacagatg cagcctgatg gaacagatcc ctcacctgaa gtccgcctct 660

ccacagatca tgcagagaac cagcgccgac cggttccgga tgaagcggag aatgcagaac 720

ctggacaatc tgggcgttcc atggccactg ctgcctggac ctctggaaaa cacacagatc 780

cccagaacaa gccctctgtg gaagatcaca atggtgtctga catacccaaa ctgcgtggtg 840

cacgtgtctga tgttctggct gcctatgaga tctctgggcg agccttggag agctggcttt 900

cagtggggag agtccccctg gcaagtgatg gctagcctga caggccccta tcctatcagc 960

gagggcctga ccatgaccac cggcagaaac atcaacagca actccctgat gaccaactgc 1020

ctgttcagcc ccatcttctt gtgccaccac gccatcatgc accggaagat gacaagccca 1080

catttcagac tgttcagcag caagatccca catcctcagg tgccatctgt ggtggccctg 1140

tgcaagtcca gagccacatt tctgtctgcc ctgtgggagt gtagtctgcc tcaagccaga 1200

ctgtgcctga tcgtgtctag aacctgtctg ctggttcagt ctgccgtcc tccacataga 1260

ctgtctggcc ctcttagatg gtccagaagc cacctggact tcagccccta ctggatgaag 1320

aaagtgaagc tggccaacgg cctgtggttc aacctgatct tcgtgtctgt caaggccgac 1380

cagagcgagt ctagcctgtc tagcggccgg aacaagaaaa caaagctgtg gttctccctc 1440

atcaacatcc accaccgcaa gaatcctctg ctgcccatga gaatccccag cctgaatgcc 1500

cagtggatgt tctgagaat cctgttcttg gcccatatgt acggttcag cacctacggc 1560

accagaaaag gcgagtgcgt ttgtctgcag tgtctgagcg gcagcagcct gttcattctg 1620

aagcagcccc tggacctgaa gatctccaag accttcatgc tgcaagctca cccacaggtg 1680

ccagctcttg ctctcaagc ttggttggcct gctagaagag gccctctgac atctgtcca 1740

tccgctcagc agtctctgac agctagccct cagattatgc agcggatgag cgccgtgaac 1800

ttcgagacaa tcatctacce tccaagcacc tgtagcctgc cttgtagagg cagaacactg 1860

gaaagcgccg gactgtttcc ttggctgcac acccagtgtg cacacccctg taccatgctg 1920

ctgccacaag gctggtggtg tacaagaggc ggcggaaaagc ggaaaaagaa aatgtgcaag 1980

gtgtccggcg gctgcaccgc ctgtgttgag agatgtcctt ggaagggcat ctgctggaag 2040
 tggccagtga cagtggctgc tcaatgggtct agcgtgacct ctctggaatg gacagcccaa 2100
 gagagaggct gcagcagctg gctgatgaag caaacatgga tgaagtcttg gtccttcgag 2160
 gaccccgagt acagatccat cctggaatac gtgtccacca gaggctgtg gatgccaca 2220
 agcaccgtgc ggagaagaaa cagcagaaag cagtctcagg tgcagctggc cattcaggtg 2280
 ctgctcgtgg acaagcaca gtactttctg ttcggcagag cccgcaaccg gaacatgaag 2340
 aaaacatga gccacctgat cgcccatcag gcctgaaga tgagcggcct gaggctgttt 2400

catcctcggc tgcigacaag aaagaagccc ggcaagtcc tgcctagcag atttccttgg 2460
 ggccctcctc ctctgtgca tctgtcttgg ctgagcccta tctccgctg tccaagactg 2520
 ctgcatatc cttttcagc gctggccctg gaagtacct ttcacctgg aacagccatg 2580
 cctcagatgc aactgcaggc cctggccatg tgggagaaag gctgggataa gcggaagaga 2640
 atgaagaccg gcgcatcca agagaagggc gctattcaag agaaaggggc catgaccaag 2700
 cggatctgcg tggtaattt cgaggcctgc agagagatgg aaagcctgag cggccctgag 2760
 aagattacc tgtttgaagc ccataatggc cgtgtcacct ccatcaatgt gctgtgtgtc 2820

agagcctctc tgatcgagaa gctgatgaaa gaaaagcgca agatgaagcg caaccaggtg 2880
 gcatccccc aaattatgca gaggctgttc attaagggt accagaaca ccacttcacc 2940
 ttccatctgc aaaacttcgc cttcttcagc agcttcggca acaacaagta catcaatac 3000
 ctgacgcggc gcaagaaaa agaggaccac tgcggactgc tgatcctgat ccagcacggc 3060
 ggcatcttca cttttcggtt ctgggtcgaa aagctgagct ggaacatctg caagaacctg 3120
 agcctgtacc tggataagtt cgtgcagcgg ctgctgtacg tgtacatcat cgagacaaac 3180
 gtgttcgtgc tgaacctgtt ccacgtgcca gtgaaccaga tcttcatgat ggccttctac 3240

ctgaagtaca ccgagaaggc ctgggtcatg gaactggaat ggctgatcca acagcaggtg 3300
 taccagaag agaagaaaag ccggaaactg atgagcagct gccgggcctt catccacaca 3360
 cctagaagcc ctggctgcag cgtgtacgcc aatatgtgtt gggccttttg gaagcctcct 3420
 agccagggca tcagctcttg tctgatgaca ggctgttggg gcagccctcc tctgcacctg 3480
 tgtcagcctc tgaggcggtg taagaaaagg ggctgtatcg cctggcggcg gagaaagtgg 3540
 cagatccggc atgtgtgaa aaacctgatc ctgtttcatg tgcggaacat cgtgtacggc 3600
 atccaagtga tctgtgtcgg caagggactg acacacctg tgcctctgaa acggacctg 3660

cagaacaaga ggaacaagaa catcaagcgg gtcaaccaga agaagggcaa catcaagagg 3720
 aagtcacatc tctgtcacct cattgtgtg aatagcccc agagcaaccc caagttcttc 3780
 ctgaccttta gccagctcga gaagaaagct acctggatga gaagaacagg cgccctgaga 3840

gccacagctc ctgctacagc agctcctcag gctcagactc ctcattggag agccgccaca 3900
acaagcagca tgagcagcag ccctagagcc gagcctacat cttctagctc ttgggccacc 3960
tgttggccca gatgctgtag ctccagctgt tactggctcc tgagtctctg gcctcctgct 4020
ggcgccgctg aggctacaaa caccagaact agaagcagag agtcccagcg gggcagaatg 4080

ctgacttggg gaagtagtct gtggctgcag ggcaccagat gttttacagg cgtgcggaca 4140
agcagcggaa gctgtggcag agcttgtagc tgcggaagag gctgtggaac ccctagaggc 4200
gattggaaga gacacctcc tcggaggaat agcgtgatcg tgcacaagat cgtgctggtg 4260
tttctgaagt cctgtccag ctacaactgc gagagaagga tcagcggcat ccagaagaga 4320
gccatcgagt ttgccgtgct gaaactgctg aatatggacc tgcaactgga ctccgcctac 4380
ctgggcagaa ctctgctggt cacctgtatc ctgtatcacc ggtggatcgt gacctccatg 4440
tgccagtctc agagatggct gaccagcacc acaagcagat ccagcgctct gatgtggacc 4500

cggcagatca atcggaggaa gctgcagaga aagaagaggc acccaagctg gccttggacc 4560
agatgcctta gaatgaggcc tcctagaagc ggctaccct acgatgtccc tgactatgcg 4620
tcc 4623

<210> 1129
<211> 4638
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 3B
<400> 1129

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60
tcgcccagcc aggaaatcca tgcccagga gctgctgctg cctcttgtca gtctcctct 120

tctcctcggg aaaccacacc tagctccgac gccaccagac ggacaagacc aattgccgct 180
cagagcaaga aaacatgac agccgccgga ctgacccta agaacaagaa gcggagaaaag 240
ctgcggccca agatgatccg gaagatccag aagagaaggc ggaccgcaa ccggcggaat 300
agcagaaggg ctacctctac aagcaaggc agcctgagaa gaaagtacct gagagtgcgg 360
ggacctctc tgcacaccg gaacatcaga aagctgatct ggaccaagca gcggagcttc 420
ctgtctctgt tcccaagct gagagccacc gagcagatga ccaatgtggg ctgctctatc 480
cctcacgtgc ccaaagccac agccgtcac tctgtgacag tgaaactgca gctgccctg 540

accttcagca ccctgctgtg ggatagcaga cacacatga gcctgagcaa catcctgatg 600

aagttccggc tgcagtctag cccatttcctg gccagatcct ggaacaccat gcagtggaac 660
aacaagaaaa tggccatgac cgtgatcgct ggcgccacc actgtcagta caagtgacc 720
tacaccaaag tgtggaagat gaactggaag aaaatgatga tcggcagcca gcattctgtg 780
ttcagccctc tggatagcag tccctgcag ctctgtctgc accctcacgg caagagatgc 840
aaccttgct gcagactgac ctggatgagc cagaacacca gaagcaccaa cctggaaaag 900
aaccccagcc tgaagaagca gagccagcgg agaggaaagc tgagcgcctt tagcggcaga 960

atcctgcacc agccagaaat ggccgccatg agactgatgc ccaagttcct gaactccacc 1020
aacagctggt ggacctgac cacactgagc ttcgtgtgta tcgaggaagc cagacagccc 1080
agcagaccta ccggcagAAC acctaccacc agactgatgg cccctgtggg cagcgtgatg 1140
agctgttctc tgcagacca gccttctcca gccagcgcct gtacaatgcc tccactgtg 1200
catccacagt gggccctca tagtgctgga ctttctccag gcgcttgag acctgcctgc 1260
acctgtatca gcatgaccac catcagcagg gccacatggg gcccagtgtc ctacgtgtgc 1320
aaccggatga acgtgtccag cgtgtgaag cccttcctgt tcaccgtgcc tatcgaggac 1380

atgagagagt gcacctggg cagaaacaga atgaatgtgt cctctgtgt gaaacctgt 1440
ctgatccctg tgccaatcag cgagaagaag aggaagctgc ccaacatcga gatcacccct 1500
cagcgttcta aggccatgct gcagaagcag tgcgtctaca acctcgtgat caagcacct 1560
ctgatcttca gaatcaacct gcggcggcag ggcaagacca aagatggcgt tgtgcagagc 1620
ctgggcttcc tcaaccagca gatcatcctg cagaaagagt tcttcatctg cctgtcatg 1680
ttcatcaagc ggtggaagcc tgccgccacc aagagcagaa agaagggcca caccaagaac 1740
agacggaagg ccaagagaaa gcccagatc tacctgttct tcctgaccgt gtgcggcttt 1800

cacctgaaaa agaccagcgc caagtggctg aagaagtcca ccaagtcag atccaacggc 1860
atggaagctt gcggcacaca cccactcct agactgagct gcctgagagt tagatgcggc 1920
ggctggctgt gtggctggac acctagaggt agaaagtccg gcgtgatgaa gtgctgggat 1980
ctgtgccccg tgcacaagaa gagaggcctg ttcagactgg attttaccc cagaagcagc 2040
tccggcaagg gaaagaacag cccctgctgc caaaagaaac tgcggtgca gaaccagggc 2100
catctgtgta tgattctgt gcacaatgac cgggtgttcc tcgtgaagat cggcgagaag 2160
ctgaagcact gtttcaagc ctggggctcc agacggaacc ggcggtacag aaagatctac 2220

ggcgagctga agatgtccct gcaggccttc ctgatccacc tgagaaaggt ggaccccac 2280
cacctccagg tggcaccaa aacagtgacc gccacaacag ccgacggcca gagaatgcgg 2340
agactgaagt gcaaggcctg ccggtgaga tgggccagac ctgaacctgc tgctcaggcc 2400
cctcctaaga gccactttcc acctatcct agcggcccca gcagaacaag tagcctgcag 2460

ctgagaagcc tgttcttttag ccactgcctg tgcagccaga agaaggaccc tgccggcaag	2520
ctgaaaaagc tgctgaagaa aagcagccag ctgcggagaa gctggcgcaa tgtgtccaga	2580
atcagcacc ctcctccact gatcctgtgg cctcaagctg ctctgtgtc cgtgatcacc	2640
atgaagctgt gggagaagca cttcaagggc ctgaattgga acctggctcgt gtggattctg	2700
aacctgaaga tgatgaccta catggaaatg cactacggcc atcaggcccc acaggtggca	2760
atgtgccta agctgtgtg cagacagatg ctgcccactc tgagcacact gcagcagaga	2820
catcctcagg gcccttgtcc tctcctgtg acacctctga gagtccagtc tgtcctgtg	2880
ctgggagtgc ctgacacagc cagaggacct agaagaaagg tctgatggt gctgtggctg	2940
cccgccaatc agtctctgca gaaaagccag gttttccagt ggggtctgcg gacagaggtg	3000
gcccctagat gtccctagatc tgccgtggac atcagccccg gacctacatc tcttagcctg	3060
gcctcttgtg cctctgtggc cattggaaag ctggcactgc ttggcgctc tgctccttgt	3120
ggtgtctgtg gcgctagaga ggccggaaga tttgtgtgc tgggcacccat ggtcatgaag	3180
ctttgtttct tctacctgt gtaccggctg cgcaccccaa gcctgaggaa gtacagacag	3240
cacctgaacc ggaagctgca cctgacaaga tctgcctga tcatctgac catgatgatg	3300
tcccagaagc tctggaagaa ccagcggaag agaatccctc tgccatctcc acggcaacat	3360
ctgtgccac agtacctct gcacccacct ccacctgtc tgcgtttgt gcacataga	3420
caccacctgg cttttctga gatggcctgt agctctcagc acaccacag catcaagatc	3480
tggatcagct tcagccatga agtggacct ccaggcagcg tgtggatact gccttgcat	3540
ctgcctcgga tctgccaat ctcttcaccc ctgcacagac cccagatgcc ttcttgacc	3600
tgcacctttc ctgccacaac ctggggcaca tgggagacac cttctacatg gggctggcgg	3660
actttcagag gcgctagcag cagcacatcc cgggacagca gatccttctt cacctctgt	3720
cacctagca ggccctgcag aatgagactg taccagtga agaagaagct cctcctgaaa	3780
ctgtgacca ccaccacaag cagccccaga agatccctg ctctgagagc aagaggcggc	3840
accacaatcg gcgaagtgc cagctgtacc aacctgagcg tgcccatgat gctgaccatc	3900
ctgatttga agcgggtgtt catcctcctg ctgagcgata agaagggcgc caagaagatc	3960
accttctgc ctattctcc acacctgaga cacctctgc tgcgtttcga gaagaaacgg	4020
cctgagtggc tgagcatgga cctggacgga atgtgacag tgatcgcca gggactcgtg	4080
ggcatgacc ctagagatct gggaacagt gcaggcgcca ccgctcagat tcagcgacct	4140
atccaggtgc agactggcgg cagactcaga agaaacctgc agagaaacct gaaggtgtc	4200
caggtgtccg tgtacagcgg caacctgtg tcttttagca gacggggcat gaagtctagc	4260

gtgcggctga aaaaccgcga gtgggagaaa cggaagcaga ttctcggagg cggcggaaag 4320

tacaaagagt acttctgaa gcgcatactc atccggaagg ctatgacagt gctggccggc 4380

gacaagaaag gactgggcag attcatgaga tgcgtgcaga gcgagacaaa ggccgtgtct 4440

ctgcaactgc ctctgggaag aaacatggaa caccggttga ccatggacag cgccctgagc 4500

ctgacaaaga gagagggacc cgagacactc aaaaagaaat acctggtcca gcaccagatg 4560

aagtgtctga ccgccgtgga ttgtctgcag gctttttggg acatgggcta cccctacgat 4620

gtccctgact atgcgtcc 4638

<210> 1130

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 4B

<400> 1130

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgccagcc aggaaatcca tgcccgaatc cagaagaaga agcagaagtc caacctggac 120

ctgcagcacc agcgagacag caaaaagaag aaggacaagg tcgagatccg gaatcggagc 180

ccaaggcca atagcacaga gtgtcagggc gagcacagca gagagcagaa cctgtctaat 240

ctggtgcagc tgaacctca cagccctcac cacagaaagg acgaagagga ccaccagaag 300

cggcaccacc accacaatca aaagaaaatg agcgtgatgg ccaagaagtc ccagcgcct 360

ctcggacagg cctttggctc tctgtgtcag ctggtgtccg ccgatttcag cgccctcaa 420

gtgaccagac tgcggagcct gaaccatctg ctgatcaacg agggcaacaa cactggcct 480

agagtggaaa tgctaccgg ttggctgtct gtgggctaca acaccagaaa cacagcccag 540

aatcctcggc tgcagcagca cctgaaacac tggcagcagt gcaccagagc cagatggtgc 600

caagagcctt gtcagacct gaccttctc catttctct tcttttcaa aacggtgtcc 660

ctgtgtgcc ccggctggtc taaaggacaa cctctccac ctggcctgaa gccttctagc 720

ctggcttctc aggtggccag aaccacaggc gtgtaccagc acgtgtggct gatctgttc 780

gtgttcttcg tgtgcgtgga aaccggcttc tgtcacgtgg ccaagtggg actcgagaga 840

ctggtgtctc tgagcggcat caccgacgtg aaccattggg cccagcctaa gccatctct 900

agcaaaggca ccggcatgaa cagacctatc ggctgagag ttggcaaagg cgtgtgggcc 960

agactgagag cctccgtgtc tttctggacc ctgctgccta caacaggcgt gcggacaaga 1020

ggaagccctc tgagactgac actgtggcct ccacggaaca tcctgaacag cctgcctagc	1080
agcatggaaa tcgccgtgct gcaagagaac cgcaagacca gaaaggccgc cagagagaag	1140
cacagaaaga ccgacaacct gcacctgtgc tactaccaca gccagagcaa ccggaacaag	1200
agccggcaga tggaaagcct gggcatgaag ctgcagagcc ctctgtggga ttgctccacc	1260
acaacaggca cacaccagg ctgtctgtgg gagatcccta gcgttacact gctggcctgc	1320
agagtgaacg ccgtggaaga actgcacagc aggcggatgt ctgtgcggat cgtgaagaac	1380
tgggtgtcct gctgttacgt gcgcctgtct gctgtgggcc tgtctacttg gagcgccctg	1440
gacgtggtca tcaacctgaa gcggctgcag aagttagcc agaagtctca gcaccactgc	1500
gccctgagaa agatcgagtg ggccacaaag ctgagcctcg gcggaaaagc tggaccccag	1560
gctcaagaga aggccaacgc caagaagatg cccttcagc ggtggatctt cagcaatcag	1620
ctgaccgtgc agatgctgtg cctgcctatt gaagccctga ctgccctgtt cacctgtcgg	1680
acagccagca tcagcgtgaa catcagcacc ctgatgagca tcctggaagc ccctctgttt	1740
tttcacggcg acctgtgcga ggaaaagaag aacggccgga tcagcagcca ggctcctctc	1800
agactttggt cttggtgcgg cacaagccag acctactttg gcagcaccgc caagaaaagc	1860
cccaccagct ttigtctcga gtggggagga caggctcacc ggagagaaaa taccggaatg	1920
gaaatcctgc tgtggattct gctcaagatg gaaattcaga tcttcaagat ttgcctgggc	1980
gagatgcagc tgtgcaccta cacacccac atctgcagac acacctgtag aggcggacct	2040
agcgccagcg atagatgctg tagctgtagc cctagcggct tcagcgccgg aagaggcaga	2100
tgtccagttc agggatgtct gcggcctcac agagtgcagc tgctgagaag atggggccct	2160
ggatctcctg ctggccagag actgtctaag ggctttcagc tgctccgttg gtggggacca	2220
ggatctccag ctctgagcc tagaaaggc ccatttcac cacctgatcc tccatggcct	2280
gtgaccgtg tgacagtgat ggctggctct gtgcctagcg ctcagtctgt ggatgctctg	2340
gaaagccctg gacctctggc actggaagga cctagcagcc ccagaaacct gctctggcgg	2400
gaaatgagca tcttctgccc tggcatcttc acctctcgga ttctgaacct gcaagtgtg	2460
aagaagatcc tgcggagctt tatgaagctg taccactctc tggcatgtg cctgcggctg	2520
cggaccaagc tggaaaaagc tctgagcgt ctgttcatct ggccccagca cagctacaag	2580
cagaggcctc ctctgcagcc tgtgcaggtc gtgctcagac tgggaaacct gcctccattc	2640
ttcagaggca gcgagggtcc ctttctaga ccttgccgga ccaagatgct gaaccagaag	2700
tgtctggccc ctttcatcac acaccattc gcctctcagc ccctgggaca agagatgccc	2760
aacaacaccc agatcagact gctgaagccc ctgctgaccc ctgacaccag atggatcttc	2820

tccaaccagc tgcagacagt ccagatgctc tgtctgccac ctctgaagca gggcgagaga	2880
atcatttggc cctcggcgg ctttcagatc cccaacttct tttggagcct cggaatcggc	2940
cacactggcg cctggtggca tactggaagg cggagaagag aatggggcgg ctccaccgtg	3000
tctagaagcc cactgtggat cagctccatg atctacctga gaggcattggc cttcgccagc	3060
gacagctcca tcagaaccac cagagtgtcc tgggtgcagaa gatcgggcgc caaatctgcc	3120
gtgctctcca gctcaagaa gaaaccccg gacatctgtc ggatcagcga ctctaagaag	3180
atgaccaga agcgcgagag caccctgggc aatttctgga tgaagctcct ccagctgcca	3240
gacaagaaga agaagtctac cgaaaagacc aagatcatca agaagatgaa gaaacggatc	3300
atggtccaca tgtgcagctc cctggctctg ccaacaggcc tgacatctct gatcctgcca	3360
agcagcgatc tggccgtgct gatctctagc tccaccagcc actttctgat gcggagccca	3420
gtgctgccta gctccagact gacttgtgcc tctccacagc tgcccagaat gtggacctgg	3480
tccagctggc tgaagtggct gaaaaactgg aagcgggtca agcttaaaaa gaagtacatc	3540
ctggccatga cgctgacct gaacgggcat ccaagaaccg cctctatcac cctgcctacc	3600
accagcctga agggctctag aaccagctgt tgccccagat ctacccccag actgcctagg	3660
acaaagtggc ctctgcagtg cctgtgtcac agcctgggaa caactggaac actcgtgtgg	3720
gaaaggggcg tgtgcagat gagaagtctg gaagctcact gccctctgca gacctccac	3780
ctccaccact gtagaactca gccagctct tgcctcctg catggattct gtaccaagga	3840
cagtggagcg gagccgtcgt gggacttaga cctgtggctc accatctgcc aagacctatt	3900
cagggcctgc actgcccaca ggctccacat caaccagctc tgtcttgggg caagtggccc	3960
gtgggaatga caggacctgc cagatgttgc cgttggccta gacgggaact caaaaagaat	4020
ctgctgtcc cctgccgtg cagacgcgag tatagagtga caatggcca agccttcggc	4080
agcttttagc ccgactttag cgctccccag gtgttgaaga agaatcgga gcagaacaag	4140
attatctgca agggccaccg catcacaagc ctgacctga gctttcagcg cgtgaaactt	4200
aagaagaaag tcaacgcctg ctctcccgcc tgcacctcta aagcctggac tcccagaaag	4260
ctcgtgggga gagccgtcag aagaaaggc atcatctgta tcaagaatat gtccctgcag	4320
cgaagggtt tctgaacct gagccacgtg gaaaagtctg tgcctcttc tctcctctg	4380
gctctcgcc ctagaatgca gctctgtacc cagctggccc ggttcttccc tatcacacct	4440
cctgtgtggc acatcctggg acctcagagg cacaccctt gtcaaaagaa ggtgcctcc	4500
gctagcccat ggggccttag accatctcct tgcttagct ggtcctccag aattgtggcc	4560

cctggacacg ccctgagctg tcggactaga agaagatggt ccagcaaggg ctacccttac 4620
gatgtccctg actatgcgtc c 4641
<210> 1131
<211> 5250
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 1A
<400> 1131
atgcatcgac ggcgctcacg gagttgccgg gaagacaaa agcctgtgat ggacgatcag 60
cgggacctta tttctaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
ccaaagcccg tctccaaat gaggatggcg acaccgctcc ttatgcaagc ccttcccatg 360
ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
catgtcatgc atttgcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480
agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540
tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
ggcgtcacia agcaagacct gggaccctg ccgatgaccg agatccagct gaccatgaac 720
gacagcaagc acaagctgga aagccccgct ctgaaacagg tgtcaccagc ctctccacct 780
actcagcagc ctacagacc tcaggattct agacaggtgc tggccctggc caagaaaacc 840
ctgacaaatg cctccagagc cggacagttt cctgtgtggc ggagaacaag cagaggcatg 900
agcctgcagt ggaagtccgg caatgcctgc acacctctga gatgccttag cagaagccct 960
gccacattcc tgacagccct gaatggctgg cacagatctg gcctgagagc ccagatgcct 1020
agctcttggt ctagcagcgg cagaacactg aagctggccc ctctgcaagt gaccaccact 1080
ctgaagctga tcttggtcat gctggaaatc gtgaccgagc gctccctgct gtactccaga 1140
atgtgtctgg tgcagatccc cacacacacc tgggagcccg attacttcgt gtccctgcct 1200
atgatgttca gctgggccac acagtctttt cccgtgggag cctgttttct gaccagacct 1260
gccattcctt gctgcagctg taccagccac agcaaccctt ggagccagag caatcagcag 1320
ctgaagtgga cccctcacat cctgaagtcc gccagcttcg acaagaaagg cttcgtgatc 1380

ctgagccggc ggagcaagat tgaggcctct cctatcggct ctatcgccag ctctcctgga 1440

catcctctgg gacctacact ggccatcaga ttcacagcg cccctcagcc tagcagctct 1500

acagtgacag ctgcccctag cggccagtac tttatcgcca agaagcggat caagctgcgg 1560

cggacaata tgggcgga cagatccatc tgctgacca gaaagcgaa gagagagaag 1620

cggagccaga agtccaggca gaacctctg cagctgaaa gctgcagacg gaagatcagc 1680

aactggtcca agctgagaag cccctggatc ttcaccaagt gcgagatctg cgtgaagaac 1740

accgccatcc tggctatcac cctgatcacc cctcaggacc ctcatctgga ccctgtgtgt 1800

cacctcata gaaggcctgg atggaagggc caccatagag tgggtttctc tcaccatcct 1860

agcggcagca caaagagcca ctggcagcaa agagaacgag gaggcggcag acgcgagaag 1920

aagggatgta gagaacagcg gaaggtggtc aagaaccctc ctgagcccg gcctctgaga 1980

aacgatggca tcaccaacgg caacgactcc accagaagct gctccatcag cctgaagaaa 2040

agcctggaaa agatgccct gatgcggaga gccagaccta ccagctgtag cacctgtaga 2100

atgtgtgga agggcaagaa acggcgga gaaatcgtgc ctatgagcct ggcctgcagc 2160

atcacgtgt cttttgtggg acagatcagc accctggtgc tggatgtgtc tagcatcagc 2220

cattggcggc tgcctgtaa agtgaccgag agcagctcca gcttcttcta caccagcgac 2280

aggaccctc tgagcatcag cagaccaacc agcagagcta gacagagctg ttgtctgccc 2340

ggactgacac accctgtca ccaacctctg ggacagatga gcactagaag agagatgcca 2400

agccaggcca caccttctc accctggacct tggagagccg ctctgggcaa agaagtgaag 2460

agatccaga gcaagctgag cctgagaaac acaagccctg gggagaagaa cgatctccag 2520

ctgttctgta tgagcgacac cacctacaag atctactgga cagtatcct gctgaacccc 2580

tgcggcaacc tgcacctgaa aacaacatca ctgcagcggc cacctcggag catcctgtct 2640

ctgaatggaa tctgggaagt gatgccccgg aactggaag gctgcatcag cgtgaaggat 2700

cacagaacca gccagaacca cagcaagtgc atcacgaat gtgtcggac tgcctgaac 2760

gtgtccaaga agagactgcc taagctgatg aagaagaagg acagcaccat ctatcatcaac 2820

aaagtgcgc agaacttcaa gcgcaacttc aagaagaaga aaccctcac tttagcccc 2880

agcagacgga tgactcggag aacctgaca accacaaaa tgatgatgat gcggcggacc 2940

aagcggagaa ggcgcaaaa gcggagaatg accatgatga ccagacggac cctgctgaca 3000

aagaaaacct gtctgacccc tagaaccagc gccgccaca aagctctgcc tagacagacc 3060

atcagccagc ggaggcctat tcagaccca cctggaacat ctctggccat ctggggcaga 3120

acaagactga ccctgacagg caccagatcc agcggaaaca gagcctctcc ttccgccgtg 3180
 tgcctgtgtt gttggacctg tccaagcaga agcttcccag ccgcttctcc tagtggactg 3240
 agagcacctg ttggagccca ggctcctcct gaagtgcac tgagagcctc ttgtgcctct 3300
 agcgcctcta aagcctgtgc tggactttgg ccttggggag cccaagtctg agttggagct 3360
 ggaacaggcg gaggacctgc ttgtgttcct gtggctgaag cttctacagg cgcattggaca 3420
 gctgaaggcg ccgctggaac aagatgtaga gcctctagag ccccttgccg ccaacttct 3480
 gctagctccc ctaccaagtg tgaaatttgt gtgaagcgca gacggcggag aaagagaagc 3540

agccagtcta gaagccccgt gcctaaaaag cgcgagagga tgatgctgcc tgtgcgggcc 3600
 agaacagcta gatctgcaat tcctcagggc agagcacctc tggaagggat gctgcttcct 3660
 agagcactgc ctacgctgct gaggagaatg cctgccagaa gagagtcccg gttttggctg 3720
 gctctgcagg cacttggact cagacctcca catctgccta gctgtcatcc tctgcctcaa 3780
 ctgttgggcc ctccacctcc tcatcaggcc ccaatgcac tgaaggccct ggtaagacc 3840
 tggacacagt tccgcaacta cccagagcc gacaagaaga atgtccggtc taccgccttc 3900
 ttctgctgg acatcatcct gggcgattgc ccaagaacaa tggccggacc ttctgcctct 3960

ctgcatcctg catctggcag agcctccaga aagacctggc agagaaggct gagagcttgt 4020
 agagcaggcg gacctgctgg atgggctaga caggcctatc ctactgtaa aaccttcggc 4080
 gtgccccctg gctctattct gtgtctggcc ggagcctgt ccacaatgat gatcattagc 4140
 accaccagac aagagtgcgg caggcgggct tctgtgcctt gtagacctat gatcggaagc 4200
 gccagaccag gaccttggcg gacatctgct atgcctagtg ccatgggagt cgccctgcct 4260
 acctcttgtg aaagcggaag atctctcct gccaccggcg gaagaatgcc aggatctcag 4320
 tctatcatga tgagctggat gcctccactg gctccatgtg ccgcttgtcc atgttctccc 4380

gtcctacac tgtgcccagc acatcctgct agagcaccaa cagccgtgcc tgcctttaca 4440
 cctctgtctg ctcatcctgt gccagtgtg tctggatgtc acctggccgt cagaacctcc 4500
 atgtgcacac tgtgcccct ggaagccaaa aagagcatga agcggtccaa cgctaagaaa 4560
 atggaagata tgatctggga gagccggctg cactgaggc cacaagagg acctagacct 4620
 ctgcacagat ggctgcagca gacaaccggc ttagccaga ggccggtcgt gttctttctg 4680
 gccccatact tccctggca cctcacaga tctccacaa catcttgcct acctctgctg 4740
 gaagctttcc cactgccaag agcttctctg agggccacag tgccaagaca tagctctgtt 4800

ctgccaccg gtctgcacct ccacagacag atttctctgc cctgagagg attcctcctg 4860
 caccaaccac tgccaggaca gcatctgtgg ctgtctcaca gactgaggt gagactgccc 4920
 aggacacagc catctttgcc tggaccatgt gcaagcctgc tgtccacct gtctcagcca 4980

ccacctcagg ctccatctca agtgtggact gccgctacac tgagatgtcc tgctgttcct 5040
gcagctgcct gtctctctgc tctgagatcc atgcctaaga gccggaacca ggtgctgttc 5100
agacggaatc tgacccaag ccagctgaga aactggccc caccttatat gctgctgccc 5160
cagtctctgt cccagagcct gagtagaaag cagatcccta gccagtccat gctcgtgggc 5220

taccctacg atgtccctga ctatgcgtcc 5250

<210> 1132
<211> 5232
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 2A
<400> 1132

atgcatcgac ggcgctcacg gagggtccgg gaagacaaa agcctgtgat ggacgatcag 60
cgggacctta tttctaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
gagtcgaagt gtcttagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
ctggcgggac aggcacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
ccaaagcccg tctcaaaat gaggatggcg acaccgctcc ttatgcaagc ctttcccatg 360
ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
catgtcatgc atttgcttca aaacgtgat ccccttaaag tttaccctcc tctgaagggg 480
agctttccag aaaaattctg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540
tttgagagct ggatgcacca ttggctcttg ttcgagatgt cccggcattc tctggagcaa 600
aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggaccgag tagtgggctg 660

ggcgtcaca agcaagacct gggaccctg ccgatgagaa agatgcagag cctgaatcac 720
cccagcagac tgaccaatgg ctctctctca ctgcacctgt gccagcctct gagaatgagc 780
agaaccctc ctagaagagt gtgcgccgt cctccacata gactgctggg cccttcaga 840
tggaaccctc ggagaaagac ctggaagatg cggaagaagt acgcccagaa gcctagccag 900
aagaaccacc tgtacggcgg caagaagcgc tctaagtca gcagaagcca cctggacttc 960
agcccctact ggatgaagaa agtgaaggtg ctgttcaagg ccgaccagag cgagtctagc 1020
ctgagcagcg gaagatgcag cctgatggaa cagatccctc acctgaagtc tcggcggaag 1080

tggcagatca gacacgtgct gaagaacctg tggctgcca tgagaagcct gggagaacct 1140

tggagagccg gctttcagtg gggagagtct ccttggcaag tgatggcctc tctgaccggc	1200
agagccacat ttctgctggc cctttgggaa tgtagcctgc ctcaggcaag actgtgcctg	1260
atcgtgtcta gaacctgct gctggtgcag agccggaaca agaaaacaaa gctgtggttc	1320
agcctgatca acatccacca ccggaagaac ccactgctgc ctatgagatg gtggtgtacc	1380
agaggcggcg gaaagcggaa aaagaaaatg tgcaagggtg ccggcggctg caccgcctgt	1440
gttgagagat gtccttggaa gggcatctgc tggaagtggc ctgtgacagt ggccgccatt	1500
agaatgtgtg ccctgtctca ccctagcttc tacatcagca gcaccgtgtg ctttctgagc	1560
aagcactgca tgaccgcctg caccagaaag agaatgaaga ccggcgccat ccaagagaag	1620
ggcgctattc aagagaaagg ggccatgacc aagcggatct gcgtggtcaa ttctgaggcc	1680
tgcagagaga tggaaagcct gagcgccctt gagaagatca ccctgtttga agcccacatg	1740
gccccgtgca cctccatcaa tgtgctgtgt gtgcgggcca gcctgattga gaagctgatg	1800
aaagaaaagc gcaagatgaa gcggaaccag gtggcctctc cacagatcat gcagcggctg	1860
ttcatcaagg gctaccagaa caaccattc acctccatc tgcaaaactt cgccttcttc	1920
agctccttcg gcaacaacaa gtacatcaat atcctgacca tctgtttcca cgtgcggaac	1980
atcgtgtacg gcatccaagt gatgtgtgtc gctagccctc agattatgca gagaaccagc	2040
gccgaccggt tccggatgaa gagaagaatg cagaatctgg acaacctggg cgtgccatgg	2100
cctctgttgc ctggaatccc atctctgaac gcccagtgga tgttctgag aatcgcatcc	2160
ccgcaaatca tgcagaggat gagcgccgtg aacttcgaga caatccgggc cagaaaccgg	2220
aacatgaaga aaaccatgag ccacctgatc gcccatcagg ccctgaagat gagcggcctg	2280
agactgtttc accccagact gctgacacgg aagaagcccg gaaaactgct gctcgcccat	2340
atgtacggct tcagcaccta cggcacccag aaaggcgagt gcgtttgtct gcagtgtctg	2400
agcggcagca gcctgttcat tctgaagcag cccctggacc tgaagatcag caagaccttc	2460
atgggccaca gagaggcgag cgagtctgat aatctgggcc tgctgtatag cttccctcca	2520
ccttatecta tcagcgaggg cctgaccatg accaccggca gaaacatcaa cagcaactcc	2580
ctgatgacca actgcctgtt cagecccatc ttctgtgcc accacgcat catgcacaga	2640
aagatgacaa gccctcactt caggctgttc agcagcaaga tcccacatcc tcaggtgcca	2700
tctgtggtgg cctgtgcaa gttccgggcc ttcatccaca cacctagaag ccttggtgc	2760
agcgtgtacg ccaatatgtg ctggcccaag ttcttctga ccttcagcca gcagtgttcc	2820
agcgtgacat ctctggaatg gacagcccaa gagagaggct gcagcagctg gctgatgaag	2880
cagacatgga tgaagtcttg gagcctgcgg gacccagct acagatccat cctggaatac	2940
gtgtccacca gagtgcctgt gatgcctacc tctaccgtgc tgcaggctca tccacaagtt	3000

ccagctctgg ctctcaagc ctgggtggcct gctagaagag gacctctgac atctgcccc	3060
tccgtctcagc agtccctgac cagagagaag attatcaacc ccaccatcag ctgccccctt	3120
cagagcccc ccaagagact gatctaccct cctagcacct gttctctgcc ctgcagaggc	3180
ttcctgccta gcagatttcc ttggggccca cctcctctga acagcgtgat cgtgcacaag	3240
atcgtctggt ttttctgaa gtccctgtcc agctacaact gcgagcggag aatcagcggc	3300
atccagaaga gagccatcga gttcggcgtg ctgaaactgc tgaatatgga cctgcctctc	3360
gagaacacac agatccccag aacaagccca ctgtggaaga tcacaatggt gctgacatac	3420
cccaactgcg tgggtgatgt gctgatgttt ggcgccctga gagccacagc tctgtctaca	3480
gctgcacctc aggtctcagc ccctcattgg agagctgcca caacaagcag catgagcagc	3540
agccctagag ccgagcctac atcttctagc tcttgggcca cctgttggcc cagatgctgc	3600
tccagctctt gttactggtc actgtctagc tggcctccag ctggcgccgc tgaagctaca	3660
aataccagaa ccagaagccg cgagagccag aggggtagaa tgctgacttg gagaagctcc	3720
ctgtggttgc agggcaccag atgttttaca ggctgtcgga ccagctccag atacaagaaa	3780
agaggcgtga tcgctggcg gagacagatc aatagacgga agctgcagag aaagaagcac	3840
tggaacacgc cctacctggg cagaacactg ctggtcacct gtatcctgta tcaccgttgg	3900
atcgtgacct ccatgtgtca gtcccagaga ttgctgacca gcaccacaag tagatctagc	3960
gccctgatgt ggaccgagct gagcctggaa ccatggattc cctacctgca tcagcagaaa	4020
accagcggga cactggaatc cgccggactg tttccttggc tgcacacca gtgccaagag	4080
aagaaaagca gaaagctgat gtccagctgc acacaccct gcacaatgct gctgccacag	4140
ggatgtcatc ctgcctggct gagccctatc tctgcctgtc caagactgct gccatatcct	4200
tttcactgtc tggtcttggg agtgaccttt cctcctggaa ccgccatgcc tcagatgcag	4260
ttgcaggctc ttgctatgtg ggagaaaggc tgggataagc ctggcaccag cctgcagtgc	4320
tacctgaaca gaagaagaaa cagccggaag cagagccagg tgcaactggc cattcaggtg	4380
ctgctcgtgg acaagcaca gtactttctg ttcggccaaa agaaaggcca catgatcttt	4440
agcctggcca acggcctgtg gtttaacctg attttcaact cccggaagaa actgctcgag	4500
gacatgaagc aaaatggctt caccggcaaa ggctgtacac acccgtgcc tctgaagcgg	4560
actctgcaga aaaaaagaaa caagaatatc aaacgcgtca accagaagaa gggcaacatc	4620
aagcggaagt ccatcctgct gcacctgatt gtgctgaata gcccagagag caacctgatc	4680
ctgatccagc atggcggcat cttcaccttt cggttctggg tcgagaagct gtcttggaa	4740
atctgcaaga acctgagcct gtacctggac aagttcgtgc agagactgct gtacgtgtac	4800

atcatcgaga caaacgtgtt cgtgctgaac ctgtttcatg tgcccgtgaa ccagatcttc 4860

atgatggcct tctacctgaa gtacaccgag aaggcctggg tcatggaact ggaatggctg 4920

atccaacagc agtgctatca gggcagctgc ggcagagctt gttcttgttg aagaggctgt 4980

ggcacccta gaggcgattg gaagagacat cctcctcgga gagccttctg gaagcctcct 5040

agccagggca tctctagctg tctgatgacc ggctgttggc tcgagaagaa agctacctgg 5100

atgcggcgga cccgccggaa gaagaggga gatcattgcg gactgagaca ccccagctgg 5160

ccttgacaa gatgtctgag gatgaggcct ccaagaagcg gctacccta cgatgtcctt 5220

gactatgcgt cc 5232

<210> 1133

<211> 5247

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 3A

<400> 1133

atgcatcgac ggcgctcag gagttgccgg gaagacaaa agcctgtgat ggacgatcag 60

cgggacctta ttctaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120

gagtccaagt gtctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180

ctggcgggac aggcacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

cttacagtta catccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300

ccaaagcccg tctcaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360

ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaatat gacagaggat 420

catgtcatgc atttcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480

agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540

tttgagagct ggatgcacca ttggtcctg ttcgagatgt cccggcattc tctggagcaa 600

aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggaccgag tagtgggctg 660

ggcgtcacia agcaagacct gggaccctg ccgatgggag ctgctgctgc ctcttctcag 720

tctcctcctt ctctcggga aaccacacct agctccgacg ccaccagacg gacaagacct 780

attgccgctc agagcaagaa aaccatgaca gccgccggac tgaccctat gatccggaag 840

atccagaagc ggcggagaac cgccaaccgg tgtctgagag ttagatgtgg cggctggctg 900

tgtggctgga cacctagagg acagaacacc agaagcacca acctggaaaa gaacccagc 960

ctgaagaagc agagccagcg gagaggaaag ctgagcagcc tgttcttcag ccactgcctg	1020
tgccggaaca gcagaagggc cacacctaca tctaaggga gcctgcggcg gaagtacctg	1080
agagtgccta ttctccaca cctgagacac cctctgctgc tgatggacct ggacggaatg	1140
ctgaccgtga tcggacaggg actcgtgggc atgacccta gagatctggg aacagtggct	1200
ggcgccaccg ctgagattca gaggcctatt caggtgcaga ccggcggcag acttacacct	1260
cctcctctga ttctgtggcc tcaggccgct cctgttgatc ctctggctc tgtgtggatt	1320
ctgccctgca agaacaagaa gcggagaaag ctgcggccca agcggctgga ctttcacct	1380
agatcttcta gcggcgtgct cgtgatacc atgaagctgt gggagaagca cttcaagggc	1440
ctgaactgga acctggctgt ctggattctg aacctgaaga tgatgaacat cgagatcacc	1500
cctcagcgga gcaaggccag aaagtccggc gtgatgaagt gctgggatct gtgccccagc	1560
gagaagaaga ggaagctgcc tctgcctctg accttcagca cctgctgtg ggactctaga	1620
catagaggcg ccagctccag caccagcaga gactccagaa gctttttcac cagcgtcac	1680
cccagcagac cctgcagaat gagactgtac cagtctctga tccacctgag aaaggtggac	1740
accaccatc tgcaggtcgt gaccaagacc gtgacagcca caacagctga cggccagaga	1800
atgcggagac tgaagtcaa ggcctgccgg ctgagatggg ctgacctga acctgtgct	1860
caggccctc caaagagcca ctttcacct catctagcg gccctagcag aaccagttct	1920
ctgcagctgc ggagcatccc tcacgtgcca aaagccacag ccgtcacag cgtgacagtg	1980
aagctgcaga agggaaagaa cagccctgc tgccaaaaga aactgcgggt gcagaatcag	2040
ggccatctgc tgatgatcct gctgcacaat acctacatgg aaatgacta cggccatcag	2100
gccccacagg tggccatgct gcctaagctg ctgtgcagac agatgctgcc cactctgagc	2160
acactgcagc aaagacacc acagggccct tgcctccac ctgtgacacc actgagagtc	2220
cagtctgtcc tgetgtggg agtgcctcag acagctgcta gacagcctag cagaccacc	2280
ggcagaacc ctaccacaag actgatggc cctgtcggca gcgtgatgag ctgttctctg	2340
ctgacccagc cttctccagc cagcgctgt acaatgcctc cactgtgca tctcagtg	2400
gccccacatt ctgctggatt gtctccggc gcttgacagc ctgcctgtac ctgtatcagc	2460
atgaccacca tctccagagc cactggcag gtttcctgt acagcggca tctgctgagc	2520
ttctccagc ggggcatgaa gtagcgtg cgctgaaaa acagccggcg gaacagacgg	2580
tacagaaaga tctacggcga gctgaagatg tcctgcagg ccgtggctcc tagatgtcct	2640
agatctgccg tggacatcag ccccgacct acctctcta gcctggcctc ttgtgcctct	2700
gtggccattg gaaaactggc cctgttggc gcttctgccc ctttgtgtgc tgctggcgt	2760

agagaggctg gaagatttgc cgtgctgggc accatggtca tgaagcacct gaaccgcaag 2820

ctgcatctga cccggtcctg cctgatcgat ctgacatga tgatgagcca gaagctctgg 2880

aagaaccagc ggaagagaat ccctctgcca tctcctagac agcatctgct ccctcagtac 2940

cctctgcacc ctctccacc ttgtctgctg ctgctccacc acagacacca cctggccttt 3000

ctggaaatgg cctgcagcag ccagcacacc cactccatca agatctggat cagcttttagc 3060

cacgagcaga gcagcccatc cctggccaga tcctggaaca ccatgcagtg gaacaacaag 3120

aaaatggcca tgacagtgat cgctggcgcc caccactgtc agtacaagct gacctacacc 3180

aaagtgtgga agatgaattg gaagaaaatg atgacggct cccagcacct cctgttcagc 3240

cctctggata gcctccact gcaactgctg cttcacctc acggcaagag atgcaaccct 3300

tgctgcagac tgacatggat gtccatgctg cagaaacagt gctgctaca cctcgtgatc 3360

aagcaccac tgatcttcag aatcaacctg cggagacagg gcaagaccaa ggatggcgtt 3420

gtgcagagcc tgggcttctt gaaccagcag atcatcctgc agaaagagtt cttcatctgc 3480

ctgctcatgt ttatcaagcg gtggaagcct gccgccacca agagagagtg ggagaaacgc 3540

aagcagatcc tcggcggagg cggcaagtac aaagagtact tcctgaagcg catcctgatt 3600

cggaaggcca tgactgtgct ggccggcgac aagaaaggcc tgggcagatt catgagatgc 3660

gtgcagagcg agacaaaggc cgtagcctg cagctccac tcggaagagg ccctgtgtac 3720

tacgtgtgca accggatgaa cgtgtccagc gtgctgaagc ccttctgtt caccgtgcct 3780

atcgaggaca tgagagagtg cactctgggc cgcaacagaa tgaatgtgct ctctgtgctg 3840

aaacctgtc tgatccctgt gccaatcgac ctgcctcgga tgctgccaat cagcagccca 3900

ctgcacagac ccagatgcc attctggacc tgcaccttc ctgccacaac atggggcacc 3960

tgggagacac cttctacatg gggctggcgg acctttcggg gccctagaag aaaagtgtg 4020

atggtgctgt ggctgccgc caaccagagt ctgcagaaaa gccaaagtgt ccagtgggtc 4080

ctgcggaccg agaacatccg gaagctgatc tggaccaagc agcggagctt cctgtctctg 4140

ttccccaagc tgagagccac cgaacagatg accaatgtgg gctgcgcctt cagcggccgg 4200

attctgcatc aacctgaaat ggccgcatg cggtgatgc ccaagttcct gaatagcacc 4260

aacagctggt ggacctgtac caacctgagc gtgccatga tgctgacat tctgatttgg 4320

aagcgggtgt tcatttctct gctgtccgac aagaagctgc tgaagaagtc tagccagctg 4380

aggcggctct ggagaaacgt gtcccgatc agccaccaga tgaagtgtct gaccgccgtg 4440

gactgtctgc aggccttctg ggacatgaac atggaacacc ggctgacat ggacagcgcc 4500

ctgagcctga caaagagaga gggacccgag acttgcaaga agaagctcct gctgaaactg 4560
ctgacaatga gcctgagcaa catcctgatg aagttccggc tgcggctgag aatcccaagc 4620
ctgaggaagt atcgccagca tctgaaaaag accagcgcca agggcgagaa gctgaagcac 4680
tgctttaagg ctiggggcag aggcccacct ctgcacacaa gaagccagaa gaaagaccct 4740
gccggcaagc tgaaaaaact gaccacactg agcttcgtgc tgatcgagga acggcggaac 4800
ctgcagcgga atctgaaagt cctgtggctc aagaaaagca ccaagagccg gtatctgttc 4860
ttcctgaccg tgtgcggctt cttcgagaag aaacggcctg agtggctgtc ctccagaaag 4920

aaggacaca caaagaatcg gaggaaggcc aagcggaagc ccagatcgt gcacaagaag 4980
agaggcctgt tctcaaaaa gaaatacttg gtgcaggcg ccaagaagat caccttcctg 5040
tccaacggca tggaagcttg cggcacacac cccacaccaa gactgagcga cagagtgttc 5100
ctggtcaaga tcaccaccac cacaagcagc cccagaagaa gcccgact gagagctaga 5160
ggcggcacca caattggcga agtgaccagc ctgtgcttct tctacctgt gtacggctac 5220
ccctacgatg tccctgacta tgcgtcc 5247

<210> 1134

<211> 5250

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 4A

<400> 1134

atgcatcgac ggcgctcacg gaggttccgg gaagaccaa agcctgtgat ggacgatcag 60
cgggacctta tttctaacaa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
gagtccaagt gtictagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
ccaaagcccg tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360

ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
catgtcatgc atttgcttca aaacgtgat ccccttaaag tttaccctcc tctgaagggg 480
agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540
tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
ggcgtcacia agcaagacct gggacccgtg ccgatgatcc agaagaagaa acagaaatcc 720

atggccaaga agtcccagca gcctctggtg ctgaagaaga accggaagca agagtgggga 780

ggacaggccc acagacagag aaacaacgcc aagaagatgc cttccaaga ggaaaagaag 840

aacggccgga tcagcagcag cctgatcctg agcttccaga gagtgaagga cagcaagaaa 900

atgaccaga agatgtgcag ctctctggcc ctgcctacag gcctgacatc tctgatcctg 960

cctagcagcg atctggccgt gctgatctct agcagcacca gccactttct gatgcggagc 1020

cctgtgctgc caagctccag actgacatgt gcctctccac agctgccccg gatgtggaca 1080

tggctctagct ggctgaagca cccagaacc gctagcatca cactgcctac cacaagcctg 1140

aagggcagca gaaccagctg ctgccaaga tctcaccca gactgcctag gaccaagtgg 1200

cctctgcagt gtctgctgca cagcctggga acaacaggca cactcgtttg ggaaaggggc 1260

gtgctgcaga tgagaagcct cgaagcccat tgtcctctgc agaccttcca tctgcaccac 1320

tgcagaacct agccaagctc ttgtcctcct gcctggattc tgtaccaagg ccagtggagc 1380

ggagccgtcg ttggacttag acccgtggct caccatctgc ctgacctat ccagggcctg 1440

cactgtctc aggtcctca tcaacctgct ctgagctggg gaaagtggcc cgtgggaatg 1500

acaggacctg ccagatgctg tcggtggccc cgcagatctc agaagtctca gcatcactgc 1560

gccctgcgga agatcgagtg ggccacaaaa ctgtctctcg gcggaaaagc cggaccacag 1620

gctcaagaga aggccagacc ttctccttgc ctgtcctggt ccagcagaat tgtggccct 1680

ggacacgccc tgagctgtcg gactcgtaga agatggtcct ccaagtgcag aggcgccct 1740

agcggccagc atagatgttg tagctgtagc ccagcggct tcagcgccgg aagagcaga 1800

tgtcctgtgc agggatgtct gaggccacac agagttcagc tgcctgagaag atggggccca 1860

ggatctcctg ctggccagag actgtctaag ggcttccaac tgcctcgctg gtggggacct 1920

ggatctccag ctctgagcc tagaaaggc ccatttctc cactgatcc tccatggcct 1980

gtgaccgtg tgacagtgat ggctggctct gtgcctagcg cacagtctgt ggatgcctg 2040

gaatctcctg gacctctggc tctggaaggc cctagcagcc ctgaaacct gctgtggcgg 2100

gaaatgagca tctttctgcc cggcattctc tgccaaaaga aggtgccatc tgccagcccc 2160

tggggacttg ttctccttc tccaccactc gctctgggcc ctagaatgca gctgtgtacc 2220

cagctcgcca gattcttccc catcacacct ccagtgtggc acatcctggg acctcagaga 2280

cacacacctc aggtggctct gagactgggc aacctgcctc cattcttcag aggcagcgag 2340

gtgcccttct ctagaccttg ccggaccaag aacgaggga acaatcactg gccagagtg 2400

gaaatgccta ccggctggct gctcgtgggc tacaacacca gaaacacagc ccagaatcct 2460

cggctgcagc agcatctgaa acactggcag cagtgcacac gggccagatg gtgtcaagag 2520
 ccttgctaga ccttgacctt cttccacttc ttcttctttt tcaaaacggt gtccctgtgt 2580
 tgtcccggct ggtccaaagg acaacctcca cctcctggcc tgaagccttc tagcctggct 2640
 tctcaggtgg ccagaaccac aggcgtgtac cagcacgtgt ggctgatctg cttcgtgttc 2700
 ttcgtgtgcg tggaaaccgg cttctgtcac gtggcacaag tgggcctcga gagactggtt 2760
 tctctgagcg gcataccga cgtgaacat tgggccagc ctaagccatc tcctagcaaa 2820
 ggcaccggca tgaacagacc catcggcctg agagtggca aaggcgtgtg ggccagactg 2880

 ctcaagaaga agcctagaga catctgtcgg atctccaaca gaaagacccg gaaggccgcc 2940
 agagagaagc accgcaaac agatagagcc agcgtgtcct tctggactct gctgcctaca 3000
 acaggcgtgc ggacaagagg aagccctctg agactgactc tgtggcctcc tagatgcaga 3060
 tgcagacgcg agtacagagt gaccatgaac atcctgaaca gcctgccaag cagcatggaa 3120
 atcgccgtgc tgcaagaac cgccaagaaa agccctacca gcttctgtg caacctggac 3180
 ctgcagcatc agcgagacg caaaaagaag aaagacaagg tcgagatccg gaatcggagc 3240
 cccaaggcca atagcacaga gtgtcagggc gagcacagca gagagcagaa tctgtgtaat 3300

 ctggtgcagc tgaatcctca cagccctcac caccggaagg acgaagagga ccaccagaag 3360
 agacaccacc accacaatca aaagaagatg agcgtccac tgttcttcca cggcgacctg 3420
 tgtagagaga gcacctggg caatttctgg atgaagctgc tccagctgcc tcagaggcct 3480
 ccaactgcaac cagtgaccgg aatggaaatc ctgctttgga ttctgctgaa gatggaaatt 3540
 cagatcttca agatttgcct gggcgagatg cagctctgca cctctcgat tctgaacctg 3600
 caagtgtga aaaagatcct gcggagcttt atgaagctgt accacagcct cgtgatgtgc 3660
 ctgcggctga ggaccaagct ggaaaaggct ctgagcgccc tgttcatctg gcctcagcac 3720

 tcctacaaga tcacacacc attcgccagc cagccactgg gacaagagat gccaacaac 3780
 accagatcc ggctgtgaa gcccgacaag aagaagaaaa gcaccgaaaa gaccaaaggc 3840
 caggctttcg gcagcttctc gcgcgatttt tcagccctc aaggacagc ttttggtcc 3900
 ctgtgtcagc tgggtgtcgc cgactttagc gccccacaag tgaccagact gcggagcctg 3960
 aacctctgc tgatttggct gaagaattgg aagcggttca agctcaaaaa gaaatatcag 4020
 gcccctctgc ggctgtggc ttgggtcgga acaagccaga cctacttcgg cagcatcatc 4080
 tgtatcaaga atatgttct gcagcggaag ggtttctga acctgagcca cgtggaaaag 4140

 ttcgagctta agaagaatct tctgtctccc gtctgatca acctgaagag actgcagaaa 4200
 ttcagtctga accagaagt cctggctcca ttctctgcct gcaccagcaa agcctggaca 4260
 ccagaaaaac tcgtgggcag agccgtgcgg agaaaggga tttggccat gacactgacc 4320

ctgaacggaa tcgaggccct gacagccctg tttaacctga gaaccgcctc catcagcgtg 4380
aacatcagca cctgatgag catcctggaa gccatcatca agaagatgaa gaaacggatc 4440
atggtgcacc ggtggatctt ctccaatcag ctgaccgtgc agatgctctg cctgcctctg 4500
ctgaccctg acaccagatg gatctttagt aatcagctgc agacagtga aatgctgtgt 4560

ctgccacctc tgaagcagg cgagagaatc atttgccac tcggcggtt tcagatcccc 4620
aattttctt ggtccctcgg catcggacac actggcgcat ggtggcatc tggtagaagg 4680
cggagagagt gggcggtc taccgtgtct agaagccac tgtggatcag ctccatgatc 4740
tacctgagag gcatggcctt cgccagcgac agctccatca gaaccaccag agtgtcctgg 4800
tgtcggagat gtggcgcaa gtctgccga gcctcttctt ctccactgtg ggattgcagc 4860
accacaaccg gcacacacca cggatgcctg tgggagatcc ctagcggtac cctgctggct 4920
aacctgcacc tgtgtacta ccactctcag agcaacagaa acaagagccg ccagatggaa 4980

tccctgggca tgaagctcca acttaaaaag aaagtgaacg cctgcagcac ctacacaccc 5040
cacatctgca gacacacctg tcgcgtgaac gccgtcgagg aactgcactc tagaaggatg 5100
tccgtgcgga tcgtgaaaaa ttgggtgtcc tgtgtctacg tgcggctgtc agctgtggga 5160
ctgtctactt ggagcgctct ggacaacaag atcatctgca agggccacag aatcacccgc 5220
taccctacg atgtccctga ctatgcgtcc 5250

<210> 1135

<211> 5250

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP

polypeptide 1B

<400> 1135

atgcatcgac ggcgctcacg gagttgccgg gaagacaaaa agcctgtgat ggacgatcag 60
cgggacctta ttctaataa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
gagtccaagt gtcttagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
ccaaagcccc tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ccttcccatg 360
ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420

catgtcatgc atttgcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480

agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540
 tttagagact ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
 aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
 ggcgtcacia agcaagacct gggacccgtg ccgatgaccg agatccaatt gaccatgaac 720
 gacagcaagc acaagctgga aagccccgtc ctgaaacagg tgtcaccagc ctctccacct 780
 actcagcagc ctgagacacc tcaggatagc agacaggtgc tggccatgcc tagcagctgg 840

 tctagctctg gcagaaccca gcggaaggtg gtcaagaatc ctagccagcc tgtgcctctg 900
 agaaacgacg gcatcaccaa cggcaacgac tccaccagaa gctgcagcat cagcctgaag 960
 aaaagcctgg aaaagatgcc cctcatgatg aagaagaagg acagcaccat cttcatcgtg 1020
 cccatgagcc tggcctgtag catcaccgtg tctttcgtgg gccagatcag cacactgggtg 1080
 ctggatgtgt ccagcatctc ccactggaac aaagtgcggc agaacttcaa gcggaacgcc 1140
 gacaagaaga acgttcggag cggcgagaag aacgacctgc agctgtttgt gatgagcgac 1200
 accacctaca agatctactg gaccgtgatc ctgctgaacc cctgcggcaa tctgcacctg 1260

 aaaaccacca gcctgggcca ctgtcctaga acaatggccg gaccttctgc ctctctgcac 1320
 cctgcatctg gcagagcctc tagaaagacc tggcagagaa ggctgagagc ctgtagagct 1380
 ggtggacctg ctggatgggc cagacaggcc ttcgataaga aaggctttgt gatcctgagc 1440
 gtcggagccg gaacaggcgg aggacctgct tgtgttcctg tggctgaagc ttctacaggc 1500
 gcttggacag ctgaaggcgc cgctggaaca agatgtagag cttctagagc cccttgcaga 1560
 cagctgcctg ccagctctcc taccaagtgc gagatctgcg tgaagcgagc acggcggaga 1620
 aagagaagca gccagtctag aagccccgtg cctaagaaac gcgagagaat gatgctgccc 1680

 gtgcgggcca gaacagctag atctgcactt cctcagggga gagccctctt tgagggaatg 1740
 ctgcttecta gagcactgcc cagcctgctg tctagaatgc cagccagaag agagagccgg 1800
 ttttggtcgg ctctgcaggc acttggactc agacctccac atctgcctag ctgtcatcct 1860
 ctgcctcaac tgcctggccc tccacctcct catcaggccc ctacagcttt cttcctgctg 1920
 gacatcattc tgcggctgcc ctgcaaagtg accgagtcta gcaatatggg cggcaacaga 1980
 tccatctgcc tgaccaacgc caagaaaatg gaagatatga tctgggagag cacgccctg 2040
 agcatcagca gacctacatc tagagccagg cagagctgtt gtctgcccgg actgacacat 2100

 cctgctcacc agccactggg atctatgacc ctggccatca gattcatcag cgctcctcag 2160
 cctagctcca gcacagtac agctgctcct agcggccagt acttcaaggc caagaagcgg 2220
 cggaagaga tcttcaagaa gaagaaaccc ctgacattca gccccagcct ggccaaaaag 2280
 accctgacca atagcagctt cttctacacc agcgaccgag aggccaagaa atctatgaag 2340

cggagcatga ccctgaaggc cctggtaag acctggacac agttcagaaa ctaccccaga	2400
gcctctcttc ctggacaccc tctgggacct aatggcatct gggaagtgat gcccagaaca	2460
ctggaaggct gcatctccgt gaaggaccac agaacaagcc agaaccacag caagtgcac	2520
accgagtgtg tgcggacagc cctgaacaga agaagcaaga tcgaggcctc tcctatcggc	2580
tctatcgccc tgagatccat gcctaagagc agaaaccagg tgctgttcag acggaatctg	2640
acccaagcc agctgagaac tctggccctt ctttatatgc tgctgcccga gtctctgagc	2700
cagagcctga gcagaaagca gatccctagc cagtccatgc tggtagcctc tagagcagga	2760
cagtttctg tgtggcggag aaccagcaga ggaatgagcc tgcagtggaa gtccggcaat	2820
gcctgcacac ctctgagatg ccctagcaga agccctgcca cattcctgac agctctgaac	2880
ggctggcaca gatctggact gagagcccag agaaagcgca agcgcgagaa gagaagccag	2940
aagtccaggc agaaccatct gcagctgaag tctgcccgc gcaagatctc caactggtec	3000
aagctgagaa gcccctggat cttctgtgcc aagaagagac tgccaagct gaccaagtgt	3060
gaaatctgtg tcaagaacac cgccatcctg gctatcacc tgatcacccc tcaggaccct	3120
catctggacc ctgtgtgta ccctcataga aggcctggat ggaagggcca ccacagagtg	3180
gtgttttctc atcaccttag cggcagcacc aagagccact ggagcaaaag agaacgcgga	3240
ggcggcagac gggaaaagaa gggctgtaga gagagatccc tgctgtactc cagaatgtgc	3300
ctggtgcaga tcccacaca cacctgggag cccgattact tcgtgtctct gcccatgatg	3360
ttcagctggg ccacacagtc attccccgtg ggagccgtgt ttctgaccag acctgccatt	3420
ccttctgtga gctgcacaag ccacagcaac ccttgagtc agagcagaca cccacacaga	3480
agcccaccta cctctgtcc tccgtgtctg gaagccttc cactgcctag agcatccctg	3540
agagccaccg tgccaagaca tagctctgtg ctggcaaccg gactgcatct gcacagacag	3600
atttctctgc cctgagagg attctgtctg catcaaccac tgccaggcca gcatctgtgg	3660
ctgtctcata gactgcggct gagactgcca agaactcagc ggctcctag atccatcctg	3720
agccttagac tgccactgag gccacagaga ggaccagac ctctgcatag atggctgcag	3780
cagaccacag gctgtagcca gagaagatac cccagactga aaaccttcgg cgtgccactg	3840
ggctccattc tgtgtctggc tggatctctg agcaccatga tgatcattag caccaccaga	3900
caagagtgtg gcaggcgggc atctgtgccc ttagaccta tgatcggaag cgccagacca	3960
ggaccttgga gaacatctgc tatgcctagc gccatgggcg tcgactgcc tacaagctgt	4020
gaatccggaa gatctctcc tgccaccggc ggaagaatgc ctggaagcca gagcattatg	4080
atgagctgga tgcctctctt ggctccttgt gccgttgtc cttgttctcc cgctcctaca	4140

ctgtgtcccc ctcatcctgc tagagcacct acagccgtgc ctgcctttac acctctgtct 4200

gcacatcctg tgctgtgct gtctggatgt cacctggccg tcagaacctc catgtgaca 4260

ctgtgccta tgetgaagct ggccccactg caagtgacca ccacctgaa getgatcctg 4320

gtcatgctgg aaatcgtgac cgagagcact cggagagaga tgccttctca ggccacacct 4380

tctccacctg gaccttggcg agccgctctg ggcaaagaag tgaagagatc ccagagcaag 4440

ctgcgcctga gaaacacaag ccccatcgtg ttttttctgg ccccatactt cccagacgg 4500

atgaccagac ggacatgac aaccaccaa atgatgatga tgcggcggac caagcggaga 4560

aggcgcaaaa ggcggaagaat gacaatgatg acaaggcgga ccctgctgac aaagaaaacc 4620

tgtctgacct ctagaaccag cgccgtacc aaagctctgc caaggcagac aatctcccag 4680

cggaggccta ttcagacccc tcttgaaca tctctggcca tctggggcaa ccagcagctg 4740

aatggacctc ctacatcct gaagtcgcc agcagaaggg ccagacctac cagctgtagc 4800

acctglagaa tttgggtgat cgccaaaaag cggatcaagc tgcggcggaa cagaaccaga 4860

ctgacactga caggcacaag aagcagcggc accagagctt ctccatccgc cgtttgcctg 4920

tgttctgga cctgtcctc cagaagcttc ccagccgctt ctccaagcgg attgagagca 4980

cctgttggag cacaggcccc tccagaagt acactgagag ctactgtgac ctccagcgcc 5040

tctaaggctt gtgctggact ttggccttgg ggagcacaag ttcggcaacc atctttgcct 5100

ggacatgcg ctctctgct gagcacactg tctcagccac ctccacaggc tccatctcaa 5160

gtgtggacag ccgaacact gagatgtcct gctgttccag ctgtgcctg tctcctggc 5220

taccctacg atgtcctga ctatcgctcc 5250

<210> 1136

<211> 5232

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide encoding the hinv- and ha-extended poly-fsp
polypeptide 2b

<400> 1136

atgcatcgac ggcgctcacg gagggtccgg gaagaccaa agcctgtgat ggacgatcag 60

cgggacctta ttctaacaa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120

gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180

ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

cttacagtta catccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300

ccaaagcccg tctccaaaat gaggatggcg acaccgctcc ttatgcaagc ccttcccatg 360
 ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
 catgtcatgc atttgcctca aaacgctgat ccccttaaag tttaccctcc tctgaagggg 480

 agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540
 tttagagact ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
 aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
 ggcgtcacia agcaagacct gggacccgtg ccgatgagaa agatgcagag cctgaatcac 720
 cccagcagac tgaccaacat gagcagaaca cctccaagac gcgtgtgcaa ccctcggaga 780
 aagacctgga agatgcggaa gaagtacgcc cagaagccta gccagaagaa ccacctgtac 840
 aacagccgga agaaactgct cgaggacatg aagcagaatg gcttcacagg ccacagagag 900

 ggcagcagat ctgataatct gggcctgctg tactccttcc ctcctatccg gatgtgcgcc 960
 ctgtctcacc ctagcttcta catcagcagc accgtgtgct tctgagcaa gcactgcatg 1020
 accgcctgca caaaaagaa aggccacatg atcttcagcc gcgagaagat catcaacccc 1080
 accatcagct gccccttcca gagccccaca aagcggtctg aactgagcct ggaaccttgg 1140
 attccttacc tgcaccagca gaaaacccaa ggcggcaaga agagaagcaa gttccctggc 1200
 accagcctgc agtgctacct gaacagatgc agcctgatgg aacagatccc tcacctgaag 1260
 tccgcctctc cacagatcat gcagagaacc agcgccgacc ggttccggat gaagcggaga 1320

 atgcagaacc tggacaatct gggcggtcca tggccactgc tgcttgacc tctggaaaac 1380
 acacagatcc ccagaacaag ccctctgtgg aagatcacia tgggtgctgac ataccccaac 1440
 tgcgtggtgc acgtgctgat gttctggctg cctatgagat ctctgggca gccttgagaa 1500
 gctggcttcc agtggggaga gtcccttgg caagtatgg ctagcctgac agggccctat 1560
 cctatcagcg agggcctgac catgaccacc ggcagaaaca tcaacagcaa ctccctgatg 1620
 accaactgcc tgttcagccc catcttctg tgccaccacg ccatcatgca ccggaagatg 1680
 acaagccac acttcagact gttcagcagc aagatccac atcctcaggt gccatctgtg 1740

 gtggccctgt gcaagttcag agccacattt ctgctcgccc tgtgggagtg tagtctgcct 1800
 caagccagac tgtgcctgat cgtgtctaga accctgctgc tggttcagtc tgccgtcct 1860
 ccacatagac tcttgggccc ttctagatgg tccagaagcc acctggactt cagccctac 1920
 tggatgaaga aagtgaagct ggccaacggc ctgtggttca acctgatctt cgtgctgttc 1980
 aaggccgacc agagcgagtc tagcctgtct agcgcccgga acaagaaaac aaagctgtgg 2040
 ttctccctca tcaacatcca ccaccgaag aatcctctgc tgcccatgag aatccccagc 2100

ctgaatgcc agtggatgtt cctgagaatc ctgcttctgg cccatatgta cggcttcagc 2160

acctacggca cccagaaagg cgagtgcgtt tgtctgcagt gtctgagcgg cagcagcctg 2220

ttcattctga agcagccctt ggacctgaag atctccaaga cttcatgct gcaagctcac 2280

ccacaggtgc cagctcttgc tctcaagct tggtagcctg ctagaagagg ccctctgaca 2340

tctgtccat ccgtcagca gtctctgaca gctagccctc agattatgca gcggatgagc 2400

gccgtgaact tcgagacaat catctaccct ccaagcacct gtagcctgcc ttgtagaggc 2460

agaacactgg aaagcgccgg actgtttcct tggctgcaca cccagtgtac acaccctgt 2520

accatgctgc tgccacaagg ctgggtggtgt acaagaggcg gcggaaagcg gaaaaagaaa 2580

atgtgcaagg tgiccgccgg ctgcaccgcc tgtgttgaga gatgtcctt gaaggccatc 2640

tgctggaagt ggccagtgc agtggtgct cagtgtctta gcgtgacct tctggaatgg 2700

acagcccaag agagaggtg cagcagctgg ctgatgaagc aaacatggat gaagtcttgg 2760

tccctgcggg accccagcta cagatccatc ctggaatag tgtccaccag agtgcttgg 2820

atgccacaa gcaccgtgc gagaagaaac agcagaaagc agtctcaggt gcagctggcc 2880

attcaggtgc tgctcgtgga caagcacaag tactttctgt tcggcagagc ccgcaaccgg 2940

aacatgaaga aaacatgag ccacctgatc gcccatcagg cctgaagat gagcggcctg 3000

aggctgtttc atcctcggt gctgacaaga aagaagcccg gcaagttcct gcctagcaga 3060

tttcttggg gccctctcc tctgtgtcat cctgttggc tgagccctat ctccgcctgt 3120

ccaagactgc tgccatacc ttttcactg ctggccctgg aagtacctt tccacctgga 3180

acagccatgc ctcatgca actgcaggcc ctggccatgt gggagaaagg ctgggataag 3240

cggaagagaa tgaagaccgg cgccatcaa gagaaggcg ctattcaaga gaaaggggcc 3300

atgaccaagc ggtctgctt ggtcaattc gaggcctgca gagagatgga aagcctgagc 3360

gccctgaga agattacct gtttgaagc catatggccc ggtgcacctc catcaatgtg 3420

ctgtgtgtca gagcctctct gatcgagaag ctgatgaaag aaaagcgcaa gatgaagcgc 3480

aaccaggtgg catccccaca aattatgcag aggtgttca ttaagggtc ccagaacaac 3540

cattcacct tccatctgca aaacttcgcc ttcttcagca gcttcggcaa caacaagtac 3600

atcaatatcc tgacggcg caagaaaaga gaggaccact gcggactgct gatcctgatc 3660

cagcagggc gcatcttcac ctttcggtt tgggtcgaag agctgagctg gaacatctgc 3720

aagaacctga gcctgtacct ggataagttc gtgcagcggc tgctgtacgt gtacatcatc 3780

gagacaaacg tgttcgtgct gaacctgtt cactgtccag tgaaccagat cttcatgatg 3840

gcctttctacc tgaagtacac cgagaaggcc tgggtcatgg aactggaatg gctgatccaa 3900
cagcagtgtt accagcaaga gaagaaaagc cggaaactga tgagcagctg cggggccttc 3960
atccacacac ctagaagccc tggctgcagc gtgtacgcca atatgtgctg ggccttttgg 4020
aagcctccta gccagggcac cagctcttgt ctgatgacag gctgttgggg cagccctcct 4080
ctgcacctgt gtcagcctct gaggcggtat aagaaaagg gctgatcgc ctggcgcgcg 4140
agaaagtggc agatccggca tgtgtgaaa aacctgatcc tgtttcatgt gcggaacatc 4200
gtgtacggca tccaagtgat gctgtcggc aagggactga cacaccctgt gcctctgaaa 4260

cggaccctgc agaacaagag gaacaagaac atcaagcggg tcaaccagaa gaagggaac 4320
atcaagagga agtccatcct gctgcacctc attgtgctga atagccccga gagcaacccc 4380
aagtcttcc tgacctttag ccagctcgag aagaaagcta cctggatgag aagaacaggc 4440
gccctgagag ccacagctcc tgctacagca gctcctcagg ctgagactcc tcattggaga 4500
gccgccacaa caagcagcat gagcagcagc cctagagccg agcctacatc ttctagctct 4560
tgggccacct gttggccag atgctgtagc tccagctgtt actggtcctt gatttcttgg 4620
cctctgctg gcgccgctga ggctacaaac accagaacta gaagcagaga gtcccagcgg 4680

ggcagaatgc tgacttggag aagtagtctg tggctgcagg gcaccagatg ttttacaggc 4740
gtgcggacaa gcagcggag ctgtggcaga gctttagct gcggaagagg ctgtggaacc 4800
cctagaggcg attggaagag acaccctcct cggaggaata gcgtgatcgt gcacaagatc 4860
gtgctggtgt ttctgaagtc cctgtccagc tacaactgcg agagaaggat cagcggcatc 4920
cagaagagag ccatcgagtt tgccgtgctg aaactgctga atatggacct gcaactggaac 4980
tccgcctacc tgggcagaac tctgtggtc acctgtatcc tgtatcacgg gtggatcgtg 5040
acctcatgt gccagtctca gagatggctg accagacca caagcagatc cagcgtctgt 5100

atgtggacct ggcagatcaa tcggaggaag ctgcagagaa agaagaggca cccaagctgg 5160
ccttggacca gatgccttag aatgaggcct cctagaagcg gctacccta cgatgtcctt 5220
gactatgcgt cc 5232

<210> 1137
<211> 5247
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 3B
<400> 1137
atgcatcgac ggcgctcacg gattgcccga gaagacaaa agcctgtgat ggacgatcag 60

cgggacctta ttictaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120

 gagtccaagt gtcttagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
 ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
 cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
 ccaaagcccc tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360
 ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
 catgtcatgc atttgcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480
 agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaagggtg 540

 tttagagact ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
 aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
 ggcgtcacaa agcaagacct gggacccgtg ccgatgggag ctgctgctgc ctcttgctag 720
 tctcctcctt ctctcggga aaccacacct agctccgacg ccaccagacg gacaagacca 780
 attgccgctc agagcaagaa aaccatgaca gccgccggac tgaccctaa gaacaagaag 840
 cggagaaagc tgcggcccaa gatgatccgg aagatccaga agagaaggcg gaccgccaac 900
 cggcggaata gcagaagggc taccctaca agcaagggca gcctgagaag aaagtacctg 960

 agagtgcggg gacctcctct gcacaccgg aacatcagaa agctgatctg gaccaagcag 1020
 cggagcttcc tgctctgtt cccaagctg agagccaccg agcagatgac caatgtgggc 1080
 tgctctatcc ctacgtgcc caaagccaca gccgctcact ctgtgacagt gaaactgcag 1140
 ctgcccctga cttcagcac cctgctgtgg gatagcagac acaccatgag cctgagcaac 1200
 atcctgatga agttccggct gcagtctagc ccattcctgg ccagatcctg gaacaccatg 1260
 cagtgaaca acaagaaaa ggccatgacc gtgatcgtg gcgcccacca ctgtcagtac 1320
 aagctgacct acaccaaagt gtggaagatg aactggaaga aaatgatgat cggcagccag 1380

 catctgctgt tcagccctct ggatagcagt ccctgcagc tcctgctgca ccctcacggc 1440
 aagagatgca acccttgctg cagactgacc tggtatgagc agaacaccag aagcaccaac 1500
 ctggaaaaga accccagcct gaagaagcag agccagcgga gaggaaagct gagcgctttt 1560
 agcggcagaa tcctgcacca gccagaaatg gccgcatga gactgatgcc caagttcctg 1620
 aactccacca acagctgggtg gacctgacc aactgagct tcgtgctgat cgaggaagcc 1680
 agacagccca gcagacctac cggcagaaca cctaccacca gactgatggc ccctgtgggc 1740
 agcgtgatga gctgttctct gctgaccag ctttctccag ccagcgctg tacaatgcct 1800

ccactgctgc atccacagtg ggccctcat agtgctggac tttctcagg cgcttgcaga 1860
cctgcctgca cctgtatcag catgaccacc atcagcaggg ccacatgggg cccagtgtac 1920
tacgtgtgca accggatgaa cgtgtccagc gtgtctgaagc ccttcctgtt caccgtgcct 1980
atcgaggaca tgagagagtg caccctgggc agaaacagaa tgaatgtgtc ctctgtgctg 2040
aaacctgtc tgatccctgt gccaatcagc gagaagaaga ggaagctgcc caacatcgag 2100
atcacccctc agcgggtctaa ggccatgctg cagaagcagt gctgtctaaa cctcgtgatc 2160
aagcacccctc tgatcttcag aatcaacctg cggcggcagg gcaagaccaa agatggcgtt 2220

gtgcagagcc tgggcttctt caaccagcag atcatcctgc agaaagagtt ctcatctgc 2280
ctgtcatgt tcatcaagcg gtggaagcct gccgccacca agagcagaaa gaagggccac 2340
accaagaaca gacggaaggc caagagaaag cccagatctt acctgttctt cctgaccgtg 2400
tgcggctttt acctgaaaaa gaccagcgcc aagtggctga agaagtcac caagtcaga 2460
tccaacggca tggaagcttg cggcacacac cccactccta gactgagctg cctgagagtt 2520
agatgcggcg gctggctgtg tggctggaca cctagaggta gaaagtcgg cgtgatgaag 2580
tgctggggtc tgtgccccgt gcacaagaag agaggcctgt tcagactgga ttttcacccc 2640

agaagcagct ccggcaaggg aaagaacagc cctgtctgcc aaaagaaact gcgggtgcag 2700
aaccagggcc atctgtgat gattctgtg cacaatgacc gggtgttctt cgtgaagatc 2760
ggcgagaagc tgaagcactg tttcaaggcc tggggctcca gacggaaccg gcggtacaga 2820
aagatctacg gcgagctgaa gatgtccctg caggccttcc tgatccacct gagaaaggtg 2880
gacaccacc acctccaggt ggtcaccaaa acagtgaccg ccacaacagc cgacggccag 2940
agaatgcgga gactgaagtg caaggcctgc cggctgagat gggccagacc tgaacctgct 3000
gctcaggccc ctctaagag ccactttcca cctcatccta gcggccccag cagaacaagt 3060

agcctgcagc tgagaagcct gttcttttagc cactgcctgt gcagccagaa gaaggacctt 3120
gccggcaagc tgaaaaagct gctgaagaaa agcagccagc tgcggagaag ctggcgcaat 3180
gtgtccagaa tcagcaccct tcttccactg atcctgtggc ctcaagctgc tctgtgtcc 3240
gtgatcacca tgaagctgtg ggagaagcac ttcaagggcc tgaattggaa cctggctgtg 3300
tggattctga acctgaagat gatgacctac atggaaatgc actacggcca tcaggcccca 3360
caggtggcaa tctgtcctaa gctgtgtgtc agacagatgc tgcccactct gagcacactg 3420
cagcagagac atctcaggg cccttgtctt cctcctgtga cacctctgag agtccagtct 3480

gtcctgctgc tgggagtgcc tcagacagcc agaggaccta gaagaaaggt cctgatgggtg 3540
ctgtggctgc ccgccaatca gtctctgcag aaaagccagg ttttcagtg ggtgctgcgg 3600
acagaggtgg cccttagatg tcttagatct gccgtggaca tcagccccgg acctacatct 3660

cctagcctgg ccctttgtgc ctctgtggcc attggaaagc tggcactgct tggcgctct 3720
gctccttgtg gtgtgtctgg cgctagagag gccggaagat ttgtgtgtct gggcaccatg 3780
gtcatgaagc tttgtttctt ctacctgtg taccggtgc gcatcccaag cctgaggaag 3840
tacagacagc acctgaaccg gaagctgcac ctgacaagat cctgcctgat cgatctgacc 3900

atgatgatgt ccagaagct ctggaagaac cagcggaaga gaatccctct gccatctcca 3960
cggcaacatc tgetgccaca gtacctctg caccacctc caccttgtct gctgttgctg 4020
caccatagac accacctggc ctttctcgag atggcctgta gctctcagca caccacagc 4080
atcaagatct ggatcagctt cagccatgaa gtggaccctc caggcagcgt gtggatactg 4140
ccttgcgac tgcctcggat gctgccaatc tcttaccctc tgcacagacc ccagatgcct 4200
ttctggacct gcacctttcc tgccacaacc tggggcacat gggagacacc ttctacatgg 4260
ggctggcgga ctttcagagg cgctagcagc agcacatccc gggacagcag atccttcttc 4320

acctctgctc acctagcag gccctgcaga atgagactgt accagtcaa gaagaagctc 4380
ctctgaaac tctgaccac caccacaagc agccccagaa gatccctgc tctgagagca 4440
agaggcgga ccacaatcg cgaagtgacc agctgtacca acctgagcgt gccatgatg 4500
ctgaccatcc tgatttgaa gcgggtgttc atcctcctgc tgagcgataa gaaggcgcc 4560
aagaagatca ctttctgcc tattctcca cacctgagac acctctgtct gctgttcgag 4620
aagaaacggc ctgagtggct gagcatggac ctggacggaa tctgacagt gatcgccag 4680
ggactcgtgg gcatgacccc tagagatctg ggaacagtgg caggcgccac cgctcagatt 4740

cagcgaccta tccaggtgca gactggcggc agactcagaa gaaacctgca gagaaacctg 4800
aaggtgctcc aggtgtccgt gtacagcggc aacctgtgt ctttagcag acggggcatg 4860
aagtctagcg tgcggctgaa aaaccgcgag tgggagaaac ggaagcagat tctcgaggc 4920
ggcggaaagt acaaagagta cttctgaag cgcattctca tccggaaggc tatgacagtg 4980
ctggccggcg acaagaaagg actgggcaga ttcattgagat gcgtgcagag cgagacaaag 5040
gccgtgtctc tgcaactgcc tctgggaaga aacatggaac accggttgac catggacagc 5100
gccctgagcc tgacaaagag agagggacct gagacactca aaaagaaata cctggtccag 5160

caccagatga agtgtctgac cgccgtggat tgtctgcagg ctttttggga catgggctac 5220
ccctacgatg tccctgacta tgcgtcc 5247

<210> 1138
<211> 5250
<212> DNA
<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 4B

<400> 1138

atgcatcgac ggcgctcacg gagttgccgg gaagacaaaa agcctgtgat ggacgatcag	60
cgggacctta tttctaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca	120
gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg	180
ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag	240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc	300
ccaaagcccc tctccaaaat gaggatggcg acaccgctcc ttatgcaagc ctttcccatg	360
ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat	420
catgtcatgc atttgcttca aaacgctgat ccccttaaag ttaccctcc tctgaagggg	480
agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg	540
tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa	600
aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggaccgag tagtgggctg	660
ggcgtcacia agcaagacct gggacccgtg ccgatgatcc agaagaagaa gcagaagtcc	720
aacctggacc tgcagcacca gcgcagacgc aaaaagaaga aggacaaggt cgagatccgg	780
aatcggagcc ccaaggccaa tagcacagag tgcagggcg agcacagcag agagcagaac	840
ctgctgaatc tgggtgcagt gaacctcac agccctcacc acagaaagga cgaagaggac	900
caccagaagc ggcaccacca ccacaatcaa aaaaaatga gcgtgatggc caagaagtcc	960
cagcagcctc tcggacaggc ctttggctct ctgtgtcagc tgggtgccgc cgatttcagc	1020
gcccccaag tgaccagact gcggagcctg aaccatctgc tgatcaacga gggcaacaac	1080
cactggccta gactggaat gcctaccggt tggctgctcg tgggtacaa caccagaaac	1140
acagcccaga atctcggct gcagcagcac ctgaaacact ggcagcagt caccagagcc	1200
agatggtgcc aagagccttg tcagaccctg accttcttcc atttcttctt ctttttcaa	1260
acggtgtccc tgtgtgtccc cggtgtgtct aaaggacaac ctctccacc tggcctgaag	1320
ccttctagcc tggcttctca ggtggccaga accacaggcg tgtaccagca cgtgtggctg	1380
atctgtctcg tgttcttctg gtgcgtggaa accggcttct gtcacgtggc ccaagtggga	1440
ctcgagagac tgggtgtctct gagcggcatc accgacgtga accattgggc ccagcctaag	1500
ccatctccta gcaaaggcac cggcatgaac agaccatcg gcctgagagt tggcaaaggc	1560
gtgtgggcca gactgagagc ctccgtgtct ttctggacce tgcctcctac aacaggcgtg	1620
cggacaagag gaagccctct gagactgaca ctgtggcctc cacggaacat cctgaacagc	1680

ctgcctagca gcatggaat cgccgtgctg caagagaacc gcaagaccag aaaggccgcc	1740
agagagaagc acagaaagac cgacaacctg cacctgtgct actaccacag ccagagcaac	1800
cggaacaaga gccggcagat ggaaagcctg ggcatgaagc tgcagagccc tctgtgggat	1860
tgctccacca caacaggcac acaccacggc tgctgtggg agatccctag cgttacactg	1920
ctggcctgca gaggtaacgc cgtggaagaa ctgcacagca ggcggtatgc tgtgcggatc	1980
gtgaagaact ggggtgtcctg ctgttacctg cgcctgtctg ctgtgggcct gtctacttgg	2040
agcgcccttg acgtggatcat caacctgaag cggtgcaga agttcagcca gaagtctcag	2100
cacctgtgc cctgagaaa gatcgagtgg gccacaaagc tgcgcctcgg cggaaaagct	2160
ggacccagg ctcaagagaa ggccaacgcc aagaagatgc ccttcagcg gtggatcttc	2220
agcaatcagc tgaccgtgca gatgtgtgct ctgcctattg aagccctgac tgccctgttc	2280
acctgtcgga cagccagcat cagcgtgaac atcagcacc tgatgagcat cctggaagcc	2340
cctctgtttt ttacggcgga cctgtgcgag gaaaagaaga acggccggat cagcagccag	2400
gtcctctca gactttggtc ttggtgcggc acaagccaga cctactttgg cagcaccgcc	2460
aagaaaagcc ccaccagctt ttgctgcgag tggggaggac aggtcaccc gcagagaaat	2520
accggaatgg aaatcctgct gtggattctg ctcaagatgg aaattcagat cttcaagatt	2580
tgctgggcg agatgcagct gtgcacctac acacccaca tctgcagaca cacctgtaga	2640
ggcggaccta gcgccagcga tagatgctgt agctgtagcc ctacggcctt cagcgccgga	2700
agaggcagat gtccagtcca gggatgtctg cggcctcaca gaggcagct gctgagaaga	2760
tggggccctg gatctcctgc tggccagaga ctgtctaagg gctttcagct gctccgttgg	2820
tggggaccag gatctccagc tcttagcct agaaagggcc catttcacc acctgatcct	2880
ccatggcctg tgaccgtgt gacagtgtg gctggctctg tgcctagcgc tcagtctgtg	2940
gatgtcttgg aaagccctgg acctctggca ctggaaggac ctacgagccc cagaaacctg	3000
ctctggcggg aaatgagcat cttcctgcct ggcatcttca cctctcgat tctgaacctg	3060
caagtgtga agaagatcct gcggagcttt atgaagctgt accactctct ggtcatgtgc	3120
ctgcggctgc ggaccaagct ggaaaaagct ctgagcgctc tgttcatctg gccccagcac	3180
agctacaagc agaggcctcc tctgcagcct gtgcaggtcg tgctcagact gggaaacctg	3240
cctccattct tcagaggcag cgaggtgccc ttctctagac cttgccggac caagatgctg	3300
aaccagaagt gtctggcccc ttctatcaca caccattcg cctctcagcc cctgggacaa	3360
gagatgccc acaacaccca gatcagactg ctgaagcccc tgctgacccc tgacaccaga	3420
tggatcttct ccaaccagct gcagacagtc cagatgtctt gtctgccacc tctgaagcag	3480

ggcgagagaa tcatttggcc cctcggcggc tticagatcc ccaacttctt ttggagcctc 3540

ggaatcggcc acactggcgc ctggtggcat actggaaggc ggagaagaga atggggcggc 3600

tccaccgtgt ctagaagccc actgtggatc agctccatga tctacctgag aggcatggcc 3660

ttcgccagcg acagctccat cagaaccacc agagtgtcct ggtgcagaag atgcggcggc 3720

aaatctgccg ctgcctccag cctcaagaag aaaccccggg acatctgtcg gatcagcgac 3780

tctaagaaga tgaccagaa gcgcgagagc accctgggca atttctggat gaagctcctc 3840

cagctgccag acaagaagaa gaagtctacc gaaaagacca agatcatcaa gaagatgaag 3900

aaacggatca tgggccacat gtgcagctcc ctggctctgc caacaggcct gacatctctg 3960

atcctgccaa gcagcgatct ggccgtgctg atctctagct ccaccagcca ctttctgatg 4020

cggagcccag tgctgcctag ctccagactg acttgtgcct ctccacagct gcccagaatg 4080

tggacctggt ccagctggct gaagtggctg aaaaactgga agcggttcaa gcttaaaaag 4140

aagtacatcc tggccatgac gctgacctg aacgggcac caagaaccgc ctctatcacc 4200

ctgcctacca ccagcctgaa gggctctaga accagctgtt gcccagatc tcacccaga 4260

ctgcctagga caaagtggcc tctgcagtgc ctgctgcaca gcctgggaac aactggaaca 4320

ctcgtgtggg aaaggggcgt gctgcagatg agaagtctgg aagctcactg ccctctgcag 4380

accttcacc tcaccactg tagaactcag ccagctctt gccctctgc atggattctg 4440

taccaaggac agtggagcgg agccgtcgtg ggacttagac ctgtggctca ccatctgcca 4500

agacatttc agggcctgca ctgcccacag gctccacac aaccagctct gtcttggggc 4560

aagtggcccg tgggaatgac aggacctgcc agatgttgc ggtggcctag acgggaactc 4620

aaaaagaatc tgctgtccc ctgccggtgc agacgcgagt atagagtgc aatgggcca 4680

gccttcggca gctttagcg cgactttagc gctccccagg tgttgaagaa gaatcggaag 4740

cagaacaaga ttatctgcaa gggccaccgc atcacaagcc tgatcctgag ctttcagcgc 4800

gtgaaactta agaagaaagt caacgcctgc tctccgcct gcacctctaa agcctggact 4860

cccagaaagc tcgtggggag agccgtcaga agaaaggga tcactgttat caagaatatg 4920

ttcctgcagc ggaagggttt cctgaacctg agccacgtgg aaaagtctgt gcctccttct 4980

cctcctctgg ctctcggccc tagaatgcag ctctgtaccc agctggcccg gttcttcct 5040

atcacacctc ctgtgtggca catctggga cctcagagge acacccttg tcaaaagaag 5100

gtgccctccg ctagcccatg gggccttaga ccatctcctt gcctgagctg gtcctccaga 5160

attgtggccc ctggacacgc cctgagctgt cgactagaa gaagatggtc cagcaagggc 5220

taccctacg atgtccctga ctatgcgtcc 5250

<210> 1139

<211> 4690

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 1A

<400> 1139

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg 60

ctgctgtgt gtggagcagt ctctgtttcg cccagccagg aaatccatgc ccgaaccgag 120

atccagctga ccatgaacga cagcaagcac aagctggaaa gccccgtct gaaacaggtg 180

tcaccagcct ctccacctac tcagcagcct cagacacctc aggattctag acaggtgctg 240

gccctggcca agaaaaccct gacaaatgcc tccagagccg gacagtttcc tgtgtggcgg 300

agaacaagca gaggcattgag cctgcagtgg aagtccggca atgcctgcac acctctgaga 360

tgccctagca gaagccctgc cacattctcg acagccctga atggctggca cagatctggc 420

ctgagagccc agatgcctag ctcttggtct agcagcggca gaacctgaa gctggcccct 480

ctgcaagtga ccaccactct gaagctgatc ctggtcatgc tggaaatcgt gaccgagcgc 540

tccctgctgt actccagaat gtgtctggtg cagatcccca cacacacctg ggagcccgat 600

tacttcgtgt cctgcctat gatgttcagc tgggccacac agtcttttcc cgtgggcgcc 660

gtgtttctga ccagacctgc cattccttgc tgcagctgta ccagccacag caacccttgg 720

agccagagca atcagcagct gaagtggacc cctcacatcc tgaagtccgc cagcttcgac 780

aagaaaggct tcgtgatcct gagccggcgg agcaagattg aggctctcc tatcggtctt 840

atgccagct ctcttgaca tctctggga cctacactgg ccatcagatt catcagcgcc 900

cctcagccta gcagctctac agtgacagct gcccttagcg gccagtactt tatcgccaag 960

aagcggatca agctgcggcg gaacaatatg ggcggcaaca gatccatctg cctgaccaga 1020

aagcgcaaga gagagaagcg gagccagaag tccaggcaga accatctgca gctgaaaagc 1080

tgcagacgga agatcagcaa ctggccaag ctgagaagcc cctggatctt caccaagtgc 1140

gagatctgcg tgaagaacac cgccatctg gctatcacc tgatcacc tcaggacct 1200

catctggacc ctgtgtgtca ccctcataga aggctggat ggaagggcca ccatagagt 1260

gtgttctctc accatctag cggcagcaca aagagccact ggcagcaaag agaacgcgga 1320

ggcggcagac gcgagaagaa gggatgtaga gaacagcgga aggtggtcaa gaacccctct 1380

cagcccgctg ctctgagaaa cgatggcatc accaacggca acgactccac cagaagctgc 1440

tccatcagcc tgaagaaaag cctggaaaag atgccctga tgcggagagc cagacctacc 1500

agctgtagca cctgtagaat gtgggtggaag ggcaagaaac ggcggaaga aatcgtgcct 1560

atgagcctgg cctgcagcat caccgtgtct tttgtgggac agatcagcac cctgggtctg 1620

gatgtgtcta gcatcagcca ttggcggtg cctgttaaag tgaccgagag cagctccagc 1680

ttcttttaca ccagcgacag gacccctctg agcatcagca gaccaaccag cagagctaga 1740

cagagctgtt gtctgcccgg actgacacac cctgtcacc aacctctggg cagcatgagc 1800

actagaagag agatgccaag ccaggccaca ctttctccac ctggaccttg gagagccgt 1860

ctgggcaaag aagtgaagag atcccagagc aagctgcgcc tgagaaacac aagccctggg 1920

gagaagaacg atctccagct gtctgtgatg agcgacacca cctacaagat ctactggaca 1980

gtgatcctgc tgaacccctg cggcaacctg cacctgaaaa caacatcact gcagcggcca 2040

cctcggagca tctgtctct gaattggaatc tgggaagtga tgccccggac actggaaggc 2100

tgcatcagcg tgaaggatca cagaaccagc cagaaccaca gcaagtgcac caccgaatgt 2160

gtgcggactg cctgaacgt gtccaagaag agactgccta agctgatgaa gaagaaggac 2220

agcaccatct tcatcaacaa agtgcgccag aacttcaagc gcaacttcaa gaagaagaaa 2280

cccctcactt tcagccccag cagacggatg actcggagaa ccatgacaac caccaaatg 2340

atgatgatgc ggcggaacca gcggagaagg cgcaaaaggc ggagaatgac catgatgacc 2400

agacggacc tctgacaaa gaaaacctgt ctgacccta gaaccagcg cgccacaaaa 2460

gtctgccta gacagacat cagccagcgg aggcctattc agacccacc tggacatct 2520

ctggccatct ggggcagaac aagactgacc ctgacaggca ccagatccag cggaacaaga 2580

gcctctcctt ccgccgtgtg cctgtgtgtg ttgacctgtc caagcagaag ctctccagcc 2640

gtctctccta gtggactgag agcacctgtt ggagcccagg ctctctctga agtgacactg 2700

agagcctctt gtgcctctag cgcctctaaa gcctgtgtg gactttggcc ttggggagcc 2760

caagttcgag ttggagctgg aacaggcgga ggacctgctt gtgttctgt ggctgaagct 2820

tctacaggcg catggacagc tgaaggcgcc gctggaacaa gatglagagc ctctagagcc 2880

ccttgccgcc aacttctgc tagctccct accaagtgtg aaatttgtgt gaagcgcaga 2940

cggcggagaa agagaagcag ccagtctaga agccccgtgc ctaaaaagcg cgagaggatg 3000

atgtgcctg tgcgggccag aacagctaga tctgcacttc ctgaggcag agcacctctg 3060

gaagggatgc tcttcttag agcactgcct agcctgtga gcagaatgcc tgccagaaga 3120

gagtcgccgt ttggctggc tctgcaggca cttggactca gacctccaca tctgcctagc 3180

tgtatcttc tgcctcaact gttgggcct ccacctctc atcaggcccc aatgacactg 3240

aaggccctgg ttaagacctg gacacagttc cgcaactacc ccagagccga caagaagaat 3300
gtccggctcta ccgccttctt cctgctggac atcatcctgg gcgattgccc aagaacaatg 3360
gccggacctt ctgcctctct gcatcctgca tctggcagag cctccagaaa gacctggcag 3420
agaaggctga gagctttagt agcaggcggg cctgctggat gggctagaca ggcctatcct 3480
agactgaaaa ccttcggcgt gcccttgggc tctattctgt gtctggccgg cagcctgtcc 3540
acaatgatga tcattagcac caccagacaa gagtgcggca ggccggcttc tgtgccttgt 3600
agacctatga tcggaagcgc cagaccagga ccttggcgga catctgctat gcctagtgcc 3660

atgggagtcg ccttgcctac ctcttgtgaa agcgggaagat ctctctctgc caccggcgga 3720
agaatgccag gatctcagtc tatcatgatg agctggatgc ctccactggc tccatgtgcc 3780
gcttgtccat gtctccccg tcttacctg tgcccagcac atcctgctag agcaccaaca 3840
gccgtgcctg cctttacacc tctgtctgct catcctgtgc cagtgtctgc tggatgtcac 3900
ctggccgtca gaacctccat gctgacactg ctgcccattg aagccaaaaa gagcatgaag 3960
cgggtccaacg ctaagaaaat ggaagatatg atctgggaga gccggctgcc actgaggcca 4020
caaagaggac ctagacctct gcacagatgg ctgcagcaga caaccggctg tagccagagg 4080

cggatcgtgt tctttctggc ccatacttc cctcggcacc ctacagatc tccaccaaca 4140
tcttggccac ctctgtgga agctttccca ctgccaagag cttctctgag ggccacagtg 4200
ccaagacata gctctgttct cgccaccggt ctgcacctcc acagacagat ttctctgccc 4260
ctgagaggat tctcctgca ccaaccactg ccaggacagc atctgtggct gtctcacaga 4320
ctgaggctga gactgcccag gacacagcca tctttgcctg gaccatgtgc aagcctgtctg 4380
tccacactgt ctacgccacc acctcaggct ccatctcaag tgtggactgc cgctacactg 4440
agatgtcctg ctgttctgc agctgcctgt cctcctgctc tgagatccat gcctaagagc 4500

cggaaccagg tgctgttcag acggaatctg accccaagcc agctgagaac actggcccca 4560
ccttatatgc tgctgcccc gctctgtgcc cagagcctga gtagaaagca gatccctagc 4620
cagtccatgc tcgtgggcta cccctacgat gtcctgact atgcgtccta aaggcgcgcc 4680
tagcggccgc 4690
<210> 1140
<211> 4672
<212> DNA
<213> Artificial Sequence
<220><223> Cloning cassette hTPA 2A
<400> 1140
gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggtc ctgctgtgtg 60

ctgctgctgt gtggagcagt cttcgtttcg ccagccagg aaatccatgc ccgaagaaag 120

atgcagagcc tgaatcacc cagcagactg accaatggct ctctccact gcacctgtgc 180

cagcctctga gaatgagcag aacccctcct agaagagtgt gcgcgcgtcc tccacataga 240

ctgctgggccc cttccagatg gaaccctcgg agaaagacct ggaagatgcg gaagaagtac 300

gcccagaagc ctagccagaa gaaccacctg tacggcggca agaagcgctc taagttcagc 360

agaagccacc tggacttcag cccctactgg atgaagaaag tgaaggtgct gttcaaggcc 420

gaccagagcg agtctagcct gagcagcgga agatgcagcc tgatggaaca gatccctcac 480

ctgaagtctc ggcggaagtg gcagatcaga cacgtgctga agaacctgtg gctgcccattg 540

agaagcctgg gagaaccttg gagagccggc ttccagtggg gagagtctcc ttggcaagtg 600

atggcctctc tgaccggcag agccacattt ctgctggccc ttggggaatg tagcctgcct 660

caggcaagac tgtgcctgat cgtgtctaga accctgctgc tgggtgcagag ccggaacaag 720

aaaacaaagc tgtggttcag cctgatcaac atccaccacc ggaagaacct actgctgcct 780

atgagatggt ggtgtaccag aggcggcgga aagcggaata agaaatgtg caaggtgtcc 840

ggcggtctga ccgcctgtgt tgagagatgt ccttggaagg gcatctgctg gaagtggcct 900

gtgacagtgg ccgccattag aatgtgtgcc ctgtctcacc ctactttcta catcagcagc 960

accgtgtgct ttctgagcaa gcaactgcatg accgcctgca ccagaaagag aatgaagacc 1020

ggcgccatcc aagagaaggg cgctattcaa gagaaagggg ccatgaccaa gcggatctgc 1080

gtggtcaatt tcgaggcctg cagagagatg gaaagcctga gcgccctga gaagatcacc 1140

ctgtttgaag ccacatggc ccggtgcacc tccatcaatg tgctgtgtgt gcgggccagc 1200

ctgattgaga agctgatgaa agaaaagcgc aagatgaagc ggaaccaggt ggcctctcca 1260

cagatcatgc agcggtgtt catcaagggc taccagaaca accacttcac cttccatctg 1320

caaaacttcg cttctctcag ctcttcggc aacaacaagt acatcaatat cctgaccatc 1380

ctgttccacg tgcggaacat cgtgtacggc atccaagtga tgctgtgcgc tagccctcag 1440

attatgcaga gaaccagcgc gcaccggttc cgatgaaga gaagaatgca gaatctggac 1500

aacctgggcg tgccatggcc tctgttcct ggaatcccat ctctgaacgc ccagtggatg 1560

ttcttgagaa tcgcatcccc gcaaatcatg cagaggatga gcgccgtgaa cttcgagaca 1620

atccgggcca gaaaccggaa catgaagaaa accatgagcc acctgatcgc ccatcaggcc 1680

ctgaagatga gcggcctgag actgtttcac ccagactgc tgacacggaa gaagcccga 1740

aaactgctgc tcgcccattat gtacggcttc agcacctacg gcaccagaa aggcgagtgc 1800

gtttgtctgc agtgtctgag cggcagcagc ctgttcattc tgaagcagcc cctggacctg 1860
aagatcagca agaccttcat gggccacaga gagggcagcg agtctgataa tctgggcctg 1920
ctgtatatgt tccctccacc ttatcctatc agcagaggcc tgaccatgac caccggcaga 1980
aacatcaaca gcaactccct gatgaccaac tgcctgttca gcccctctt cctgtgccac 2040
cacgccatca tgcacagaaa gatgacaagc cctcacttca ggctgttcag cagcaagatc 2100
ccacatcctc aggtgccatc tgtgtgtggc ctgtgcaagt tccgggcctt catccacaca 2160
cctagaagcc ctggctgcag cgtgtacgcc aatatgtgt ggcccaagtt cttcctgacc 2220

ttcagccagc agtgggtccag cgtgacatct ctggaatgga cagcccaaga gagaggctgc 2280
agcagctggc tgatgaagca gacatggatg aagtcttga gcctgcggga cccagctac 2340
agatccatcc tggaaatcgt gtccaccaga gtgctgtgga tgcctacctc taccgtgctg 2400
caggctcacc cacaagtcc agctctggct cctcaagcct ggtggcctgc tagaagagga 2460
cctctgacat ctgccccatc cgctcagcag tccctgacca gagagaagat tatcaacccc 2520
accatcagct gcccttttca gagccccacc aagagactga tctacctcc tagcacctgt 2580
tctctgcct gcagaggctt cctgcctagc agatttcctt ggggcccacc tcctctgaac 2640

agcgtgatcg tgcacaagat cgtgtgtgtg ttctgaagt cctgtccag ctacaactgc 2700
gagcggagaa tcagcggcat ccagaagaga gccatcgagt tcgccgtgct gaaactgctg 2760
aatatggacc tgcctctcga gaacacacag atccccagaa caagcccact gtggaagatc 2820
acaatggtgc tgacataccc caactgcgtg gtgcatgtgc tgatgtttgg cgccctgaga 2880
gccacagctc ctgctacagc tgcacctcag gctcagacc ctcattggag agctgccaca 2940
acaagcagca tgagcagcag ccctagagcc gagcctacat cttctagctc ttgggccacc 3000
tgttggccca gatgctgctc cagctcttgt tactggtcac tgtctagctg gcctccagct 3060

ggcgccgctg aagctacaaa taccagaacc agaagccgcg agagccagag gggtagaatg 3120
ctgacttga gaagctccct gtggttgagc ggcaccagat gttttacagg cgtgcggacc 3180
agctccagat acaagaaaag aggcgtgatc gcctggcgga gacagatcaa tagacggaag 3240
ctgcagagaa agaagcactg gaacagcgcc tacctgggca gaacactgct ggtcacctgt 3300
atcctgtatc accggtggat cgtgacctcc atgtgtcagt cccagagatg gctgaccagc 3360
accacaagta gatctagcgc cctgatgtgg accgagctga gcctggaacc atggattccc 3420
tacctgcatc agcagaaaac ccagcggaca ctggaatccg ccggactgtt tccttggtg 3480

cacacccagt gccaagagaa gaaaagcaga aagctgatgt ccagctgcac acaccctgc 3540
acaatgctgc tgccacaggg atgtcatcct gcctggtga gccctatctc tgcctgtcca 3600
agactgctgc catatccttt tcacgtgctg gctctggaag tgacctttcc tcctggaacc 3660

gccatgcctc agatgcagtt gcaggctctg gctatgtggg agaaaggctg ggataagcct 3720
 ggaccagcc tgcagtgccta cctgaacaga agaagaaaca gccggaagca gagccaggtg 3780
 caactggcca ttcaggtgct gctcgtggac aagcacaagt actttctgtt cggccaaaag 3840
 aaaggccaca tgatctttag cctggccaac ggcctgtggt ttaacctgat tttcaactcc 3900

cggaagaaac tgctcgagga catgaagcaa aatggcttca ccggcaaagg cctgacacac 3960
 cccgtgcctc tgaageggac tctgcagaac aaaagaaaca agaatatcaa acgcgtcaac 4020
 cagaagaagg gcaacatcaa gcggaagtcc atcctgctgc acctgattgt gctgaatagc 4080
 cccgagagca acctgatcct gatccagcat ggcgcatct tcacctttcg gttctgggtc 4140
 gagaagctgt cctggaacat ctgcaagaac ctgagcctgt acctggacaa gttcgtgcag 4200
 agactgctgt acgtgtacat catcgagaca aacgtgttcg tgctgaacct gtttcattgtg 4260
 cccgtgaacc agatcttcat gatggccttc tacctgaagt acaccgagaa ggcctgggtc 4320

atggaactgg aatggctgat ccaacagcag tgctatcagg gcagctgcgg cagagcttgt 4380
 tcttgtggaa gaggtgtgg caccctaga ggcgattgga agagacatcc tcctcggaga 4440
 gccttctgga agcctcctag ccagggcctc tctagctgtc tgatgaccgg ctgttggctc 4500
 gagaagaaag ctacctggat gcggcggacc cgccggaaga agagggaaga tcattgcgga 4560
 ctgagacacc ccagctggcc ttggacaaga tgtctgagga tgaggcctcc aagaagcggc 4620
 taccctacg atgtccctga ctatgcgtcc taaaggcgcg cctagcggcc gc 4672

<210> 1141

<211> 4687

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 3A

<400> 1141

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggtc ctgctgtgtg 60
 ctgctgctgt gtggagcagt cttcgttttcg ccagccagg aaatccatgc ccgaggagct 120
 gctgctgcct cttgtcagtc tctccttct cctcgggaaa ccacacctag ctccgacgcc 180
 accagacgga caagacctat tgccgctcag agcaagaaaa ccatgacagc cgccggactg 240
 acccctatga tccggaagat ccagaagcgg cgagaaaccg ccaaccggtg tctgagagtt 300
 agatgtggcg gctggctgtg tggctggaca cctagaggac agaacaccag aagcaccaac 360

ctggaaaaga accccagcct gaagaagcag agccagcggg gaggaaagct gagcagcctg 420
 ttcttcagcc actgcctgtg ccggaacagc agaaggcca cacctacatc taagggcagc 480

ctgcggcgga agtacctgag agtgcctatt cctccacacc tgagacaccc tctgctgctg	540
atggacctgg acggaatgct gaccgtgatc ggacaggacgac tcgtgggcat gaccctaga	600
gatctgggaa cagtggctgg cgccaccgct cagattcaga ggccatttca ggtgcagacc	660
ggcggcagac ttacacctcc tcctctgatt ctgtggcctc aggcgcgtcc tgttgatcct	720
cctggctctg tgtggattct gccctgcaag aacaagaagc ggagaaagct gcggcccaag	780
cggtctggact ttcacctag atcttctagc ggctgtccg tgatcaccat gaagctgtgg	840
gagaagcact tcaagggcct gaactggaac ctggctgtct ggattctgaa cctgaagatg	900
atgaacatcg agatcacccc tcagcggagc aaggccagaa agtccggcgt gatgaagtgc	960
tgggatctgt gcccagcga gaagaagagg aagctgcctc tgcctctgac ctccagcacc	1020
ctgctgtggg actctagaca tagaggcgcc agctccagca ccagcagaga ctccagaagc	1080
tttttaccac gcgtcaccc cagcagaccc tgcagaatga gactgtacca gttcctgac	1140
cacctgagaa aggtggacac ccaccatctg caggctcgtga ccaagaccgt gacagccaca	1200
acagctgacg gccagagaat gcggagactg aagtgaagg cctgccggct gagatgggct	1260
agacctgaac ctgctgtcca ggcccctcca aagagccact ttcacctca tctagcggc	1320
cctagcagaa ccagttctct gcagctgcgg agcatccctc acgtgcaaaa agccacagcc	1380
gctcacagcg tgacagtga gctgcagaag ggaaagaaca gccctgctg ccaaaagaaa	1440
ctgcgggtgc agaatacagg ccattctgtg atgatcctgc tgcacaatac ctacatggaa	1500
atgactacg gccatcaggg ccacaggtg gccatgctgc ctaagctgct gtgcagacag	1560
atgtgcccc ctctgagcac actgcagcaa agacacccac agggcccttg tcctccacct	1620
gtgacaccac tgagagtcca gtctgtcctg ctgctgggag tgcctcagac agctgctaga	1680
cagcctagca gaccaccgg cagaaccct accacaagac tgatggcccc tctcggcagc	1740
gtgatgagct gttctctgct gaccagcct tctccagcca gcgcctgtac aatgcctcca	1800
ctgctgcatc ctgagtggc ccacattct gctggattgt ctcccgcgct ttgcagacct	1860
gcctgtacct gtatcagcat gaccaccatc tccagagcca cctggcaggt ttccgtgtac	1920
agcggcaatc tctgagctt ctccagacgg ggcatgaaga gtagcgtgcg gctgaaaaac	1980
agccggcgga acagacggt cagaaagatc tacggcgagc tgaagatgtc cctgcaggcc	2040
gtggctccta gatgtcctag atctgccgtg gacatcagcc ccggacctac ctctcctagc	2100
ctggcctctt gtgcctctgt ggccattgga aaactggccc tgcttggcgc ttctgcccct	2160
tgtggtgctg ctggcgctag agaggctgga agatttgccg tgctgggcac catggtcatg	2220
aagcacctga accgcaagct gcattgacc cggctcctgcc tgatcgatct gaccatgatg	2280
atgagccaga agctctggaa gaaccagcgg aagagaatcc ctctgccatc tctagacag	2340

catctgctcc ctcagtacc	tctgcaccct cctccacctt	gtctgctgct gctccaccac	2400
agacaccacc tggcctttct	ggaaatggcc tgcagcagcc	agcacacca ctccatcaag	2460
atctggatca gctttagcca	cgagcagagc agcccatcc	tggccagatc ctggaacacc	2520
atgcagtggc acaacaagaa	aatggccatg acagtgatcg	ctggcgccca ccactgtcag	2580
tacaagtga cctacaccaa	agtgtggaag atgaattgga	agaaaatgat gatcggtcc	2640
cagcacctcc tgttcagccc	tctggatagc tctccactgc	aactgctgct tcacctcac	2700
ggcaagagat gcaacccttg	ctgcagactg acatggatgt	ccatgctgca gaaacagtgc	2760
tgctacaacc tctgatcaa	gcaccactg atcttcagaa	tcaacctgcg gagacagggc	2820
aagaccaagg atggcgttgt	gcagagcctg ggcttcctga	accagcagat catcctgcag	2880
aaagagttct tcatctgcct	gctcatgttt atcaagcgg	ggaagcctgc cgccaccaag	2940
agagagtggg agaaacgcaa	cgagatcctc ggcgaggcg	gcaagtacaa agagtacttc	3000
ctgaagcgca tctgatctcg	gaaggccatg actgtgctgg	ccggcgacaa gaaaggcctg	3060
ggcagattca tgagatgcgt	gcagagcgag acaaaggccg	ttagcctgca gctccactc	3120
ggaagaggcc ctgtgtacta	cggtgtgcaac cggatgaacg	tgtccagcgt gctgaagccc	3180
ttcctgttca ccgtgcctat	cgaggacatg agagagtgc	cactgggccc caacagaatg	3240
aatgtgtcct ctgtgtgaa	accctgtctg atccctgtgc	caatcgacct gcctcggatg	3300
ctgccaatca gcagcccact	gcacagaccc cagatgccat	tctggacctg cacctttcct	3360
gccacaacat ggggcacctg	ggagacacct tctacatggg	gctggcgac ctttcggggc	3420
cctagaagaa aagtgtgat	gggtgtgtgg ctgcccga	accagagtct gcagaaaagc	3480
caagtgttcc agtgggtcct	gcggaccgag aacatccgga	agctgatctg gaccaagcag	3540
cggagcttcc tgtctctgtt	cccaagctg agagccaccg	aacagatgac caatgtgggc	3600
tgcgccttca gcggcggat	tctgcatcaa cctgaaatgg	ccgcatgcg gctgatgccc	3660
aagttctga atagcaccaa	cagctgggtg accctgtacca	acctgagcgt gcccagatg	3720
ctgaccattc tgatttgga	gcgggtgttc attctctgc	tgtccgacaa gaagctgctg	3780
aagaagtcta gccagctgag	gcggctcttg agaaacgtgt	cccggatcag ccaccagatg	3840
aagtgtctga ccgccgtgga	ctgtctgcag gccttctggg	acatgaacat ggaacaccgg	3900
ctgaccatgg acagcgccct	gagcctgaca aagagagagg	gacccgagac ttgcaagaag	3960
aagctcctgc tgaacctgct	gacaatgagc ctgagcaaca	tcctgatgaa gttccggctg	4020
cggctgagaa tccaagcct	gaggaagtat cgccagcatc	tgaaaaagac cagcgccaag	4080

ggcgagaagc tgaagcactg ctttaaggct tggggcagag gcccacctct gcacacaaga 4140

agccagaaga aagaccctgc cggcaagctg aaaaaactga ccacactgag cttcgtgctg 4200

atcgaggaac ggcggaacct gcagcggaat ctgaaagtcc tgtggctcaa gaaaagcacc 4260

aagagccggt atctgttctt cctgaccgtg tgcggcttct tcgagaagaa acggcctgag 4320

tggctgtcct ccagaaagaa gggacacaca aagaatcgga ggaaggccaa gcggaagccc 4380

cagatcgtgc acaagaagag aggctgttc ctcaaaaaga aatacctggt gcaggcgcc 4440

aagaagatca ccttcctgtc caacggcatg gaagcttgcg gcacacacc cacaccaaga 4500

ctgagcgaca gagtgttctt ggtcaagatc accaccacca caagcagccc cagaagaagc 4560

ccagcactga gagctagagg cggcaccaca attggcgaag tgaccagcct gtgcttcttc 4620

tacctgtgt acggctaccc ctacgatgtc cctgactatg cgtcctaaag gcgcgcctag 4680

cggccgc 4687

<210> 1142

<211> 4690

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 4A

<400> 1142

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg 60

ctgctgtgt gtggagcagt cttcgtttcg ccagccagg aaatccatgc ccgaatccag 120

aagaagaaac agaaatccat ggccaagaag tcccagcagc ctctgggtgt gaagaagaac 180

cggaagcaag agtggggagg acaggccac agacagagaa acaacgcaa gaagatgccc 240

ttccaagagg aaaagaagaa cggccggatc agcagcagcc tgatcctgag cttccagaga 300

gtgaaggaca gcaagaaat gaccagaag atgtgcagct ctctggccct gcctacaggc 360

ctgacatctc tgatcctgcc tagcagcgat ctggccgtgc tgatctctag cagcaccagc 420

cactttctga tgcggagccc tgtgtgccca agctccagac tgacatgtgc ctctccacag 480

ctgccccgga tgtggacatg gtctagctgg ctgaagcacc ccagaaccgc tagcatcaca 540

ctgcctacca caagcctgaa gggcagcaga accagctgct gccaagatc tcacccaga 600

ctgcctagga ccaagtggcc tctgcagtgt ctgctgcaca gcctgggaac aacaggcaca 660

ctcgtttggg aaaggggctg gctgcagatg agaagcctcg aagccattg tcctctgcag 720

accttccatc tgcaccactg cagaaccag ccaagctctt gtcctctgc ctggattctg 780

taccaaggcc agtggagcgg agccgtcgtt ggacttagac ccgtggctca ccatctgcct 840

agacctatcc agggcctgca ctgtcctcag gtcctcatc aacctgtctt gagctgggga 900
 aagtggcccc tgggaatgac aggacctgcc agatgtctgc ggtggccccg cagatctcag 960
 aagtctcagc atcactgcgc cctgcggaag atcgagtggg ccacaaaact gtctctcggc 1020

 ggaaaagccg gaccacagcg tcaagagaag gccagacctt ctcttgcct gtcctggtcc 1080
 agcagaattg tggccccggg acacgccctg agctgtcggg ctctagaag atggtcctcc 1140
 aagtgcagag ggggccctag cgccagcgat agatgttgta gctgtagccc cagcggttc 1200
 agcgccggaa gaggcagatg tctgtgcag gtagtctga ggccacacag agttcagctg 1260
 ctgagaagat gggggccagg atctctgtct ggccagagac tgtctaaggg cttccaactg 1320
 ctgcgttggg ggggacctgg atctccagct cctgagccta gaaagggcc atttctcca 1380
 cctgatctc catggcctgt gaccgtgtg acagtgatgg ctggctctgt gcctagcgca 1440

 cagtctgtgg atgccctgga atctcctgga cctctggctc tggaaggccc tagcagccct 1500
 agaaacctgc tgtggcggga aatgagcatc ttctgcccg gcatcttctg caaaagaag 1560
 gtgccatctg ccagcccctg gggacttgtt cctcttctc caccactcgc tctgggccct 1620
 agaatgcagc tgtgtacca gctgccaga ttcttccca tcacacctcc agtgtggcac 1680
 atcctgggac ctgagagaca cacacctcag gtggtcctga gactgggcaa cctgcctcca 1740
 ttcttcagag gcagcgaggt gccctttct agaccttgc ggaccaagaa cgagggcaac 1800
 aatcactggc ccagagtgga aatgcctacc ggtggctgc tcgtgggcta caacaccaga 1860

 aacacagccc agaatcctcg gctgcagcag catctgaaac actggcagca gtgcacacgg 1920
 gccagatggt gtcaagagcc ttgtcagacc ctgaccttct tccacttctt ctctttttc 1980
 aaaacggtgt cctgtgttg tcccggtgg tcaaaggac aacctccacc tctggcctg 2040
 aagccttcta gcctggcttc tcaggtggcc agaaccacag gcgtgtacca gcacgtgtgg 2100
 ctgatctgct tcgtgttctt cgtgtgcgtg gaaaccggct tctgtcacgt ggcacaagtg 2160
 ggccctgaga gactggtttc tctgagcggc atcaccgacg tgaaccattg ggcccagcct 2220
 aagccatctc ctagcaaagg caccggcatg aacagacca tcggcctgag agttggcaaa 2280

 ggcgtgtggg ccagactgct caagaagaag cctagagaca tctgtcggat ctccaacaga 2340
 aagaccggga aggccgccag agagaagcac cgcaaacag atagagccag cgtgtccttc 2400
 tggactctgc tcctacaac aggcgtgcgg acaagaggaa gccctctgag actgactctg 2460
 tggcctccta gatgcagatg cagacgcgag tacagagtga ccatgaacat cctgaacagc 2520
 ctgccaagca gcatggaaat cgccgtgtg caagaaaccg ccaagaaaag ccctaccagc 2580
 ttctgtgca acctggacct gcagcatcag cgcagacgca aaaagaagaa agacaaggtc 2640

gagatccgga atcggagccc caaggccaat agcacagagt gtcagggcga gcacagcaga 2700

gagcagaatc tgctgaatct ggtgcagctg aatcctcaca gccctcacca ccggaaggac 2760

gaagaggacc accagaagag acaccaccac cacaatcaaa agaagatgag cgtcccactg 2820

ttcttccacg gcgacctgtg tagagagagc accctgggca atttctggat gaagctgctc 2880

cagctgcctc agaggcctcc actgcaacca gtgaccggaa tggaaatcct gctttggatt 2940

ctgtgaaga tggaaattca gatcttcaag atttgcttgg gcgagatgca gctctgcacc 3000

tctcggattc tgaacctgca agtgtctgaa aagatcctgc ggagctttat gaagctgtac 3060

cacagcctcg tgatgtgcct gcggctgagg accaagctgg aaaaggctct gagcgccctg 3120

ttcatctggc ctcagcactc ctacaagatc acacacccat tcgccagcca gccactggga 3180

caagagatgc ccaacaacac ccagatccgg ctgtctgaagc ccgacaagaa gaagaaaagc 3240

accgaaaaga ccaaaggcca ggctttcggc agcttctccg ccgatttttc agccctcaa 3300

ggacaggctt ttggctccct gtgtcagctg gtgtccggc actttagcgc cccacaagtg 3360

accagactgc ggagcctgaa ccatctgctg atttggtga agaattggaa gcggttcaag 3420

ctcaaaaaga aatatcaggc ccctctgcgg ctgtggtctt ggtgcggaac aagccagacc 3480

tacttcggca gcatcatctg tatcaagaat atgttctctg agcggaaggg tttcctgaac 3540

ctgagccacg tggaaaagtt cgagcttaag aagaatcttc tgctccccgt cgtgatcaac 3600

ctgaagagac tgcagaaatt catgtgaac cagaagtgc tggctccatt tcctgcctgc 3660

accagcaaag cctggacacc cagaaaactc gtgggcagag ccgtgcggag aaagggcatt 3720

ctggccatga cactgacct gaacggaatc gaggcctga cagccctgtt tacctgtaga 3780

accgcctcca tcagcgtgaa catcagcacc ctgatgagca tcctggaagc catcatcaag 3840

aagatgaaga aacggatcat ggtgcaccgg tggatcttct ccaatcagct gaccgtgcag 3900

atgctctgcc tgcctctgct gaccctgac accagatgga tctttagtaa tcagctgcag 3960

acagtgcaaa tgctgtgtct gccacctctg aagcagggcg agagaatcat ttggccactc 4020

ggcggttttc agatcccaa tttcttctgg tcctcggca tcggacacac tggcgcatgg 4080

tggcactactg gtagaaggcg gagagagtgg ggcggctcta ccgtgtctag aagccactg 4140

tggatcagct ccatgatcta cctgagaggc atggccttcg ccagcgacag ctccatcaga 4200

accaccagag tgccttggtg tcggagatgt ggcgccaagt ctgccgcagc ctcttcttct 4260

ccactgtggg attgccagc cacaaccggc acacaccag gatgcctgtg ggagatccct 4320

agcgttacc tgctggctaa cctgcacctg tgctactacc actctcagag caacagaaac 4380

aagagccgcc agatggaatc cctgggcatg aagctccaac ttaaaaagaa agtgaacgcc 4440
 tgcagcacct acacacccca catctgcaga cacacctgtc gcgtgaacgc cgtcgaggaa 4500
 ctgcactcta gaaggatgtc cgtgcggatc gtgaaaaatt gggtgtcctg ctgctacgtg 4560
 cggctgtcag ctgtgggact gtctacttgg agcgtcttgg acaacaagat catctgcaag 4620
 ggccacagaa tcaccggcta cccctacgat gtcctgact atgcgtccta aaggcgcgcc 4680
 tagcgccgc 4690

<210> 1143

<211> 4690

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 1B

<400> 1143

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg 60
 ctgctgtgtg gtggagcagt cttcgtttcg ccagccagg aatccatgc ccgaaccgag 120
 atccaattga ccatgaacga cagcaagcac aagctggaaa gcccgcgtct gaaacaggtg 180
 tcaccagcct ctccacctac tcagcagcct cagacacctc aggatagcag acaggtgctg 240
 gccatgccta gcagctggtc tagctctggc agaaccagc ggaaggtggt caagaatcct 300
 agccagcctg tgctctgag aaacgacggc atcaccaacg gcaacgactc caccagaagc 360

tgcagcatca gcctgaagaa aagcctggaa aagatgcccc tcatgatgaa gaagaaggac 420
 agcaccatct tcatcgtgcc catgagcctg gcctgtagca tcaccgtgtc tttcgtgggc 480
 cagatcagca cactggtgct ggatgtgtcc agcatctccc actggaacaa agtgcggcag 540
 aacttcaagc ggaacgccga caagaagaac gttcggagcg gcgagaagaa cgacctgcag 600
 ctgtttgtga tgagcgacac cacctacaag atctactgga ccgtgatcct gctgaacccc 660
 tgcggcaatc tgcacctgaa aaccaccagc ctggcgact gtcctagaac aatggccgga 720
 ctttctgctt ctctgcaccc tgcacttggc agagcctcta gaaagacctg gcagagaagg 780

ctgagagcct gtagagctgg tggacctgct ggatgggcca gacaggcctt cgataagaaa 840
 ggctttgtga tctgagcgt cggagccgga acaggcggag gacctgcttg tgttctgtg 900
 gctgaagctt ctacaggcgc ttggacagct gaaggcggc ctggaacaag atgtagagct 960
 tctagagccc ctgacagaca gctgcctgcc agctctccta ccaagtgcga gatctgcgtg 1020
 aagcgcagac ggccggagaaa gagaagcagc cagtctagaa gcccgtgcc taagaaacgc 1080
 gagagaatga tgctgccctg gcgggccaga acagctagat ctgcacttcc tcaggggaga 1140

gccccctcttg agggaatgct gcttcctaga gcactgcca gcctgctgtc tagaatgcca 1200

gccagaagag agagccggtt ttggctggct ctgcaggcac ttggactcag acctccacat 1260

ctgcctagct gtcatectct gcctcaactg cttggccctc cacctctca tcaggccct 1320

acagctttct tctgctgga catcattctg cggctgcct gcaaagtac cgagtctagc 1380

aatatggcg gcaacagatc catctgcctg accaacgcca agaaaatgga agatatgatc 1440

tgggagagca cggccctgag catcagcaga cctacatcta gagccaggca gagctgttgt 1500

ctgcccggac tgacacatcc tgctcaccag cactgggat ctatgacct ggccatcaga 1560

ttcatcagcg ctctcagcc tagctccagc acagtgacag ctgctctag cggccagtac 1620

ttcaaggga agaagcggcg gaaagagatc ttcaagaaga agaaaccct gacattcagc 1680

cccagcctgg caaaaagac cctgaccaat agcagcttct tctacaccag cgaccgcgag 1740

gccaagaaat ctatgaagcg gagcatgacc ctgaaggccc tggtaagac ctggacacag 1800

ttcagaaact accccagagc ctctctctc ggacacctc tgggacctaa tggcatctgg 1860

gaagtgatgc ccagaacact ggaaggctgc atctccgtga aggaccacag aacaagccag 1920

aaccacagca agtgcatcac cgagtgtgtg cggacagccc tgaacagaag aagcaagatc 1980

gaggcctctc ctatcggtc tatcgccctg agatccatgc ctaagagcag aaaccaggtg 2040

ctgttcagac ggaatctgac cccaagccag ctgagaactc tggccctcc ttatatgctg 2100

ctgccccagt ctctgagcca gagcctgagc agaaagcaga tccctagcca gtccatgctg 2160

gtggcctcta gagcaggaca gtttctgtg tggcggagaa ccagcagagg aatgagcctg 2220

cagtggaaat ccggcaatgc ctgcacacct ctgagatgcc ctagcagaag ccctgccaca 2280

ttctgacag ctctgaacgg ctggcacaga tctggactga gagcccagag aaagcgcaag 2340

cgcgagaaga gaagccagaa gtccaggcag aacctctgc agtgaagtc ctgccggcgc 2400

aagatctcca actggtccaa gctgagaagc cctggatct tcgtgtccaa gaagagactg 2460

ccaagctga ccaagtgtga aatctgtgtc aagaacaccg ccatcctggc tatcacctg 2520

atcacccctc aggacctca tctggacct gtgtgtcacc ctcatagaag gcctggatgg 2580

aagggccacc acagagtggg gttttctcat caccctagcg gcagcaccaa gagccactgg 2640

cagcaaagag aacgcggagg cggcagacgg gaaaagaagg gctgtagaga gagatccctg 2700

ctgtactcca gaatgtgctt ggtgcagatc cccacacaca cctgggagcc cgattacttc 2760

gtgtctctgc ccatgatgtt cagctgggcc acacagtcac tcccgtggg agccgtgttt 2820

ctgaccagac ctgccattcc ttgctgtagc tgcacaagcc acagcaacct ttggagttag 2880

agcagacacc cacacagaag cccacctacc tcttgtcttc cgctgctgga agcctttcca 2940
 ctgcctagag catccctgag agccaccgtg ccaagacata gctctgtgct ggcaaccgga 3000
 ctgcatctgc acagacagat ttctctgccc ctgagaggat tcttctgtca tcaaccactg 3060
 ccaggccagc atctgtggct gtctcataga ctgcggctga gactgccaag aactcagcgg 3120
 cctcctagat ccacctgag ccttagactg ccactgaggc cacagagagg acccagacct 3180
 ctgcatagat ggctgcagca gaccacaggc tgtagccaga gaagataccc cagactgaaa 3240
 accttcggcg tgccactggg ctccattctg tgtctggctg gatctctgag caccatgatg 3300

 atcattagca ccaccagaca agagtgtggc aggcgggcat ctgtgccctg tagacctatg 3360
 atcggaagcg ccagaccagg accttggaaga acatctgcta tgcctagcgc catgggcgtc 3420
 gcactgccta caagctgtga atccggaaga tctcctcctg ccaccggcgg aagaatgcct 3480
 ggaagccaga gcattatgat gagctggatg cctcctctgg ctcttctgtc cgtttgtcct 3540
 tgtttctccg ctctacact gtgtcccgt catcctgcta gagcacctac agccgtgcct 3600
 gcctttacac ctctgtctgc acatcctgtg cctgtgtgt ctggatgtca cctggccgtc 3660
 agaacctcca tgcctgacct gctgcctatg ctgaagctgg cccactgca agtgaccacc 3720

 aactgaagc tgatcctggt catgttgaa atcgtgaccg agagcactcg gagagagatg 3780
 ctttctcagg ccacaccttc tccacctgga ccttggcgag ccgctctggg caaagaagtg 3840
 aagagatccc agagcaagct gcgcctgaga aacacaagcc ccacgtgtt ctttctggcc 3900
 ccatacttcc ccagacggt gaccagacgg accatgacaa ccacaaaat gatgatgatg 3960
 cggcggaaca agcggagaag gcgcaaaagg cggagaatga caatgatgac aaggcggacc 4020
 ctgtgacaa agaaaacctg tctgacctt agaaccagcg ccgctacaa agctctgcca 4080
 aggcagacaa tctcccagcg gaggcctatt cagaccctc ctggaacatc tctggccatc 4140

 tggggcaacc agcagctgaa atggacctt cacatcctga agtccgccag cagaagggcc 4200
 agacctacca gctgtagcac ctgtagaatg tggtagatcg ccaaaaagcg gatcaagctg 4260
 cggcggaaca gaaccagact gacactgaca ggcacaagaa gcagcggcac cagagcttct 4320
 ccacccgccc ttgtcctgtg ttgtggacc tgccttcca gaagcttccc agccgttct 4380
 ccaagcggat tgagagcacc tgttgagca caggccctc cagaagtac actgagagct 4440
 agctgtgct ccagcctc taagcttgt gctggacttt ggccttgggg agcacaagtt 4500
 cggaacat ctttgctgg acctgcgt tctctgtga gcacactgtc tcagccacct 4560

 ccacaggctc catctcaagt gtggacagcc gcaacactga gatgtcctgc tgttcagct 4620
 gctgcctgtc ctcttgcta cccctacgat gtcctgact atgcgtcta aaggcgcgcc 4680
 tagcgccgc 4690

<210> 1144

<211> 4672

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 2B

<400> 1144

```

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg      60
ctgctgtgtg gtggagcagt cttcgtttcg cccagccagg aatccatgc ccgaagaaag      120
atgcagagcc tgaatcacc cagcagactg accaacaatga gcagaacacc tccaagacgc      180

gtgtgcaacc ctcgagaaaa gacctggaag atcggaaga agtacgcca gaagcctagc      240
cagaagaacc acctgtacaa cagccggaag aaactgctcg aggacatgaa gcagaatggc      300
ttcacaggcc acagagaggg cagcgagtct gataatctgg gcctgctgta ctcctttcct      360
cctatccgga tgtgcgcctt gtctcacctt agcttttaca tcagcagcac cgtgtgcttt      420
ctgagcaagc actgcatgac cgctgcaca caaaagaaag gccacatgat cttcagccgc      480
gagaagatca tcaacccac catcagctgc ccttttcaga gcccacaaa gcggctggaa      540
ctgagcctgg aaccttgat tccctacctg caccagcaga aaaccaagg cggcaagaag      600

agaagcaagt tccctggcac cagcctgcag tgctacctga acagatgcag cctgatggaa      660
cagatccctc acctgaagtc cgctctcca cagatcatgc agagaaccag cgccgaccgg      720
ttccggatga agcggagaat gcagaacctg gacaatctgg gcgttccatg gccactgctg      780
cctggacctc tggaaaacac acagatcccc agaacaagcc ctctgtggaa gatcacaatg      840
gtgctgacat accccaactg cgtggtgcac gtgctgatgt tctggctgcc tatgagatct      900
ctgggcgagc cttggagagc tggctttcag tggggagagt ccccttgca agtgatggct      960
agcctgacag gccctatcc tatcagcgag ggcctgacca tgaccaccgg cagaaacatc     1020

aacagcaact cctgatgac caactgctg ttcagcccca tcttctgtg ccaccagcc      1080
atcatgcacc ggaagatgac aagccacac ttcagactgt tcagcagcaa gatccacat      1140
cctcaggtgc catctgttgt ggccctgtgc aagttcagag ccacatttct gctcgccctg      1200
tgggagtgtg gtctgcctca agccagactg tgctgatcg tgtctagaac cctgctgctg      1260
gttcagtctg ccgtcctcc acatagactg ctgggccctt ctgatggtc cagaagccac      1320
ctggacttca gccctactg gatgaagaaa gtgaagctgg ccaacggcct gtggttcaac      1380
ctgatcttcg tctgtttcaa ggccgaccag agcagctcta gcctgtctag cgcccggaac      1440

aagaaaacaa agctgtggtt ctccctcatc aacatccacc accgaagaa tcctctgctg      1500

```

cccatgagaa tccccagcct gaatgcccag tggatgttcc tgagaatcct gcttctggcc 1560
 catatgtacg gcttcagcac ctacggcacc cagaaaggcg agtgcgtttg tctgcagtgt 1620
 ctgagcggca gcagcctgtt cattctgaag cagccccctgg acctgaagat ctccaagacc 1680
 ttcattgctgc aagctcacc acaggtgcca gctcttgctc ctcaagcttg gtggcctgct 1740
 agaagaggcc ctctgacatc tgctccatcc gctcagcagt ctctgacagc tagccctcag 1800
 attatgcagc ggatgagcgc cgtgaacttc gagacaatca tctaccctcc aagcacctgt 1860

 agcctgcctt gtagaggcag aacactggaa agcgccggac tgtttccttg gctgcacacc 1920
 cagtgtacac acccctgtac catgctgctg ccacaaggct ggtggtgtac aagaggcggc 1980
 ggaaagcgga aaaagaaaat gtgcaagggtg tccggcggct gcaccgcctg tgttgagaga 2040
 tgtccttgga agggcatctg ctggaagtgg ccagtgcagc tggctgctca gtggtctagc 2100
 gtgacctctc tggaatggac agcccaagag agaggctgca gcagctggct gatgaagcaa 2160
 acatggatga agtcttggtc cctgcgggac cccagctaca gatccatcct ggaatacgtg 2220
 tccaccagag tgctgtggat gcccacaagc accgtgcgga gaagaaacag cagaaagcag 2280

 tctcaggtgc agctggccat tcaggtgctg ctctgggaca agcacaagta ctttctgttc 2340
 ggcagagccc gcaaccggaa catgaagaaa accatgagcc acctgatcgc ccatcaggcc 2400
 ctgaagatga gcggcctgag gctgtttcat cctcggctgc tgacaagaaa gaagcccggc 2460
 aagttctgc ctagcagatt tccttggggc cctcctctc tgtgtcatcc tgcttggctg 2520
 agccctatct ccgcctgtcc aagactgctg ccatatcctt ttcacgtgct ggccctggaa 2580
 gtgacctttc cacctggaac agccatgcct cagatgcaac tgcaggccct ggccatgtgg 2640
 gagaaaggct gggataagcg gaagagaatg aagaccggcg ccatccaaga gaaggcgct 2700

 attcaagaga aaggggccat gaccaagcgg atctgcgtgg tcaatttcga ggcctgcaga 2760
 gagatggaaa gcctgagcgc ccctgagaag attacctgt ttgaagcca tatggcccgg 2820
 tgcacctcca tcaatgtgct gtgtgtcaga gcctctctga tcgagaagct gatgaaagaa 2880
 aagcgcaaga tgaagcgcaa ccaggtggca tccccacaaa ttatgcagag gctgttcatt 2940
 aagggtacc agaacaacca cttcaccttc catctgcaaa acttcgcctt cttcagcagc 3000
 ttcggcaaca acaagtacat caatatcctg acgcggcgca agaaaagaga ggaccactgc 3060
 ggactgctga tctgatcca gcacggcggc atcttcacct ttcggttctg ggtcgaaaag 3120

 ctgagctgga acatctgcaa gaacctgagc ctgtacctgg ataagttcgt gcagcggctg 3180
 ctgtactgtg acatcatcga gacaaacgtg ttcgtgctga acctgttcca cgtgccagtg 3240
 aaccagatct tcatgatggc cttctacctg aagtacaccg agaaggcctg ggtcatggaa 3300
 ctggaatggc tgatccaaca gcagtgttac cagcaagaga agaaaagccg gaaactgatg 3360

agcagctgcc gggccttcat ccacacacct agaagccctg gctgcagcgt gtacgccaat 3420
 atgtgtctggg ccttttggaa gcctcctagc cagggcacatca gctcttgtct gatgacaggc 3480
 tgttggggca gccctcctct gcacctgtgt cagcctctga ggcggtataa gaaaaggggc 3540

 gtgatcgctt ggcgcgaggag aaagtggcag atccggcatg tgctgaaaaa cctgatcctg 3600
 tttcatgtgc ggaacatcgt gtacggcatc caagtgtatg tgtgcggcaa gggactgaca 3660
 caccctgtgc ctctgaaacg gacctgcag aacaagagga acaagaacat caagcgggtc 3720
 aaccagaaga agggcaacat caagaggaag tccatcctgc tgcacctcat tgtgtgaat 3780
 agccccgaga gcaaccccaa gttcttctctg accttttagcc agctcgagaa gaaagctacc 3840
 tggatgagaa gaacaggcgc cctgagagcc acagctcctg ctacagcagc tcctcaggct 3900
 cagactcctc attggagagc cgccacaaca agcagcatga gcagcagccc tagagccgag 3960

 cctacatctt ctagctcttg ggccacctgt tggcccagat gctgtagctc cagctgttac 4020
 tggctcctga gttcttggcc tctgctggc gccgctgagg ctacaaacac cagaactaga 4080
 agcagagagt ccagcggggg cagaatgctg acttggagaa gtagtctgtg gctgcagggc 4140
 accagatgtt ttacaggcgt gcggacaagc agcgggaagct gtggcagagc ttgtagctgc 4200
 ggaagaggct gtggaacccc tagaggcgat tggaagagac accctcctcg gaggaatagc 4260
 gtgatcgtgc acaagatcgt gctggtgttt ctgaagtccc tgtccagcta caactgcgag 4320
 agaaggatca gcggcatcca gaagagagcc atcgagtttg ccgtgctgaa actgctgaat 4380

 atggacctgc actggaactc cgcctacctg ggcagaactc tgctggtcac ctgtatcctg 4440
 tatcaccggt ggalcgtgac ctccatgtgc cagtctcaga gatggctgac cagcaccaca 4500
 agcagatcca gcgctctgat gtggacccgg cagatcaatc ggaggaagct gcagagaaag 4560
 aagaggcacc caagctggcc ttggaccaga tgccttagaa tgaggcctcc tagaagcggc 4620
 taccctacg atgtccctga ctatcgctcc taaaggcgcg cctagcggcc gc 4672

 <210> 1145
 <211> 4687
 <212> DNA
 <213> Artificial Sequence
 <220><223> Cloning cassette hTPA 3B
 <400> 1145
 gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggct ctgctgtgtg 60

 ctgctgtgtg gtggagcagt cttcgttttcg ccagccagg aaatccatgc ccgaggagct 120
 gctgtgcct ctgtcagtc tctccttct cctcgggaaa ccacacctag ctccgacgcc 180

accagacgga caagaccaat tgccgctcag agcaagaaaa ccatgacagc cgccggactg	240
acccctaaga acaagaagcg gagaaagctg cgGCCCaaga tgatccgga gatccagaag	300
agaagcgga ccGCCaaccg gcggaatagc agaagggcta cccctacaag caagggcagc	360
ctgagaagaa agtacctgag agtgcgggga cctcctctgc acacccgga catcagaaag	420
ctgatctgga ccaagcagcg gagcttctg tctctgttcc ccaagctgag agccaccgag	480
cagatgacca atgtgggctg ctctatccct cacgtgccca aagccacagc cgctcactct	540
gtgacagtga aactgcagct gcccctgacc ttcagcacc tgctgtggga tagcagacac	600
accatgagcc tgagcaacat cctgatgaag ttcggctgc agtctagccc attcctggcc	660
agatcctgga acacatgca gtggaacaac aagaaaatgg ccatgaccgt gatcgctggc	720
gcccaccact gtcagtacaa gctgacctac accaaagtgt ggaagatgaa ctggaagaaa	780
atgatgatcg gcagccagca tctgtgttc agccctctgg atagcagtcc cctgcagctc	840
ctgtgcacc ctcacggcaa gagatgcaac ccttgctgca gactgacctg gatgagccag	900
aacaccagaa gcaccaacct ggaaaagaac ccagccctga agaagcagag ccagcggaga	960
ggaaagctga gcgccttag cggcagaatc ctgcaccagc cagaaatggc cgccatgaga	1020
ctgatgccca agttcctgaa ctccaccaac agctgggtgga cctgaccac actgagcttc	1080
gtgtgatcg aggaagccag acagcccagc agacctaccg gcagaacacc taccaccaga	1140
ctgatggccc ctgtgggagc cgtgatgagc tgttctctgc tgaccagcc ttctccagcc	1200
agcgccctgta caatgcctcc actgtgcat ccacagtggg cccctcatag tgctggactt	1260
tctccaggcg cttgcagacc tgctgcacc tgtatcagca tgaccacat cagcagggcc	1320
acatggggcc cagtgtacta cgtgtgcaac cggatgaacg tgtccagcgt gctgaagccc	1380
ttcctgttca ccgtgcctat cgaggacatg agagagtga ccctgggcag aaacagaatg	1440
aatgtgtcct ctgtgtgaa accctgtctg atccctgtgc caatcagca gaagaagagg	1500
aagtgccca acatcgagat caccctcag cggcttaagg ccatgctgca gaagcagtgc	1560
tgctacaacc tcgtgatcaa gcacctctg atcttcagaa tcaacctgcg gcggcagggc	1620
aagaccaaag atggcgttgt gcagagcctg ggcttctca accagcagat catcctgcag	1680
aaagagttct tcatctgcct gctcatgttc atcaagcggg ggaagcctgc cgccaccaag	1740
agcagaaaga agggccacac caagaacaga cggaaggcca agagaaagcc ccagatctac	1800
ctgtttctcc tgaccgtgtg cggtttcac ctgaaaaaga ccagcgccaa gtggctgaag	1860
aagtccacca agtccagatc caacggcatg gaagcttgcg gcacacacc cactcctaga	1920
ctgagctgcc tgagagttag atcgggcggc tggctgtgtg gctggacacc tagaggtaga	1980
aagtcggcg tgatgaagtg ctgggatctg tgccccgtgc acaagaagag aggcctgttc	2040

agactggatt ttcaccccag aagcagctcc ggcaaggga agaacagccc ctgctgccaa	2100
aagaaactgc ggggtgcagaa ccaggggccat ctgctgatga ttctgctgca caatgaccgg	2160
gtgttcctcg tgaagatcgg cgagaagctg aagcactgtt tcaaggcctg gggctccaga	2220
cggaaaccggc ggtacagaaa gatctacggc gagctgaaga tgtccctgca ggccttcctg	2280
atccacctga gaaaggtgga caccaccac ctccaggtgg tcacaaaaac agtgaccgcc	2340
acaacagccg acggccagag aatgcggaga ctgaagtga aggcctgccg gctgagatgg	2400
gccagacctg aacctgtgc tcaggcccct cctaagagcc actttccacc tcctcctagc	2460
ggccccagca gaacaagtag cctgcagctg agaagcctgt tctttagcca ctgcctgtgc	2520
agccagaaga aggaccctgc cggcaagctg aaaaagctgc tgaagaaaag cagccagctg	2580
cggagaagct ggcgcaatgt gtccagaatc agcaccctc ctccactgat cctgtggcct	2640
caagctgctc ctgtgtccgt gatcccatg aagctgtggg agaagcactt caagggcctg	2700
aattggaacc tggtcgtgtg gattctgaac ctgaagatga tgacctacat ggaaatgcac	2760
tacggccatc agggcccaca ggtggcaatg ctgcctaagc tgctgtgcag acagatgctg	2820
cccactctga gcacactgca gcagagacat cctcagggcc cttgtcctcc tcctgtgaca	2880
cctctgagag tccagtctgt cctgtgtctg ggagtgcctc agacagccag aggacctaga	2940
agaaaggtcc tgatggtgct gtggctgccc gccaatcagt ctctgcagaa aagccaggtt	3000
ttccagtggg tgctgcggac agaggtggcc cctagatgtc ctatgctgc cgtggacatc	3060
agccccggac ctacatctcc tagcctggcc tcttgtgcct ctgtggccat tggaaagctg	3120
gcactgcttg gcgcctctgc tccttgtggt gctgctggcg cttagagagc cggaagattt	3180
gctgtgctgg gcacatggt catgaagctt tgtttcttct acctgctgta cggctgcgc	3240
atcccaagcc ttaggaagta cagacagcac ctgaaccgga agctgcacct gacaagatcc	3300
tgctgatcg atctgacat gatgatgtcc cagaagctct ggaagaacca gcggaagaga	3360
atccctctgc catctccag gcaacatctg ctgccacagt accctctgca cccacctcca	3420
ccttgtctgc tgttgtgca ccatagacac cacctggcct ttctcgagat ggctgtagc	3480
tctcagcaca cccacagcat caagatctgg atcagcttca gccatgaagt ggacctcca	3540
ggcagcgtgt ggatactgcc ttgcgatctg cctcgatgc tgccaatctc ttcaccctg	3600
cacagacccc agatgccttt ctggacctgc acctttcttg ccacaacctg gggcacatgg	3660
gagacacctt ctacatgggg ctggcggact ttcagaggcg cttagcagcag cacatccgg	3720
gacagcagat ctttcttcac ctctgtcac cctagcaggc cctgcagaat gagactgtac	3780

cagtgcaga agaagctcct cctgaaactg ctgaccacca ccacaagcag cccagaaga 3840

tcccctgctc tgagagcaag aggcggcacc acaatcggcg aagtgaccag ctgtaccaac 3900

ctgagcgtgc ccatgatgct gaccatcctg atttggaagc ggggtgtcat cctcctgctg 3960

agcgataaga agggcgccaa gaagatcacc ttctgccta ttctccaca cctgagacac 4020

cctctgctgc tgttcgagaa gaaacggcct gagtggctga gcatggacct ggacggaatg 4080

ctgacagtga tcggccaggg actcgtgggc atgacccta gagatctggg aacagtggca 4140

ggcgccaccg ctgagattca gcgacctatc caggtgcaga ctggcggcag actcagaaga 4200

aacctgcaga gaaacctgaa ggtgctccag gtgtccgtgt acagcggcaa cctgctgtcc 4260

tttagcagac ggggcatgaa gtctagcgtg cggctgaaaa accgcgagtg ggagaaacgg 4320

aagcagattc tcggaggcgg cggaagtac aaagagtact tcctgaagcg catcctcatc 4380

cggaaggcta tgacagtgtt ggccggcgac aagaaaggac tgggcagatt catgagatgc 4440

gtgcagagcg agacaaaggc cgtgtctctg caactgcctc tgggaagaaa catggaacac 4500

cggttgacca tggacagcgc cctgagcctg acaaagagag agggaccga gacactcaaa 4560

aagaaatacc tggtcagca ccagatgaag tgtctgaccg ccgtggattg tctgcaggt 4620

ttttgggaca tgggctaccc ctacgatgtc cctgactatg cgtcctaag gcgcgcctag 4680

cggccgc 4687

<210> 1146

<211> 4690

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 4B

<400> 1146

gaattcggat cccgcgactt cgccgcatg gatgcaatga agagagggt ctgctgtgtg 60

ctgctgtgt gtggagcagt ctctgtttcg ccagccagg aatccatgc ccgaatccag 120

aagaagaagc agaagtccaa cctggacctg cagcaccagc gcagacgcaa aaagaagaag 180

gacaaggtcg agatccggaa tcggagcccc aaggccaata gcacagagtg tcagggcgag 240

cacagcagag agcagaacct gctgaatctg gtgcagctga accctcacag ccctcaccac 300

agaaaggacg aagaggacca ccagaagcgg caccaccacc acaatcaaaa gaaaatgagc 360

gtgatggcca agaagtccca gcagcctctc ggacaggcct ttggctctct gtgtcagctg 420

gtgtccgccg atttcagcgc ccctcaagtg accagactgc ggagcctgaa ccatctgctg 480

atcaacgagg gcaacaacca ctggcctaga gtggaaatgc ctaccggttg gctgctcgtg 540

ggctacaaca ccagaaacac agcccagaat cctcggctgc agcagcacct gaaacactgg 600
 cagcagtgc cagagccag atggtgccaa gagccttgtc agaccctgac cttcttccat 660
 ttctttttct ttttcaaac ggtgtccctg tctgccccg gctggtctaa aggacaacct 720

 cctccacctg gcctgaagcc ttctagcctg gcttctcagg tggccagaac cacaggcgtg 780
 taccagcacg tgttgctgat ctgcttcgtg ttcttcgtgt gcgtggaaac cggtttctgt 840
 cacgtggccc aagtgggact cgagagactg gtgtctctga gcggcatcac cgacgtgaac 900
 cattgggccc agcctaagcc atctcctagc aaaggcaccg gcatgaacag acctatcggc 960
 ctgagagttg gcaaaggcgt gtgggccaga ctgagagcct ccgtgtcttt ctggaccctg 1020
 ctgcctacaa caggcgtgcg gacaagagga agccctctga gactgacact gtggcctcca 1080
 cggaacatcc tgaacagcct gcctagcagc atggaaatcg ccgtgctgca agagaaccgc 1140

 aagaccagaa aggccgccag agagaagcac agaaagaccg acaacctgca cctgtgctac 1200
 taccagacc agagcaaccg gaacaagagc cggcagatgg aaagcctggg catgaagctg 1260
 cagagccctc tgtgggattg ctccaccaca acaggcacac accacggctg tctgtgggag 1320
 atccctagcg ttacactgct ggcctgcaga gtgaacgccg tggaagaact gcacagcagg 1380
 cggatgtctg tgcggatcgt gaagaactgg gtgtcctgct gttacgtgcg cctgtctgct 1440
 gtgggcctgt ctacttgag cgccctggac gtggtcatca acctgaagcg gctgcagaag 1500
 ttcagccaga agtctcagca ccactgcgcc ctgagaaaga tcgagtgggc cacaagctg 1560

 agcctcggcg gaaaagctgg accccaggct caagagaagg ccaacgcaa gaagatgccc 1620
 ttccagcggg ggaatttcag caatcagctg accgtgcaga tgctgtgcct gcctattgaa 1680
 gccctgactg cctgtttcac ctgtcggaca gccagcatca gcgtgaacat cagcacctg 1740
 atgagcatcc tggaagcccc tctgtttttt cacggcgacc tgtgcgagga aaagaagaac 1800
 ggccggatca gcagccaggc tcctctcaga ctttggtctt ggtgcggcac aagccagacc 1860
 tactttggca gcaccgcaa gaaaagcccc accagctttt gctgcgagtg gggaggacag 1920
 gctcaccggc agagaaatc cggaatggaa atcctgtctg ggattctgct caagatggaa 1980

 attcagatct tcaagatttg cctggcgag atgcagctgt gcacctacac accccacatc 2040
 tgcagacaca cctgtagagg cggacctagc gccagcgata gatgctgtag ctgtagccct 2100
 agcggcttca gcgccggaag aggcagatgt ccagttcagg gatgtctgcg gcctcacaga 2160
 gtgcagctgc tgagaagatg gggccctgga tctcctgctg gccagagact gtctaagggc 2220
 tttcagctgc tccgttggtg gggaccagga tctccagctc ctgagcctag aaagggccca 2280
 ttccaccac ctgactctcc atggcctgtg accgtgtga cagtgatggc tggctctgtg 2340

cctagcgctc agtctgtgga tgctctggaa agccctggac ctctggcact ggaaggacct 2400

agcagcccca gaaacctgct ctggcgggaa atgagcatct tctgcctgg catcttcacc 2460

tctcggtatc tgaacctgca agtgcctgaag aagatcctgc ggagctttat gaagctgtac 2520

cactctctgg tcatgtgcct gcggctgcgg accaagctgg aaaaagctct gagcgctctg 2580

ttcatctggc cccagcacag ctacaagcag aggcctcctc tgcagcctgt gcaggtcgtg 2640

ctcagactgg gaaacctgcc tccattcttc agaggcagcg aggtgccctt tcctagacct 2700

tgccggacca agatgctgaa ccagaagtgt ctggccctt tcatcacaca cccattcgcc 2760

tctcagcccc tgggacaaga gatgcccaac aacaccaga tcagactgct gaagcccctg 2820

ctgaccctg acaccagatg gatcttctcc aaccagctgc agacagtcca gatgctctgt 2880

ctgccacctc tgaagcaggc cgagagaatc atttgcccc tcggcggctt tcagatcccc 2940

aacttctttt ggagcctcgg aatcggccac actggcgctt ggtggcatac tggaggcg 3000

agaagagaat gggcggtc caccgtgtct agaagccac tgtggatcag ctccatgac 3060

tacctgagag gcatggcctt cgccagcgac agtccatca gaaccaccag agtgtcctgg 3120

tgcagaagat gcggcgccaa atctgccgt gcctccagcc tcaagaagaa accccgggac 3180

atctgtcgga tcagcgactc taagaagatg acccagaagc gcgagagcac cctgggcaat 3240

ttctggatga agtctctcca gctgccagac aagaagaaga agtctaccga aaagaccaag 3300

atcatcaaga agatgaagaa acggatcatg gtccacatgt gcagctccct ggctctgcca 3360

acaggcctga catctctgat cctgccaagc agcgatctgg ccgtgctgat ctctagctcc 3420

accagccact ttctgatgcg gagccctagt ctgcctagct ccagactgac ttgtgcctct 3480

ccacagctgc ccagaatgtg gacctggtcc agctggctga agtggctgaa aaactggaag 3540

cggttcaagc ttaaaaagaa gtacatctg gccatgacgc tgacctgaa cgggcatcca 3600

agaaccgct ctatcacct gcctaccacc agcctgaagg gctctagaac cagctgttgc 3660

cccagatctc accccagact gcctaggaca aagtggcctc tgcagtgcct gctgcacagc 3720

ctgggaacaa ctggaacct cgtgtgggaa aggggcgtgc tgcagatgag aagtctggaa 3780

gtcactgcc ctctgcagac cttccacct caccactgta gaactcagcc cagctcttgc 3840

cctctgcat ggattctgta ccaaggacag tggagcggag ccgtcgtggg acttagacct 3900

gtggctcacc atctgccaag acctattcag ggctgcact gccacaggc tccacatcaa 3960

ccagctctgt ctiggggcaa gtggccctg ggaatgacag gacctgccag atgttgccgg 4020

tggcctagac gggaactcaa aaagaatctg ctgctccct gccggtgcag acgcgagtat 4080

agagtgacaa tgggccaagc cttcggcagc tttagcgccg actttagcgc tccccaggtg 4140
 ttgaagaaga atcggaagca gaacaagatt atctgcaagg gccaccgcat cacaagcctg 4200
 atcctgagct ttcagcgctt gaaacttaag aagaaagtca acgcctgctc tcccgcctgc 4260
 acctctaaag cciggactcc cagaaagctc gtggggagag ccgtcagaag aaagggcac 4320
 atctgtatca agaatatgtt cctgcagcgg aagggtttcc tgaacctgag ccacgtggaa 4380
 aagttcgtgc ctctttctcc tctctggct ctcggcccta gaatgcagct ctgtaccag 4440
 ctggccccgt tcttcctat cacacctct gtgtggcaca tctgggacc tcagaggcac 4500

 acccctgtgc aaaagaaggt gccctccgct agcccatggg gccttagacc atctccttgc 4560
 ctgagctggt cctccagaat tgtggccct ggacacgccc tgagctgtcg gactagaaga 4620
 agatggtcca gcaaggcta cccctacgat gtccctgact atgcgtccta aaggcgcgcc 4680
 tagcgccgc 4690

 <210> 1147
 <211> 5299
 <212> DNA
 <213> Artificial Sequence
 <220><223> Cloning cassette hINV 1A
 <400> 1147

 gaattcggat cccgcgactt cgccccaatg catcgacggc gtcacggag ttgccgggaa 60
 gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120

 atgcttggtg ggcggcctgg agcaccagag tccaagtgtt ctaggggagc cctgtacact 180
 ggtttctcca tctcgtgac actgttctg gcgggacagg caacaactgc gtatttcttg 240
 tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300
 aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360
 ccgtcctta tgcaagcctt tcccatgggg gctctgcccc aaggccaat gcagaacgt 420
 acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
 cttaaagttt accctctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540

 acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gtcctgttc 600
 gagatgtccc ggcatctct ggagcaaaag ccgacggacg cacctccca ggaagcctg 660
 gaattggagg acccgagtag tgggtgggc gtcacaaagc aagacctggg acccgtgccg 720
 atgaccgaga tccagtgac catgaacgac agcaagcaca agctggaaag ccccgctctg 780
 aaacaggtgt caccagctc tccactact cagcagctc agacacctca ggattctaga 840
 caggtgctgg ccctggccaa gaaaacctg acaaatgcct ccagagccgg acagtttct 900

gtgtggcgga gaacaagcag aggcattgagc ctgcagtgga agtccggcaa tgcctgcaca 960

cctctgagat gccctagcag aagccctgcc acattcctga cagccctgaa tggctggcac 1020

agatctggcc tgagagccca gatgcctagc tcttgggtcta gcagcggcag aacactgaag 1080

ctggcccctc tgcaagtgc caccactctg aagctgatcc tggatcatgct ggaaatcgtg 1140

accgagcgct ccttctgtga ctccagaatg tgtctgggtgc agatccccac acacacctgg 1200

gagcccgatt acttctgtgc cctgcctatg atgttcagct gggccacaca gtcttttccc 1260

gtgggcgcgcg tgtttctgac cagacctgcc attccttctg gcagctgtac cagccacagc 1320

aacccttggg gccagagcaa tcagcagctg aagtggaccc ctacatcct gaagtccgcc 1380

agcttcgaca agaaaggctt cgtgatccctg agccggcgga gcaagattga ggcctctcct 1440

atcggtctta tcgccagctc tcttggacat cctctgggac ctacactggc catcagattc 1500

atcagcgccc ctacgctag cagctctaca gtgacagctg ccctagcgg ccagtacttt 1560

atcgccaaga agcggatcaa gctgcggcgg aacaatatgg gcggcaacag atccatctgc 1620

ctgaccagaa agcgcaagag agagaagcgg agccagaagt ccaggcagaa ccatctgcag 1680

ctgaaaaagt gcagacggaa gatcagcaac tggccaagc tgagaagccc ctggatcttc 1740

accaagtgcg agatctgcgt gaagaacacc gccatcctgg ctatcacct gatcacccct 1800

caggaccctc atctggaccc tgtgtgtcac cctcatagaa ggcctggatg gaaggccac 1860

catagagtgg tgttctctca ccatcctagc ggagcagcaa agagccactg gcagcaaaga 1920

gaacgcggag gcggcagacg cgagaagaag ggatgtagag aacagcggaa ggttgtcaag 1980

aaccctctc agcccgctgc tctgagaaac gatggcatca ccaacggcaa cgactccacc 2040

agaagctgct ccatcagcct gaagaaaagc ctggaaaaga tgcccctgat gcggagagcc 2100

agacctacca gctgtagcac ctgtagaatg tgggtggaagg gcaagaaacg gcggaaagaa 2160

atcgtgccta tgagcctggc ctgcagcatc accgtgtctt ttgtgggaca gatcagcacc 2220

ctggtgctgg atgtgtctag catcagccat tggcggtgc cctglaaagt gaccgagagc 2280

agctccagct tcttctacac cagcgacagg accctctga gcatcagcag accaaccagc 2340

agagctagac agagctgttg tctgcccggg ctgacacacc ctgctacca acctctgggc 2400

agcatgagca ctagaagaga gatccaagc caggccacac cttctccacc tggaccttgg 2460

agagccgctc tgggcaaaga agtgaagaga tcccagagca agctgcgcct gagaaacaca 2520

agccctgggg agaagaacga tctccagctg ttcgtgatga gcgacaccac ctacaagatc 2580

tactggacag tgatcctgct gaaccctgc ggcaacctgc acctgaaaac aacatcactg 2640

cagcggccac ctcgagcat cctgtctctg aatggaatct gggaagtgat gccccggaca 2700
 ctggaaggct gcatcagcgt gaaggatcac agaaccagcc agaaccacag caagtgcac 2760
 accgaatgtg tgcggactgc cctgaacgtg tccaagaaga gactgcctaa gctgatgaag 2820
 aagaaggaca gcaccatctt catcaacaaa gtgcgccaga acttcaagcg caacttcaag 2880
 aagaagaaac ccttcacttt cagccccagc agacggatga ctcgagaaac catgacaacc 2940
 accaaaatga tgatgatgcg gcggaccaag cggagaaggc gcaaaaggcg gagaatgacc 3000
 atgatgacca gacggaccct gctgacaaaag aaaacctgtc tgacccttag aaccagcgcc 3060

 gccacaaaag ctctgcctag acagaccatc agccagcggg ggcctattca gacccacct 3120
 ggaacatctc tggccatctg gggcagaaca agactgaccc tgacaggcac cagatccagc 3180
 ggaacaagag cctctccttc cgccgtgtgc ctgtgttgtt ggacctgtcc aagcagaagc 3240
 tccccagccg ctctccttag tggactgaga gcacctgttg gagcccagcg tcctcctgaa 3300
 gtgacactga gagcctcttg tgcctctagc gcctctaaag cctgtgtctg actttggcct 3360
 tggggagccc aagttcaggt tggagctgga acaggcggag gacctgcttg tgttcctgtg 3420
 gctgaagctt ctacaggcgc atggacagct gaaggcggcg ctggaacaag atgtagagcc 3480

 tctagagccc ctigccgcca acttcctgct agctccccta ccaagtgtga aatttgtgtg 3540
 aagcgcagac ggccggagaaa gagaagcagc cagtctagaa gccccgtgcc taaaaagcgc 3600
 gagaggatga tgctgcctgt gcgggccaga acagctagat ctgcacttcc tcagggcaga 3660
 gcacctctgg aagggatgct gcttcctaga gcactgccta gcctgctgag cagaatgcct 3720
 gccagaagag agtcccgggt ttggctggct ctgcaggcac ttggactcag acctccacat 3780
 ctgcctagct gtcatcctct gcctcaactg ttgggcccct cacctcctca tcaggcccca 3840
 atgacactga aggccctggt taagacctgg acacagtcc gcaactacc cagagccgac 3900

 aagaagaatg tccggtctac cgcttcttc ctgctggaca tcatcctggg cgattgccc 3960
 agaacaatgg ccggaccttc tgctctctg catcctgcat ctggcagagc ctccagaaag 4020
 acctggcaga gaaggctgag agcttgtaga gcaggcggac ctgctggatg ggctagacag 4080
 gcctatccta gactgaaaac cttcggcgtg cccctgggct ctattctgtg tetggccggc 4140
 agcctgtcca caatgatgat cattagcacc accagacaag agtgcggcag gcgggcttct 4200
 gtgccttgta gacctatgat cggaagcgcc agaccaggac cttggcggac atctgctatg 4260
 cctagtgcc 4320
 accggcggaa gaatgccagg atctcagtct atcatgatga gctggatgcc tccactggct 4380
 ccatgtgccg cttgtccatg ttctcccgt cctacactgt gccagcaca tctgctaga 4440
 gcaccaacag ccgtgcctgc ctttacacct ctgtctgtc atcctgtgcc agtgtgtct 4500

ggatgtcacc tggccgtcag aacctccatg ctgacactgc tgcccatgga agccaaaaag 4560
 agcatgaagc ggtccaacgc taagaaaatg gaagatatga tctgggagag cgggtgccca 4620
 ctgaggccac aaagaggacc tagacctctg cacagatggc tgcagcagac aaccggctgt 4680
 agccagaggc ggatcgtgtt ctttctggcc ccatacttcc ctcggcaccc tcacagatct 4740

 ccaccaacat cttgccacc tctgttgaa gctttccac tgccaagagc ttctctgagg 4800
 gccacagtgc caagacatag ctctgttctc gccaccggc tgcacctca cagacagatt 4860
 tctctgcccc tgagaggatt cctcctgcac caaccactgc caggacagca tctgtggctg 4920
 tctcacagac tgaggctgag actgcccagg acacagccat ctttgctgg accatgtgca 4980
 agcctgctgt ccacactgtc tcagccacca cctcaggctc catctcaagt gtggactgcc 5040
 gctacactga gatgtcctgc tgttctgca gctgcctgtc ctctgtctct gagatccatg 5100
 cctaagagcc ggaaccaggt gctgttcaga cggaatctga cccaagcca gctgagaaca 5160

 ctggccccac cttatatgct gctgccccag tctctgtccc agagcctgag tagaaagcag 5220
 atccctagcc agtccatgct cgtgggctac ccctacgatg tccctgacta tgcgtcctaa 5280
 aggcgcgcct agcggccgc 5299

 <210> 1148
 <211> 5281
 <212> DNA
 <213> Artificial Sequence
 <220><223> Cloning cassette hINV 2A
 <400> 1148

 gaattcggat cccgcgactt cgccgcatg catcgacggc gtcacggag ttgccgggaa 60
 gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
 atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180

 ggttttctca tctcgtgac actgttctg gcgggacagg caacaactgc gtatttcttg 240
 tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300
 aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360
 ccgtctctta tgcaagccct tccatgggg gctctgcccc aaggccaat gcagaacgt 420
 acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
 cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
 acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600

 gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctccaa ggaaagcctg 660

gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720
 atgagaaaga tgcagagcct gaatcacccc agcagactga ccaatggctc tcctccactg 780
 cacctgtgcc agcctctgag aatgagcaga acccctccta gaagagtgtg cgccgctcct 840
 ccacatagac tgctgggccc ttccagatgg aaccctcgga gaaagacctg gaagatgcgg 900
 aagaagtacg cccagaagcc tagccagaag aaccacctgt acggcggcaa gaagcgtctt 960
 aagttcagca gaagccacct ggacttcagc ccctactgga tgaagaaagt gaaggtgctg 1020

 ttcaaggccg accagagcga gtctagcctg agcagcggaa gatgcagcct gatggaacag 1080
 atccctcacc tgaagtctcg gcggaagtgg cagatcagac acgtgctgaa gaacctgtgg 1140
 ctgccatga gaagcctggg agaaccttgg agagccggct ttcagtgggg agagtctcct 1200
 tggcaagtga tggcctctct gaccggcaga gccacatttc tgctggccct ttgggaatgt 1260
 agcctgcctc agcgaagact gtgcctgata gtgtctagaa ccctgctgct ggtgcagagc 1320
 cggaacaaga aaacaaagct gtggttcagc ctgatcaaca tccaccaccg gaagaaccca 1380
 ctgctgccta tgagatgggt gtgtaccaga ggcggcggaa agcggaaaaa gaaaatgtgc 1440

 aaggtgtccg gcggctgcac cgcctgtgtt gagagatgtc cttggaaggg catctgctgg 1500
 aagtggcctg tgacagtggc cgccattaga atgtgtgccc tgtctcacc tagcttctac 1560
 atcagcagca ccgtgtgctt tctgagcaag cactgcatga ccgctgcac cagaaagaga 1620
 atgaagaccg gcgccatcca agagaagggc gctattcaag agaaaggggc catgaccaag 1680
 cggatctgcg tggtaattt cgaggcctgc agagagatgg aaagcctgag cggccctgag 1740
 aagatcacc tgittgaagc ccacatggcc cgggtgcacct ccatcaatgt gctgtgtgtg 1800
 cgggccagcc tgattgagaa gctgatgaaa gaaaagcgca agatgaagcg gaaccaggtg 1860

 gcctctccac agatcatgca gcggtgtt atcaagggt accagaacaa ccacttcacc 1920
 ttccatctgc aaaacttcgc cttcttcagc tccttcggca acaacaagta catcaatata 1980
 ctgaccatcc tgttccacgt gcggaacatc gtgtacggca tccaagtat gctgtgctgt 2040
 agccctcaga ttatgcagag aaccagcgcc gaccggttcc ggatgaagag aagaatgcag 2100
 aatctggaca acctgggcgt gccatggcct ctgttgctg gaatcccatc tetgaacgcc 2160
 cagtggatgt tcctgagaat cgcatccccg caaatcatgc agaggatgag cgccgtgaac 2220
 ttcgagacaa tccgggccag aaaccggaac atgaagaaaa ccatgagcca cctgatcgcc 2280

 catcaggccc tgaagatgag cggcctgaga ctgtttcacc ccagactgct gacacggaag 2340
 aagcccgga aactgtgtct cgcccatatg tacggcttca gcacctacgg caccagaaa 2400
 ggcgagtgcg tttgtctgca gtgtctgagc ggacgagcc tgttcattct gaagcagccc 2460
 ctggacctga agatcagcaa gaccttcata ggccacagag agggcagcga gtctgataat 2520

ctgggcctgc tgiatagctt cctccacct tatcctatca gcgagggcct gaccatgacc 2580
accgcgagaa acatcaacag caactccctg atgaccaact gcctgttcag ccccatcttc 2640
ctgtgccacc acgccatcat gcacagaaag atgacaagcc ctcaattcag gctgttcagc 2700

agcaagatcc cacatcctca ggtgccatct gtggtggccc tgtgcaagtt ccgggccttc 2760
atccacacac ctagaagccc tggctgcagc gtgtacgcca atatgtgctg gcccagttc 2820
ttcctgacct tcagccagca gtggtccagc gtgacatctc tggaatggac agcccaagag 2880
agaggctgca gcagctggct gatgaagcag acatggatga agtcttgag cctgcgggac 2940
cccagctaca gatccatcct ggaatacgtg tccaccagag tgctgtggat gcctacctct 3000
accgtgctgc aggtcatcc acaagtcca gctctggctc ctcaagcctg gtggcctgct 3060
agaagaggac ctctgacatc tgcccatcc gctcagcagt ccctgaccag agagaagatt 3120

atcaacccca ccatcagctg cccctttcag agccccacca agagactgat ctacctcct 3180
agcacctgtt ctctgccctg cagaggcttc ctgcctagca gatttccttg gggccacct 3240
cctctgaaca gcgtgatcgt gcacaagatc gtgctggtgt tcctgaagtc cctgtccagc 3300
tacaactgcg agcggagaaat cagcggcatc cagaagagag ccatcgagtt cgccgtgctg 3360
aaactgctga atatggacct gcctctcgag aacacacaga tccccagAAC aagccactg 3420
tggaagatca caatggtgct gacatacccc aactgcgtgg tgcatgtgct gatgtttggc 3480
gccctgagag ccacagctcc tgctacagct gcacctcagg ctcaagcccc tcattggaga 3540

gctgccacaa caagcagcat gagcagcagc cctagagccg agcctacatc ttctagctct 3600
tgggccacct gttggcccag atgctgctcc agctcttggt actggcact gtctagctgg 3660
cctccagctg gcgccgctga agctacaaat accagaacca gaagccgcga gagccagagg 3720
ggtagaatgc tgacttgag aagctccctg tggttgcagg gcaccagatg ttttacaggc 3780
gtgcggacca gctccagata caagaaaaga ggcgtgatcg cctggcggag acagatcaat 3840
agacggaagc tgacagagaa gaagcactgg aacagcgctt acctgggcag aacactgctg 3900
gtcacctgta tctgtatca ccggtggatc gtgacctcca tgtgtcagtc ccagagatgg 3960

ctgaccagca ccacaagtag atctagcgcc ctgatgtgga ccgagctgag cctggaacca 4020
tggaattcct acctgcatca gcagaaaacc cagcggacac tggaatccgc cggactgttt 4080
ccttggtgctg acaccagtg ccaagagaag aaaagcagaa agctgatgtc cagctgcaca 4140
caccctgca caatgctgct gccacaggga tgcatcctg cctggctgag ccctatctct 4200
gcctgtccaa gactgctgcc atatcctttt cacgtgctgg ctctggaagt gaccttcct 4260
cctggaaccg ccatgcctca gatgcagttg caggctctgg ctatgtggga gaaagctgg 4320

gataagcctg gcaccagcct gcagtgtac ctgaacagaa gaagaaacag ccggaagcag 4380

agccagggtgc aactggccat tcaggtgctg ctctgtggaca agcacaagta ctttctgttc 4440

ggccaaaaga aaggccacat gatcttttagc ctggccaacg gcctgtggtt taacctgatt 4500

ttcaactccc ggaagaaact gctcgaggac atgaagcaaa atggcttcac cggcaaaggc 4560

ctgacacacc ccgtgcctct gaagcggact ctgcagaaca aaagaaacaa gaatatcaaa 4620

cgcgtcaacc agaagaaggg caacatcaag cggaagtcca tcttctgtca cctgattgtg 4680

ctgaatatgcc ccgagagcaa cctgatcctg atccagcatg gcggcatctt cacctttcgg 4740

ttctgggtcg agaagctgtc ctggaacatc tgcaagaacc tgagcctgta cctggacaag 4800

ttctgtcaga gactgtctga cgtgtacatc atcgagacaa acgtgttcgt gctgaacctg 4860

tttcatgtgc ccgtgaacca gatcttcatg atggccttct acctgaagta caccgagaag 4920

gcctgggtca tggaactgga atggctgac caacagcagt gctatcaggg cagctgcggc 4980

agagcttggt cttgtggaag aggctgtggc acccctagag gcgattggaa gagacatcct 5040

cctcggagag ctttctggaa gcctcctagc cagggcacat ctagctgtct gatgaccggc 5100

tggttggtcg agaagaaagc tacctggatg cggcggaccc gccggaagaa gagggaagat 5160

cattgcggac tgagacaccc cagctggcct tggacaagat gtctgaggat gaggcctcca 5220

agaagcggct acccctacga tgctcctgac tatgcgtcct aaaggcgcgc ctagcggccg 5280

c 5281

<210> 1149

<211> 5296

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 3A

<400> 1149

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60

gacccaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttcg 120

atgcttggta ggccgcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180

ggtttctcca tctctgtgac actgttctg gcgggacagg caacaactgc gtatttcttg 240

tatcagcagc aaggaagact ggataagctt acagttacat ccagaatct ccaacttgaa 300

aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaaatgag gatggcgaca 360

ccgtcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt 420

acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480

cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
 acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600
 gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctcccaa ggaaagcctg 660

 gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720
 atgggagctg ctgctgcctc ttgtcagtct cctccttctc ctcgggaaac cacacctagc 780
 tccgacgcca ccagacggac aagacctatt gccgctcaga gcaagaaaac catgacagcc 840
 gccggactga cccctatgat ccggaagatc cagaagcggc ggagaaccgc caaccggtgt 900
 ctgagagtta gatgtggcgg ctggctgtgt ggctggacac ctaggagaca gaacaccaga 960
 agcaccaacc tggaaaagaa ccccgacctg aagaagcaga gccagcggag aggaaagctg 1020
 agcagcctgt tcttcagcca ctgcctgtgc cggaacagca gaaggccac acctacatct 1080

 aagggcagcc tgcggcgga gtaacctgaga gtgcctattc ctcacacct gagacacct 1140
 ctgctgctga tggacctgga cggaatgctg accgtgatcg gacagggact cgtgggcatg 1200
 acccctagag atctgggaac agtggctggc gccaccgctc agattcagag gcctattcag 1260
 gtgcagaccg gcggcagact tacacctct cctctgattc tgtggcctca ggccgctcct 1320
 gttgatcctc ctggctctgt gtggattctg cctgcaaga acaagaagcg gagaaagctg 1380
 cggccaagc ggcctgactt tcacctaga tcttctagcg gcgtgtccgt gatcaccatg 1440
 aagctgtggg agaagcactt caaggcctg aactggaacc tggctgctg gattctgaac 1500

 ctgaagatga tgaacatga gatcacccct cagcggagca agccagaaa gtccggcgtg 1560
 atgaagtgtt gggatctgtg ccccgagcag aagaagagga agctgcctct gcctctgacc 1620
 ttcagcacc tgcgtgtgga ctctagacat agaggcgcca gctccagcac cagcagagac 1680
 tccagaagct ttttcaccag cgctcacccc agcagacct gcagaatgag actgtaccag 1740
 ttctgatcc acctgagaaa ggtggacacc caccatctgc aggtcgtgac caagaccgtg 1800
 acagccaaa cagctgacgg ccagagaatg cggagactga agtgcaaggc ctgccggctg 1860
 agatgggcta gacctgaacc tctgctcag gccctccaa agagccactt tccacctcat 1920

 cctagcggcc ctacgagaac cagtctctg cagctgcgga gcatccctca cgtgccaaaa 1980
 gccacagccg ctacagcgt gacagtgaag ctgcagaagg gaaagaacag cccctgctgc 2040
 caaaagaaa tgcgggtgca gaatcaggc catctgtga tgatcctgct gcacaatacc 2100
 tacatggaaa tgcactacgg ccatcaggcc ccacaggtgg ccatgctgcc taagctgctg 2160
 tgcagacaga tctgcccac tctgagcaca ctgcagcaa gacaccaca gggcccttgt 2220
 cctccacctg tgacaccact gagagtccag tctgtctgc tgcctggagt gcctcagaca 2280

gctgctagac agcctagcag acccaccggc agaacccta ccacaagact gatggcccct	2340
gtcggcagcg tgatgagctg ttctctgctg acccagcctt ctccagccag cgectgtaca	2400
atgcctccac tgcctgcatc tcagtgggcc ccacattctg ctggattgtc tcccggcgct	2460
tgcagacctg ccgtacctg tatcagcatg accaccatct ccagagccac ctggcaggtt	2520
tccgtgtaca ggggcaatct gctgagcttc tccagacggg gcatgaagag tagcgtgcgg	2580
ctgaaaaaca gccggcgga cagacggtag agaaagatct acggcgagct gaagatgtcc	2640
ctgcaggccg tggctcctag atgtcctaga tctgccgtgg acatcagccc cggacctacc	2700
tctcctagcc tggcctcttg tgccctctgt gccattggaa aactggccct gcttggcgct	2760
tctgcccctt gtggtgctgc tggcgctaga gaggtggaa gatttgccgt gctgggcacc	2820
atggtcatga agcacctgaa ccgcaagctg catctgacct ggtcctgcct gatcgatctg	2880
accatgatga tgagccagaa gctctggaag aaccagcgga agagaatccc tctgccatct	2940
cctagacagc atctgtcccc tcagtaacct ctgcacctc ctccaccttg tctgtgctg	3000
ctccaccaca gacaccacct ggccctttctg gaaatggcct gcagcagcca gcacaccac	3060
tccatcaaga tctggatcag ctttagccac gagcagagca gccattcct ggccagatec	3120
tggaacacca tgcatggaa caacaagaaa atggccatga cagtgatcgc tggcgccac	3180
cactgtcagt acaagctgac ctacacaaa gtgtggaaga tgaattgga gaaaatgatg	3240
atcggtcccc agcacctcct gttcagccct ctggatagct ctccactgca actgctgctt	3300
cacctcacg gcaagagatg caaccttgc tgcagactga catggatgtc catgctgcag	3360
aaacagtgt gctacaacct cgtgatcaag caccactga tcttcagaat caacctgcgg	3420
agacagggca agaccaagga tggcgttgtg cagagcctgg gcttcctgaa ccagcagatc	3480
atcctgcaga aagagtctct catctgcctg ctcatgttta tcaagcgtg gaagcctgcc	3540
gccaccaaga gagagtggga gaaacgcaag cagatcctcg gcggaggcgg caagtacaaa	3600
gagtacttcc tgaagcgcat cctgattcgg aaggccatga ctgtgctggc cggcgacaag	3660
aaaggcctgg gcagattcat gagatgcgtg cagagcgaga caaaggccgt tagcctgcag	3720
ctccactcg gaagaggccc tgtgtactac gtgtgcaacc ggatgaacgt gtccagcgtg	3780
ctgaagccct tctgtttcac cgtgcctatc gaggacatga gagagtgcac actgggccgc	3840
aacagaatga atgtgtcctc tgtgtgaaa cctgtctga tccctgtgcc aatcgacctg	3900
cctcgatgc tgccaatcag cagccactg cacagacccc agatgccatt ctggacctgc	3960
acctttcctg ccacaacatg gggcacctgg gagacacctt ctacatgggg ctggcggacc	4020

tttcggggcc ctagaagaaa agtgctgatg gtgctgtggc tgcccgcctg	4080
cagaaaaacc aagtgttcca gtgggtcctg cggaccgaga acatccggaa gctgatctgg	4140
accaagcagc ggagcttctt gtctctgttc cccaagctga gagccaccga acagatgacc	4200
aatgtgggct ggccttcag cggccggatt ctgcatcaac ctgaaatggc cgccatgcgg	4260
ctgatccca agttcctgaa tagcaccaac agctgggtga cctgtacaa cctgagcgtg	4320
cccatgatgc tgaccattct gatttgaag cgggtgttca ttctcctgct gtccgacaag	4380
aagctgctga agaagtctag ccagctgagg cggctcttga gaaacgtgtc ccggtcagc	4440
caccagatga agtgtctgac cgccgtggac tgtctgcagg cttcttggga catgaacatg	4500
gaacaccggc tgaccatgga cagcgccctg agcctgacaa agagagaggg acccgagact	4560
tgcaagaaga agctcctgct gaaactgctg acaatgagcc tgagcaacat cctgatgaag	4620
ttccggctgc ggctgagaat cccaagcctg aggaagtatc gccagcatct gaaaaagacc	4680
agcgccaagg gcgagaagct gaagcactgc ttttaaggctt ggggcagagg cccacctctg	4740
cacacaagaa gccagaagaa agaccctgcc ggcaagctga aaaaactgac cactgagc	4800
ttcgtgctga tcgaggaacg gcggaacctg cagcggaatc tgaaagtcct gtggctcaag	4860
aaaagcacca agagccggtg tctgttcttc ctgaccgtgt gcggcttctt cgagaagaaa	4920
cggcctgagt ggtgtctctc cagaaagaag ggacacacaa agaatcggag gaaggccaag	4980
cggaagcccc agatcgtgca caagaagaga ggctgttcc tcaaaaagaa atacctggtg	5040
cagggcgcca agaagatcac cttctgttcc aacggcatgg aagcttgcgg cacacacccc	5100
acaccaagac tgagcgacag agtgttctg gtcaagatca ccaccaccac aagcagcccc	5160
agaagaagcc cagcactgag agctagaggc ggaccacaa ttggcgaagt gaccagcctg	5220
tgcttcttct acctgctgta cggtacccc tacgatgtcc ctgactatgc gtctaaagg	5280
cgcgctagc ggccgc	5296
<210> 1150	
<211> 5299	
<212> DNA	
<213> Artificial Sequence	
<220><223> Cloning cassette hINV 4A	
<400> 1150	
gaattcggat ccgcgactt cgccgcatg catcgacggc gctcacggag ttgccgggaa	60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg	120
atgcttggtg ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact	180
ggtttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg	240

tatcagcagc aaggaagact ggataagcitt acagttacat cccagaatct ccaacttgaa 300

aacctcagaa tgaagcttcc gaagcccca aagcccgctc ccaaatgag gatggcgaca 360

ccgtcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt 420

acaaagtatg gaaatatgac agaggatcat gtcattgatt tgcttcaaaa cgctgatccc 480

cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540

acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600

gagatgtccc ggcatctctt ggagcaaaag ccgacggacg cacctccaa ggaaagcctg 660

gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720

atgatccaga agaagaaaca gaaatccatg gccaaagaat cccagcagcc tctgggtctg 780

aagaagaacc ggaagcaaga gtggggagga caggcccaca gacagagaaa caacccaag 840

aagatgccct tccaagagga aaagaagaac ggccggatca gcagcagcct gatcctgagc 900

ttccagagag tgaaggacag caagaaaatg acccagaaga tgtgcagctc tctggccctg 960

cctacaggcc tgacatctct gatcctgcct agcagcgatc tggccgtgct gatctctagc 1020

agcaccagcc actttctgat gcggagccct gtgctgcaa gctccagact gacatgtgcc 1080

tctccacagc tgccccggat gtggacatgg tctagctggc tgaagcacc cagaaccgt 1140

agcatcacac tgcctaccac aagcctgaag ggagcagaa ccagctgctg cccaagatct 1200

cacccagac tgcctaggac caagtggcct ctgcagtgc tgctgcacag cctgggaaca 1260

acaggcacac tcgtttggga aagggcgctg ctgcagatga gaagcctga agccattgt 1320

cctctgcaga ctttccatct gcaccactgc agaaccagc caagctcttg tctcctgcc 1380

tggattctgt accaaggcca gtggagcgga gccgtcgttg gacttagacc cgtggctcac 1440

catctgccta gacctatcca gggcctgcac tgcctcagg ctctcatca acctgctctg 1500

agctggggaa agtggcccggt gggaatgaca ggacctgcca gatgctgtcg gtggccccgc 1560

agatctcaga agtctcagca tcactgcgcc ctgcggaaga tcgagtgggc caaaaactg 1620

tctctcgcg gaaaagccgg accacaggct caagagaagg ccagacctc tccttgccctg 1680

tcctggctca gcagaattgt ggccctgga cagccctga gctgtcggac tcgtagaaga 1740

tggctctcca agtgcagagg cggccctagc gccagcgata gatgtttag ctgtagcccc 1800

agcggcttca gcgccggaag aggcagatgt cctgtgcagg gatgtctgag gccacacaga 1860

gttcagctgc tgagaagatg gggcccagga tctcctgctg gccagagact gtctaagggc 1920

ttccaactgc tgcgttggtg gggacctgga tctccagctc ctgagcctag aaaggccca 1980

tttctccac ctgactctcc atggcctgtg accgctgtga cagtgatggc tggctctgtg	2040
cctagcgac agtctgtgga tgccctggaa tctcctggac ctctggctct ggaaggccct	2100
agcagcccta gaaacctgct gtggcgggaa atgagcatct ttctgcccgg catcttctgc	2160
caaaagaagg tgccatctgc cagccctgg ggacttggtc ctcttctcc accactcgct	2220
ctgggccta gaatgcagct gtgtaccag ctgccagat tcttcccat cacactcca	2280
gtgtggcaca tctgggacc tcagagacac acacctcagg tggctctgag actgggcaac	2340
ctgcctccat tctcagagg cagcgagggt ccctttccta gacctgccc gaccaagaac	2400
gagggaaca atcactggcc cagagtggaa atgcctaccg gctggctgct cgtgggctac	2460
aacaccagaa acacagccca gaatcctcgg ctgcagcagc atctgaaaca ctggcagcag	2520
tgcacacggg ccagatgggt tcaagagcct tgcagacc tgaccttctt ccacttcttc	2580
ttctttttca aaacggtgct cctgtgtgtt ccggctgggt ccaaaggaca acctccacct	2640
cctggcctga agccttctag cctggcttct cagggtggcca gaaccacagg cgtgtaccag	2700
cacgtgtggc tgatctgctt cgtgttcttc gtgtgcgtgg aaaccggctt ctgtcacgtg	2760
gcacaagtgg gcctcgagag actggtttct ctgagcggca tcaccgacgt gaaccattgg	2820
gcccagccta agccatctcc tagcaaaggc accggcatga acagacccat cggcctgaga	2880
gttggcaaag gcgtgtgggc cagactgtct aagaagaagc ctagagacat ctgtcggatc	2940
tccaacagaa agaccgggaa ggccgccaga gagaagcacc gcaaacaga tagagccagc	3000
gtgtccttct ggactctgct gcctacaaca ggctgtcgga caagaggaag ccctctgaga	3060
ctgactctgt ggcctcctag atgcagatgc agacgcgagt acagagtgc catgaacatc	3120
ctgaacagcc tgccaagcag catggaaatc gccgtgctgc aagaaaccgc caagaaaagc	3180
cctaccagct tctgctgcaa cctggacctg cagcatcagc gcagacgcaa aaagaagaaa	3240
gacaaggctg agatccggaa tcggagcccc aaggccaata gcacagagtg tcagggcgag	3300
cacagcagag agcagaatct gctgaatctg gtgcagctga atcctcacag ccctcaccac	3360
cggaggagc aagaggacca ccagaagaga caccaccacc acaatcaaaa gaagatgagc	3420
gtcccactgt tttccacgg cgacctgtgt agagagagca ccctgggcaa tttctggatg	3480
aagctgtcc agctgcctca gaggcctcca ctgcaaccag tgaccggaat ggaaatcctg	3540
ctttggattc tgctgaagat ggaaattcag atcttcaaga ttgcctggg cgagatgcag	3600
ctctgcacct ctcgattct gaacctgcaa gtgctgaaaa agatcctgcg gagctttatg	3660
aagctgtacc acagcctcgt gatgtgcctg cgctgagga ccaagctgga aaaggtctg	3720
agcgccctgt tcatctggcc tcagcactcc tacaagatca cacaccatt cgccagccag	3780
ccactgggac aagagatgcc caacaacacc cagatccggc tgctgaagcc cgacaagaag	3840

aagaaaagca ccgaaaagac caaaggccag gctttcggca gcttctccgc cgatttttca 3900
 gcccctcaag gacaggcttt tggctccctg tgtcagctgg tgtccgccga ctttagcgcc 3960
 ccacaagtga ccagactgcg gagcctgaac catctgctga tttggctgaa gaattggaag 4020
 cggttcaagc tcaaaaagaa atatcaggcc cctctgcggc tgtggtcttg gtgcggaaca 4080

agccagacct acttcggcag catcatctgt atcaagaata tgttcctgca gcggaagggt 4140
 ttctgaacc tgagccacgt ggaaaagtgc gagcttaaga agaattttct gctccccgtc 4200
 glgatcaacc tgaagagact gcagaaattc atgctgaacc agaagtgcct ggctccattt 4260
 cctgcctgca ccagcaaagc ctggacaccc agaaaactcg tgggcagagc cgtgcggaga 4320
 aagggcattc tggccatgac actgacctg aacggaatcg aggcctgac agccctgttt 4380
 acctgtagaa ccgcctccat cagcgtgaac atcagcacc tgatgagcat cctggaagcc 4440
 atcatcaaga agatgaagaa acggatcatg gtgcaccggt ggatcttctc caatcagctg 4500

accgtgcaga tgctctgcct gcctctgctg acccctgaca ccagatggat ctttagtaat 4560
 cagctgcaga cagtgcacat gctgtgtctg ccacctctga agcagggcga gagaatcatt 4620
 tggccactcg gcggctttca gatecccaat ttcttctggt ccctcgcat cggacacact 4680
 ggcgcatggt ggcatactgg tagaaggcgg agagagtggg gcggtcttac cgtgtctaga 4740
 agcccactgt ggatcagctc catgatctac ctgagaggca tggccttcgc cagcgacagc 4800
 tccatcagaa ccaccagagt gtcttggtgt cggagatgtg gcgccaagtc tgccgcagcc 4860
 tcttcttctc cactgtggga ttgcagcacc acaaccggca cacaccagg atgcctgtgg 4920

gagatcccta gcgttacct gctggctaac ctgcacctgt gctactacca ctctcagagc 4980
 aacagaaaca agagccgcc gatggaatcc ctgggcatga agctccaact taaaaagaaa 5040
 gtgaacgct gcagcaccta cacacccac atctgcagac acacctgtcg cgtgaacgcc 5100
 gtcgaggaac tgcactctag aaggatgtcc gtgcggatcg tgaaaaattg ggtgtcctgc 5160
 tgctactgtc ggctgtcagc tgtgggactg tctacttga gcgctctgga caacaagatc 5220
 atctgcaagg gccacagaat caccggctac cctacgatg tccctgacta tgcgtcctaa 5280
 aggcgcgcct agcggccgc 5299

<210> 1151

<211> 5299

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 1B

<400> 1151

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
ggttttccca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg 240
tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300
aacctcagaa tgaagcttcc gaagcccca aagcccgtct ccaaatgag gatggcgaca 360

ccgctcctta tgcaagccct tcccatgggg gctctgcccc aagggccaat gcagaacgct 420
acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600
gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctccaa ggaaagcctg 660
gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720
atgaccgaga tccaattgac catgaacgac agcaagcaca agctggaaag ccccgctctg 780

aaacaggtgt caccagctc tccacctact cagcagctc agacacctca ggatagcaga 840
caggtgctgg ccatgcctag cagctggtct agctctggca gaaccagcg gaagtggtc 900
aagaatccta gccagcctgt gcctctgaga aacgacggca tcaccaacgg caacgactcc 960
accagaagct gcagcatcag cctgaagaaa agcctggaaa agatgccct catgatgaag 1020
aagaaggaca gcaccatctt catcgtgccc atgagcctgg cctglagcat caccgtgtct 1080
ttcgtgggcc agatcagcac actggtgctg gatgtgtcca gcatctccca ctggaacaaa 1140
gtgcggcaga acttcaagcg gaacgccgac aagaagaacg ttcgagcgg cgagaagaac 1200

gacctgcagc tgtttgtgat gagcgacacc acctacaaga tctactggac cgtgatcctg 1260
ctgaaccctt gcggcaatct gcacctgaaa accaccagcc tgggcgactg tctagaaca 1320
atggccggac ctctgcctc tctgcacct gcatctggca gagcctctag aaagacctgg 1380
cagagaaggc tgagagcctg tagagctggt ggacctgctg gatgggccag acaggccttc 1440
gataagaaag gcttttgtat cctgagcgtc ggagccggaa caggcggagg acctgcttgt 1500
gttcctgtgg ctgaagcttc tacaggcgct tggacagctg aaggcgccgc tggacaaga 1560
tgtagagctt ctagagcccc ttgcagacag ctgcctgcca gctctctac caagtgcgag 1620

atctgcgtga agcgacagc gcggagaaa agaaagcagcc agtctagaag ccccgctcct 1680
aagaaacgcg agagaatgat gctgcccgtg cgggccagaa cagctagatc tgcacttcct 1740
caggggagag cccctcttga gggaatgctg ctctctagag cactgcccag cctgctgtct 1800
agaatgccag ccagaagaga gagccggttt tggctggctc tgcaggcact tggactcaga 1860

cctccacatc tgcctagctg tcatcctctg cctcaactgc ttggccctcc acctcctcat	1920
caggccctca cagcttttctt cctgtctggac atcattctgc ggctgccctg caaagtgacc	1980
gagtctagca atatgggcgg caacagatcc atctgcctga ccaacgcca gaaaatggaa	2040
gatatgatct gggagagcac gccctgagc atcagcagac ctacatctag agccaggcag	2100
agctgttgtc tgcccgact gacacatcct gctcaccagc cactgggac tatgaccctg	2160
gccatcagat tcatcagcgc tcctcagcct agctccagca cagtgcagc tgctcctagc	2220
ggccagtact tcaagggcaa gaagcggcgg aaagagatct tcaagaagaa gaaaccctg	2280
acattcagcc ccagcctggc caaaaagacc ctgaccaata gcagcttctt ctacaccagc	2340
gaccgcgagg ccaagaaatc tatgaagcgg agcatgaccc tgaaggccct ggtcaagacc	2400
tggacacagt tcagaaacta cccagagcc tcctctcctg gacaccctct gggacctaat	2460
ggcatctggg aagtgatgcc cagaacactg gaaggctgca tctccgtgaa ggaccacaga	2520
acaagccaga accacagcaa gtgcatcacc gagtgtgtgc ggacagccct gaacagaaga	2580
agcaagatcg aggcctctcc tateggctct atcgccctga gatccatgcc taagagcaga	2640
aaccaggcgc tgctcagacg gaatctgacc ccaagccagc tgagaactct ggccctcct	2700
tatatgctgc tgccccagtc tctgagccag agcctgagca gaaagcagat ccctagccag	2760
tccatgctgg tggcctctag agcaggacag tttcctgtgt ggcgagaaac cagcagagga	2820
atgagcctgc agtggaaagtc cggcaatgcc tgcacacctc tgagatgccc tagcagaagc	2880
cctgccacat tcctgacagc tctgaacggc tggcacagat ctggactgag agcccagaga	2940
aagcgcaagc gcgagaagag aagccagaag tccaggcaga accatctgca gctgaagtc	3000
tgccggcgca agatctccaa ctggccaag ctgagaagcc cctggatctt cgtgtccaag	3060
aagagactgc ccaagctgac caagtgtgaa atctgtgtca agaaccgc catcctggct	3120
atcacctga tcacctca ggacctcat ctggacctg tgtgtcacc tcatagaagg	3180
cctggatgga agggccacca cagagtggcg tttctcatc accctagcgg cagcaccaag	3240
agccactggc agcaaagaga acgcggaggc ggcagacggg aaaagaaggg ctgtagagag	3300
agatccctgc tgiactccag aatgtgcctg gtgcagatcc ccacacacac ctgggagccc	3360
gattacttcg tgtctctgcc catgatgttc agctgggcca cacagtcatt cccctggga	3420
gccgtgtttc tgaccagacc tgccattcct tegtgtagct gcacaagcca cagcaacct	3480
tggagtcaga gcagacacc acacagaagc ccacctacct cttgtcctcc gctgttgaa	3540
gcctttccac tgcctagagc atccctgaga gccaccgtgc caagacatag ctctgtgctg	3600
gcaaccggac tgcatctgca cagacagatt tctctgcccc tgagaggatt cctgtgcat	3660

caaccactgc caggccagca tctgtggctg tctcatagac tgcggctgag actgccaaga 3720

actcagcggc ctcttagatc catcctgagc cttagactgc cactgaggcc acagagagga 3780

cccagacctc tgcatagatg gctgcagcag accacaggct gtagccagag aagatacccc 3840

agactgaaaa ccttcggcgt gccactgggc tccattctgt gtctggctgg atctctgagc 3900

accatgatga tcattagcac caccagacaa gagtgtggca ggcgggcatc tgtgccctgt 3960

agacctatga tcggaagcgc cagaccagga ccttgagaa catctgctat gcctagcgc 4020

atggcgctcg cactgcctac aagctgtgaa tccggaagat ctctctctgc caccggcgga 4080

agaatgcctg gaagccagag cattatgatg agctggatgc ctctctggc tccttgtgcc 4140

gcttgtcctt gtctccgc tctacactg tgcctcctc atcctgctag agcacctaca 4200

gccgtgcctg cctttacacc tctgtctgca catcctgtgc ctgtgctgtc tggatgtcac 4260

ctggcctga gaacctccat gctgacactg ctgcctatgc tgaagctggc cccactgcaa 4320

gtgaccacca cactgaagct gatcctggtc atgctggaaa tcgtgaccga gagcactcgg 4380

agagagatgc ctctcaggc cacaccttct ccacctggac cttggcgagc cgctctgggc 4440

aaagaagtga agagatccca gagcaagctg cgcctgagaa acacaagccc catcgtgttc 4500

tttctggccc catacttccc cagacggatg accagacgga ccatgacaac caccaaatg 4560

atgatgatgc ggcggaccaa gcggagaagg cgcaaaaggc ggagaatgac aatgatgaca 4620

aggcggacc cgtgtgacaaa gaaaacctgt ctgaccctta gaaccagcgc cgctacaaa 4680

gctctgcaa ggcagacaa ctcccagcg aggccattc agaccctcc tggaaatct 4740

ctggccatct ggggcaacca gcagctgaaa tggaccctc acatcctgaa gtccgccagc 4800

agaagggcca gacctaccag ctgtagcacc tglagaatgt ggtggatcgc caaaaagcgg 4860

atcaagctgc ggcggaacag aaccagactg aactgacag gcacaagaag cagcggcacc 4920

agagcttctc catccgcgt ttgcctgtgt tgcggacct gtccttcag aagcttccca 4980

gccgttctc caagcggatt gagagcacct gttggagcac aggccctcc agaagtaca 5040

ctgagagcta gctgtgcctc cagcgctct aagccttggt ctggactttg gccttgggga 5100

gcacaagtgc ggcaaccatc ttgctctgga ccatgcgctt ctctgctgag cacactgtct 5160

cagccacctc cacaggctcc atctcaagtg tggacagccg caaactgag atgtcctgct 5220

gttcagctg ctgcctgtcc tctggctac cctacgatg tccctgacta tgcgtcctaa 5280

aggcgcgct agcggccgc 5299

<210> 1152

<211> 5281

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 2B

<400> 1152

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa	60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg	120
atgcttggtg ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact	180
ggtttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg	240
tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa	300
aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca	360
ccgctcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt	420
acaaagtatg gaaatatgac agaggatcat gtcattgatt tgcttcaaaa cgctgatccc	480
cttaaagttt acctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac	540
acgatggaaa cgattgactg gaagtggtt gagagctgga tgcaccattg gtcctgttc	600
gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctccaa ggaaagcctg	660
gaattggagg acccgagtag tgggtgggc gtcacaaagc aagacctggg accgtgccg	720
atgagaaaga tgcagagcct gaatcaccac agcagactga ccaacatgag cagaacacct	780
ccaagacgcg tgtgcaacc tcggagaaag acctggaaga tgcggaagaa gtacgccag	840
aagcctagcc agaagaacca cctgtacaac agccggaaga aactgctcga ggacatgaag	900
cagaatggct tcacaggcca cagagagggc agcgagtctg ataactctgg cctgctgtac	960
tcctttctc ctatccggat gtgcgccctg tctcaccta gcttctacat cagcagcacc	1020
gtgtgctttc tgagcaagca ctgcatgacc gcctgcacac aaaagaaagg ccacatgac	1080
ttcagccgcg agaagatcat caaccacc atcagctgcc ctttcagag cccacaaaag	1140
cggctggaac tgagcctgga accttggtt cctacctgc accagcagaa aaccaaggc	1200
ggcaagaaga gaagcaagtt cctggcacc agcctgcagt gctacctgaa cagatgcagc	1260
ctgatggaac agatccctca cctgaagtcc gcctctccac agatcatgca gagaaccagc	1320
gccgaccggt tccggatgaa gcggagaatg cagaacctgg acaatctggg cgttccatgg	1380
ccactgctgc ctggacctt ggaaaaacaca cagatccca gaacaagccc tctgtggaag	1440
atcacaatgg tgctgacata cccaactgc gtggtgcacg tgctgatgtt ctggctgcct	1500
atgagatctc tgggcgagcc ttggagagct ggctttcagt ggggagagtc cccttgcaa	1560

gtgatggcta gcctgacagg cccctatcct atcagcgagg gcctgacat gaccaccggc 1620

agaaacatca acagcaactc cctgatgacc aactgcctgt tcagcccat cttcctgtgc 1680

caccacgcca tcatgcaccg gaagatgaca agcccacact tcagactgtt cagcagcaag 1740

atccacatc ctgagtgcc atctgtgggt gccctgtgca agttcagagc cacatttctg 1800

ctcgccctgt gggagtgtag tctgcctcaa gccagactgt gcctgatcgt gtctagaacc 1860

ctgctgctgg ttgagtctgc cgctcctcca catagactgc tgggcccttc tagatggtec 1920

agaagccacc tggacttcag cccctactgg atgaagaaag tgaagctggc caacggcctg 1980

tggttcaacc tgatcttcgt gctgttcaag gccgaccaga gcgagtctag cctgtctagc 2040

ggccggaaca agaaaacaaa gctgtggttc tccctcatca acatccacca ccgcaagaat 2100

cctctgctgc ccatgagaat cccagcctg aatgccagt ggatgttcct gagaatcctg 2160

cttctggccc atatgtacgg ctccagcacc tacggcacc agaaaggcga gtgcgtttgt 2220

ctgcagtgtc tgagcggcag cagcctgttc attctgaagc agcccctgga cctgaagatc 2280

tccaagacct tcatgtgca agctcaccca caggtgccag ctcttgctcc tcaagcttgg 2340

tggcctgcta gaagaggccc tctgacatct gctccatccg ctccagcagc tctgacagct 2400

agccctcaga ttatgcagcg gatgagcgcc gtgaacttcg agacaatcat ctaccctcca 2460

agcacctgta gccctgcttg tagaggcaga aacttgaaa gcgccggact gtttccttgg 2520

ctgcacacc agtgtacaca cccctgtacc atgctgctgc cacaaggctg gtggtgtaca 2580

agaggcggcg gaaagcggaa aaagaaaatg tgcaagggtg ccggcggctg caccgcctgt 2640

gttgagagat gtccttgaa gggcatctgc tggaagtggc cagtacagct ggctgctcag 2700

tggcttagcg tgacctctt ggaatggaca gcccaagaga gaggtgacag cagctggctg 2760

atgaagcaaa catggatgaa gtcttggtcc ctgcgggacc ccagctacag atccatcctg 2820

gaatacgtgt ccaccagagt gctgtggatg cccacaagca ccgtgcggag aagaaacagc 2880

agaaagcagt ctgagtgca gctggccatt caggtgctgc tcgtggaca gcacaagtac 2940

tttctgttcg gcagagcccg caaccggaac atgaagaaaa ccatgagcca cctgatcgcc 3000

catcaggccc tgaagatgag cggcctgagg ctgtttcatc ctccgctgct gacaagaaag 3060

aagcccgga agttcctgcc tagcagattt ccttggggcc ctccctctct gtgtcatcct 3120

gcttggtgta gccctatctc cgctgtcca agactgctgc cataccttt tcacgtgctg 3180

gccctggaag tgacctttcc acctggaaca gccatgcctc agatgcaact gcaggccctg 3240

gccatgtggg agaaaggctg ggataagcgg aagagaatga agaccggcgc catccaagag 3300

aagggcgcta ttcaagagaa aggggccatg accaagcgga tctgcgtggt caatttcgag 3360
gcctgcagag agatggaag cctgagcgcc cctgagaaga ttaccctgtt tgaagcccat 3420
atggcccgtg gcacctccat caatgtgctg tgtgtcagag cctctctgat cgagaagctg 3480
atgaaagaaa agcgcaagat gaagcgcaac caggtggcat cccacaaaat tatgcagagg 3540
ctgttcatta agggctacca gaacaaccac ttacattcc atctgcaaaa cttcgccttc 3600
ttcagcagct tcggcaacaa caagtacatc aatctctga cgcggcgcaa gaaaagagag 3660
gaccactgcg gactgctgat cctgatccag cacggcggca tcttcacctt tcggttctgg 3720

gtcgaagagc tgagctggaa catctgcaag aacctgagcc tgtacctgga taagtctgtg 3780
cagcggctgc tgiactgta catcatcgag acaaacgtgt tcgtgctgaa cctgttcac 3840
gtgccagtga accagatctt catgatggcc ttctacctga agtacaccga gaaggcctgg 3900
gtcatggaac tggaatggct gatccaacag cagtgttacc agcaagagaa gaaaagccgg 3960
aaactgatga gcagctgccg ggccttcac cacacaccta gaagccctgg ctgcagcgtg 4020
tacgccaata tgtgtgggc cttttggaag cctcctagcc agggcatcag ctcttgtctg 4080
atgacaggct gttggggcag ccctcctctg cacctgtgtc agcctctgag gcggtataag 4140

aaaagggcg tgatcgctg gcggcggaga aagtggcaga tccggcatgt gctgaaaaac 4200
ctgatcctgt ttcatgtcg gaacatcgtg tacggcatcc aagtgtgct gtgcggcaag 4260
ggactgacac accctgtgcc tctgaaacgg accctgcaga acaagaggaa caagaacatc 4320
aagcgggtca accagaagaa gggcaacatc aagaggaagt ccatcctgct gcacctcatt 4380
gtgtgaata gccccgagag caacccaag ttcttctga cctttagcca gctcgagaag 4440
aaagctacct ggatgagaag aacagcgcc ctgagagcca cagctcctgc tacagcagct 4500
cctcaggctc agactcctca ttggagagcc gccacaacaa gcagcatgag cagcagccct 4560

agagccgagc ctacatcttc tagctcttgg gccacctgtt ggcccagatg ctgtagctcc 4620
agctgttact ggtccctgag ttcttggcct cctgctggcg ccgctgaggc tacaacacc 4680
agaactagaa gcagagagtc ccagcggggc agaattgtga cttggagaag tagtctgtgg 4740
ctgcagggca ccagatgttt tacaggcgtg cggacaagca gcggaagctg tggcagagct 4800
tgtagctgcg gaagaggctg tggaaccct agaggcgatt ggaagagaca ccctcctcgg 4860
aggaatagcg tgatcgtgca caagatcgtg ctggtgtttc tgaagtcct gtccagctac 4920
aactgcgaga gaaggatcag cggcatccag aagagagcca tcgagtttgc cgtgctgaaa 4980

ctgtgaata tggacctgca ctggaactcc gcctacctgg gcagaactct gctggtcacc 5040
tgtatcctgt atcacgggtg gatcgtgacc tccatgtgcc agtctcagag atggctgacc 5100
agcaccacaa gcagatccag cgctctgatg tggaccggc agatcaatcg gaggaagctg 5160

cagagaaaga agaggcaccc aagctggcct tggaccagat gccttagaat gaggcctcct 5220
agaagcggct acccctacga tgtccctgac tatgcgtcct aaaggcgcgc ctageggccg 5280
c 5281

<210> 1153

<211> 5296

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 3B

<400> 1153

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttcg 120
atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
ggtttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg 240
tatcagcagc aaggaagact ggataagctt acagttacat ccagaatct ccaacttgaa 300
aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360

ccgtcctta tgcaagccct tcccatgggg gctctgcccc aagggccaat gcagaacgt 420
acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
acgatggaaa cgattgactg gaagtggtt gagagctgga tgcaccattg gctcctgttc 600
gagatgtccc ggcattctct ggagcaaaaag ccgacggacg cacctccaa ggaaagcctg 660
gaattggagg acccgagtag tgggtgggc gtcacaaagc aagacctggg accgtgccg 720
atgggagctg ctgctgcctc ttgtcagtct cctcttctc ctcgggaaac cacacctagc 780

tccgacgcca ccagacggac aagaccaatt gccgtcaga gcaagaaaac catgacagcc 840
gccggactga cccctaagaa caagaagcgg agaaagctgc ggccaagat gatccggaag 900
atccagaaga gaaggcggac cgccaaccgg cggaatagca gaagggtac ccctacaagc 960
aagggcagcc tgagaagaaa gtacctgaga gtgcggggac ctctctgca caccggaac 1020
atcagaaagc tgatctggac caagcagcgg agcttctgt ctctgttccc caagctgaga 1080
gccaccgagc agatgaccaa tgtgggctgc tctatccctc acgtgccccaa agccacagcc 1140
gctcactctg tgacagtga actgcagctg ccctgacct tcagcacct gctgtgggat 1200

agcagacaca ccatgagcct gagcaacatc ctgatgaagt tccggctgca gtctagccca 1260
ttcctggcca gatcctggaa caccatgcag tggaacaaca agaaaatggc catgaccgtg 1320

atcgctggcg cccaccactg tcagtacaag ctgacctaca ccaaagtggt gaagatgaac	1380
tggaagaaaa tgatgatcgg cagccagcat ctgctgttca gccctctgga tagcagtcct	1440
ctgcagctcc tgctgcaccc tcacggcaag agatgcaacc cttgctgcag actgacctgg	1500
atgagccaga acaccagaag caccaacctg gaaaaagaacc ccagcctgaa gaagcagagc	1560
cagcggagag gaaagctgag cgccttttagc ggcagaatcc tgcaccagcc agaaatggcc	1620
gccatgagac tgatgcccaa gtctctgaac tccaccaaca gctggtggac cctgaccaca	1680
ctgagcttcg tgctgatcga ggaagccaga cagcccagca gacctaccgg cagaacacct	1740
accaccagac tgatggcccc tgtgggcagc gtgatgagct gttctctgct gaccagcct	1800
tctccagcca ggcctgtac aatgcctcca ctgctgcac cacagtgggc cctcatagt	1860
gctggacttt ctccaggcgc ttgcagacct gcctgcacct gtatcagcat gaccaccatc	1920
agcagggcca catggggccc agtgtactac gtgtgcaacc ggatgaacgt gtccagcgtg	1980
ctgaagccct tctgtttcac cgtgcctatc gaggacatga gagagtgcac cctgggcaga	2040
aacagaatga atgtgtcctc tgtgtgaaa cctgtctga tccctgtgcc aatcagcgag	2100
aagaagagga agctgcccaa catcgagatc acccctcagc ggtctaaggc catgctgcag	2160
aagcagtgtc gctacaacct cgtgatcaag caccctctga tcttcagaat caacctgcgg	2220
cggcagggca agaccaaaga tggcgttgtg cagagcctgg gcttctcaa ccagcagatc	2280
atcctgcaga aagagttctt catctgcctg ctcatgttca tcaagcgtg gaagcctgcc	2340
gccaccaaga gcagaaagaa gggccacacc aagaacagac ggaaggccaa gagaaagccc	2400
cagatctacc tgtttcttct gaccgtgtgc ggctttcacc tgaaaaagac cagcgccaag	2460
tggctgaaga agtccaccaa gtccagatcc aacggcatgg aagcttgcgg cacacacccc	2520
actcctagac tgagctgcct gagagttaga tgcggcggct ggctgtgtgg ctggacacct	2580
agaggtagaa agtccggcgt gatgaagtgc tgggatctgt gcccctgca caagaagaga	2640
ggcctgttca gactggattt tcaccccaga agcagctccg gcaagggaag gaacagcccc	2700
tgctgcaaaa agaaactgag ggtgcagaac cagggccatc tgctgatgat tctgtgcac	2760
aatgaccggg tgttctctgt gaagatcggc gagaagctga agcactgttt caaggcctgg	2820
ggctccagac ggaaccggcg gtacagaaag atctacggcg agctgaagat gtccctgcag	2880
gccttctga tccacctgag aaaggtggac acccaccacc tccaggtggt caccaaaaca	2940
gtgaccgcca caacagccga cggccagaga atgcggagac tgaagtgcaa ggcctgccgg	3000
ctgagatggg ccagacctga acctgtgtct caggccctc ctaagagcca ctttccacct	3060
catcctagcg gcccagcag aacaagtagc ctgcagctga gaagcctgtt ctttagccac	3120
tgctgtgca gccagaagaa ggacctgcc ggcaagctga aaaagctgct gaagaaaagc	3180

agccagctgc ggagaagctg gcgcaatgtg tccagaatca gcacccctcc tccactgac	3240
ctgtggcctc aagctgctcc tgtgtccgtg atcaccatga agctgtggga gaagcacttc	3300
aagggcctga attggaacct ggtcgtgtgg attctgaacc tgaagatgat gacctacatg	3360
gaaatgcact acggccatca ggccccacag gtggcaatgc tgcctaagct gctgtgcaga	3420
cagatgctgc ccactctgag cacactgcag cagagacatc ctcagggccc ttgtctctct	3480
cctgtgacac ctctgagagt ccagtctgtc ctgctgctgg gactgcctca gacagccaga	3540
ggacctagaa gaaaggtcct gatgggtgtg ttgctgcccc ccaatcagtc tctgcagaaa	3600
agccaggttt tccagtgggt gctgcggaca gaggtggccc ctatagatgcc tagatctgcc	3660
gtggacatca gccccggacc tacatctcct agcctggcct cttgtgcctc tgtggccatt	3720
ggaaagctgg cactgcttgg cgcctctgct ccttgtgtgtg ctgctggcgc tagagaggcc	3780
ggaagatttg ctgtgctggg caccatggtc atgaagcttt gtttcttcta cctgctgtac	3840
cggctgcgca tccaagcct gaggaagtac agacagcacc tgaaccgga gctgcacctg	3900
acaagatcct gcctgatcga tctgacctg atgatgtccc agaagctctg gaagaaccag	3960
cggaagagaa tccctctgcc atctccacgg caacatctgc tgccacagta ccctctgcac	4020
ccacctccac ctgtctgct gttgtgtcac catagacacc acctggcctt tctcgagatg	4080
gcctgtagct ctgcagcac ccacagcatc aagatctgga tcagcttcag ccatgaagtg	4140
gacctccag gcagcgtgtg gatactgcct tgcgatctgc ctcggatgct gccaatctct	4200
tcacctctgc acagaccca gatgcctttc tggacctgca ctttctctgc cacaacctgg	4260
ggcacatggg agacaccttc tacatggggc tggcggactt tcagaggcgc tagcagcagc	4320
acatcccggg acagcagatc cttcttcacc tctgttcacc ctagcaggcc ctgcagaatg	4380
agactgtacc agtgcaagaa gaagctctc ctgaaactgc tgaccaccac cacaagcagc	4440
cccagaagat ccctgtctct gagagcaaga ggcgccacca caatcggcga agtgaccagc	4500
tgtaccaacc tgagcgtgcc catgatgtg accatcctga tttggaagcg ggtgttcac	4560
ctctgctga gcgataagaa gggcgccaag aagatcacct tctgcctat tcctccacac	4620
ctgagacacc ctctgctgct gtctgagaag aaacggcctg agtggctgag catggacctg	4680
gacggaatgc tgacagtgat cggccaggga ctctgtggga tgaccttag agatctggga	4740
acagtggcag gcgccaccgc tcagattcag cgacctatcc aggtgcagac tggcggcaga	4800
ctcagaagaa acctgcagag aaacctgaag gtgctccagg tgtccgtgta cagcggcaac	4860
ctgctgtcct ttagcagacg gggcatgaag tctagcgtgc ggctgaaaaa ccgcgagtgg	4920

gagaaacgga agcagattct cggaggcggc ggaaagtaca aagagtactt cctgaagcgc 4980

atcctcatcc ggaaggctat gacagtgtg gccggcgaca agaaaggact gggcagattc 5040

atgagatgcg tgcagagcga gacaaaggcc gtgtctctgc aactgcctct gggaagaaac 5100

atggaacacc gggtgacat ggacagcgcc ctgagcctga caaagagaga gggacccgag 5160

acactcaaaa agaaatacct ggtccagcac cagatgaagt gtctgaccgc cgtggattgt 5220

ctgcaggctt ttggggacat gggctacccc tacgatgtcc ctgactatgc gtcctaaagg 5280

cgcgcctagc ggccgc 5296

<210> 1154

<211> 5299

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 4B

<400> 1154

gaattcggat cccgcgactt cgccgcatg catcgacggc gctcacggag ttgccgggaa 60

gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120

atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180

ggttttctcca tctcgtgac actgttgtctg gcgggacagg caacaactgc gtattttctt 240

tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300

aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360

ccgctcctta tgcaagcctt tcccatgggg gctctgcccc aagggccaat gcagaacgct 420

acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480

cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540

acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gtcctgttc 600

gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctccaa ggaaagcctg 660

gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720

atgatccaga agaagaagca gaagtccaac ctggacctgc agcaccagcg cagacgcaaa 780

aagaagaagg acaaggtcga gatccggaat cgagagccca aggccaatag cacagagtgt 840

cagggcgagc acagcagaga gcagaacctg ctgaatctgg tgcagctgaa ccctcacagc 900

cctcaccaca gaaaggacga agaggaccac cagaagcggc accaccacca caatcaaaag 960

aaaatgagcg tgatggccaa gaagtcccag cagcctctcg gacaggcctt tggctctctg 1020

tgtcagctgg tgtccgccga ttccagcgcc cctcaagtga ccagactgcg gagcctgaac 1080

catctgctga tcaacgaggg caacaaccac tggcctagag tggaaatgcc taccggttgg	1140
ctgctcgtgg gctacaacac cagaaacaca gccagaatc ctcggctgca gcagcacctg	1200
aaacactggc agcagtgcac cagagccaga tggtgccaag agccttgtca gaccctgacc	1260
ttcttccatt tcttcttctt ttcaaaacg gtgtccctgt gctgccccgg ctggtctaaa	1320
ggacaacctc ctccacctgg cctgaagcct tctagcctgg cttctcaggt ggccagaacc	1380
acaggcgtgt accagcacgt gtggctgata tgcctcgtgt tcttcgtgtg cgtggaaacc	1440
ggcttctgtc acgtggccca agtgggactc gagagactgg tgtctctgag cggcatcacc	1500
gacgtgaacc attgggcccc gcctaagcca tctcctagca aaggcaccgg catgaacaga	1560
cccatcggcc tgagagtgg caaaggcgtg tgggccagac tgagagcctc cgtgtctttc	1620
tggaccctgc tgcctacaac aggcgtgcgg acaagaggaa gccctctgag actgacactg	1680
tggcctccac ggaacatcct gaacagcctg cctagcagca tggaaatcgc cgtgctgcaa	1740
gagaaccgca agaccagaaa ggccgccaga gagaagcaca gaaagaccga caacctgcac	1800
ctgtgtact accacagcca gagcaaccgg aacaagagcc ggcatatgga aagcctgggc	1860
atgaagtgc agagccctct gtgggattgc tccaccacaa caggcacaca ccacggctgt	1920
ctgtgggaga tccctagcgt tacactgctg gcctgcagag tgaacgccgt ggaagaactg	1980
cacagcaggc ggatgtctgt gcggatcgtg aagaactggg tgtcctgctg ttacgtgcgc	2040
ctgtctgctg tgggcctgtc tacttggagc gcctggacg tggcatcaa cctgaagcgg	2100
ctgcagaagt tcagccagaa gtctcagcac cactgcgccc tgagaaagat cgagtgggcc	2160
acaaagctga gcctcgccgg aaaagctgga cccaggtc aagagaaggc caacgccaag	2220
aagatgccct tccagcgggtg gatcttcagc aatcagctga ccgtgcagat gctgtgcctg	2280
cctattgaag cctgactgc cctgttcacc tgcggacag ccagcatcag cgtgaacatc	2340
agcacctga tgagcatcct ggaagccct ctgttttttc acggcgacct gtgcgaggaa	2400
aagaagaacg gccggatcag cagccaggct cctctcagac tttggtcttg gtgcgcaca	2460
agccagacct actttggcag caccgccaag aaaagcccca ccagcttttg ctgcgagtgg	2520
ggaggacagg ctaccggca gagaataacc ggaatggaaa tcctgctgtg gattctgctc	2580
aagatggaaa ttcagatctt caagatttgc ctggcgaga tgcagctgtg cacctacaca	2640
ccccacatct gcagacacac ctgtagaggc ggacctagcg ccagcgatag atgctgtagc	2700
tgtagcccta gcggcttcag cgccggaaga ggcagatgtc cagttcaggg atgtctcgcg	2760
cctcacagag tgcagctgct gagaagatgg ggccctggat ctctgctgg ccagagactg	2820

tctaagggct ttcagctgct ccgttggtgg ggaccaggat ctccagctcc tgagcctaga	2880
aagggcccat ttccaccacc tgatcctcca tggcctgtga ccgctgtgac agtgatggct	2940
ggctctgtgc ctacgctca gtctgtggat gctctggaaa gccctggacc tctggcactg	3000
gaaggaccta gcagccccag aaacctgctc tggcgggaaa tgagcatctt cctgcctggc	3060
atcttcacct ctcgattct gaacctgcaa gtgctgaaga agatcctgcg gagctttatg	3120
aagctgtacc actctctggt catgtgcctg cggctgcgga ccaagctgga aaaagctctg	3180
agcgtctgtg tcatctggcc ccagcacagc tacaagcaga ggctcctct gcagcctgtg	3240
caggtcgtgc tcagactggg aaacctgcct ccattcttca gaggcagcga ggtgcccttt	3300
cctagacctt gccggacca gatgctgaac cagaagtgtc tggccccctt catcacacac	3360
ccattgcct ctacgccct gggacaagag atgccaaca acaccagat cagactgctg	3420
aagccccgc tgacccctga caccagatgg atcttctcca accagctgca gacagtccag	3480
atgctctgtc tgccacctct gaagcagggc gagagaatca tttggcccc cggcggcttt	3540
cagatccca acttcttttg gacccctgga atcgccaca ctggcgctg gtggcatact	3600
ggaaggcgga gaagagaatg gggcggtcc accgtgtcta gaagccact gtggatcagc	3660
tccatgatct acctgagagg catggccttc gccagcgaca gctccatcag aaccaccaga	3720
gtgtcctggt gcagaagatg cggcgccaaa tctgccgtg cctccagcct caagaagaaa	3780
ccccgggaca tctgtcggat cagcgactct aagaagatga ccagaagcg cgagagcacc	3840
ctgggcaatt tctggatgaa gctcctccag ctgccagaca agaagaagaa gtctaccgaa	3900
aagaccaaga tcatcaagaa gatgaagaaa cggatcatgg tccacatgtg cagctccctg	3960
gtcttgccaa caggcctgac atctctgac ctgccaagca gcgatctggc cgtgctgac	4020
tctagctcca ccagccactt tctgatgcgg agcccagtgc tgcctagctc cagactgact	4080
tgtgcctctc cacagctgcc cagaatgtgg acctggtcca gctggctgaa gtggctgaaa	4140
aactggaagc ggttcaagct taaaagaag tacatcctgg ccatgacgt gaccctgaac	4200
gggcatccaa gaaccgcctc taccacctg cctaccacca gcctgaaggg ctctagaacc	4260
agctgttgcc ccagatctca cccagactg cctaggacaa agtggcctct gcagtgcctg	4320
ctgcacagcc tgggaacaac tggaaactc gtgtgggaaa ggggcgtgct gcagatgaga	4380
agtctggaag ctactgccc tctgcagacc ttccacctc accactgtag aactcagccc	4440
agctcttgcc ctctgcatg gattctgtac caaggacagt ggagcggagc cgtcgtggga	4500
cttagacctg tggtcacca tctgccaaga cctattcagg gcctgcactg cccacaggct	4560

ccacatcaac cagctctgtc ttggggcaag tggcccgtgg gaatgacagg acctgccaga 4620
 tgttgccggt ggcctagacg ggaactcaaa aagaatctgc tgctcccctg ccggtgcaga 4680
 cgcgagtata gagtgacaat gggccaagcc ttgggcagct ttagcgccga ctttagcgct 4740
 ccccagggtg tgaagaagaa tcggaagcag aacaagatta tctgcaaggg ccaccgcac 4800
 acaagcctga tctgagctt tcagcgctg aaacttaaga agaaagtcaa cgctgctct 4860
 cccgcctgca cctctaaagc ctggactccc agaaagctcg tggggagagc cgtcagaaga 4920
 aagggcac 4980

cacgtggaaa agttcgtgcc tcttctcct cctctggctc tcggccctag aatgcagctc 5040
 tgtaccagc tggcccggtt cttccctatc acacctctg tgtggcacat cctgggacct 5100
 cagaggcaca ccccttgta aaagaagggt cctccgcta gcccatgggg ccttagacca 5160
 tctccttgcc tgagctggc ctcagaatt gtggccctg gacacgcct gagctgtcgg 5220
 actagaagaa gatgtccag caagggtac cctacgatg tccctgacta tgcgtcctaa 5280
 aggcgcgcct agcgccgc 5299

<210> 1155

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 1C

<400> 1155

Ser Thr Arg Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro Gly
 1 5 10 15
 Pro Trp Arg Ala Ala Leu Gly Lys Glu Val Lys Arg Ser Gln Ser Lys
 20 25 30
 Leu Arg Leu Arg Asn Thr Ser Pro Thr Glu Ile Gln Leu Thr Met Asn
 35 40 45
 Asp Ser Lys His Lys Leu Glu Ser Pro Ala Leu Lys Gln Val Ser Pro
 50 55 60
 Ala Ser Pro Pro Thr Gln Gln Pro Gln Thr Pro Gln Asp Ser Arg Gln
 65 70 75 80
 Val Leu Ala Ala Ser Ser Pro Gly His Pro Leu Gly Pro Gly Asp Cys
 85 90 95
 Pro Arg Thr Met Ala Gly Pro Ser Ala Ser Leu His Pro Ala Ser Gly

100 105 110
Arg Ala Ser Arg Lys Thr Trp Gln Arg Arg Leu Arg Ala Cys Arg Ala

115 120 125
Gly Gly Pro Ala Gly Trp Ala Arg Gln Ala Met Thr Leu Lys Ala Leu

130 135 140
Val Lys Thr Trp Thr Gln Phe Arg Asn Tyr Pro Arg Val Gly Ala Gly

145 150 155 160
Thr Gly Gly Gly Pro Ala Cys Val Pro Val Ala Glu Ala Ser Thr Gly

165 170 175
Ala Trp Thr Ala Glu Gly Ala Ala Gly Thr Arg Cys Arg Ala Ser Arg

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

195 200 205
Cys Val Lys Arg Arg Arg Arg Arg Lys Arg Ser Ser Gln Ser Arg Ser

210 215 220
Pro Val Pro Lys Lys Arg Glu Arg Met Met Leu Pro Val Arg Ala Arg

225 230 235 240
Thr Ala Arg Ser Ala Leu Pro Gln Gly Arg Ala Pro Leu Glu Gly Met

245 250 255
Leu Leu Pro Arg Ala Leu Pro Ser Leu Leu Ser Arg Met Pro Ala Arg

260 265 270
Arg Glu Ser Arg Phe Trp Leu Ala Leu Gln Ala Leu Gly Leu Arg Pro

275 280 285
Pro His Leu Pro Ser Cys His Pro Leu Pro Gln Leu Leu Gly Pro Pro

290 295 300
Pro Pro His Gln Ala Pro Phe Asp Lys Lys Gly Phe Val Ile Leu Ser

305 310 315 320
Lys Gly Lys Lys Arg Arg Lys Glu Ile Arg Arg Met Thr Arg Arg Thr

325 330 335
Met Thr Thr Thr Lys Met Met Met Met Arg Arg Thr Lys Arg Arg Arg

340 345 350

Arg Lys Arg Arg Arg Met Thr Met Met Thr Arg Arg Thr Leu Leu Thr
355 360 365

Lys Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu

370 375 380

Pro Arg Gln Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro Gly
385 390 395 400

Thr Ser Leu Ala Ile Trp Gly Arg Leu Pro Leu Arg Pro Gln Arg Gly
405 410 415

Pro Arg Pro Leu His Arg Trp Leu Gln Gln Thr Thr Gly Cys Ser Gln
420 425 430

Arg Arg Ile Ala Lys Lys Arg Ile Lys Leu Arg Arg Asn Thr Leu Ala

435 440 445

Ile Arg Phe Ile Ser Ala Pro Gln Pro Ser Ser Ser Thr Val Thr Ala
450 455 460

Ala Pro Ser Gly Gln Tyr Phe Ser Ser Phe Phe Tyr Thr Ser Asp Arg
465 470 475 480

Thr Lys Cys Glu Ile Cys Val Lys Asn Thr Ala Ile Leu Ala Ile Thr
485 490 495

Leu Ile Thr Pro Gln Asp Pro His Leu Asp Pro Val Cys His Pro His

500 505 510

Arg Arg Pro Gly Trp Lys Gly His His Arg Val Val Phe Ser His His
515 520 525

Pro Ser Gly Ser Thr Lys Ser His Trp Gln Gln Arg Glu Arg Gly Gly
530 535 540

Gly Arg Arg Glu Lys Lys Gly Cys Arg Glu Met Pro Ser Ser Trp Ser
545 550 555 560

Ser Ser Gly Arg Thr Ala Asp Lys Lys Asn Val Arg Ser Arg Thr Arg

565 570 575

Leu Thr Leu Thr Gly Thr Arg Ser Ser Gly Thr Arg Ala Ser Pro Ser
580 585 590

Ala Val Cys Leu Cys Cys Trp Thr Cys Pro Ser Arg Ser Phe Pro Ala

595 600 605
 Ala Ser Pro Ser Gly Leu Arg Ala Pro Val Gly Ala Gln Ala Pro Pro
 610 615 620
 Glu Val Thr Leu Arg Ala Ser Cys Ala Ser Ser Ala Ser Lys Ala Cys

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

 690 695 700
 Ser Leu Ser Gln Ser Leu Ser Arg Lys Gln Ile Pro Ser Gln Ser Met
 705 710 715 720
 Leu Val Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu Arg Ser Leu Leu
 725 730 735
 Tyr Ser Arg Met Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro
 740 745 750
 Asp Tyr Phe Val Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser

 755 760 765
 Phe Pro Val Gly Ala Val Phe Leu Thr Arg Pro Ala Ile Pro Cys Cys
 770 775 780
 Ser Cys Thr Ser His Ser Asn Pro Trp Ser Gln Ser Phe Lys Lys Lys
 785 790 795 800
 Lys Pro Leu Thr Phe Ser Pro Ser Val Pro Met Ser Leu Ala Cys Ser
 805 810 815
 Ile Thr Val Ser Phe Val Gly Gln Ile Ser Thr Leu Val Leu Asp Val

 820 825 830
 Ser Ser Ile Ser His Trp Arg Lys Arg Lys Arg Glu Lys Arg Ser Gln
 835 840 845

Lys Ser Arg Gln Asn His Leu Gln Leu Lys Ser Cys Arg Arg Lys Ile
 850 855 860
 Ser Asn Trp Ser Lys Leu Arg Ser Pro Trp Ile Phe Tyr Pro Arg Leu
 865 870 875 880
 Lys Thr Phe Gly Val Pro Leu Gly Ser Ile Leu Cys Leu Ala Gly Ser
 885 890 895
 Leu Ser Thr Met Met Ile Ile Ser Thr Thr Arg Gln Glu Cys Gly Arg
 900 905 910
 Arg Ala Ser Val Pro Cys Arg Pro Met Ile Gly Ser Ala Arg Pro Gly
 915 920 925
 Pro Trp Arg Thr Ser Ala Met Pro Ser Ala Met Gly Val Ala Leu Pro
 930 935 940
 Thr Ser Cys Glu Ser Gly Arg Ser Pro Pro Ala Thr Gly Gly Arg Met
 945 950 955 960
 Pro Gly Ser Gln Ser Ile Met Met Ser Trp Met Pro Pro Leu Ala Pro
 965 970 975
 Cys Ala Ala Cys Pro Cys Ser Pro Ala Pro Thr Leu Cys Pro Ala His
 980 985 990
 Pro Ala Arg Ala Pro Thr Ala Val Pro Ala Phe Thr Pro Leu Ser Ala
 995 1000 1005
 His Pro Val Pro Val Leu Ser Gly Cys His Leu Ala Val Arg Thr
 1010 1015 1020
 Ser Met Leu Thr Leu Leu Pro Met Arg His Pro His Arg Ser Pro
 1025 1030 1035
 Pro Thr Ser Cys Pro Pro Leu Leu Glu Ala Phe Pro Leu Pro Arg
 1040 1045 1050
 Ala Ser Leu Arg Ala Thr Val Pro Arg His Ser Ser Val Leu Ala
 1055 1060 1065
 Thr Gly Leu His Leu His Arg Gln Ile Ser Leu Pro Leu Arg Gly
 1070 1075 1080
 Phe Leu Leu His Gln Pro Leu Pro Gly Gln His Leu Trp Leu Ser

1085	1090	1095
His Arg Leu Arg Leu Arg Leu	Pro Arg Thr Gly Glu	Lys Asn Asp
1100	1105	1110
Leu Gln Leu Phe Val Met Ser	Asp Thr Thr Tyr Lys	Ile Tyr Trp
1115	1120	1125
Thr Val Ile Leu Leu Asn Pro	Cys Gly Asn Leu His	Leu Lys Thr

1130	1135	1140
Thr Ser Leu Arg Arg Ala Arg	Pro Thr Ser Cys Ser	Thr Cys Arg
1145	1150	1155
Met Trp Trp Leu Lys Leu Ala	Pro Leu Gln Val Thr	Thr Thr Leu
1160	1165	1170
Lys Leu Ile Leu Val Met Leu	Glu Ile Val Thr Glu	Glu Ala Lys
1175	1180	1185
Lys Ser Met Lys Arg Ser Arg	Arg Ser Lys Ile Glu	Ala Ser Pro

1190	1195	1200
Ile Gly Ser Ile Met Lys Lys	Lys Asp Ser Thr Ile	Phe Ile Asn
1205	1210	1215
Gln Gln Leu Lys Trp Thr Pro	His Ile Leu Lys Ser	Ala Ser Val
1220	1225	1230
Ser Lys Lys Arg Leu Pro Lys	Leu Asn Gly Ile Trp	Glu Val Met
1235	1240	1245
Pro Arg Thr Leu Glu Gly Cys	Ile Ser Val Lys Asp	His Arg Thr

1250	1255	1260
Ser Gln Asn His Ser Lys Cys	Ile Thr Glu Cys Val	Arg Thr Ala
1265	1270	1275
Leu Asn Gln Arg Lys Val Val	Lys Asn Pro Ser Gln	Pro Val Pro
1280	1285	1290
Leu Arg Asn Asp Gly Ile Thr	Asn Gly Asn Asp Ser	Thr Arg Ser
1295	1300	1305
Cys Ser Ile Ser Leu Lys Lys	Ser Leu Glu Lys Met	Pro Leu Met

1310	1315	1320

Asn Ala	Lys Lys Met Glu Asp	Met Ile Trp Glu Ser	Asn Met Gly
1325	1330	1335	
Gly Asn	Arg Ser Ile Cys Leu	Thr Arg Leu Pro Cys	Lys Val Thr
1340	1345	1350	
Glu Ser	Ser Gln Arg Pro Pro	Arg Ser Ile Leu Ser	Leu Ala Ser
1355	1360	1365	
Arg Ala	Gly Gln Phe Pro Val	Trp Arg Arg Thr Ser	Arg Gly Met
1370	1375	1380	
Ser Leu	Gln Trp Lys Ser Gly	Asn Ala Cys Thr Pro	Leu Arg Cys
1385	1390	1395	
Pro Ser	Arg Ser Pro Ala Thr	Phe Leu Thr Ala Leu	Asn Gly Trp
1400	1405	1410	
His Arg	Ser Gly Leu Arg Ala	Gln Gln Pro Ser Leu	Pro Gly Pro
1415	1420	1425	
Cys Ala	Ser Leu Leu Ser Thr	Leu Ser Gln Pro Pro	Pro Gln Ala
1430	1435	1440	
Pro Ser	Gln Val Trp Thr Ala	Ala Thr Leu Arg Cys	Pro Ala Val
1445	1450	1455	
Pro Ala	Ala Ala Cys Pro Pro	Ile Val Phe Phe Leu	Ala Pro Tyr
1460	1465	1470	
Phe Pro	Thr Pro Leu Ser Ile	Ser Arg Pro Thr Ser	Arg Ala Arg
1475	1480	1485	
Gln Ser	Cys Cys Leu Pro Gly	Leu Thr His Pro Ala	His Gln Pro
1490	1495	1500	
Leu Gly	Ser Met		
1505			
<210>	1156		
<211>	1501		
<212>	PRT		
<213>	Artificial Sequence		
<220><223>	Assembled poly-FSP polypeptide 2C		
<400>	1156		

Arg Gln Ile Asn Arg Arg Lys Leu Gln Arg Lys Lys Arg Arg Lys Lys
 1 5 10 15
 Arg Glu Asp His Cys Gly Leu Arg Ala Arg Asn Arg Asn Met Lys Lys
 20 25 30
 Thr Met Ser His Leu Ile Ala His Gln Ala Leu Lys Met Ser Gly Leu
 35 40 45
 Arg Leu Phe His Pro Arg Leu Leu Thr Arg Lys Lys Pro Gly Lys Asn
 50 55 60
 Pro Arg Arg Lys Thr Trp Lys Met Arg Lys Lys Tyr Ala Gln Lys Pro
 65 70 75 80
 Ser Gln Lys Asn His Leu Tyr Gly Lys Gly Leu Thr His Pro Val Pro
 85 90 95
 Leu Lys Arg Thr Leu Gln Asn Lys Arg Asn Lys Asn Ile Lys Arg Val
 100 105 110
 Asn Gln Lys Lys Gly Asn Ile Lys Arg Lys Ser Ile Leu Leu His Leu
 115 120 125
 Ile Val Leu Asn Ser Pro Glu Ser Asn Leu Gln Ala His Pro Gln Val
 130 135 140
 Pro Ala Leu Ala Pro Gln Ala Trp Trp Pro Ala Arg Arg Gly Pro Leu
 145 150 155 160
 Thr Ser Ala Pro Ser Ala Gln Gln Ser Leu Thr Phe Leu Pro Ser Arg
 165 170 175
 Phe Pro Trp Gly Pro Pro Pro Leu His Trp Asn Ser Ala Tyr Leu Gly
 180 185 190
 Arg Thr Leu Leu Val Thr Cys Ile Leu Tyr His Arg Trp Ile Val Thr
 195 200 205
 Ser Met Cys Gln Ser Gln Arg Trp Leu Thr Ser Thr Thr Ser Arg Ser
 210 215 220
 Ser Ala Leu Met Trp Thr Gln Trp Ser Ser Val Thr Ser Leu Glu Trp
 225 230 235 240
 Thr Ala Gln Glu Arg Gly Cys Ser Ser Trp Leu Met Lys Gln Thr Trp

245 250 255
 Met Lys Ser Trp Ser Leu Arg Asp Pro Ser Tyr Arg Ser Ile Leu Glu
 260 265 270
 Tyr Val Ser Thr Arg Val Leu Trp Met Pro Thr Ser Thr Val Gly Ala
 275 280 285
 Leu Arg Ala Thr Ala Pro Ala Thr Ala Ala Pro Gln Ala Gln Thr Pro

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

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

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

 485 490 495

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

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

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

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

740 745 750
 Ile Tyr Pro Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly Ile Arg Met
 755 760 765
 Cys Ala Leu Ser His Pro Ser Phe Tyr Ile Ser Ser Thr Val Cys Phe
 770 775 780
 Leu Ser Lys His Cys Met Thr Ala Cys Thr Arg Glu Lys Ile Ile Asn
 785 790 795 800
 Pro Thr Ile Ser Cys Pro Phe Gln Ser Pro Thr Lys Arg Leu Gly His

 805 810 815
 Arg Glu Gly Ser Glu Ser Asp Asn Leu Gly Leu Leu Tyr Ser Phe Pro
 820 825 830
 Pro Trp Leu Pro Met Arg Ser Leu Gly Glu Pro Trp Arg Ala Gly Phe
 835 840 845
 Gln Trp Gly Glu Ser Pro Trp Gln Val Met Ala Ser Leu Thr Gly Asn
 850 855 860
 Ser Val Ile Val His Lys Ile Val Leu Val Phe Leu Lys Ser Leu Ser

 865 870 875 880
 Ser Tyr Asn Cys Glu Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile
 885 890 895
 Glu Phe Ala Val Leu Lys Leu Leu Asn Met Asp Leu Ala Ser Pro Gln
 900 905 910
 Ile Met Gln Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg Arg Met
 915 920 925
 Gln Asn Leu Asp Asn Leu Gly Val Pro Trp Pro Leu Leu Pro Gly Ala

 930 935 940
 Ala Pro Pro His Arg Leu Leu Gly Pro Ser Arg Trp Ile Leu Phe His
 945 950 955 960
 Val Arg Asn Ile Val Tyr Gly Ile Gln Val Met Leu Cys Arg Arg Arg
 965 970 975
 Asn Ser Arg Lys Gln Ser Gln Val Gln Leu Ala Ile Gln Val Leu Leu
 980 985 990

Val Asp Lys His Lys Tyr Phe Leu Phe Gly Pro Tyr Pro Ile Ser Glu

995	1000	1005
Gly Leu Thr Met Thr Thr Gly Arg Asn Ile Asn Ser Asn Ser Leu		
1010	1015	1020
Met Thr Asn Cys Leu Phe Ser Pro Ile Phe Leu Cys His His Ala		
1025	1030	1035
Ile Met His Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe Ser		
1040	1045	1050
Ser Lys Ile Pro His Pro Gln Val Pro Ser Val Val Ala Leu Cys		

1055	1060	1065
Lys Phe Leu Ala Asn Gly Leu Trp Phe Asn Leu Ile Phe Gln Lys		
1070	1075	1080
Lys Gly His Met Ile Phe Ser Pro Lys Phe Phe Leu Thr Phe Ser		
1085	1090	1095
Gln Arg Thr Leu Glu Ser Ala Gly Leu Phe Pro Trp Leu His Thr		
1100	1105	1110
Gln Cys Arg Asn Lys Lys Thr Lys Leu Trp Phe Ser Leu Ile Asn		

1115	1120	1125
Ile His His Arg Lys Asn Pro Leu Leu Pro Met Arg Met Ser Arg		
1130	1135	1140
Thr Pro Pro Arg Arg Val Cys Gly Ser Pro Pro Leu His Leu Cys		
1145	1150	1155
Gln Pro Leu Arg Gly Gly Lys Lys Arg Ser Lys Phe Ala Phe Trp		
1160	1165	1170
Lys Pro Pro Ser Gln Gly Ile Ser Ser Cys Leu Met Thr Gly Cys		

1175	1180	1185
Trp Gly Ser Cys Gly Arg Ala Cys Ser Cys Gly Arg Gly Cys Gly		
1190	1195	1200
Thr Pro Arg Gly Asp Trp Lys Arg His Pro Pro Arg Arg Glu Leu		
1205	1210	1215
Ser Leu Glu Pro Trp Ile Pro Tyr Leu His Gln Gln Lys Thr Gln		

1220 1225 1230
Arg Lys Arg Met Lys Thr Gly Ala Ile Gln Glu Lys Gly Ala Ile

1235 1240 1245
Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe

1250 1255 1260
Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro Glu Lys Ile

1265 1270 1275
Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile Asn Val

1280 1285 1290
Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu Lys

1295 1300 1305
Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln

1310 1315 1320
Arg Leu Phe Ile Lys Gly Tyr Gln Asn Asn His Phe Thr Phe His

1325 1330 1335
Leu Gln Asn Phe Ala Phe Phe Ser Ser Phe Gly Asn Asn Lys Tyr

1340 1345 1350
Ile Asn Ile Leu Thr Arg Ala Phe Ile His Thr Pro Arg Ser Pro

1355 1360 1365
Gly Cys Ser Val Tyr Ala Asn Met Cys Trp Arg Lys Met Gln Ser

1370 1375 1380
Leu Asn His Pro Ser Arg Leu Thr Asn Cys His Pro Ala Trp Leu

1385 1390 1395
Ser Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe His

1400 1405 1410
Val Leu Ala Leu Glu Val Thr Phe Pro Pro Gly Thr Ala Met Pro

1415 1420 1425
Gln Met Gln Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp

1430 1435 1440
Lys Gln Glu Lys Lys Ser Arg Lys Leu Met Ser Ser Cys Leu Glu

1445 1450 1455

Lys Lys Ala Thr Trp Met Arg Arg Thr Pro Gly Thr Ser Leu Gln

1460 1465 1470

Cys Tyr Leu Asn Thr His Pro Cys Thr Met Leu Leu Pro Gln Gly

1475 1480 1485

Ile Pro Ser Leu Asn Ala Gln Trp Met Phe Leu Arg Ile

1490 1495 1500

<210> 1157

<211> 1506

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 3C

<400> 1157

Pro Ile Pro Pro His Leu Arg His Pro Leu Leu Lys Asn Lys Lys

1 5 10 15

Arg Arg Lys Leu Arg Pro Lys Ser Arg Lys Lys Gly His Thr Lys Asn

20 25 30

Arg Arg Lys Ala Lys Arg Lys Pro Gln Ile Arg Asn Ser Arg Arg Ala

35 40 45

Thr Pro Thr Ser Lys Gly Ser Leu Arg Arg Lys Tyr Leu Arg Val Gly

50 55 60

Ala Ala Ala Ala Ser Cys Gln Ser Pro Pro Ser Pro Arg Glu Thr Thr

65 70 75 80

Pro Ser Ser Asp Ala Thr Arg Arg Thr Arg Pro Ile Ala Ala Gln Ser

85 90 95

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

100 105 110

Pro Ala Gly Lys Leu Lys Lys Gln Val Ser Val Tyr Ser Gly Asn Leu

115 120 125

Leu Ser Phe Ser Arg Arg Gly Met Lys Ser Ser Val Arg Leu Lys Asn

130 135 140

Cys Thr Asn Leu Ser Val Pro Met Met Leu Thr Ile Leu Ile Trp Lys

145	150							155							160						
Arg	Val	Phe	Ile	Leu	Leu	Leu	Ser	Asp	Lys	Lys	Ser	Ile	Pro	His	Val						
165								170				175									
Pro	Lys	Ala	Thr	Ala	Ala	His	Ser	Val	Thr	Val	Lys	Leu	Gln	Ser	Arg						
180								185				190									
Arg	Asn	Arg	Arg	Tyr	Arg	Lys	Ile	Tyr	Gly	Glu	Leu	Lys	Met	Ser	Leu						
195								200				205									
Gln	Ala	Ser	Asn	Gly	Met	Glu	Ala	Cys	Gly	Thr	His	Pro	Thr	Pro	Arg						
210								215				220									
Leu	Ser	Val	Ser	Val	Ile	Thr	Met	Lys	Leu	Trp	Glu	Lys	His	Phe	Lys						
225				230				235				240									
Gly	Leu	Asn	Trp	Asn	Leu	Val	Val	Trp	Ile	Leu	Asn	Leu	Lys	Met	Met						
245								250				255									
Leu	Lys	Lys	Lys	Tyr	Leu	Val	Gln	Arg	Glu	Trp	Glu	Lys	Arg	Lys	Gln						
260								265				270									
Ile	Leu	Gly	Gly	Gly	Gly	Lys	Tyr	Lys	Glu	Tyr	Phe	Leu	Lys	Arg	Ile						
275								280				285									
Leu	Ile	Arg	Lys	Ala	Met	Thr	Val	Leu	Ala	Gly	Asp	Lys	Lys	Gly	Leu						
290				295				300													
Gly	Arg	Phe	Met	Arg	Cys	Val	Gln	Ser	Glu	Thr	Lys	Ala	Val	Ser	Leu						
305				310				315				320									
Gln	Leu	Pro	Leu	Gly	Arg	Met	Asp	Leu	Asp	Gly	Met	Leu	Thr	Val	Ile						
325								330				335									
Gly	Gln	Gly	Leu	Val	Gly	Met	Thr	Pro	Arg	Asp	Leu	Gly	Thr	Val	Ala						
340								345				350									
Gly	Ala	Thr	Ala	Gln	Ile	Gln	Arg	Pro	Ile	Gln	Val	Gln	Thr	Gly	Gly						
355				360				365													
Arg	Leu	Arg	Gly	Pro	Arg	Arg	Lys	Val	Leu	Met	Val	Leu	Trp	Leu	Pro						
370				375				380													
Ala	Asn	Gln	Ser	Leu	Gln	Lys	Ser	Gln	Val	Phe	Gln	Trp	Val	Leu	Arg						
385				390				395				400									

Thr Glu Leu Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser Arg His
405 410 415

Asp Leu Pro Arg Met Leu Pro Ile Ser Ser Pro Leu His Arg Pro Gln
420 425 430

Met Pro Phe Trp Thr Cys Thr Phe Pro Ala Thr Thr Trp Gly Thr Trp
435 440 445

Glu Thr Pro Ser Thr Trp Gly Trp Arg Thr Phe Ala Arg Gln Pro Ser
450 455 460

Arg Pro Thr Gly Arg Thr Pro Thr Thr Arg Leu Met Ala Pro Val Gly
465 470 475 480

Ser Val Met Ser Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala
485 490 495

Cys Thr Met Pro Pro Leu Leu His Pro Gln Trp Ala Pro His Ser Ala
500 505 510

Gly Leu Ser Pro Gly Ala Cys Arg Pro Ala Cys Thr Cys Ile Ser Met
515 520 525

Thr Thr Ile Ser Arg Ala Thr Trp Arg Arg Asn Leu Gln Arg Asn Leu
530 535 540

Lys Val Leu Arg Leu Arg Ile Pro Ser Leu Arg Lys Tyr Arg Gln Gln
545 550 555 560

Asn Thr Arg Ser Thr Asn Leu Glu Lys Asn Pro Ser Leu Lys Lys Gln
565 570 575

Ser Gln Arg Arg Gly Lys Leu Ser Leu Thr Thr Leu Ser Phe Val Leu
580 585 590

Ile Glu Glu Leu Leu Lys Lys Ser Ser Gln Leu Arg Arg Ser Trp Arg
595 600 605

Asn Val Ser Arg Ile Ser Asn Ile Arg Lys Leu Ile Trp Thr Lys Gln
610 615 620

Arg Ser Phe Leu Ser Leu Phe Pro Lys Leu Arg Ala Thr Glu Gln Met
625 630 635 640

Thr Asn Val Gly Cys Arg Leu Asp Phe His Pro Arg Ser Ser Ser Gly

645	650	655	
Asp Arg Val Phe Leu Val Lys Ile Gln Ser Ser Pro Phe Leu Ala Arg			
660	665	670	
Ser Trp Asn Thr Met Gln Trp Asn Asn Lys Lys Met Ala Met Thr Val			
675	680	685	
Ile Ala Gly Ala His His Cys Gln Tyr Lys Leu Thr Tyr Thr Lys Val			
690	695	700	
Trp Lys Met Asn Trp Lys Lys Met Met Ile Gly Ser Gln His Leu Leu			
705	710	715	720
Phe Ser Pro Leu Asp Ser Ser Pro Leu Gln Leu Leu Leu His Pro His			
725	730	735	
Gly Lys Arg Cys Asn Pro Cys Cys Arg Leu Thr Trp Met Ser His Leu			
740	745	750	
Asn Arg Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu Thr Met			
755	760	765	
Met Met Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile Pro Leu			
770	775	780	
Pro Ser Pro Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His Pro Pro			
785	790	795	800
Pro Pro Cys Leu Leu Leu Leu His His Arg His His Leu Ala Phe Leu			
805	810	815	
Glu Met Ala Cys Ser Ser Gln His Thr His Ser Ile Lys Ile Trp Ile			
820	825	830	
Ser Phe Ser His Glu Thr Met Ser Leu Ser Asn Ile Leu Met Lys Phe			
835	840	845	
Arg Leu Thr Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg			
850	855	860	
Ala Arg Gly Gly Thr Thr Ile Gly Glu Val Thr Ser Ser Leu Phe Phe			
865	870	875	880
Ser His Cys Leu Cys Val Ala Pro Arg Cys Pro Arg Ser Ala Val Asp			
885	890	895	

Ile Ser Pro Gly Pro Thr Ser Pro Ser Leu Ala Ser Cys Ala Ser Val
 900 905 910

Ala Ile Gly Lys Leu Ala Leu Leu Gly Ala Ser Ala Pro Cys Gly Ala
 915 920 925

Ala Gly Ala Arg Glu Ala Gly Arg Phe Ala Val Leu Gly Thr Met Val
 930 935 940

Met Lys Asn Met Glu His Arg Leu Thr Met Asp Ser Ala Leu Ser Leu
 945 950 955 960

Thr Lys Arg Glu Gly Pro Glu Thr Gly Pro Val Tyr Tyr Val Cys Asn
 965 970 975

Arg Met Asn Val Ser Ser Val Leu Lys Pro Phe Leu Phe Thr Val Pro
 980 985 990

Ile Glu Asp Met Arg Glu Cys Thr Leu Gly Arg Asn Arg Met Asn Val
 995 1000 1005

Ser Ser Val Leu Lys Pro Cys Leu Ile Pro Val Pro Ile Cys Lys
 1010 1015 1020

Lys Lys Leu Leu Leu Lys Leu Leu Arg Gly Ala Ser Ser Ser Thr
 1025 1030 1035

Ser Arg Asp Ser Arg Ser Phe Phe Thr Ser Ala His Pro Ser Arg
 1040 1045 1050

Pro Cys Arg Met Arg Leu Tyr Gln Met Leu Gln Lys Gln Cys Cys
 1055 1060 1065

Tyr Asn Leu Val Ile Lys His Pro Leu Ile Phe Arg Ile Asn Leu
 1070 1075 1080

Arg Arg Gln Gly Lys Thr Lys Asp Gly Val Val Gln Ser Leu Gly
 1085 1090 1095

Phe Leu Asn Gln Gln Ile Ile Leu Gln Lys Glu Phe Phe Ile Cys
 1100 1105 1110

Leu Leu Met Phe Ile Lys Arg Trp Lys Pro Ala Ala Thr Lys Lys
 1115 1120 1125

Gly Lys Asn Ser Pro Cys Cys Gln Lys Lys Leu Arg Val Gln Asn

1130	1135	1140
Gln Gly His Leu Leu Met Ile Leu Leu His Asn Arg Gly Pro Pro		
1145	1150	1155
Leu His Thr Arg Phe Glu Lys Lys Arg Pro Glu Trp Leu Ser Arg		
1160	1165	1170
Lys Ser Gly Val Met Lys Cys Trp Asp Leu Cys Pro Ala Phe Ser		
1175	1180	1185
Gly Arg Ile Leu His Gln Pro Glu Met Ala Ala Met Arg Leu Met		
1190	1195	1200
Pro Lys Phe Leu Asn Ser Thr Asn Ser Trp Trp Thr Val His Lys		
1205	1210	1215
Lys Arg Gly Leu Phe His Gln Met Lys Cys Leu Thr Ala Val Asp		
1220	1225	1230
Cys Leu Gln Ala Phe Trp Asp Met Ser Glu Lys Lys Arg Lys Leu		
1235	1240	1245
Pro Met Ile Arg Lys Ile Gln Lys Arg Arg Arg Thr Ala Asn Arg		
1250	1255	1260
Asn Ile Glu Ile Thr Pro Gln Arg Ser Lys Ala His Leu Lys Lys		
1265	1270	1275
Thr Ser Ala Lys Gly Ala Lys Lys Ile Thr Phe Leu Cys Leu Arg		
1280	1285	1290
Val Arg Cys Gly Gly Trp Leu Cys Gly Trp Thr Pro Arg Gly Trp		
1295	1300	1305
Leu Lys Lys Ser Thr Lys Ser Arg Leu Cys Phe Phe Tyr Leu Leu		
1310	1315	1320
Tyr Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe Thr Pro Pro Pro		
1325	1330	1335
Leu Ile Leu Trp Pro Gln Ala Ala Pro Gly Glu Lys Leu Lys His		
1340	1345	1350
Cys Phe Lys Ala Trp Gly Val Asp Pro Pro Gly Ser Val Trp Ile		
1355	1360	1365

Leu Pro Cys Phe Leu Ile His Leu Arg Lys Val Asp Thr His His
 1370 1375 1380
 Leu Gln Val Val Thr Lys Thr Val Thr Ala Thr Thr Ala Asp Gly
 1385 1390 1395
 Gln Arg Met Arg Arg Leu Lys Cys Lys Ala Cys Arg Leu Arg Trp
 1400 1405 1410

Ala Arg Pro Glu Pro Ala Ala Gln Ala Pro Pro Lys Ser His Phe
 1415 1420 1425
 Pro Pro His Pro Ser Gly Pro Ser Arg Thr Ser Ser Leu Gln Leu
 1430 1435 1440
 Arg Thr Tyr Met Glu Met His Tyr Gly His Gln Ala Pro Gln Val
 1445 1450 1455
 Ala Met Leu Pro Lys Leu Leu Cys Arg Gln Met Leu Pro Thr Leu
 1460 1465 1470

Ser Thr Leu Gln Gln Arg His Pro Gln Gly Pro Cys Pro Pro Pro
 1475 1480 1485
 Val Thr Pro Leu Arg Val Gln Ser Val Leu Leu Leu Gly Val Pro
 1490 1495 1500

Gln Thr Ala
 1505

<210> 1158

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 4C

<400> 1158

Asp Ser Lys Lys Met Thr Gln Lys Asn Arg Lys Thr Arg Lys Ala Ala
 1 5 10 15

Arg Glu Lys His Arg Lys Thr Asp Asn Leu Asp Leu Gln His Gln Arg
 20 25 30

Arg Arg Lys Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro
 35 40 45

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

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

Lys Ser Arg Gln Met Glu Ser Leu Gly Met Lys Leu Gln Ile Thr His
 545 550 555 560
 Pro Phe Ala Ser Gln Pro Leu Gly Gln Glu Met Pro Asn Asn Thr Gln
 565 570 575
 Ile Arg Leu Leu Lys Pro Gly Gln Ala Phe Gly Ser Phe Ser Ala Asp
 580 585 590

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

 Leu Trp Asp Cys Ser Thr Thr Thr Gly Thr His His Gly Cys Leu Trp
 660 665 670
 Glu Ile Pro Ser Val Thr Leu Leu Ala Thr Ala Lys Lys Ser Pro Thr
 675 680 685
 Ser Phe Cys Cys Gln Arg Pro Pro Leu Gln Pro Val Glu Glu Lys Lys
 690 695 700
 Asn Gly Arg Ile Ser Ser Val Pro Pro Ser Pro Pro Leu Ala Leu Gly
 705 710 715 720

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

 Leu Gly Gly Phe Gln Ile Pro Asn Phe Phe Trp Ser Leu Gly Ile Gly

785	790	795	800
His Thr Gly Ala Trp	Trp His Thr Gly Arg Arg Arg Arg Glu Trp Gly		
	805	810	815
Gly Ser Thr Val Ser Arg Ser Pro Leu Trp Ile Ser Ser Met Ile Tyr			
	820	825	830
Leu Arg Gly Met Ala Phe Ala Ser Asp Ser Ser Ile Arg Thr Thr Arg			
	835	840	845
Val Ser Trp Cys Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala Ser Ser			
	850	855	860
Asp Lys Lys Lys Lys Ser Thr Glu Lys Thr Lys Asn Lys Ile Ile Cys			
	865	870	875
Lys Gly His Arg Ile Thr Gln Val Val Leu Arg Leu Gly Asn Leu Pro			
	885	890	895
Pro Phe Phe Arg Gly Ser Glu Val Pro Phe Pro Arg Pro Cys Arg Thr			
	900	905	910
Lys Cys Gln Lys Lys Val Pro Ser Ala Ser Pro Trp Gly Leu His Pro			
	915	920	925
Arg Thr Ala Ser Ile Thr Leu Pro Thr Thr Ser Leu Lys Gly Ser Arg			
	930	935	940
Thr Ser Cys Cys Pro Arg Ser His Pro Arg Leu Pro Arg Thr Lys Trp			
	945	950	955
Pro Leu Gln Cys Leu Leu His Ser Leu Gly Thr Thr Gly Thr Leu Val			
	965	970	975
Trp Glu Arg Gly Val Leu Gln Met Arg Ser Leu Glu Ala His Cys Pro			
	980	985	990
Leu Gln Thr Phe His Leu His His Cys Arg Thr Gln Pro Ser Ser Cys			
	995	1000	1005
Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln Trp Ser Gly Ala Val			
	1010	1015	1020
Val Gly Leu Arg Pro Val Ala His His Leu Pro Arg Pro Ile Gln			
	1025	1030	1035

Gly Leu	His Cys	Pro Gln	Ala	Pro His	Gln Pro	Ala	Leu Ser	Trp
1040			1045			1050		
Gly Lys	Trp Pro	Val Gly	Met	Thr Gly	Pro Ala	Arg	Cys Cys	Arg
1055			1060			1065		
Trp Pro	Arg Arg	Met Cys	Ser	Ser Leu	Ala Leu	Pro	Thr Gly	Leu
1070			1075			1080		
Thr Ser	Leu Ile	Leu Pro	Ser	Ser Asp	Leu Ala	Val	Leu Ile	Ser
1085			1090			1095		
Ser Ser	Thr Ser	His Phe	Leu	Met Arg	Ser Pro	Val	Leu Pro	Ser
1100			1105			1110		
Ser Arg	Leu Thr	Cys Ala	Ser	Pro Gln	Leu Pro	Arg	Met Trp	Thr
1115			1120			1125		
Trp Ser	Ser Trp	Leu Lys	Glu	Trp Gly	Gly Gln	Ala	His Arg	Gln
1130			1135			1140		
Arg Asn	Cys Arg	Val Asn	Ala	Val Glu	Glu Leu	His	Ser Arg	Arg
1145			1150			1155		
Met Ser	Val Arg	Ile Val	Lys	Asn Trp	Val Ser	Cys	Cys Tyr	Val
1160			1165			1170		
Arg Leu	Ser Ala	Val Gly	Leu	Ser Thr	Trp Ser	Ala	Leu Asp	Ser
1175			1180			1185		
Leu Ile	Leu Ser	Phe Gln	Arg	Val Lys	Thr Ser	Arg	Ile Leu	Asn
1190			1195			1200		
Leu Gln	Val Leu	Lys Lys	Ile	Leu Arg	Ser Phe	Met	Lys Leu	Tyr
1205			1210			1215		
His Ser	Leu Val	Met Cys	Leu	Arg Leu	Arg Thr	Lys	Leu Glu	Lys
1220			1225			1230		
Ala Leu	Ser Ala	Leu Phe	Ile	Trp Pro	Gln His	Ser	Tyr Lys	Gly
1235			1240			1245		
Gln Ala	Phe Gly	Ser Leu	Cys	Gln Leu	Val Ser	Ala	Asp Phe	Ser
1250			1255			1260		
Ala Pro	Gln Val	Thr Arg	Leu	Arg Ser	Leu Asn	His	Leu Leu	Ile

1265	1270	1275
Arg Trp Ile Phe Ser Asn Gln	Leu Thr Val Gln Met	Leu Cys Leu
1280	1285	1290
Pro Ile Ile Lys Lys Met Lys	Lys Arg Ile Met Val	His Val Leu
1295	1300	1305
Lys Lys Asn Arg Lys Gln Ile	Ile Cys Ile Lys Asn	Met Phe Leu
1310	1315	1320
Gln Arg Lys Gly Phe Leu Asn	Leu Ser His Val Glu	Lys Phe Arg
1325	1330	1335
Glu Ser Thr Leu Gly Asn Phe	Trp Met Lys Leu Leu	Gln Leu Pro
1340	1345	1350
Pro Ala Cys Thr Ser Lys Ala	Trp Thr Pro Arg Lys	Leu Val Gly
1355	1360	1365
Arg Ala Val Arg Arg Lys Gly	Val Val Ile Asn Leu	Lys Arg Leu
1370	1375	1380
Gln Lys Phe Arg Ala Ser Val	Ser Phe Trp Thr Leu	Leu Pro Thr
1385	1390	1395
Thr Gly Val Arg Thr Arg Gly	Ser Pro Leu Arg Leu	Thr Leu Trp
1400	1405	1410
Pro Pro Arg Ser Gln Lys Ser	Gln His His Cys Ala	Leu Arg Lys
1415	1420	1425
Ile Glu Trp Ala Thr Lys Leu	Ser Leu Gly Gly Lys	Ala Gly Pro
1430	1435	1440
Gln Ala Gln Glu Lys Ala Asn	Ile Leu Asn Ser Leu	Pro Ser Ser
1445	1450	1455
Met Glu Ile Ala Val Leu Gln	Glu Met Leu Asn Gln	Lys Cys Leu
1460	1465	1470
Ala Pro Phe Glu Leu Lys Lys	Asn Leu Leu Leu Pro	Thr Tyr Thr
1475	1480	1485
Pro His Ile Cys Arg His Thr	Leu Lys Lys Lys Pro	Arg Asp Ile
1490	1495	1500

Cys Arg Ile Ser

1505

<210> 1159

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 1D

<400> 1159

Ala Asp Lys Lys Asn Val Arg Ser Ala Ser Ser Pro Gly His Pro Leu

1 5 10 15

Gly Pro Arg Arg Met Thr Arg Arg Thr Met Thr Thr Thr Lys Met Met

20 25 30

Met Met Arg Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg Arg Met Thr

35 40 45

Met Met Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu Thr Pro

50 55 60

Arg Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile Ser Gln

65 70 75 80

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

85 90 95

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

100 105 110

Ser Ile Ser Arg Pro Thr Ser Arg Ala Arg Gln Ser Cys Cys Leu Pro

115 120 125

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

130 135 140

Gly Thr Gly Gly Gly Pro Ala Cys Val Pro Val Ala Glu Ala Ser Thr

145 150 155 160

Gly Ala Trp Thr Ala Glu Gly Ala Ala Gly Thr Arg Cys Arg Ala Ser

165 170 175

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

180	185	190	
Ile Cys Val Lys Arg Arg Arg Arg Arg Lys Arg Ser Ser Gln Ser Arg			
195	200	205	
Ser Pro Val Pro Lys Lys Arg Glu Arg Met Met Leu Pro Val Arg Ala			
210	215	220	
Arg Thr Ala Arg Ser Ala Leu Pro Gln Gly Arg Ala Pro Leu Glu Gly			
225	230	235	240
Met Leu Leu Pro Arg Ala Leu Pro Ser Leu Leu Ser Arg Met Pro Ala			
245	250	255	
Arg Arg Glu Ser Arg Phe Trp Leu Ala Leu Gln Ala Leu Gly Leu Arg			
260	265	270	
Pro Pro His Leu Pro Ser Cys His Pro Leu Pro Gln Leu Leu Gly Pro			
275	280	285	
Pro Pro Pro His Gln Ala Pro Gly Glu Lys Asn Asp Leu Gln Leu Phe			
290	295	300	
Val Met Ser Asp Thr Thr Tyr Lys Ile Tyr Trp Thr Val Ile Leu Leu			
305	310	315	320
Asn Pro Cys Gly Asn Leu His Leu Lys Thr Thr Ser Leu Asn Ala Lys			
325	330	335	
Lys Met Glu Asp Met Ile Trp Glu Ser Asn Gln Gln Leu Lys Trp Thr			
340	345	350	
Pro His Ile Leu Lys Ser Ala Ser Ile Ala Lys Lys Arg Ile Lys Leu			
355	360	365	
Arg Arg Asn Ser Thr Arg Arg Glu Met Pro Ser Gln Ala Thr Pro Ser			
370	375	380	
Pro Pro Gly Pro Trp Arg Ala Ala Leu Gly Lys Glu Val Lys Arg Ser			
385	390	395	400
Gln Ser Lys Leu Arg Leu Arg Asn Thr Ser Pro Phe Asp Lys Lys Gly			
405	410	415	
Phe Val Ile Leu Ser Asn Met Gly Gly Asn Arg Ser Ile Cys Leu Thr			
420	425	430	

Ile Val Phe Phe Leu Ala Pro Tyr Phe Pro Met Pro Ser Ser Trp Ser
435 440 445

Ser Ser Gly Arg Thr Arg Leu Pro Leu Arg Pro Gln Arg Gly Pro Arg
450 455 460

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

Gly Asp Cys Pro Arg Thr Met Ala Gly Pro Ser Ala Ser Leu His Pro
485 490 495

Ala Ser Gly Arg Ala Ser Arg Lys Thr Trp Gln Arg Arg Leu Arg Ala
500 505 510

Cys Arg Ala Gly Gly Pro Ala Gly Trp Ala Arg Gln Ala Arg Lys Arg
515 520 525

Lys Arg Glu Lys Arg Ser Gln Lys Ser Arg Gln Asn His Leu Gln Leu
530 535 540

Lys Ser Cys Arg Arg Lys Ile Ser Asn Trp Ser Lys Leu Arg Ser Pro
545 550 555 560

Trp Ile Phe Glu Ala Lys Lys Ser Met Lys Arg Ser Gln Arg Pro Pro
565 570 575

Arg Ser Ile Leu Ser Leu Phe Lys Lys Lys Lys Pro Leu Thr Phe Ser
580 585 590

Pro Ser Val Ser Lys Lys Arg Leu Pro Lys Leu Lys Gly Lys Lys Arg
595 600 605

Arg Lys Glu Ile Gln Arg Lys Val Val Lys Asn Pro Ser Gln Pro Val
610 615 620

Pro Leu Arg Asn Asp Gly Ile Thr Asn Gly Asn Asp Ser Thr Arg Ser
625 630 635 640

Cys Ser Ile Ser Leu Lys Lys Ser Leu Glu Lys Met Pro Leu Met Arg
645 650 655

Ser Leu Leu Tyr Ser Arg Met Cys Leu Val Gln Ile Pro Thr His Thr
660 665 670

Trp Glu Pro Asp Tyr Phe Val Ser Leu Pro Met Met Phe Ser Trp Ala

675	680	685	
Thr Gln Ser Phe Pro Val Gly Ala Val Phe Leu Thr Arg Pro Ala Ile			
690	695	700	
Pro Cys Cys Ser Cys Thr Ser His Ser Asn Pro Trp Ser Gln Ser Thr			
705	710	715	720
Leu Ala Ile Arg Phe Ile Ser Ala Pro Gln Pro Ser Ser Ser Thr Val			
725	730	735	
Thr Ala Ala Pro Ser Gly Gln Tyr Phe Ala Leu Arg Ser Met Pro Lys			
740	745	750	
Ser Arg Asn Gln Val Leu Phe Arg Arg Asn Leu Thr Pro Ser Gln Leu			
755	760	765	
Arg Thr Leu Ala Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln			
770	775	780	
Ser Leu Ser Arg Lys Gln Ile Pro Ser Gln Ser Met Leu Val Arg Thr			
785	790	795	800
Arg Leu Thr Leu Thr Gly Thr Arg Ser Ser Gly Thr Arg Ala Ser Pro			
805	810	815	
Ser Ala Val Cys Leu Cys Cys Trp Thr Cys Pro Ser Arg Ser Phe Pro			
820	825	830	
Ala Ala Ser Pro Ser Gly Leu Arg Ala Pro Val Gly Ala Gln Ala Pro			
835	840	845	
Pro Glu Val Thr Leu Arg Ala Ser Cys Ala Ser Ser Ala Ser Lys Ala			
850	855	860	
Cys Ala Gly Leu Trp Pro Trp Gly Ala Gln Val Arg Met Lys Lys Lys			
865	870	875	880
Asp Ser Thr Ile Phe Ile Tyr Pro Arg Leu Lys Thr Phe Gly Val Pro			
885	890	895	
Leu Gly Ser Ile Leu Cys Leu Ala Gly Ser Leu Ser Thr Met Met Ile			
900	905	910	
Ile Ser Thr Thr Arg Gln Glu Cys Gly Arg Arg Ala Ser Val Pro Cys			
915	920	925	

Arg Pro Met Ile Gly Ser Ala Arg Pro Gly Pro Trp Arg Thr Ser Ala
930 935 940

Met Pro Ser Ala Met Gly Val Ala Leu Pro Thr Ser Cys Glu Ser Gly
945 950 955 960

Arg Ser Pro Pro Ala Thr Gly Gly Arg Met Pro Gly Ser Gln Ser Ile
965 970 975

Met Met Ser Trp Met Pro Pro Leu Ala Pro Cys Ala Ala Cys Pro Cys
980 985 990

Ser Pro Ala Pro Thr Leu Cys Pro Ala His Pro Ala Arg Ala Pro Thr
995 1000 1005

Ala Val Pro Ala Phe Thr Pro Leu Ser Ala His Pro Val Pro Val
1010 1015 1020

Leu Ser Gly Cys His Leu Ala Val Arg Thr Ser Met Leu Thr Leu
1025 1030 1035

Leu Pro Met Met Thr Leu Lys Ala Leu Val Lys Thr Trp Thr Gln
1040 1045 1050

Phe Arg Asn Tyr Pro Arg Arg His Pro His Arg Ser Pro Pro Thr
1055 1060 1065

Ser Cys Pro Pro Leu Leu Glu Ala Phe Pro Leu Pro Arg Ala Ser
1070 1075 1080

Leu Arg Ala Thr Val Pro Arg His Ser Ser Val Leu Ala Thr Gly
1085 1090 1095

Leu His Leu His Arg Gln Ile Ser Leu Pro Leu Arg Gly Phe Leu
1100 1105 1110

Leu His Gln Pro Leu Pro Gly Gln His Leu Trp Leu Ser His Arg
1115 1120 1125

Leu Arg Leu Arg Leu Pro Arg Thr Thr Glu Ile Gln Leu Thr Met
1130 1135 1140

Asn Asp Ser Lys His Lys Leu Glu Ser Pro Ala Leu Lys Gln Val
1145 1150 1155

Ser Pro Ala Ser Pro Pro Thr Gln Gln Pro Gln Thr Pro Gln Asp

1160	1165	1170
Ser Arg Gln Val Leu Ala Val	Pro Met Ser Leu Ala	Cys Ser Ile
1175	1180	1185
Thr Val Ser Phe Val Gly Gln	Ile Ser Thr Leu Val	Leu Asp Val
1190	1195	1200
Ser Ser Ile Ser His Trp Asn	Gly Ile Trp Glu Val	Met Pro Arg
1205	1210	1215
Thr Leu Glu Gly Cys Ile Ser	Val Lys Asp His Arg	Thr Ser Gln
1220	1225	1230
Asn His Ser Lys Cys Ile Thr	Glu Cys Val Arg Thr	Ala Leu Asn
1235	1240	1245
Thr Lys Cys Glu Ile Cys Val	Lys Asn Thr Ala Ile	Leu Ala Ile
1250	1255	1260
Thr Leu Ile Thr Pro Gln Asp	Pro His Leu Asp Pro	Val Cys His
1265	1270	1275
Pro His Arg Arg Pro Gly Trp	Lys Gly His His Arg	Val Val Phe
1280	1285	1290
Ser His His Pro Ser Gly Ser	Thr Lys Ser His Trp	Gln Gln Arg
1295	1300	1305
Glu Arg Gly Gly Gly Arg Arg	Glu Lys Lys Gly Cys	Arg Glu Ala
1310	1315	1320
Ser Arg Ala Gly Gln Phe Pro	Val Trp Arg Arg Thr	Ser Arg Gly
1325	1330	1335
Met Ser Leu Gln Trp Lys Ser	Gly Asn Ala Cys Thr	Pro Leu Arg
1340	1345	1350
Cys Pro Ser Arg Ser Pro Ala	Thr Phe Leu Thr Ala	Leu Asn Gly
1355	1360	1365
Trp His Arg Ser Gly Leu Arg	Ala Gln Thr Ala Phe	Phe Leu Leu
1370	1375	1380
Asp Ile Ile Leu Arg Arg Ala	Arg Pro Thr Ser Cys	Ser Thr Cys
1385	1390	1395

Arg Met Trp Trp Arg Leu Pro Cys Lys Val Thr Glu Ser Ser Leu
1400 1405 1410

Ala Lys Lys Thr Leu Thr Asn Gln Pro Ser Leu Pro Gly Pro Cys
1415 1420 1425

Ala Ser Leu Leu Ser Thr Leu Ser Gln Pro Pro Pro Gln Ala Pro
1430 1435 1440

Ser Gln Val Trp Thr Ala Ala Thr Leu Arg Cys Pro Ala Val Pro
1445 1450 1455

Ala Ala Ala Cys Pro Pro Leu Lys Leu Ala Pro Leu Gln Val Thr
1460 1465 1470

Thr Thr Leu Lys Leu Ile Leu Val Met Leu Glu Ile Val Thr Glu
1475 1480 1485

Asn Lys Val Arg Gln Asn Phe Lys Arg Asn Ser Ser Phe Phe Tyr
1490 1495 1500

Thr Ser Asp Arg
1505

<210> 1160

<211> 1501

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 2D

<400> 1160

Arg Lys Met Gln Ser Leu Asn His Pro Ser Arg Leu Thr Asn Asn Pro
1 5 10 15

Arg Arg Lys Thr Trp Lys Met Arg Lys Lys Tyr Ala Gln Lys Pro Ser
20 25 30

Gln Lys Asn His Leu Tyr Arg Gln Ile Asn Arg Arg Lys Leu Gln Arg
35 40 45

Lys Lys Ser Arg Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys
50 55 60

Val Lys Arg Ala Arg Asn Arg Asn Met Lys Lys Thr Met Ser His Leu
65 70 75 80

Ile Ala His Gln Ala Leu Lys Met Ser Gly Leu Arg Leu Phe His Pro
85 90 95

Arg Leu Leu Thr Arg Lys Lys Pro Gly Lys Gln Lys Lys Gly His Met
100 105 110

Ile Phe Ser Arg Arg Lys Trp Gln Ile Arg His Val Leu Lys Asn Leu
115 120 125

Ile Pro Ser Leu Asn Ala Gln Trp Met Phe Leu Arg Ile Ala Ser Pro
130 135 140

Gln Ile Met Gln Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg Arg
145 150 155 160

Met Gln Asn Leu Asp Asn Leu Gly Val Pro Trp Pro Leu Leu Pro Gly
165 170 175

Leu Leu Leu Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr Gln Lys
180 185 190

Gly Glu Cys Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu Phe Ile
195 200 205

Leu Lys Gln Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met Ala Ser
210 215 220

Pro Gln Ile Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr Ile Leu
225 230 235 240

Gln Ala His Pro Gln Val Pro Ala Leu Ala Pro Gln Ala Trp Trp Pro
245 250 255

Ala Arg Arg Gly Pro Leu Thr Ser Ala Pro Ser Ala Gln Gln Ser Leu
260 265 270

Thr Arg Thr Leu Glu Ser Ala Gly Leu Phe Pro Trp Leu His Thr Gln
275 280 285

Cys Arg Ala Phe Ile His Thr Pro Arg Ser Pro Gly Cys Ser Val Tyr
290 295 300

Ala Asn Met Cys Trp Arg Tyr Lys Lys Arg Gly Val Ile Ala Trp Arg
305 310 315 320

Ile Tyr Pro Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly Leu Ile Leu

325	330	335	
Ile Gln His Gly Gly Ile Phe Thr Phe Arg Phe Trp Val Glu Lys Leu			
340	345	350	
Ser Trp Asn Ile Cys Lys Asn Leu Ser Leu Tyr Leu Asp Lys Phe Val			
355	360	365	
Gln Arg Leu Leu Tyr Val Tyr Ile Ile Glu Thr Asn Val Phe Val Leu			
370	375	380	
Asn Leu Phe His Val Pro Val Asn Gln Ile Phe Met Met Ala Phe Tyr			
385	390	395	400
Leu Lys Tyr Thr Glu Lys Ala Trp Val Met Glu Leu Glu Trp Leu Ile			
405	410	415	
Gln Gln Gln Cys Tyr Gln Arg Lys Arg Met Lys Thr Gly Ala Ile Gln			
420	425	430	
Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys			
435	440	445	
Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro			
450	455	460	
Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile			
465	470	475	480
Asn Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu			
485	490	495	
Lys Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln			
500	505	510	
Arg Leu Phe Ile Lys Gly Tyr Gln Asn Asn His Phe Thr Phe His Leu			
515	520	525	
Gln Asn Phe Ala Phe Phe Ser Ser Phe Gly Asn Asn Lys Tyr Ile Asn			
530	535	540	
Ile Leu Thr Phe Leu Pro Ser Arg Phe Pro Trp Gly Pro Pro Pro Leu			
545	550	555	560
Gly Ala Leu Arg Ala Thr Ala Pro Ala Thr Ala Ala Pro Gln Ala Gln			
565	570	575	

Thr Pro His Trp Arg Ala Ala Thr Thr Ser Ser Met Ser Ser Ser Pro
 580 585 590
 Arg Ala Glu Pro Thr Ser Ser Ser Ser Trp Ala Thr Cys Trp Pro Arg
 595 600 605
 Cys Cys Ser Ser Ser Cys Tyr Trp Ser Leu Ser Ser Trp Pro Pro Ala
 610 615 620

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

 Met Lys Gln Asn Gly Phe Thr Arg Arg Arg Asn Ser Arg Lys Gln Ser
 690 695 700
 Gln Val Gln Leu Ala Ile Gln Val Leu Leu Val Asp Lys His Lys Tyr
 705 710 715 720
 Phe Leu Phe Gly Arg Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys Ser
 725 730 735
 Leu Pro Gln Ala Arg Leu Cys Leu Ile Val Ser Arg Thr Leu Leu Leu
 740 745 750

 Val Gln Ser Arg His Pro Ser Trp Pro Trp Thr Arg Cys Leu Arg Met
 755 760 765
 Arg Pro Pro Arg Ser His Trp Asn Ser Ala Tyr Leu Gly Arg Thr Leu
 770 775 780
 Leu Val Thr Cys Ile Leu Tyr His Arg Trp Ile Val Thr Ser Met Cys
 785 790 795 800
 Gln Ser Gln Arg Trp Leu Thr Ser Thr Thr Ser Arg Ser Ser Ala Leu
 805 810 815

 Met Trp Thr Trp Trp Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys

820	825	830	
Met Cys Lys Val Ser Gly Gly Cys Thr Ala Cys Val Glu Arg Cys Pro			
835	840	845	
Trp Lys Gly Ile Cys Trp Lys Trp Pro Val Thr Val Ala Ala Met Ser			
850	855	860	
Arg Thr Pro Pro Arg Arg Val Cys Gly His Arg Glu Gly Ser Glu Ser			
865	870	875	880
Asp Asn Leu Gly Leu Leu Tyr Ser Phe Pro Pro Val Leu Phe Lys Ala			
885	890	895	
Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly Asn Ser Val Ile Val His			
900	905	910	
Lys Ile Val Leu Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn Cys Glu			
915	920	925	
Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile Glu Phe Ala Val Leu			
930	935	940	
Lys Leu Leu Asn Met Asp Leu Gly Lys Gly Leu Thr His Pro Val Pro			
945	950	955	960
Leu Lys Arg Thr Leu Gln Asn Lys Arg Asn Lys Asn Ile Lys Arg Val			
965	970	975	
Asn Gln Lys Lys Gly Asn Ile Lys Arg Lys Ser Ile Leu Leu His Leu			
980	985	990	
Ile Val Leu Asn Ser Pro Glu Ser Asn Arg Glu Lys Ile Ile Asn Pro			
995	1000	1005	
Thr Ile Ser Cys Pro Phe Gln Ser Pro Thr Lys Arg Leu Gly Ser			
1010	1015	1020	
Pro Pro Leu His Leu Cys Gln Pro Leu Arg Pro Tyr Pro Ile Ser			
1025	1030	1035	
Glu Gly Leu Thr Met Thr Thr Gly Arg Asn Ile Asn Ser Asn Ser			
1040	1045	1050	
Leu Met Thr Asn Cys Leu Phe Ser Pro Ile Phe Leu Cys His His			
1055	1060	1065	

Ala Ile Met His Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe		
1070	1075	1080
Ser Ser Lys Ile Pro His Pro Gln Val Pro Ser Val Val Ala Leu		
1085	1090	1095
Cys Lys Phe Thr His Pro Cys Thr Met Leu Leu Pro Gln Gly Ala		
1100	1105	1110
Phe Trp Lys Pro Pro Ser Gln Gly Ile Ser Ser Cys Leu Met Thr		
1115	1120	1125
Gly Cys Trp Gln Trp Ser Ser Val Thr Ser Leu Glu Trp Thr Ala		
1130	1135	1140
Gln Glu Arg Gly Cys Ser Ser Trp Leu Met Lys Gln Thr Trp Met		
1145	1150	1155
Lys Ser Trp Ser Leu Arg Asp Pro Ser Tyr Arg Ser Ile Leu Glu		
1160	1165	1170
Tyr Val Ser Thr Arg Val Leu Trp Met Pro Thr Ser Thr Val Pro		
1175	1180	1185
Lys Phe Phe Leu Thr Phe Ser Gln Ile Arg Met Cys Ala Leu Ser		
1190	1195	1200
His Pro Ser Phe Tyr Ile Ser Ser Thr Val Cys Phe Leu Ser Lys		
1205	1210	1215
His Cys Met Thr Ala Cys Thr Pro Gly Thr Ser Leu Gln Cys Tyr		
1220	1225	1230
Leu Asn Leu Ala Asn Gly Leu Trp Phe Asn Leu Ile Phe Arg Asn		
1235	1240	1245
Lys Lys Thr Lys Leu Trp Phe Ser Leu Ile Asn Ile His His Arg		
1250	1255	1260
Lys Asn Pro Leu Leu Pro Met Arg Leu Glu Lys Lys Ala Thr Trp		
1265	1270	1275
Met Arg Arg Thr Glu Leu Ser Leu Glu Pro Trp Ile Pro Tyr Leu		
1280	1285	1290
His Gln Gln Lys Thr Gln Trp Leu Pro Met Arg Ser Leu Gly Glu		

1295	1300	1305
Pro Trp Arg Ala Gly Phe Gln Trp Gly Glu Ser Pro Trp Gln Val		
1310	1315	1320
Met Ala Ser Leu Thr Gly Arg Arg Lys Lys Arg Glu Asp His Cys		
1325	1330	1335
Gly Leu Gln Glu Lys Lys Ser Arg Lys Leu Met Ser Ser Cys Ala		
1340	1345	1350
Ala Pro Pro His Arg Leu Leu Gly Pro Ser Arg Trp Gly Ser Cys		
1355	1360	1365
Gly Arg Ala Cys Ser Cys Gly Arg Gly Cys Gly Thr Pro Arg Gly		
1370	1375	1380
Asp Trp Lys Arg His Pro Pro Arg Arg Ile Leu Phe His Val Arg		
1385	1390	1395
Asn Ile Val Tyr Gly Ile Gln Val Met Leu Cys Cys His Pro Ala		
1400	1405	1410
Trp Leu Ser Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro		
1415	1420	1425
Phe His Val Leu Ala Leu Glu Val Thr Phe Pro Pro Gly Thr Ala		
1430	1435	1440
Met Pro Gln Met Gln Leu Gln Ala Leu Ala Met Trp Glu Lys Gly		
1445	1450	1455
Trp Asp Lys Pro Leu Glu Asn Thr Gln Ile Pro Arg Thr Ser Pro		
1460	1465	1470
Leu Trp Lys Ile Thr Met Val Leu Thr Tyr Pro Asn Cys Val Val		
1475	1480	1485
His Val Leu Met Phe Gly Gly Lys Lys Arg Ser Lys Phe		
1490	1495	1500
<210> 1161		
<211> 1506		
<212> PRT		
<213> Artificial Sequence		

<220><223> Assembled poly-FSP polypeptide 3D

<400> 1161

Gln Asn Thr Arg Ser Thr Asn Leu Glu Lys Asn Pro Ser Leu Lys Lys

1 5 10 15

Gln Ser Gln Arg Arg Gly Lys Leu Ser Ser Arg Lys Lys Gly His Thr

20 25 30

Lys Asn Arg Arg Lys Ala Lys Arg Lys Pro Gln Ile Ser Gln Lys Lys

35 40 45

Asp Pro Ala Gly Lys Leu Lys Lys His Leu Asn Arg Lys Leu His Leu

50 55 60

Thr Arg Ser Cys Leu Ile Asp Leu Thr Met Met Met Ser Gln Lys Leu

65 70 75 80

Trp Lys Asn Gln Arg Lys Arg Ile Pro Leu Pro Ser Pro Arg Gln His

85 90 95

Leu Leu Pro Gln Tyr Pro Leu His Pro Pro Pro Pro Cys Leu Leu Leu

100 105 110

Leu His His Arg His His Leu Ala Phe Leu Glu Met Ala Cys Ser Ser

115 120 125

Gln His Thr His Ser Ile Lys Ile Trp Ile Ser Phe Ser His Glu Asp

130 135 140

Leu Pro Arg Met Leu Pro Ile Ser Ser Pro Leu His Arg Pro Gln Met

145 150 155 160

Pro Phe Trp Thr Cys Thr Phe Pro Ala Thr Thr Trp Gly Thr Trp Glu

165 170 175

Thr Pro Ser Thr Trp Gly Trp Arg Thr Phe Gly Pro Val Tyr Tyr Val

180 185 190

Cys Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Phe Leu Phe Thr

195 200 205

Val Pro Ile Glu Asp Met Arg Glu Cys Thr Leu Gly Arg Asn Arg Met

210 215 220

Asn Val Ser Ser Val Leu Lys Pro Cys Leu Ile Pro Val Pro Ile Leu

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

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

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

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

Ala Val Asp Cys Leu Gln Ala Phe Trp Asp Met Met Ile Arg Lys Ile
485 490 495

Gln Lys Arg Arg Arg Thr Ala Asn Arg Leu Lys Lys Lys Tyr Leu Val
500 505 510

Gln Cys Thr Asn Leu Ser Val Pro Met Met Leu Thr Ile Leu Ile Trp
515 520 525

Lys Arg Val Phe Ile Leu Leu Leu Ser Asp Lys Lys Cys Leu Arg Val
530 535 540

Arg Cys Gly Gly Trp Leu Cys Gly Trp Thr Pro Arg Gly Lys Asn Lys
545 550 555 560

Lys Arg Arg Lys Leu Arg Pro Lys His Leu Lys Lys Thr Ser Ala Lys
565 570 575

Val Ser Val Ile Thr Met Lys Leu Trp Glu Lys His Phe Lys Gly Leu
580 585 590

Asn Trp Asn Leu Val Val Trp Ile Leu Asn Leu Lys Met Met Trp Leu
595 600 605

Lys Lys Ser Thr Lys Ser Arg Gln Ser Ser Pro Phe Leu Ala Arg Ser
610 615 620

Trp Asn Thr Met Gln Trp Asn Asn Lys Lys Met Ala Met Thr Val Ile
625 630 635 640

Ala Gly Ala His His Cys Gln Tyr Lys Leu Thr Tyr Thr Lys Val Trp
645 650 655

Lys Met Asn Trp Lys Lys Met Met Ile Gly Ser Gln His Leu Leu Phe
660 665 670

Ser Pro Leu Asp Ser Ser Pro Leu Gln Leu Leu Leu His Pro His Gly
675 680 685

Lys Arg Cys Asn Pro Cys Cys Arg Leu Thr Trp Met Ser Arg Glu Trp
690 695 700

Glu Lys Arg Lys Gln Ile Leu Gly Gly Gly Gly Lys Tyr Lys Glu Tyr
705 710 715 720

Phe Leu Lys Arg Ile Leu Ile Arg Lys Ala Met Thr Val Leu Ala Gly

725	730	735
Asp Lys Lys Gly Leu Gly Arg Phe Met Arg Cys Val Gln Ser Glu Thr		
740	745	750
Lys Ala Val Ser Leu Gln Leu Pro Leu Gly Arg Arg Lys Ser Gly Val		
755	760	765
Met Lys Cys Trp Asp Leu Cys Pro Arg Leu Asp Phe His Pro Arg Ser		
770	775	780
Ser Ser Gly Gly Glu Lys Leu Lys His Cys Phe Lys Ala Trp Gly Leu		
785	790	795
800		
Cys Phe Phe Tyr Leu Leu Tyr Phe Glu Lys Lys Arg Pro Glu Trp Leu		
805	810	815
Ser Val Asp Pro Pro Gly Ser Val Trp Ile Leu Pro Cys Met Asp Leu		
820	825	830
Asp Gly Met Leu Thr Val Ile Gly Gln Gly Leu Val Gly Met Thr Pro		
835	840	845
Arg Asp Leu Gly Thr Val Ala Gly Ala Thr Ala Gln Ile Gln Arg Pro		
850	855	860
Ile Gln Val Gln Thr Gly Gly Arg Leu Phe Leu Ile His Leu Arg Lys		
865	870	875
880		
Val Asp Thr His His Leu Gln Val Val Thr Lys Thr Val Thr Ala Thr		
885	890	895
Thr Ala Asp Gly Gln Arg Met Arg Arg Leu Lys Cys Lys Ala Cys Arg		
900	905	910
Leu Arg Trp Ala Arg Pro Glu Pro Ala Ala Gln Ala Pro Pro Lys Ser		
915	920	925
His Phe Pro Pro His Pro Ser Gly Pro Ser Arg Thr Ser Ser Leu Gln		
930	935	940
Leu Arg Pro Ile Pro Pro His Leu Arg His Pro Leu Leu Leu Lys Gly		
945	950	955
960		
Lys Asn Ser Pro Cys Cys Gln Lys Lys Leu Arg Val Gln Asn Gln Gly		
965	970	975

His Leu Leu Met Ile Leu Leu His Asn Ala Arg Gln Pro Ser Arg Pro
 980 985 990

Thr Gly Arg Thr Pro Thr Thr Arg Leu Met Ala Pro Val Gly Ser Val
 995 1000 1005

Met Ser Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys
 1010 1015 1020

Thr Met Pro Pro Leu Leu His Pro Gln Trp Ala Pro His Ser Ala
 1025 1030 1035

Gly Leu Ser Pro Gly Ala Cys Arg Pro Ala Cys Thr Cys Ile Ser
 1040 1045 1050

Met Thr Thr Ile Ser Arg Ala Thr Trp Arg Leu Arg Ile Pro Ser
 1055 1060 1065

Leu Arg Lys Tyr Arg Gln Asn Ile Glu Ile Thr Pro Gln Arg Ser
 1070 1075 1080

Lys Ala Gln Val Ser Val Tyr Ser Gly Asn Leu Leu Ser Phe Ser
 1085 1090 1095

Arg Arg Gly Met Lys Ser Ser Val Arg Leu Lys Asn Ser Ile Pro
 1100 1105 1110

His Val Pro Lys Ala Thr Ala Ala His Ser Val Thr Val Lys Leu
 1115 1120 1125

Gln Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe Asp Arg Val Phe
 1130 1135 1140

Leu Val Lys Ile Cys Lys Lys Lys Leu Leu Leu Lys Leu Leu Arg
 1145 1150 1155

Gly Pro Arg Arg Lys Val Leu Met Val Leu Trp Leu Pro Ala Asn
 1160 1165 1170

Gln Ser Leu Gln Lys Ser Gln Val Phe Gln Trp Val Leu Arg Thr
 1175 1180 1185

Glu Thr Tyr Met Glu Met His Tyr Gly His Gln Ala Pro Gln Val
 1190 1195 1200

Ala Met Leu Pro Lys Leu Leu Cys Arg Gln Met Leu Pro Thr Leu

1205	1210	1215
Ser Thr Leu Gln Gln Arg His	Pro Gln Gly Pro Cys	Pro Pro Pro
1220	1225	1230
Val Thr Pro Leu Arg Val Gln	Ser Val Leu Leu Leu	Gly Val Pro
1235	1240	1245
Gln Thr Ala Ala Phe Ser Gly	Arg Ile Leu His Gln	Pro Glu Met
1250	1255	1260
Ala Ala Met Arg Leu Met Pro	Lys Phe Leu Asn Ser	Thr Asn Ser
1265	1270	1275
Trp Trp Thr Val Ala Pro Arg	Cys Pro Arg Ser Ala	Val Asp Ile
1280	1285	1290
Ser Pro Gly Pro Thr Ser Pro	Ser Leu Ala Ser Cys	Ala Ser Val
1295	1300	1305
Ala Ile Gly Lys Leu Ala Leu	Leu Gly Ala Ser Ala	Pro Cys Gly
1310	1315	1320
Ala Ala Gly Ala Arg Glu Ala	Gly Arg Phe Ala Val	Leu Gly Thr
1325	1330	1335
Met Val Met Lys Gly Ala Ala	Ala Ala Ser Cys Gln	Ser Pro Pro
1340	1345	1350
Ser Pro Arg Glu Thr Thr Pro	Ser Ser Asp Ala Thr	Arg Arg Thr
1355	1360	1365
Arg Pro Ile Ala Ala Gln Ser	Lys Lys Thr Met Thr	Ala Ala Gly
1370	1375	1380
Leu Thr Pro Arg Arg Asn Leu	Gln Arg Asn Leu Lys	Val Leu Gly
1385	1390	1395
Ala Lys Lys Ile Thr Phe Leu	Arg Asn Ser Arg Arg	Ala Thr Pro
1400	1405	1410
Thr Ser Lys Gly Ser Leu Arg	Arg Lys Tyr Leu Arg	Val Asn Ile
1415	1420	1425
Arg Lys Leu Ile Trp Thr Lys	Gln Arg Ser Phe Leu	Ser Leu Phe
1430	1435	1440

Pro Lys Leu Arg Ala Thr Glu Gln Met Thr Asn Val Gly Cys Leu
1445 1450 1455

Leu Lys Lys Ser Ser Gln Leu Arg Arg Ser Trp Arg Asn Val Ser
1460 1465 1470

Arg Ile Ser Asn Met Glu His Arg Leu Thr Met Asp Ser Ala Leu
1475 1480 1485

Ser Leu Thr Lys Arg Glu Gly Pro Glu Thr Ser Glu Lys Lys Arg
1490 1495 1500

Lys Leu Pro
1505

<210> 1162

<211> 1507

<212> PRT

<213> Artificial Sequence

<220><223> Assembled poly-FSP polypeptide 4D

<400> 1162

Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr Asp
1 5 10 15

Asp Lys Lys Lys Lys Ser Thr Glu Lys Thr Lys Asn Ala Lys Lys Met
20 25 30

Pro Phe Gln Gln Arg Pro Pro Leu Gln Pro Val Asn Leu Asp Leu Gln
35 40 45

His Gln Arg Arg Arg Lys Lys Lys Lys Asp Lys Val Glu Ile Arg Asn
50 55 60

Arg Ser Pro Lys Ala Asn Ser Thr Glu Cys Gln Gly Glu His Ser Arg
65 70 75 80

Glu Gln Asn Leu Leu Asn Leu Val Gln Leu Asn Pro His Ser Pro His
85 90 95

His Arg Lys Asp Glu Glu Asp His Gln Lys Arg His His His His Asn
100 105 110

Gln Lys Lys Met Ser Val Arg Ala Ser Val Ser Phe Trp Thr Leu Leu
115 120 125

Pro Thr Thr Gly Val Arg Thr Arg Gly Ser Pro Leu Arg Leu Thr Leu
130 135 140

Trp Pro Pro Arg Val Pro Pro Ser Pro Pro Leu Ala Leu Gly Pro Arg
145 150 155 160

Met Gln Leu Cys Thr Gln Leu Ala Arg Phe Phe Pro Ile Thr Pro Pro
165 170 175

Val Trp His Ile Leu Gly Pro Gln Arg His Thr Pro Gln Ala Pro Leu
180 185 190

Arg Leu Trp Ser Trp Cys Gly Thr Ser Gln Thr Tyr Phe Gly Ser Arg
195 200 205

Pro Ser Pro Cys Leu Ser Trp Ser Ser Arg Ile Val Ala Pro Gly His
210 215 220

Ala Leu Ser Cys Arg Thr Arg Arg Arg Trp Ser Ser Lys Arg Trp Ile
225 230 235 240

Phe Ser Asn Gln Leu Thr Val Gln Met Leu Cys Leu Pro Ile Thr His
245 250 255

Pro Phe Ala Ser Gln Pro Leu Gly Gln Glu Met Pro Asn Asn Thr Gln
260 265 270

Ile Arg Leu Leu Lys Pro Cys Arg Val Asn Ala Val Glu Glu Leu His
275 280 285

Ser Arg Arg Met Ser Val Arg Ile Val Lys Asn Trp Val Ser Cys Cys
290 295 300

Tyr Val Arg Leu Ser Ala Val Gly Leu Ser Thr Trp Ser Ala Leu Asp
305 310 315 320

Glu Glu Lys Lys Asn Gly Arg Ile Ser Ser Leu Lys Lys Lys Val Asn
325 330 335

Ala Cys Ser Ser Leu Ile Leu Ser Phe Gln Arg Val Lys Thr Gly Met
340 345 350

Glu Ile Leu Leu Trp Ile Leu Leu Lys Met Glu Ile Gln Ile Phe Lys
355 360 365

Ile Cys Leu Gly Glu Met Gln Leu Cys Gly Gln Ala Phe Gly Ser Phe

370 375 380
 Ser Ala Asp Phe Ser Ala Pro Gln Ile Ile Lys Lys Met Lys Lys Arg
 385 390 395 400

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

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

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

 Phe Cys His Val Ala Gln Val Gly Leu Glu Arg Leu Val Ser Leu Ser
 595 600 605
 Gly Ile Thr Asp Val Asn His Trp Ala Gln Pro Lys Pro Ser Pro Ser
 610 615 620

Lys Gly Thr Gly Met Asn Arg Pro Ile Gly Leu Arg Val Gly Lys Gly
 625 630 635 640
 Val Trp Ala Arg Leu Ile Leu Ala Met Thr Leu Thr Leu Asn Gly Met
 645 650 655

 Ala Lys Lys Ser Gln Gln Pro Leu Gln Val Val Leu Arg Leu Gly Asn
 660 665 670
 Leu Pro Pro Phe Phe Arg Gly Ser Glu Val Pro Phe Pro Arg Pro Cys
 675 680 685
 Arg Thr Lys Pro Ala Cys Thr Ser Lys Ala Trp Thr Pro Arg Lys Leu
 690 695 700
 Val Gly Arg Ala Val Arg Arg Lys Gly Ser Pro Leu Trp Asp Cys Ser
 705 710 715 720

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

 Thr Thr Gly Thr Leu Val Trp Glu Arg Gly Val Leu Gln Met Arg Ser
 785 790 795 800
 Leu Glu Ala His Cys Pro Leu Gln Thr Phe His Leu His His Cys Arg
 805 810 815
 Thr Gln Pro Ser Ser Cys Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln
 820 825 830
 Trp Ser Gly Ala Val Val Gly Leu Arg Pro Val Ala His His Leu Pro
 835 840 845

 Arg Pro Ile Gln Gly Leu His Cys Pro Gln Ala Pro His Gln Pro Ala
 850 855 860
 Leu Ser Trp Gly Lys Trp Pro Val Gly Met Thr Gly Pro Ala Arg Cys

865 870 875 880
 Cys Arg Trp Pro Arg Arg Cys Gln Lys Lys Val Pro Ser Ala Ser Pro
 885 890 895
 Trp Gly Leu Val Leu Lys Lys Asn Arg Lys Gln Met Leu Asn Gln Lys
 900 905 910

 Cys Leu Ala Pro Phe Arg Glu Ser Thr Leu Gly Asn Phe Trp Met Lys
 915 920 925
 Leu Leu Gln Leu Pro Val Val Ile Asn Leu Lys Arg Leu Gln Lys Phe
 930 935 940
 Asn Leu His Leu Cys Tyr Tyr His Ser Gln Ser Asn Arg Asn Lys Ser
 945 950 955 960
 Arg Gln Met Glu Ser Leu Gly Met Lys Leu Gln Ser Gln Lys Ser Gln
 965 970 975

 His His Cys Ala Leu Arg Lys Ile Glu Trp Ala Thr Lys Leu Ser Leu
 980 985 990
 Gly Gly Lys Ala Gly Pro Gln Ala Gln Glu Lys Ala Thr Ser Arg Ile
 995 1000 1005
 Leu Asn Leu Gln Val Leu Lys Lys Ile Leu Arg Ser Phe Met Lys
 1010 1015 1020
 Leu Tyr His Ser Leu Val Met Cys Leu Arg Leu Arg Thr Lys Leu
 1025 1030 1035

 Glu Lys Ala Leu Ser Ala Leu Phe Ile Trp Pro Gln His Ser Tyr
 1040 1045 1050
 Lys Pro Leu Phe Phe His Gly Asp Leu Cys Glu Trp Gly Gly Gln
 1055 1060 1065
 Ala His Arg Gln Arg Asn Trp Leu Lys Asn Trp Lys Arg Phe Lys
 1070 1075 1080
 Leu Lys Lys Lys Tyr Ile Gln Lys Lys Lys Gln Lys Ser Asn Lys
 1085 1090 1095

 Ile Ile Cys Lys Gly His Arg Ile Thr Ile Ile Cys Ile Lys Asn
 1100 1105 1110

Met Phe	Leu Gln Arg Lys Gly	Phe Leu Asn Leu Ser	His Val Glu
1115	1120	1125	
Lys Phe	Cys Arg Gly Gly Pro	Ser Ala Ser Asp Arg	Cys Cys Ser
1130	1135	1140	
Cys Ser	Pro Ser Gly Phe Ser	Ala Gly Arg Gly Arg	Cys Pro Val
1145	1150	1155	
Gln Gly	Cys Leu Arg Pro His	Arg Val Gln Leu Leu	Arg Arg Trp
1160	1165	1170	
Gly Pro	Gly Ser Pro Ala Gly	Gln Arg Leu Ser Lys	Gly Phe Gln
1175	1180	1185	
Leu Leu	Arg Trp Trp Gly Pro	Gly Ser Pro Ala Pro	Glu Pro Arg
1190	1195	1200	
Lys Gly	Pro Phe Pro Pro Pro	Asp Pro Pro Trp Pro	Val Thr Ala
1205	1210	1215	
Val Thr	Val Met Ala Gly Ser	Val Pro Ser Ala Gln	Ser Val Asp
1220	1225	1230	
Ala Leu	Glu Ser Pro Gly Pro	Leu Ala Leu Glu Gly	Pro Ser Ser
1235	1240	1245	
Pro Arg	Asn Leu Leu Trp Arg	Glu Met Ser Ile Phe	Leu Pro Gly
1250	1255	1260	
Ile Phe	Thr Ala Lys Lys Ser	Pro Thr Ser Phe Cys	Cys Asn Ile
1265	1270	1275	
Leu Asn	Ser Leu Pro Ser Ser	Met Glu Ile Ala Val	Leu Gln Glu
1280	1285	1290	
Asp Ser	Lys Lys Met Thr Gln	Lys Gly Gln Ala Phe	Gly Ser Leu
1295	1300	1305	
Cys Gln	Leu Val Ser Ala Asp	Phe Ser Ala Pro Gln	Val Thr Arg
1310	1315	1320	
Leu Arg	Ser Leu Asn His Leu	Leu Ile Thr Tyr Thr	Pro His Ile
1325	1330	1335	
Cys Arg	His Thr Leu Leu Thr	Pro Asp Thr Arg Trp	Ile Phe Ser

1340	1345	1350	
Asn Gln Leu Gln Thr Val Gln Met Leu Cys Leu Pro	Pro Leu Lys		
1355	1360	1365	
Gln Gly Glu Arg Ile Ile Trp Pro Leu Gly Gly Phe	Gln Ile Pro		
1370	1375	1380	
Asn Phe Phe Trp Ser Leu Gly Ile Gly His Thr Gly	Ala Trp Trp		
1385	1390	1395	
His Thr Gly Arg Arg Arg Arg Glu Trp Gly Gly Ser	Thr Val Ser		
1400	1405	1410	
Arg Ser Pro Leu Trp Ile Ser Ser Met Ile Tyr Leu	Arg Gly Met		
1415	1420	1425	
Ala Phe Ala Ser Asp Ser Ser Ile Arg Thr Thr Arg	Val Ser Trp		
1430	1435	1440	
Cys Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala Ser	Ser Ile Glu		
1445	1450	1455	
Ala Leu Thr Ala Leu Phe Thr Cys Arg Thr Ala Ser	Ile Ser Val		
1460	1465	1470	
Asn Ile Ser Thr Leu Met Ser Ile Leu Glu Ala Leu	Lys Lys Lys		
1475	1480	1485	
Pro Arg Asp Ile Cys Arg Ile Ser Cys Arg Cys Arg	Arg Glu Tyr		
1490	1495	1500	
Arg Val Thr Met			
1505			
<210>	1163		
<211>	4521		
<212>	DNA		
<213>	Artificial Sequence		
<220><223>	polynucleotide 1C		
<400>	1163		
agcaccagac gggaaatgcc ttctcaggcc acaccttctc cacctggacc ttggagagcc	60		
gctctgggca aagaagtga gcgagaccag agcaagctgc ggctgagaaa cacaagcccc	120		
accgagatcc aattgacat gaacgacagc aagcacaagc tggaaagccc cgctctgaaa	180		

caggtgtccc ctgcctctcc acctacacag cagcctcaga caccacagga tagcagacag 240
 gtgctggccg cttcttctcc tggacatcct cttggccctg gcgactgccc tagaacaatg 300
 gctggacctt ctgcctctct gcaccagca tctggcagag ccagcagaaa gacctggcag 360
 agaaggctga gagcctgtag agctgggtga cctgctggat gggctagaca ggccatgaca 420

 ctgaaggccc tggtaagac ctggacacag ttcagaaact acccagagt cggagccgga 480
 acaggcggag gacctgcttg tgttctcttg gccgaagctt ctactggcgc ctggacagct 540
 gaaggcgtg ccggaacaag atgcagagct tctagagccc cttgcagaca gctgcctgcc 600
 agctctccta ccaagtgcga gatctgcgtg aagagaaggc ggcggagaaa ggcggagcagc 660
 cagtctagat ctcccgctcc taagaaacgc gagcggatga tgctgcctgt gcgggccaga 720
 acagctagat ctgctctgcc acaaggcaga gccctcttgg aaggatgct tctgcctaga 780
 gcactgccc gctgctgag cagaatgcca gccagaagag agagccggtt ttggctggca 840

 ctgcaggctc tgggactcag acctctcat ctgcctagct gtcacctct gcctcaactg 900
 cttggacctc ctccacctca tcaggcccct ttcgacaaga aaggcttcgt gatcctgagc 960
 aagggaaga agcgccggaa agaaatccgg cggatgacca gacggacct gaccaccacc 1020
 aaaatgatga tgatgcggcg gaccaagcgg cggaggcgaa aacglagaag aatgacctg 1080
 atgaccgca gaacctgct gaccaagaaa acctgtctga cccctagaac cagcgccgcc 1140
 acaaaagctc tgccagaca gacaatcagc cagcggaggc ctatccagac acctctgga 1200
 acaagcctgg ccatctgggg cagactgcct ctcagaccac agagaggacc tcggcctctg 1260

 catagatggc tgcagcagac aacaggctgc tcccagagaa gaatcgcaa gaagcggatc 1320
 aagctgaggc ggaacacact ggccatccgg tttatctctg cccctcagcc tagcagcagc 1380
 accgttacag ctgctcctag cggccagtac ttcagcagct tcttctacac cagcgaccgg 1440
 accaagtgtg aaatctgtgt caagaacacc gccatcctgg ctatcacct gatcacctt 1500
 caggaccctc acctggacct tgtgtgtcac ccacatagaa ggcctggctg gaaggccac 1560
 cacagagtgg tgtttagcca ccatccaagc ggctccacca agagccattg gcagcagaga 1620
 gaaagaggcg gaggcgcag agaaaaaag ggtgcagag agatgccag cagctggtct 1680

 agctctggca gaaccgccga caaaaagaac gtgcggagca gaaccagact gaccctgaca 1740
 ggcacaagaa gcagcggcac aagacctct ccaagcgcg tgtgtctgtg ctgttgga 1800
 tgccctcca gaagcttccc tgcccatct ccatctggac tgagagcacc tgttgagcc 1860
 caggctctc ctgaagtac actgagagcc agctgtgcct ctagcgctc taaagcctgt 1920
 gctggacttt ggcttgggg agccaagtg cggaacaaag tgcggcagaa cttcaagcgg 1980
 aacctggcca aaaagacct gactaacgcc ctgcggagta tgccaagag cagaaaccag 2040

gtgctgttca gacggaatct gacccaagc cagctgagaa ctctggcccc tccttacatg 2100

ctgctgcccc agtctctgtc tcagagcctg tccagaaagc agatccccag ccaatcaatg 2160

ctcgtgaccg ccttcttctt gctcgacatc atcctgagaa gcctgctgta ctcccggatg 2220

tgccctgggtgc agatccctac acacacctgg gagccccgact acttcgtgtc cctgcctatg 2280

atgttcagct gggccactca gagctttcca gtgggagccg tgttcctgac cagacctgcc 2340

attccttgct gcagctgtac cagccacagc aacccttgga gccagtcctt caagaagaag 2400

aagccccctga cattcagccc cagcgtgcc aatgtctctgg cctglagcat caccgtgtcc 2460

ttcgtggggc agatcagcac actggtgctg gacgtgtcct ccattcttca ctggcgcaag 2520

cgcaagagag agaagcggtc ccagaagtcc cggcagaacc atctgcagct gaagtcctgc 2580

agacggaaga tcagcaactg gtccaagctg agatccccgt ggatcttcta ccctcggctg 2640

aaaaccttcg gcgtgccact gggctctatc ctgtgtctgg caggtccct gagcacgatg 2700

atgatcatta gcaccaccag acaagagtgt ggcagacggg cctccgtgcc ttgtagacct 2760

atgatcggca gccttagacc cggaccttgg cggacatctg ctatgccatc tgccatggga 2820

gtgcacctgc ctaccagctg tgaaagcggg agatctctc ctgccaccgg cggaagaatg 2880

cctggatctc agtctatcat gatgagctgg atgcctccac tggctccctg tgccgcttgt 2940

ccttgttctc ctgctctac actgtgccct gctcatcctg caagagcccc tacagccgtg 3000

cctgccttta cacctctgtc tgctcaccct gtgccagtgc tgtctggatg tcacctggcc 3060

gtgcgcacct ctatgtgac actgtgccc atgagacacc ctacagaag cccacctaca 3120

agctgccctc cactgtgga agctttccca ctgccaaggg ccagcctgag agctaccgtg 3180

cctagacaca gctctgtgt ggcactgga ctgcatctgc atcggcagat tagcctgcct 3240

ctgaggggct tctgtgtgca tcaacctctg cctggacaac acctgtggct gtccacaga 3300

ctgaggctga gactgccaag aacaggcgag aagaacgacc tccagctgtt cgtgatgagc 3360

gacaccacat acaagatcta ctggacagtg atcctgtgta acccctgcgg caacctgcac 3420

ctgaaaacca catctctgcg gagagccaga cctacctct gcagcacatg cagaatgtgg 3480

tggctgaagc tggccccact gcaagtgacc acaacctga agctgacat ggtcatgctg 3540

gaaatcgtga ccgaagagc caagaaatcc atgaagagat cccggcggag caagatcgag 3600

gcctctctta tcggctccat catgaagaag aaagacagca ccatttcat caaccagcag 3660

ctcaagtgga cccctcacat cctgaagtct gccagcgtgt ccaagaagag actgcccaag 3720

ctgaacggca tctgggaagt gatgccccgg aactggaag gctgcatcag cgtgaaggac 3780

caccggacaa gccagaacca cagcaagtgc atcaccgagt gtgtgcggac agccctgaac 3840
cagagaaagg tggtaagaa cccagccag ccagtccac tgagaaacga cggcatcacc 3900
aacggcaacg actccaccag atcctgctcc atcagcctga agaaaagcct ggaaaagatg 3960
cccctgatga acgccaagaa aatggaagat atgatctggg agagcaacat gggcggcaac 4020
cggctccatct gcctgacaag actgccctgc aaagtgaccg agtccagcca aagaccacct 4080
cggagcattc tgtccctggc ctctagagcc ggacagtctc ccgtttggcg gagaaccagc 4140
agaggcatgt ccctgcagtg gaagtcgggc aatgcctgca cacctctgag gtgccctagc 4200

agaagccctg ccacatttct gaccgcactg aacggctggc acagatctgg acttagggct 4260
cagcaaccta gcctgccagg accttgtgct agcctgctgt ctacactgag ccagcctcca 4320
ccacaggctc caagccaagt ttggacagcc gccacactga gatgtcccgc tgttcctgca 4380
gctgcttgcc ctctatcgt gttctttctg gccccatact tccccacacc actgagcatc 4440
agcagaccca cctctcgggc cagacagtct tgttgtctcc ccggactgac acaccctgct 4500
caccagcctc ttggctctat g 4521

<210> 1164

<211> 4503

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 2C

<400> 1164

cggcagatca acagacggaa gctgcagaga aagaagcgcc ggaagaagag agaggaccac 60
tgcggactgc gggccagaaa ccggaacatg aagaaaacca tgagccacct gatcgcccat 120
caggccctga agatgtctgg cctgagactg tttcacccca gactgctgac acggaagaag 180
cctggcaaga accctcggag aaagacctgg aagatgcgga agaagtacgc ccagaagcct 240
agccagaaga accacctgta cggcaagggc ctgacacacc ctgtgcctct gaagagaacc 300
ctgcagaaca agcggaaaca gaacatcaag cgcgtgaacc agaagaaggg caacatcaag 360
agaaagagca tctgctgca cctcatcgtg ctgaacagcc ccgagagcaa cctgcaggct 420

catectcaag ttccagcact ggctcctcag gcttggtggc ctgctagaag aggccctctg 480
acaagcgctc catctgctca gcagagcctg accttctgc ctagcagatt tccttggggc 540
cctcctccac tgactggaa ctctgcctac ctgggcagaa cactgctcgt gacctgcatc 600
ctgtaccaca gatggatcgt gaccagcatg tgccagagcc agagatggct gaccagcacc 660
acctctagaa gcagcgccct gatgtggacc cagtggctta gcgtgacaag cctggaatgg 720
acagcccaag agaggggctg tagcagctgg ctgatgaagc agacctggat gaagtcttgg 780

agcctgcggg accccagcta cagatccatc ctggaatagc tgtccaccag agtgctgtgg 840

 atgccacat ctacagtggg agccctgaga gccacagctc ctgcaacagc tgctccacag 900
 gctcagacc ctcattggag agccgccaca acaagcagca tgagcagcag ccctagagcc 960
 gagcctacaa gcctagctc ttgggccacc tgttggccca gatgttgag ctccagctgt 1020
 tactggctcc tgtcctcttg gcctcctgct ggtgctgccg aggccacaaa taccaggacc 1080
 agaagcagag agtcccagcg gggcagaatg ctgacttga gaagcagcct gtggctgcag 1140
 ggcaccagat gttttacagg cgtgcggacc tccagcagac acccttcttg gccttggacc 1200
 agatgcctga gaatcgggcc tctagaagc aacagccgga aaaagctgct cgaggacatg 1260

 aagcaaatg gcttcacccg gtacaagaaa cggggcgtga tagcctggcg gagagccact 1320
 ttcctgctgg ccctttggga gtgcagtctg cccaagcta gactgtgcct gatcgtgtct 1380
 aggaccctgc tgctggtcca gagcagatgc agcctgatgg aacagatccc tcacctgaag 1440
 tcctggtggt gtacaagagg cggcggaag cggaagaaa agatgtgcaa ggtgtccggc 1500
 ggctgcaccg cctgtgttga aagatgtcct tggaaggga tctgctggaa gtggcctgtg 1560
 acagtggcgg ctctgatcct gattcagcac ggcgcatct tcaccttccg gttctgggtc 1620
 gagaagctgt cciggaacat ctgcaagaat ctgtccctgt acctggacaa gttcgtgcag 1680

 cggtgctgt acgtgtacat catcagaca aacgtgttcg tctgaacct gttccacgtg 1740
 ccagtgaatc agatcttcac gatggccttc tacctgaagt acaccagaa ggccctgggtc 1800
 atggaactgg aatggctcat tcagcagcag tgctaccagt tgctgctggc tcatagtac 1860
 ggcttcagca cctacggcac ccagaaaggc gattgctgt gtctgcagtg tctgagcggc 1920
 agctccctgt tcacctgaa gcagccactg gacctgaaga tcagcaagac ctcatgagc 1980
 agatcccacc tggatttcag ccctattgg atgaagaaag tgaaggcctc tccacagatc 2040
 atgcagcgga tgagcgccgt gaacttcgag acaatcaggc ggaagtggca gatccggcac 2100

 gtgctgaaga acctgcctct ggaaaacaca cagatcccca ggacaagccc tctgtggaag 2160
 atcacaatgg tgctgacata cccaactgc gtggtgcatg tgctgatgtt cgtgctgttc 2220
 aaggccgacc agagcgagtc tagcctgagc agcggaatct accctcctag cacctgtagc 2280
 ctgccttgcc ggggcattag aatgtgcgcc ctgtctcacc ctagcttcta catcagcagc 2340
 accgtgtgct ttctgagcaa gcaactgcat accgctgca ccagagagaa gatcatcaac 2400
 cccaccatca gctgcccctt tcagagcccc acaaagagac tgggccacag agagggcagc 2460
 gagagcgata atctgggcct gctgtactcc ttctctctt ggctgcccac gagatccctg 2520

ggcgaaacctt ggagagctgg ctttcagtgg ggagagtccc cttggcaagt gatggctagc 2580
 ctgaccggca acagcgtgat cgtgcacaag atcgtgctgg tgtttctgaa gtctctgagc 2640
 agctacaact gcgagcggcg gatctctggc atccagaaga gagccatcga gttcgccgtc 2700
 ctgaagctgc tgaacatgga cctggctagc cctcagatta tgcagagAAC cagcgccgac 2760
 cggttccgga tgaagcggag aatgcagaac ctggataacc tgggcgtgcc ctggccattg 2820
 ctccagggtg ctgctctccc acatagactg ctgggcccct ctatagtgat tctgtttcat 2880
 gtgcggaaca tcgtgtacgg catccaagtg atgctgtgcc ggcgagagaa cagcagaaag 2940

 cagagtcagg tgcagctggc cattcaggtc ctgctcgtgg acaagcaca gtactttctg 3000
 ttcggcccct atcctatcag cgagggactg accatgacca ccggccggaa catcaacagc 3060
 aactccctga tgaccaactg cctgttcagc cccatcttcc tgtgccacca cgccatcatg 3120
 caccggaaga tgacaagccc acatttcaga ctgtttctcca gcaagatccc acatcctcag 3180
 gtgccaagtg tgggtggccct gtgcaagtgc ctggccaatg gcctgtggtt caacctgac 3240
 tttcagaaaa agggccacat gatcttttag cccaagtctt tctgacctt tagccagcgg 3300
 accctggaat ccgccggact gtttccatgg ctgcacaccc agtgccggaa caaaaagacc 3360

 aagctgtggt tttccctgat caacatccac caccgcaaga atcctctgct gcctatgaga 3420
 atgagcagaa cacctctctg gagagtgtgc ggatctccac ctctgcatct gtgccaacct 3480
 ctgagaggcg gcaagaagag aagcaagtgc gccttctgga agcctcctag ccagggcac 3540
 agctcttgct tgatgacagg ctgttggggc tctgtggca gagcttgctt ttgcggaaga 3600
 ggctgcggta caccagagg cgactggaaa agacacccac ctgcagaga gctgagcctg 3660
 gaacatgga ttccttatct gcaccagaa aagaccagc ggaagcggat gaagaccggc 3720
 gccattcaag agaaggcgct tatccaagaa aaaggcgcaa tgaccaagcg gatctgcgtg 3780

 gtcaatttcg aggcctgcag agagatggaa agcctgagcg ccctgagaa gattaccctg 3840
 ttcgaagccc acatggcccg gtgcacctcc atcaatgtgc tgtgtgtccg ggccagcctg 3900
 attgagaagc tgatgaaaga aaagcgcaag atgaagcgca accaggtggc atccctcaa 3960
 atcatgcaac ggtgtttcat caagggtac cagaacaacc acttcacgtt ccacctcaa 4020
 aactttgctt tcttcagctc cttcggcaac aacaagtata tcaacattct caccggggc 4080
 ttcattcaca cacctagaag ccttggtgt tccgtgtacg ccaatatgtg ctggcggaag 4140
 atgcagtccc tgaatcacc cagcagactg accaactgtc acccgcttg gctgagcccc 4200

 attagtgtt gtccatagct gctgcctat ctttttcacg tgctggcact ggaagtgacc 4260
 tttccacctg gcacagccat gcctcagatg caattgcagg cactggctat gtgggagaaa 4320
 ggctgggaca agcaagagaa gaaatccgc aagctgatgt cctctgcct ggaaaaaag 4380

gctacctgga tgcggagaac ccctggcaca agcctgcagt gttacctgaa cacacacccc 4440
 tgcaccatgc tgctgcctca gggaatccca tctctgaacg cccagtggat gttcctgcgg 4500
 atc 4503
 <210> 1165
 <211> 4518
 <212> DNA
 <213> Artificial Sequence
 <220><223> polynucleotide 3C
 <400> 1165
 cctattctc cacacctgag acacctctg ctgctgaaga acaagaagcg gagaaagctg 60
 cggcccaaga gcagaaagaa gggccacacc aagaaccggc ggaaggccaa gagaaagccc 120
 cagatcagaa acagccgcag agccacacct accagcaagg gcagcctgag aagaaagtac 180
 ctgagagtgg gagccgccg tgctagctgt caatctctc catctcctag agagacaacc 240
 cctagcagcg acgccaccag aagaaccaga cctatcgccg ctgagagcaa gaaaaccatg 300
 acagccgccg gactgacccc tagccagaag aaagatcctg ccggcaagct gaagaaacag 360
 gtgtccgtgt acagcggcaa cctgctgagc ttctctcgga gaggcataaa gtctagcgtg 420
 cgctgaaga actgcaccaa cctgagcgtg cccatgatgc tgaccatcct gatctggaag 480
 cgggtgttca tctgtctgt gtccgacaag aaatctatcc ctacagtgcc caaggccacc 540
 gccgtcatt ctgtgacagt gaagctgcag agccggcgga acagacggtc cagaaagatc 600
 tatggcgagc tgaagatgtc cctgcaggcc agcaatggca tggaagcctg tggcacacac 660
 cccacaccta gactgtccgt gtccgtgatc accatgaagc tgtgggagaa gcacttcaag 720
 ggctgaact ggaacctggt cgtgtggatt ctgaacctga agatgatgct caagaagaag 780
 tatctggtcc agcgcgagtg ggagaaacgg aagcagattc ttggcggcgg aggcaagtac 840
 aaagagtact tctgaagag aatctctatc cgcaaggcca tgacagtgtt ggccggcgat 900
 aagaaaggcc tgggcagatt catgagatgc gtgcagagcg agacaaaggc cgtcagtcctg 960
 cagctgcctc tgggcagaat ggacctggat ggaatgctga ccgtgatcgg ccagggactc 1020
 gtgggcatga cacctagaga tctgggaaca gtggctggcg ccaccgcaca gattcagagg 1080
 cctattcagg tgcagacagg cggcagactg agaggcccta gaagaaaggt gctgatggtg 1140
 ctgtggctgc ccgccaatca gagcctgcag aaaagccagg tgttccagtg ggtgctgaga 1200
 accgagctgc cctgacctt tagcaccctg ctgtgggaca gcagacacga cctgcctaga 1260
 atgctgcccc tcagcagccc tctgcacaga cccagatgc ctttctggac ctgcaccttt 1320

cctgccacca catggggcac atgggagaca ccttctacat ggggctggcg gacctttgcc 1380
 agacagcctt ctagaccac cggcagaacc cctaccacca gactgatggc tccagtgggc 1440
 agcgtgatga gctgtagcct gctgacacag ccattctccag ccagcgctg tacaatgcct 1500
 ccaactgctgc atcctcagtg ggccccctcat tctgctggac tttctccagg cgcttgacaga 1560
 cctgcctgta cctgcatcag catgaccaca atcagcaggg ccacctggcg cagaaacctg 1620
 cagagaaacc tgaagtgtct gcggctgaga atccccagcc tgcggaagta cagacagcag 1680

 aacacccggt ccaccaacct cgagaagaac ccattcttga agaagcagag ccagaggcgg 1740
 ggcaagctgt ctctgaccac actgagcttc gtgctgatcg aggaactgct gaaaaagagc 1800
 agccagctgc ggagaagctg gcggaacgtg tccagaatca gcaacatccg gaagctgatt 1860
 tggaccaagc agcggagctt cctgtctctg ttccccaagc tgagagccac cgagcagatg 1920
 accaatgtgg gctgtagact ggattttcac ccagaagca gctccggcga cagagtgttc 1980
 ctggtcaaga tccagagcag cccatttctg gccagatcct ggaataccat gcagtggaac 2040
 aacaagaaaa tggccatgac tgtgatcgct ggcgcccacc actgtcagta caagctgacc 2100

 tacaccaaag tgtggaagat gaattggaag aaaatgatga tcggcagcca gcacctctg 2160
 ttctccccac tggatagctc tccactccag ctgctgctgc acccacacgg caagagatgc 2220
 aaccctgtt gtcggctgac atggatgagc cacctgaatc ggaagctgca cctcaccagg 2280
 tcctgcctga tcgacctgac catgatgatg agccagaaac tgtggaagaa tcagcggaag 2340
 cgcattccctc tgccttctcc aagacagcat ctgctgcctc agtatcctct gcacctcct 2400
 ccacttgctc tgcctgtctt ccaccataga caccacctgg cattcctcga gatggcctgt 2460
 agctctcagc acaccacag catcaagatc tggatcagct tcagccacga gacaatgagc 2520

 ctgtccaaca tctgatgaa gttccggctg accaccacca caagcagccc cagaagaagc 2580
 cctgctctgc gagctagagg cggcacaaca atcgcggaag tgaccagcag cctgttcttt 2640
 agccactgcc tgtgcgtggc ccctagatgt cctagatctg ccgtggacat cagccccgga 2700
 cctacatctc ctctcttgcc ctcttgtgcc tctgtggcca ttggaagct ggcaactgtt 2760
 ggcgctctg ctcttgtgg tgcctgtggc gctagagagg ccggaagatt tgctgtgctg 2820
 ggcacatgg tcatgaagaa catggaacac agactgacca tggacagcgc cctgagcctg 2880
 acaaagagag agggccctga aacaggcccc gtgtactacg tgtgcaaccg gatgaatgtg 2940

 tcagcgtgc tgaagccttt cctgttcacc gtgcctatcg aggacatgag agagtgcacc 3000
 ctgggacgca acagaatgaa tgtctcttcc gtgctgaaac cctgtctgat ccccgctcca 3060
 atctgcaaga agaaactgct gctcaagctg ctgaggggag cctccagctc taccagcaga 3120
 gatagcagaa gctttttcac cagcgtcac ccagcagac cctgcaggat gagactgtac 3180

cagatgctgc agaagcagtg ctgctacaac ctctgatca agcacctct gatcttccgg 3240
atcaacctgc ggagacaggg caagaccaa gacggcgttg tgcagagcct gggttcctg 3300
aaccagcaga tcatctcca gaaagagttc ttcactgcc tgcgatgtt catcaagcgg 3360

tggaagccag ccgccacaa gaagggaag aacagccct gctgccagaa aaaactgcgg 3420
gtgcagaacc agggccatct gctgatgatt ctctgcaca acagagccc acctctcat 3480
accagattcg agaaaaagcg gcccagtggt ctgagcagaa aatccggcgt gatgaagtgc 3540
tgggatctgt gccctgcctt cagcggcagg attctgcacc agccagaaat ggccgcatg 3600
agactgatgc ccaagttcct gaactccacc aacagctggt ggacagtga caagaagaga 3660
ggcctgttcc accagatgaa gtgtctgacc gccgtggact gtctgcaggc cttctgggat 3720
atgagcgaga agaaacgcaa gctgcctatg attcgcaaaa tccagaagcg gcggagaacc 3780

gccaaccgga acatcgagat caccctcag agaagcaaag cccacctgaa gaaaacctcc 3840
gccaaggcgg ccaagaaaat caccctctg tgcctgagag tcagatgcgg aggtggctg 3900
tgtggctgga caccaagagg atggctgaag aagtcacca agtcagact gtgtctctc 3960
tacctgctgt actacctgtt tttctgacc gtgtgcggct tcacctcc accacttatt 4020
ctgtggcctc aggcagcccc tggcgagaag ctgaagcact gttttaagc ctggggcgtc 4080
gacctctctg gcagcgtttg gattctgcc tgcctctga ttacctgag aaaggtggac 4140
accaccacc tcaggtggt caccaaaaca gtgaccgcca caacagccga cggccagagg 4200

atgagaaggc tgaagtgcaa ggcctgccgg ctgagatggg ctagacctga acctgcagct 4260
caggccctc ctaagagcca cttccacct catctagcg gccctccag aaccagctct 4320
ctgcaattga gaacctacat ggaaatgcac tacggccatc agggcccaca ggtggcaatg 4380
ctgcctaaac tgcgtgtcgc gcagatgctc cccactctgt ctacctgca gcagagacat 4440
cctcagggcc catgtctcc tccagtgaca cctctgagag tgcagtctgt gctgctgctc 4500
ggagtgcctc aaacagct 4518

<210> 1166

<211> 4521

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 4C

<400> 1166

gacagcaaga agatgaccca gaagaaccgc aagaccgga agccgccag agagaagcac 60
agaaagaccg acaacctgga cctgcagcac cagcgagac gcaaaaagaa gaaggacaag 120

gtcgagatcc ggaatcggag ccctaaggcc aatagcaccg agtgtcaggg cgagcacagc 180
agagagcaga acctgctgaa cctgggtgcaa ttgaacctc acagccctca ccaccggaag 240
gacgaggaag atcaccagaa gagacaccac caccacaatc aaaagaagat gtccgtcaac 300
gagggcaaca accactggcc tagagtggaa atgcctaccg gctggctgct cgtgggctac 360
aacaccagaa acacagccca gaatcctcgg ctgcagcagc acctgaaaca ctggcagcag 420

tgcaccagag ccagatggtg tcaagagccc tgcagaccc tgaccttctt ccactttctt 480
ttctttttca aaacggtgtc cctgtgctgc cccggctggt ctaaaggaca acctcctcca 540
cctggcctga agccttctag cctggcttct caggtggcca gaaccacagg cgtgtaccag 600
cacgtgtggc tgatctgctt cgtgtttttc gtgtgctgg aaaccggctt ctgtcacgtg 660
gcccagtgg gactcgagag actcgttagc ctgagcggca tcaccgacgt gaaccattgg 720
gcccagccta agccatctcc tagcaaaggc accggcatga acagacccat cggcctgaga 780
gttggcaaag gcgtgtgggc tagactgtgg ctgaagaact ggaagcgggt caagctcaaa 840

aagaaataca caggcatgga aatcctgctg tggattctgc tgaagatgga aattcagatc 900
ttcaagattt gcctgggcga gatgcagctg tgcctcaaga agaaagtcaa cgcctgcagc 960
aacgccaaga aaatgccctt ccagtgccgg tgcagacgcg agtacagatg gaccatgatt 1020
cagaagaaga aacagaagtc cccgtgttcc ttccacggcg acctgtgcag accttctcct 1080
tgctgtctt ggagcagcag gatcgtggct cctggacacg cctgagctg tcggactcgt 1140
agaagatggt ccagcaagat ggccaagaag tcccagcagc ctctgtgtag aggcgccct 1200
tctgccagcg atagatgctg tagctgtagc cccagcggct ttagcgtgg aagaggcaga 1260

tgctctgtgc agggatgtct gaggccacac agagttcagc tgcigagaag atggggccct 1320
ggatctcctg ctggccagag actgtctaag ggcttccaac tgcctgcttg gtggggacca 1380
ggatctccag ctctgagcc tagaaaggc ccatttccac cacctgatcc tccatggcct 1440
gtgaccgctg tgacagtgat ggctggctct gtgcctagcg ctgagctgtg ggatgctctg 1500
gaatccctg gacctctggc tctgaaggc cctagcagcc ctgaaacct gctctggcgg 1560
gaaatgagca tcttctgcc tggcatcttc aacctgcacc tgtgtacta ccacagccag 1620
agcaaccgga acaagagccg gcagatggaa tcctgggca tgaagctgca gatcacacac 1680

ccattcgcca gccagccact gggccaagag atgccaaca acaccagat cagactgctg 1740
aagcccgcc aggcccttgg cagcttttcc gccgatttt cagccctca gcaggccct 1800
ctgagactgt ggtcttggtg cggcacaagc cagacctact tcggtctat cgaagccctg 1860
acagccctgt tcacctgtag aaccgccagc atcagctga acatcagcac cctgatgagc 1920
atcctggaag ccacctggc catgacactg acctgaatg gcagccctct gtgggactgc 1980

agcacaacaa caggcacaca ccacggctgc ctgtgggaga tcccttctgt taccctgctg 2040
 gctaccgcca aaaagagccc taccagcttc tgctgtcagc ggcctcctct gcagccagtg 2100

 gaagagaaga agaacggccg gatcagcagc gtgccacctt cteccacctt tgctctgggc 2160
 cctagaatgc agctctgcac ccagctggcc cggttcttcc ctattacacc tctgtgtgg 2220
 cacatcctgg gacctcagag acacaccctt ctgtgaccc ctgacaccag atggatcttc 2280
 tccaaccagc tgcagaccgt gcagatgctg tgtctgcctc cactgaagca gggcgagaga 2340
 atcatctggc ctctcggcgg ctttcagatc cccaacttct tttggagcct cggcatcgga 2400
 cacactggcg cctggtggca tactggaagg cggagaagag aatggggcgg cagcaccgtg 2460
 tctagaagcc cactgtggat cagctccatg atctacctga gaggcattggc cttcgctcc 2520

 gacagcagca tcagaaccac cagagtgtcc tgggtgtcga gatgtggcgc caaaagcgcc 2580
 gcagccagca gcgacaagaa gaagaaaagc accgaaaaga ccaagaacaa gatcatctgc 2640
 aagggccaca gaatcaccca ggtggtgctg agactgggca acctgcctcc attcttcaga 2700
 ggagcgagg tgccttttcc tagaccttgc cggaccaagt gccagaagaa ggttccaagc 2760
 gcctctcctt ggggactgca cccaagaaca gcctccatca cactgcctac caccagcctg 2820
 aagggcagca gaacaagctg ctgccccaga tctcaccca gactgccag aacaaagtgg 2880
 cctctgcagt gcctgtgca cagcctggga acaactggaa cactcgtgtg ggaaaggggc 2940

 gtgctgcaga tgagaagtct ggaagctcac tgcctctgc agacattcca cctccaccac 3000
 tgcagaacce agcctagctc ttgtctcca gcctggattc tgtaccaagg acagtggagc 3060
 ggagccgtcg tgggacttag acctgtggct caccatctgc caagacctat ccaggggctg 3120
 cactgtctc aggtctctca tcaaccagct ctgtcctggg gaaagtggcc cgtgggaatg 3180
 acaggaccgc ccagatgttg ccggtggcct agaagaatgt gtactctctt ggccctgcca 3240
 accggcctga catctctgat cctgcctagc agtgatctgg ccgtgctgat ctctagctcc 3300
 accagccact ttctgatgcg gagcccagtg ctgccaagca gcagactgac atgtgcctct 3360

 ccacagctgc ctcgatgtg gacatggtct agctggctga aagagtgggg aggacaggcc 3420
 cacagacagc ggaactgtag agtgaacgcc gttgaggaac tgcacagcag gcgatgtct 3480
 gtgcggatcg tgaagaattg ggtgtcctgc tgttacgtgc ggctgagtgc agtgggactg 3540
 tctacttgga gcgccctgga ttcctgatac ctgtccttcc agagagtga aaccagccgg 3600
 atactgaacc tccaggtgct gaagaagatc ctgcggagct ttatgaagct gtaccactct 3660
 ctctgatgtg gcctgcggct gcggaccaag ctggaaaaag ctctgagcgc tctgtttatc 3720

tggccccagc acagctacaa aggccaggca ttcggaagcc tgtgccagct ggtgtctgcc 3780

gatttcagcg cccctcaagt gaccagactg cggagcctga accatctgct gattcgggtgg 3840

atcttttagca atcagctgac agtccaaatg ctctgcctgc cgatcatcaa gaaaatgaag 3900

aaacggatca tggatgcacgt cttgaagaag aatcggaagc agattatctg tatcaagaat 3960

atgttctctgc agcgggaaggg attcctgaac ctgagccacg tggaaaagt cagagagagc 4020

accttgggca atttctggat gaagctcctg cagctgccac cagcttgac ctctaaggcc 4080

tggacacca gaaagcttgt ggggagagcc gtgcggagaa agggcgctct gatcaacctg 4140

aagagactgc agaaattccg ggctagcgtg tccttctgga ctctgctgcc tacaacaggc 4200

gtgcggacaa gaggtctctcc actgagactg actctgtggc ctccaagaag ccagaaaagc 4260

cagcaccact gcgccctgag aaagatcgag tgggccacaa agctgtccct cggcggcaaa 4320

gcaggaccac aggtcgaaga gaaggccaac atcctgaaca gcctgccttc ctctatggaa 4380

atcgccgtgc tgcaagaaat gctgaaccag aagtgtctgg cccctttcga gcttaagaag 4440

aacctcctgc tgccaaccta cacacccac atctgtcggc acacccttaa aaagaagccc 4500

agagacatct gcagaatcag c 4521

<210> 1167

<211> 4521

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 1D

<400> 1167

gccgacaaga aaaacgtgcg gagcgctagt tctcctggac atcctcttgg cccagaaga 60

atgaccagac ggacatgac caccacaaa atgatgatga tgcggcggac caagcggcgg 120

agaagaaaaa gacgccgat gaccatgatg accagaagaa ccctgctgac caagaaaacc 180

tgtctgacct ctagaaccag cgccgccaca aaagctctgc ccagacagac aatcagccag 240

cggaggccta tcagacacc tcctggaaca agcctggcca tctggggcag aagaagcaag 300

atcgaggcct ctctatcgg cagcatcacc cctctgagca tcagcagacc taccagcaga 360

gccagacaga gctgttgctt gcctggactg acacaccctg ctcatcagcc tctgggctct 420

atggttggag ctggaacagg cggaggacct gcttgtgtgc ctgtggccga agcttctaca 480

ggcgcttga cagctgaagg cgctgccggc acaagatgta gagccagcag agccccttgc 540

agacagctgc ctgcttctag ccctaccaag tgcgagatct gcgtgaagag aagaaggcgg 600

cgcaagcgga gcagccagtc tagatctccc gtgcctaaga aacgcgagcg gatgatgctc 660

cctgtgcggg ccagaacagc tagatctgct ctgccacaag gcagggtcc tctggaagga	720
atgcttctgc ctagagcact gccagcctg ctgagcagaa tgcctgccag aagagagagc	780
agattctggc tggccctgca ggcccttga ctcagacctc ctcatctgcc tagctgtcac	840
cctctgcctc aactgcttgg acctcctcca cctcatcagg cccctggcga gaaaaacgac	900
ctgcagctgt tcgtgatgag cgacaccacc tacaagatct actggaccgt gatcctgctg	960
aaccctgcg gcaacctgca cctgaaaacc accagcctga acgccaagaa aatggaagat	1020
atgatctggg agagcaacca gcagctgaag tggacctctc acatcctgaa gtccgcctct	1080
atcgccaaga agcggatcaa gctgcggcgg aacagcacca gacgggaaat gccttctcag	1140
gccacacctt ctccacctgg accttggaga gccgctctgg gcaaagaagt gaagcggagc	1200
cagagcaagc tgagactgag aaacacaagc cccttcgaca aaaagggtt tgtgatcctg	1260
agcaacatgg gcggcaaccg gtctatctgc ctgaccatcg tgttctttct ggcccttac	1320
ttcccatgc ctagcagctg gtctagcagc ggagaaacca gactgcctct gaggccacag	1380
agaggcccta gacctctgca tagatggctg cagcagacca ccggtgctc tcagagaaga	1440
ggcgactgcc caagaacctat ggccggacca tctgttctc tgcacctgc atctggcaga	1500
gcctccagaa agacctggca gagaaggctg agagcctgta gagcaggcgg acctgctgga	1560
tgggctagac aggccagaaa acgcaagaga gagaagcggc ccagaaagtc cagacagaac	1620
catctgcagc tgaaaagctg cagacggaag atcagcaact ggtctaagct gcggagcccc	1680
tggatcttcg aggccaaaa gagcatgaag agatcccagc ggcttctctg gagcatcctg	1740
agcctgttca agaagaagaa gcccctgaca ttcagcccca gcgtgtccaa gaagaggctg	1800
cctaagctga agggcaagaa acgccggaag gaaatccagc ggaagggtgt caagaacccc	1860
agccagcctg tgccactgag aaatgacggc atcaccaacg gcaacgacag caccggctct	1920
tgcagcatca gcctgaagaa aagcctggaa aagatgcccc tgatgcggag cctgctgtac	1980
tccagaatgt gcctggtgca gatccccaca cacacctggg agcccgacta ctttgtgtcc	2040
ctgcctatga tgttcagctg ggccacacag agctttccag tggcgccgt gtttctgacc	2100
agacctgcca ttcttctgtg tagctgtacc agccactcca atccttggag ccagtccaca	2160
ctggccatcc ggtttatctc tgccctcag ccaagcagca gcaccgttac agctgtcct	2220
agcggccagt attttgcctt gcggagtatg cccaagagcc ggaaccaggt gctgtttcgg	2280
agaaatctga cccaagcca gctgcggaca ctggccctc catatatgct gctgcctcag	2340
tctctgtccc agagcctgtc tcggaagcag atcccatctc agtccatgct cgtgcggacc	2400
aggctgacac tgacaggcac tagaagctcc ggccaccagag cctctccatc tgccgtgtgt	2460

ctgtgctgct ggacatgccc cagcagaagc tttcctgccg cctctccaag cggactgaga 2520

gcacctgttg gagcacaggc tcctccagaa gtgacactga gagccagctg tgccagctcc 2580

gccagcaaag cttgtgcagg actttggcct tggggagccc aagtgcggat gaagaagaag 2640

gacagcacca tcttcatcta ccccaggctg aaaaccttcg gcgtgccact gggcagcatt 2700

ctgtgtctgg ctggaagcct gagcacgatg atgatcatta gcaccaccag acaagagtgc 2760

ggcagacggg ccagcgtgcc ctgtagacct atgatcggaa gcgccagacc tggacatgg 2820

cggacaagtg ctatgccttc tgccatggga gtgcacctgc ctaccagctg tgaaagcggg 2880

agatctctc ctgccaccgg cggaagaatg ccaggatctc agtctatcat gatgagctgg 2940

atgcctccac tggctccctg cgctgcttgt ccttgttctc ctgctcctac actgtgccct 3000

gtcacacctg ctagagcacc aacagccgtg cctgccttta caccctgtc tgctcatcct 3060

tgccagtgct tgtctggatg tcacctggct gtgcggacct ccatgcttac cttgctgcca 3120

atgatgacct tgaaggccct ggtcaagaca tggaccagct tcagaaacta cccagacgg 3180

cacctcaca gaagcccacc aacaagctgt cctccactgc tcgaggcctt tccactgcca 3240

agagccagcc tgagagctac cgtgcctaga cactctagcg tgcctggccac aggactgcat 3300

ctgcataggg agattagcct gcctctgcgg ggcttctctg tgcatacaacc actgccagga 3360

caacacctgt ggctgtccca cagactgaga ctgcggctgc ctagaacaac cgagatccag 3420

ctgacatga acgactcaa gcacaagctg gaaagccccg ctctgaaaca ggtgtcccca 3480

gctagtctc ctacacagca gcctcagaca cccagagatt ctacacaggt gctggccgtg 3540

cctatgagcc tggcctgtag cateaccgtg tccttcgtgg gccagatctc taccctggtg 3600

ctggacgtgt cctccatcag ccactggaac ggcatctggg aagtatgcc cagaacactg 3660

gaaggctgca tctccgtgaa ggaccaccgg acatcccaga accacagcaa gtgcatcacc 3720

gagtgtgtgc ggacagccct gaacaccaag tgtgaaattt gtgtgaagaa caccgccatc 3780

ctggctatca cctgatcac cccacaggac cctcacctgg accctgtgtg tcatcccat 3840

agaaggcccc gctggaaggg acaccacaga gtggtgttta gccaccatcc ttccggcagc 3900

accaagtctc actggcagca gagagaaaga ggcggaggcc gcagagaaaa gaagggtgt 3960

agagaggcaa gcagagccgg ccagtttctt gtgtggcgga gaacatctag aggcattgctc 4020

ctgcagtgga agtccggcaa tgctgcaca cctctagat gtcccagcag atctccagcc 4080

accttctga ctgcccagaa cggctggcat agatctggac tgagggccca gaccgccttc 4140

tttctgctgg acatcatcct gcggagagcc cggcctacaa gctgcagcac atgtagaatg 4200

tggtggcggc tgccctgcaa agtgaccgaa agctccctgg ccaagaaaac cctgaccaat 4260
cagcctagct tgcccggacc ttgtgctagc ctgctgtcta cactgagcca gccaccacct 4320
caggctccta gccaagtttg gacagccgct aactgcggt gtctgtgtgt gcctgtgtgt 4380
gcatgtccac ctctgaagct ggctccactg caagtgacca caaactgaa gctgatcctg 4440
gtcatgctgg aaatcgtgac cgagaacaaa gtccggcaga acttcaagcg gaactccagc 4500
ttctttctaca ccagcgacag a 4521

<210> 1168

<211> 4503

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 2D

<400> 1168

cggaagatgc agagcctgaa tcaccccagc agactgacca acaatcctcg gagaaagacc 60
tggaagatgc ggaagaagta cgcccagaag cctagccaga agaaccacct gtaccggcag 120
atcaaccggc gcaagctgca gagaaagaag tccagaagcc acctggactt cagcccctac 180
tggatgaaga aagtgaagcg ggccagaaac cggaacatga agaaaaccat gagccacctg 240
atcgcccatc aggccctgaa gatgtctggc ctgagactgt ttcacccag actgctgacc 300
agaaagaagc ccggcaagca gaaaaagggc cacatgatct tcagccggcg gaagtggcag 360
atccggcacg tgctgaagaa tctgatccc agcctgaacg cccagtggat gttcctgaga 420

atcgctagcc cacagatcat gcagagaacc agcgcggacc ggttccggat gaagcggaga 480
atgcagaacc tggacaatct gggcgtgccc tggcctctgt tgcctggatt gctgctggcc 540
catatgtacg gcttcagcac ctacggcacc cagaaaaggcg agtgctgtg tctgcagtgt 600
ctgagcggca gcagcctgtt catcctgaag cagcccctgg acctgaagat ctccaagacc 660
ttcatggcca gccctcatat tatgcagcgg atgagcggcg tgaacttcga gacaatcctg 720
caggcccatc ctcaggtgcc agctcttctt cctcaagctt ggtggcccg tagaagaggc 780
cctctgacat ctgctccaag cgacacagcag tcctgacac ggacactgga aagcggcgga 840

ctgtttcctt ggctgcacac ccagtgccgg gccttcattc acacacctag aagccctggc 900
tgcagcgtgt acgccaacat gtgctggcgg tacaagaaac ggggagtgat cgcctggcgg 960
atctaccctc ctagcacatg cagcctgcct tgagaggcc tgatcctgat tcagcacggc 1020
ggcatcttca ccttcgggtt ctgggtcgag aagctgagct ggaacatctg caagaacctg 1080
agcctgtacc tggataagtt cgtgcagcgg ctgctgtacg tgtacatcat cgagacaaac 1140
gtgttcgtgc tgaacctgtt ccacgtgccg gtgaaccaga tcttcatgat ggccttctac 1200

ctgaagtaca ccgagaaggc ctgggtcatg gaactggaat ggctgatcca gcagcagtgc	1260
taccagcggga agagaatgaa gaccggcgcc atccaagaga agggcgctat tcaagagaaa	1320
ggggccatga ccaagcggat ctgctgtgtc aatttcgagg cctgcagaga gatggaaagc	1380
ctgagcgccc ctgagaagat caccctgttt gaagcccaca tggcccgtg caccagcatc	1440
aatgtgctgt gtgtcagggc cagcctgatc gagaaactga tgaaagaaaa gcgcaagatg	1500
aagcgcaacc aggtggcatc ccctcaaadc atgcaacggc tgttcacaa gggctaccag	1560
aacaaccact tcacgttcca cctccaaaac ttgccttct tcagctcctt cggcaacaac	1620
aagtatatca acatcctgac ctttctgccc agcagattcc cttggggacc tcctccactg	1680
ggagccctta gagctacagc tcctgttaca gctgtcccc aggcacagac acctcattgg	1740
agagccgcca ccacaagcag catgagcagc tctccaagag ccgagcctac cagctctagc	1800
tcttgggcca cttgtgtgcc tagatgtgtc agctccagct gctattggag cctgtctagc	1860
tggcctcctg ctggcgctgc cgaagccaca aataccagaa ccagaagccg cgagagccag	1920
cggggaagaa tgctgacttg gagaagctcc ctgtggctgc agggcaccag atgttttaca	1980
ggcgtgcgga ccagctccag gtgcagcctg atggaacaga tccctcacct gaagtctaac	2040
agccggaaga aactgctcga ggacatgaag cagaacggct tcaccagacg gcggaacagc	2100
agaaagcaga gccaaagtga gctggccatc caggtgtgtc tggtgacaa gcacaagtac	2160
tttctgttcg gcagagccac atttctgtct gctctgtggg agtgtagcct gcctcaggct	2220
agactgtgcc tgatcgtgtc tagaacctg ctgctcgtgc agtctagaca cccaagctgg	2280
ccttggacca gatgcctgag aatgcggcct ccacgcagcc actggaactc tgcctacctg	2340
gggagaacac tgctcgtgac ctgcatcctg taccacagat ggatcgtgac cagcatgtgc	2400
cagagccaga gatggctgac tccaccacc tctagaagct ctgccctgat gtggacctgg	2460
tgggtgtacaa gaggtggcgg caagcggaag aaaaagatgt gcaaggtgtc cggcggtgtc	2520
accgcctgtg ttgaaagatg tccttgggaag ggcatctgtt ggaagtggcc tgtgacagtg	2580
gccgccatga gcagaacacc tccaagacgc gtgtgcggcc acagagaggg cagcgagtct	2640
gataatctgg gcctgtctga ctcttttcca cctgtgtgt tcaaggccga ccagagcgaa	2700
agctctctga gcagcggcaa cagcgtgatc gtgcacaaga tcgtgtgtgt gtctctgaag	2760
tccctgagca gctacaactg cgagagaaga atcagcggca tccagaagag agccatcgag	2820
ttcgccgtcc tgaagctgct gaacatggac ctcggaagg gactgacaca ccccgctcct	2880
ctgaagagga cctgcagaa caagcggaac aagaacatca agcgggtcaa ccagaagaag	2940

ggcaacatca agaggaagtc catcctgctg catctgattg tgctgaacag ccccgagagc	3000
aaccgggaaa agatcatcaa cccaccatc agctgcccct ttcagagccc caciaagaga	3060
ctgggaagcc ctctctgca cctgtgtcag cctctgagge cctatcctat cagcgagggc	3120
ctgacatga ccaccggcag aaacatcaac agcaactccc tgatgaccaa ctgcctgttc	3180
agccccatct tctgtgcca ccacgccatc atgcaccgga agatgacaag cctcacttc	3240
agactgttct ccagcaagat cccacatcca caggteccaa gtgtggtggc cctgtgcaag	3300
tttacacacc cctgcacat gctgctgccc caaggcgctt tttggaagcc tcctagccag	3360
ggcatctcca gctgtctgat gacaggctgt tggcagtggc ccagcgtgac aagcctggaa	3420
tggacagccc aagagagagg ctgttcctcc tggctgatga agcaaactg gatgaagtct	3480
tggctccctgc gggaccccag ctacagatcc atcctggaat acgtgtccac acgggtgctg	3540
tggatgcccc cctctaccgt gcctaagtgc tttctgacct tcagccagat ccggtatgtc	3600
gccctgtctc accctagctt ctacatcagc tccaccgtgt gctttctgag caagcactgc	3660
atgaccgctt gcacacctgg aaccagcctg cagtgttacc tgaacctggc caacggcctg	3720
tggttcaacc tgatcttcg gaacaaaaag accaagctgt ggttctccct gattaacatc	3780
caccaccgca agaaccact gctgcccatt cggttggaag aaaaggccac ttggatgcgg	3840
cggaccgagc tgtctctgga accttggatt ccttacctgc atcagcagaa aaccagtg	3900
ctccccatga gaagcctggg cgagccttgg cgagctggat ttcagtgggg agagtctccc	3960
tggcaagtga tggcctctct gacaggcaga cgcaagaaaa gagaggatca ctgcggactg	4020
caagagaaaa aaagccggaa gctgatgtcc agctgcgccg ctctccaca tagactgctg	4080
ggacctagca gatggggaag ctgtgggaga gcctgttctt gtggcagagg ctgtggaacc	4140
cctagaggcg actggaagag acaccacat cggcggattc tgtttcacgt gcggaacatc	4200
gtgtacggaa tccaagtgat gctgtgctgt cccccgcct ggctgtctcc aatcagcgt	4260
tgtcctcgcc tgcctctta tccattccac gtcttgccc tggaaagtac attccctcca	4320
ggcactgcca tgcctcagat gcaattgcag gcaactggca tgtgggagaa aggctgggac	4380
aagcctctgg aaaacacaca gateccccagg acaagccac tgtggaagat cacaatggtg	4440
ctgacatacc ccaactgcgt ggtgcacgtc ctgatgttcg gcggaagaa gcggagcaag	4500
ttc	4503
<210> 1169	
<211> 4518	
<212> DNA	
<213> Artificial Sequence	

<220><223> polynucleotide 3D

<400> 1169

cagaacacca gaagcaccaa cctggaaaag aaccccagcc tgaagaagca gagccagcgg	60
agaggaaagc tgagcagcag aaagaagggc cacaccaaga accggcggaa ggccaagaga	120
aagccccaga tcagccagaa gaaggaccct gccggcaagc tgaagaaaca cctgaaccgg	180
aagctgcacc tgaccagatc ctgcctgac gacctgacca tgatgatgag ccagaagctg	240
tggagaagcc agcgcaagag aatccctctg ccttctccac ggagcagctc gctgcctcag	300
tatccactgc atctccacc tccatgcctg ctgctgctcc accacagaca ccatctggcc	360
tttctcgaga tggcctgcag cagccagcac accacagca tcaagatctg gatcagcttc	420
agccacgagg acctgcctag aatgtgtccc atcagcagcc ctctgcacag accccagatg	480
cctttctgga cctgcacctt tctgtccacc acatggggca catgggagac accttctaca	540
tggggctggc ggacattcgg ccctgtgtac tacgtgtgca accggatgaa cgtgtccagc	600
gtgtgaagc ctttctgtt caccgtgcct atcgaggaca tgagagagtg caccctgggc	660
agaaacagaa tgaatgtgtc ctctgtgtg aaacctgtc tgatccccgt gccaatctg	720
accacactga gcttcgtgt gatcgaggaa agccggcgga acagacggta cagaaagatc	780
tacggggagc tgaagatgtc cctgcaggcc ctgcctctga cctttagcac actgctgtgg	840
gacagcagac acaccaccac cacaagcagc ccagaagat cccctgctct gagagctaga	900
ggcggcacca caatcgcgga agtgacaagc agaggcgcca gcagctctac cagcagagac	960
agcagaagct ttttaccag cgctcaccac agcagaccct gcagaatgag actgtaccag	1020
agcaacggca tggaaagcctg cggcacacac cctacaccta gactgtctag aggccctcca	1080
ctgcacacca gaacatgag cctgagcaac atcctgatga agttccggct gatgctgcag	1140
aagcagtgtc gctacaacct cgtgatcaag caccctctga tcttccggat caacctgcgg	1200
agacagggca agaccaaaga cggcgttgtg cagagcctgg gcttcctgaa ccagcagatc	1260
atcctgcaga aagagttctt catctgcctg ctgatgttca tcaagcgggtg gaagccagcc	1320
gccacaaaga cactccacc actgattctg tggcctcagg ccgtcctgt gcacaagaag	1380
agaggcctgt tcagcctgtt cttctccac tgctgtgcc accagatgaa gtgcctgacc	1440
gccgtggatt gtctgcagc cttctgggac atgatgattc gcaagatcca gaagcggcgg	1500
agaacggcca accggctgaa aaagaatac ctggtgcagt gtaccaacct gagcgtgccc	1560
atgatgtga ccatcctgat ctggaagcgg gtgttcatcc tcctgctgag cgacaagaag	1620
tgtctgagag tcagatgcgg cggatggctg tgtggctgga cacctagagg caagaacaag	1680
aagcggagaa agctgcggcc caagcacctg aagaaaacca gcgccaaggt gtccgtgatc	1740

accatgaagc tctgggagaa gcacttcaag ggcctgaact ggaacctggt cgtgtggatt 1800
 ctgaacctga agatgatgtg gctcaagaag tccaccaaga gcagacagag cagcccatc 1860
 ctggctcgga gctggaatac catgcaatgg aacaacaaga aaatggccat gaccgtgatc 1920
 gctggcgccc accactgtca gtacaagctg acctacacca aagtgtggaa gatgaattgg 1980
 aagaaaatga tgatcggtc ccagcacctc ctgttttagcc cactggattc aagcccactg 2040
 cagttgctgc tgcacctca cggcaagaga tgcaaccctt gctgcagact gacctggatg 2100

 agcagagagt gggaaaagcg gaagcagatc ctcgcgagg ggcgcaagta caaagagtac 2160
 ttctgaagc ggatttctat ccggaaggct atgacagtgc tggccggcga taagaaaggc 2220
 ctgggaagat tcatgagatg cgtgcagagc gagacaaagg ccgtgtctct gcagctgcct 2280
 ctcgccgaa gaaagtccgg cgtgatgaag tgttgggac tgtccccag actggacttt 2340
 caccacagat ctactctgg cggcgagaag ctgaagcact gtttcaaagc ctggggcctg 2400
 tgcttctctt acctgctgta cttcgagaag aaacggcccg agtggctgag cgttgacctt 2460
 cctggatctg tctggattct gccctgcatg gacctggacg gaatgctgac agtgatcggc 2520

 cagggactcg tgggcatgac ccctagagat ctgggaacag tggttggcgc caccgcacag 2580
 attcagaggc ctatccaggt gcagacaggc ggcagactgt tcttgattca cctgagaaag 2640
 gtggacacc accatctgca ggtcgtgacc aagaccgtga cagccacaac agctgacggc 2700
 cagaggatgc ggagactgaa gtgcaaggcc tgtcggtga gatgggcccag acctgaacct 2760
 gctgcacagg ctctccaaa gagccacttt ccacctcatc ctacggccc ctccagaacc 2820
 tctagcctgc agctcagacc cattctcca cacctgagac acccactgct gctgaaggga 2880
 aagaacagcc cctgctgcca aaagaaactg cgggtgcaga accagggcca tctgctgatg 2940

 atcctgctgc ataacgccag acagcccagc aggcctaccg gaagaacccc taccacaaga 3000
 ctgatggccc ctgtgggcag cgtgatgtct ttagcctgc tgaccagcc atctctgcc 3060
 agcgcatgta caatgccacc actcctgcat ccacagtggg cccacatag tgctggactg 3120
 tctccaggcg cttgcagacc tgctgtacc tgcacagca tgaccacat ctccagagcc 3180
 acatggcggc tgagaatccc aagcctgagg aagtaccggc agaacatga gatcacccct 3240
 cagcggctca aggccaggt ttccgtgtac agcggcaatc tgctgagctt ctccagacgg 3300
 ggcatgaaga gtagcgtgcg gctgaagaac agcatccctc acgtgccaaa agccaccgcc 3360

 gctcactctg tgacagtga gctgcagtac ctgtttttcc tgaccgtgtg cggcttcgac 3420
 cgggtgttcc tggtaagat ctgaagaag aagctgtctc tcaagctgct gagaggcccc 3480
 agacggaaa tgctgatggt gctttggctg cccgccaacc agagtctgca gaaaagccag 3540
 gtgttcaggt ggggtgctgc gaccgaaacc tacatggaaa tgcactacgg ccatcaggcc 3600

cctcaggtgg ccatgctgcc taaactgctg tgtagacaga tgctcccccac tctgtccaca 3660
ctccagcaga ggcatcctca gggaccttgt cctcctcctg tgacacctct gagagtgcag 3720
tctgtgctgc tcttgggagt gcctcagaca gccgctttta gcggccggat tctgcaccag 3780

ccagaaatgg ccgcatgag actgatgccc aagtctcctga actccaccaa cagctggtgg 3840
acagtggccc ctagatgtcc tagaagcgcc gtggacatta gccccggacc tacatctcct 3900
agcctggcct cttgtgcctc tgtggccatt ggaaaactgg cactgctggg cgcactctgcc 3960
ccttgtggcg cagctgggtgc tagagaggct ggaagatttg ccgtgctggg caccatggtt 4020
atgaagggtg ctgccgcagc ctctgtcag tctcctccat ctccaagaga gacaaccctt 4080
agcagcgacg ccaccagacg gacaagacct attgccgctc agagcaaaaa gaccatgact 4140
gccgccggac tgaccctcgc gagaaacctg cagagaaatc tgaaggctct gggcgccaag 4200

aagatcacct tctgagaaa cagcagacgc gccacaccta cctctaaggg cagcctgaga 4260
agaaagtacc tgagagtga catccgcaag ctcatctgga ccaagcagcg gagcttctctg 4320
tctctgttcc ccaagctgag agccaccgag cagatgacca atgtgggatg cctgctcaag 4380
aaaagcagcc aattgcggcg gagctggcgc aatgtgtccc ggatcagcaa catggaacac 4440
aggctgacca tggacagcgc cctgagcctg acaaagagag agggccctga gacaagcgag 4500
aagaagagga agttgcct 4518

<210> 1170

<211> 4521

<212> DNA

<213> Artificial Sequence

<220><223> polynucleotide 4D

<400> 1170

aacagaaaga ccagaaaggc cgccagagag aagcaccgca agaccgacga caagaagaag 60
aagtccaccg aaaagaccaa gaacgccaag aagatgcctt tccagcagcg gcctcctctg 120
cagcctgtta acctggatct gcagcaccag cgcagacgca aaaagaagaa agacaaggtc 180
gaaatccgga atcgagagccc taaggccaat agcaccgagt gtcagggcga gcacagcaga 240
gagcagaacc tgctgaatct ggtgcagctg aacctcaca gccctacca cagaaaggac 300
gaagaggacc accagaagcg gcaccaccac cacaatcaaa agaaaatgag cgtgcgggct 360
agcgtgtcct tctggacact tttgccaaca accggcgtgc ggacaagagg ctctccactg 420

agactgacac tgtggcctcc acgggttcca cttctccac ctcttctctt gggccccaga 480
atgcagctgt gtaccagct cgcccgggtt ttcctatca cacctcctgt gtggcacatc 540

ctgggacctc agagacacac acctcaggct cctctgaggc tgtggtcttg gtgcggcaca 600
 agccagacct acttcggcag cagaccatct ccttgccctga gctggtccag cagaattgtg 660
 gcccctggac acgccctgag ctgtcggact agaagaagat ggtctagcaa gcggtggatc 720
 ttctccaacc agctgaccgt gcagatgctg tgcctgccaa tcacacaccc attcgctctt 780
 cagcctctgg gacaagagat gcccaacaac acccagatcc ggctgctgaa gccctgcaga 840

 gtgaacgccg tggaagaact gcacagcagg cggatgtctg tgcggatcgt gaagaactgg 900
 gtgtcctgct gttacgtgcg gctgtctgct gtgggcctgt ctacttgag tgccctggac 960
 gaggaaaaga agaacggccg gatcagcagc ctgaaaaaga aagtgaatgc ctgcagctcc 1020
 ctgatcctga gcttcacg cgtagaaaacc ggcatggaaa tcctgctgtg gattctgctg 1080
 aagatggaaa ttcagatctt caagatttgc ctggcgaga tgcagctctg cggccaggcc 1140
 tttagaagct ttagcgccga tttagcgcc cctcagatca ttaagaagat gaagaaacgg 1200
 atcatggtgc acgagctgaa gaagaatctg ctgctgccta tgtgctccag cctggctctg 1260

 ccaacaggcc tgacatctct gatcctgcct agcagcgate tggccgtgct gatctctagc 1320
 tccaccagcc actttctgat gcggagccct gtgctgccaa gcagcagact gacttgtgcc 1380
 tctccacagc tgccccggat gtggacttgg tctagctggc tgaagaacga gggcaacaac 1440
 cactggccta gagtggaaat gcctaccggc tggtgctcg tcggctacaa caccagaaac 1500
 acagcccaga atcctcggct gcagcagcac ctgaaacact ggacagcagtg caccagagcc 1560
 agatggtgtc aagagccctg tcagaccctg accttcttcc atttcttctt ctttttcaaa 1620
 acggtgtccc tgtgttgccc cggtggtct aaaggacaac ctctccacc tggcctgaag 1680

 ccttctagcc tggcttctca ggtggccaga accacaggcg tgtaccagca cgtgtggctg 1740
 atctgtttcg tgttttctgt gtgtgtggaa accggttct gtcacgtggc ccaagtggga 1800
 ctgagagac tgggtgtctt gtccggcatc accgacgtga accattgggc ccagcctaag 1860
 ccatctccta gcaaaggcac cggcatgaac agaccatcg gcctgagagt tggcaaaggc 1920
 gtgtgggcca gactgatcct ggccatgaca ctgacctga acggcatggc caagaagtcc 1980
 cagcagcctc tgcaggtcgt gctgagactg ggaaacctgc ctccattctt cagaggcagc 2040
 gaggtgccct ttctagacc ttgtcggacc aagcctgcct gcacaagcaa gccctggact 2100

 cccagaaaac tcgtggggag agccgtgcgg agaaaggat ctccactctg ggattgctcc 2160
 accacaacag gcacacacca cggatgccctg tgggagatcc catctgtgac cctgctggcc 2220
 catcctagaa ccgcctctat caccctgcct accacaagcc tgaagggtc cagaaccagc 2280
 tgctgccta gatctcacc cagactgcct aggaccaa atggccctgca gtgtctgctg 2340
 cacagcctgg gaacaaccgg aacactcgtt tgggaaagg gcgtcctgca gatgagatcc 2400

ctcgaagccc attgtccact gcagacctic catctgcacc actgcaggac ccagcctagc	2460
tcttgtcctc ctgcctggat tctgtaccaa ggacagtgga gcggagccgt cgtgggactt	2520
agacctgtgg ctccacatct gcctagacct atccagggcc tgcactgtcc acaggcacct	2580
catcaacctg ctctgagctg gggaaaatgg cccgtgggaa tgacaggccc tgccagatgt	2640
tgcagatggc ccagacggtg ccagaagaag gtcccatcag cctctccatg gggcctcgtg	2700
ctcaaaaaga accggaaaca gatgctgaac cagaagtgtc tggccccctt tagagagagc	2760
accctgggca atttctggat gaagctgctc cagctgcctg tcgtgatcaa cctgaagaga	2820
ctgcagaagt tcaacctgca cctgtgctac taccacagcc agagcaacag aaacaagagc	2880
cgccagatgg aatccctggg catgaagttg cagtcccaga aatcccagca ccactgtgcc	2940
ctgcggaaga tcgagtgggc cacaaagtgt tctctcggcg gaaaagccgg accacaggct	3000
caagagaagg ccacctctcg gattctgaac ctgcaagtgc tcaagaagat cctgcggagc	3060
tttatgaagc tgiaccactc tctggtcatg tgcttcggcg tgaggaccaa gctggaaaag	3120
gctctgagcg cctgtttcat ctggccccag cacagctaca agccccgtt ctttcacggc	3180
gacctgtgcg agtggggagg ccaggctcat agacagcgga actggctgaa aaactggaag	3240
cggttcaagc ttaaaaagaa gtacatccag aagaagaagc agaagtctaa caagatcatc	3300
tgcaagggcc accgcatcac catcatctgt atcaagaata tgttcctgca gcgcaagggc	3360
ttcctgaacc tgagccacgt ggaaaagtgc tglagaggcg gccctagcgc cagcgataga	3420
tgctgttctt gtagccccag cggcttcagt gccggcagag gaagatgtcc tgttcagggc	3480
tgtctgaggc ccacagagt tcaactgctg agaagatggg gccctggctc tctgtctgga	3540
cagaggctgt ctaagggtt tcaactgctc cgttgggtggg gaccaggatc tctgtctct	3600
gagcctagaa agggccatt tccaccacct gatcctccat ggctgtgac cgctgtgaca	3660
gtgatggctg gatctgtgcc tagtgctcag tctgtggacg ccttgaatc tcttgacct	3720
ctggctctcg aaggacctag cagccctaga aacctgttt ggagagagat gagcatcttt	3780
ctgcccgga tcttcaccgc caagaaaagc cccaccagct tttgtgcaa tatectgaac	3840
agcctgcaa gctctatgga aatcgccgtg ctgcaagagg acagcaaaaa gatgaccag	3900
aaggccaag ccttcggctc cctgtgtcag cttgtgtccg ctgacttctc tgccctcaa	3960
gtgacccggc tgcggagcct gaatcatctg ctgatcacct acacaccca catctgcaga	4020
cacacctgc tgaccctga caccagatgg atcttttagca atcagctgca gacagtccag	4080
atgctctgtc tgcctccact gaagcagggc gagagaatca tttggccct cggcggttt	4140

cagatcccca acttcttttg gagcctcggc atcggacaca ctggcgctg gtggcatact 4200

ggaaggcggga gaagagaatg gggcggcagc accgtgtcta gaagccctct gtggatcagc 4260

tccatgatct acctgagagg catggccttc gccagcgaca gcagcatcag aaccaccaga 4320

gtgtcctggt gcagaagatg cggcgccaaa agcgtgccg ccagctctat tgaagctctg 4380

accgtctgt ttacctgccg gaccgccagc atcagcgtga acatcagcac cctgatgtcc 4440

atcctggaag cacttaagaa gaaaccaga gacatctgcc gcacagctg ccggtgtaga 4500

cgcgagtaca gattgactat g 4521

<210> 1171

<211> 1547

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 1C

<400> 1171

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Ser Thr Arg

20 25 30

Arg Glu Met Pro Ser Gln Ala Thr Pro Ser Pro Pro Gly Pro Trp Arg

35 40 45

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

50 55 60

Arg Asn Thr Ser Pro Thr Glu Ile Gln Leu Thr Met Asn Asp Ser Lys

65 70 75 80

His Lys Leu Glu Ser Pro Ala Leu Lys Gln Val Ser Pro Ala Ser Pro

85 90 95

Pro Thr Gln Gln Pro Gln Thr Pro Gln Asp Ser Arg Gln Val Leu Ala

100 105 110

Ala Ser Ser Pro Gly His Pro Leu Gly Pro Gly Asp Cys Pro Arg Thr

115 120 125

Met Ala Gly Pro Ser Ala Ser Leu His Pro Ala Ser Gly Arg Ala Ser

130 135 140

Arg Lys Thr Trp Gln Arg Arg Leu Arg Ala Cys Arg Ala Gly Gly Pro
 145 150 155 160
 Ala Gly Trp Ala Arg Gln Ala Met Thr Leu Lys Ala Leu Val Lys Thr
 165 170 175
 Trp Thr Gln Phe Arg Asn Tyr Pro Arg Val Gly Ala Gly Thr Gly Gly

 180 185 190
 Gly Pro Ala Cys Val Pro Val Ala Glu Ala Ser Thr Gly Ala Trp Thr
 195 200 205
 Ala Glu Gly Ala Ala Gly Thr Arg Cys Arg Ala Ser Arg Ala Pro Cys
 210 215 220
 Arg Gln Leu Pro Ala Ser Ser Pro Thr Lys Cys Glu Ile Cys Val Lys
 225 230 235 240
 Arg Arg Arg Arg Arg Lys Arg Ser Ser Gln Ser Arg Ser Pro Val Pro

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

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

 370 375 380
 Arg Arg Met Thr Met Met Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr

385 390 395 400
 Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln
 405 410 415
 Thr Ile Ser Gln Arg Arg Pro Ile Gln Thr Pro Pro Gly Thr Ser Leu
 420 425 430
 Ala Ile Trp Gly Arg Leu Pro Leu Arg Pro Gln Arg Gly Pro Arg Pro

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

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

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

 625 630 635 640

Ser Gly Leu Arg Ala Pro Val Gly Ala Gln Ala Pro Pro Glu Val Thr
 645 650 655
 Leu Arg Ala Ser Cys Ala Ser Ser Ala Ser Lys Ala Cys Ala Gly Leu
 660 665 670
 Trp Pro Trp Gly Ala Gln Val Arg Asn Lys Val Arg Gln Asn Phe Lys
 675 680 685
 Arg Asn Leu Ala Lys Lys Thr Leu Thr Asn Ala Leu Arg Ser Met Pro
 690 695 700
 Lys Ser Arg Asn Gln Val Leu Phe Arg Arg Asn Leu Thr Pro Ser Gln
 705 710 715 720
 Leu Arg Thr Leu Ala Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser
 725 730 735
 Gln Ser Leu Ser Arg Lys Gln Ile Pro Ser Gln Ser Met Leu Val Thr
 740 745 750
 Ala Phe Phe Leu Leu Asp Ile Ile Leu Arg Ser Leu Leu Tyr Ser Arg
 755 760 765
 Met Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro Asp Tyr Phe
 770 775 780
 Val Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser Phe Pro Val
 785 790 795 800
 Gly Ala Val Phe Leu Thr Arg Pro Ala Ile Pro Cys Cys Ser Cys Thr
 805 810 815
 Ser His Ser Asn Pro Trp Ser Gln Ser Phe Lys Lys Lys Lys Pro Leu
 820 825 830
 Thr Phe Ser Pro Ser Val Pro Met Ser Leu Ala Cys Ser Ile Thr Val
 835 840 845
 Ser Phe Val Gly Gln Ile Ser Thr Leu Val Leu Asp Val Ser Ser Ile
 850 855 860
 Ser His Trp Arg Lys Arg Lys Arg Glu Lys Arg Ser Gln Lys Ser Arg
 865 870 875 880
 Gln Asn His Leu Gln Leu Lys Ser Cys Arg Arg Lys Ile Ser Asn Trp

885	890	895	
Ser Lys Leu Arg Ser Pro Trp Ile Phe Tyr Pro Arg Leu Lys Thr Phe			
900	905	910	
Gly Val Pro Leu Gly Ser Ile Leu Cys Leu Ala Gly Ser Leu Ser Thr			
915	920	925	
Met Met Ile Ile Ser Thr Thr Arg Gln Glu Cys Gly Arg Arg Ala Ser			
930	935	940	
Val Pro Cys Arg Pro Met Ile Gly Ser Ala Arg Pro Gly Pro Trp Arg			
945	950	955	960
Thr Ser Ala Met Pro Ser Ala Met Gly Val Ala Leu Pro Thr Ser Cys			
965	970	975	
Glu Ser Gly Arg Ser Pro Pro Ala Thr Gly Gly Arg Met Pro Gly Ser			
980	985	990	
Gln Ser Ile Met Met Ser Trp Met Pro Pro Leu Ala Pro Cys Ala Ala			
995	1000	1005	
Cys Pro Cys Ser Pro Ala Pro Thr Leu Cys Pro Ala His Pro Ala			
1010	1015	1020	
Arg Ala Pro Thr Ala Val Pro Ala Phe Thr Pro Leu Ser Ala His			
1025	1030	1035	
Pro Val Pro Val Leu Ser Gly Cys His Leu Ala Val Arg Thr Ser			
1040	1045	1050	
Met Leu Thr Leu Leu Pro Met Arg His Pro His Arg Ser Pro Pro			
1055	1060	1065	
Thr Ser Cys Pro Pro Leu Leu Glu Ala Phe Pro Leu Pro Arg Ala			
1070	1075	1080	
Ser Leu Arg Ala Thr Val Pro Arg His Ser Ser Val Leu Ala Thr			
1085	1090	1095	
Gly Leu His Leu His Arg Gln Ile Ser Leu Pro Leu Arg Gly Phe			
1100	1105	1110	
Leu Leu His Gln Pro Leu Pro Gly Gln His Leu Trp Leu Ser His			
1115	1120	1125	

Arg Leu Arg Leu Arg Leu Pro Arg Thr Gly Glu Lys Asn Asp Leu

1130 1135 1140

Gln Leu Phe Val Met Ser Asp Thr Thr Tyr Lys Ile Tyr Trp Thr

1145 1150 1155

Val Ile Leu Leu Asn Pro Cys Gly Asn Leu His Leu Lys Thr Thr

1160 1165 1170

Ser Leu Arg Arg Ala Arg Pro Thr Ser Cys Ser Thr Cys Arg Met

1175 1180 1185

Trp Trp Leu Lys Leu Ala Pro Leu Gln Val Thr Thr Thr Leu Lys

1190 1195 1200

Leu Ile Leu Val Met Leu Glu Ile Val Thr Glu Glu Ala Lys Lys

1205 1210 1215

Ser Met Lys Arg Ser Arg Arg Ser Lys Ile Glu Ala Ser Pro Ile

1220 1225 1230

Gly Ser Ile Met Lys Lys Lys Asp Ser Thr Ile Phe Ile Asn Gln

1235 1240 1245

Gln Leu Lys Trp Thr Pro His Ile Leu Lys Ser Ala Ser Val Ser

1250 1255 1260

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

1265 1270 1275

Arg Thr Leu Glu Gly Cys Ile Ser Val Lys Asp His Arg Thr Ser

1280 1285 1290

Gln Asn His Ser Lys Cys Ile Thr Glu Cys Val Arg Thr Ala Leu

1295 1300 1305

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

1310 1315 1320

Arg Asn Asp Gly Ile Thr Asn Gly Asn Asp Ser Thr Arg Ser Cys

1325 1330 1335

Ser Ile Ser Leu Lys Lys Ser Leu Glu Lys Met Pro Leu Met Asn

1340 1345 1350

Ala Lys Lys Met Glu Asp Met Ile Trp Glu Ser Asn Met Gly Gly

1355 1360 1365
Asn Arg Ser Ile Cys Leu Thr Arg Leu Pro Cys Lys Val Thr Glu

1370 1375 1380
Ser Ser Gln Arg Pro Pro Arg Ser Ile Leu Ser Leu Ala Ser Arg

1385 1390 1395
Ala Gly Gln Phe Pro Val Trp Arg Arg Thr Ser Arg Gly Met Ser

1400 1405 1410
Leu Gln Trp Lys Ser Gly Asn Ala Cys Thr Pro Leu Arg Cys Pro

1415 1420 1425
Ser Arg Ser Pro Ala Thr Phe Leu Thr Ala Leu Asn Gly Trp His

1430 1435 1440
Arg Ser Gly Leu Arg Ala Gln Gln Pro Ser Leu Pro Gly Pro Cys

1445 1450 1455
Ala Ser Leu Leu Ser Thr Leu Ser Gln Pro Pro Pro Gln Ala Pro

1460 1465 1470
Ser Gln Val Trp Thr Ala Ala Thr Leu Arg Cys Pro Ala Val Pro

1475 1480 1485
Ala Ala Ala Cys Pro Pro Ile Val Phe Phe Leu Ala Pro Tyr Phe

1490 1495 1500
Pro Thr Pro Leu Ser Ile Ser Arg Pro Thr Ser Arg Ala Arg Gln

1505 1510 1515
Ser Cys Cys Leu Pro Gly Leu Thr His Pro Ala His Gln Pro Leu

1520 1525 1530
Gly Ser Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser

1535 1540 1545

<210> 1172

<211> 1541

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 2C

<400> 1172

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

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

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

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

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

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

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

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

Ser Arg Cys Ser Leu Met Glu Gln Ile Pro His Leu Lys Ser Trp Trp

500 505 510

Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys Met Cys Lys Val Ser

515 520 525

Gly Gly Cys Thr Ala Cys Val Glu Arg Cys Pro Trp Lys Gly Ile Cys

530 535 540

Trp Lys Trp Pro Val Thr Val Ala Ala Leu Ile Leu Ile Gln His Gly

545 550 555 560

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

565 570 575

Cys Lys Asn Leu Ser Leu Tyr Leu Asp Lys Phe Val Gln Arg Leu Leu

580 585 590

Tyr Val Tyr Ile Ile Glu Thr Asn Val Phe Val Leu Asn Leu Phe His

595 600 605

Val Pro Val Asn Gln Ile Phe Met Met Ala Phe Tyr Leu Lys Tyr Thr

610 615 620

Glu Lys Ala Trp Val Met Glu Leu Glu Trp Leu Ile Gln Gln Gln Cys

625 630 635 640

Tyr Gln Leu Leu Leu Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr

645 650 655

Gln Lys Gly Glu Cys Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu

660 665 670

Phe Ile Leu Lys Gln Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met

675 680 685

Ser Arg Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys Val Lys

690 695 700

Ala Ser Pro Gln Ile Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr

705 710 715 720

Ile Arg Arg Lys Trp Gln Ile Arg His Val Leu Lys Asn Leu Pro Leu

725 730 735

Glu Asn Thr Gln Ile Pro Arg Thr Ser Pro Leu Trp Lys Ile Thr Met

740 745 750
Val Leu Thr Tyr Pro Asn Cys Val Val His Val Leu Met Phe Val Leu

755 760 765
Phe Lys Ala Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly Ile Tyr Pro

770 775 780
Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly Ile Arg Met Cys Ala Leu

785 790 795 800
Ser His Pro Ser Phe Tyr Ile Ser Ser Thr Val Cys Phe Leu Ser Lys

805 810 815
His Cys Met Thr Ala Cys Thr Arg Glu Lys Ile Ile Asn Pro Thr Ile

820 825 830
Ser Cys Pro Phe Gln Ser Pro Thr Lys Arg Leu Gly His Arg Glu Gly

835 840 845
Ser Glu Ser Asp Asn Leu Gly Leu Leu Tyr Ser Phe Pro Pro Trp Leu

850 855 860
Pro Met Arg Ser Leu Gly Glu Pro Trp Arg Ala Gly Phe Gln Trp Gly

865 870 875 880
Glu Ser Pro Trp Gln Val Met Ala Ser Leu Thr Gly Asn Ser Val Ile

885 890 895
Val His Lys Ile Val Leu Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn

900 905 910
Cys Glu Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile Glu Phe Ala

915 920 925
Val Leu Lys Leu Leu Asn Met Asp Leu Ala Ser Pro Gln Ile Met Gln

930 935 940
Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg Arg Met Gln Asn Leu

945 950 955 960
Asp Asn Leu Gly Val Pro Trp Pro Leu Leu Pro Gly Ala Ala Pro Pro

965 970 975
His Arg Leu Leu Gly Pro Ser Arg Trp Ile Leu Phe His Val Arg Asn

980 985 990

Ile Val Tyr Gly Ile Gln Val Met	Leu Cys Arg Arg Arg	Asn Ser Arg
995	1000	1005
Lys Gln Ser Gln Val Gln Leu	Ala Ile Gln Val Leu	Leu Val Asp
1010	1015	1020
Lys His Lys Tyr Phe Leu Phe	Gly Pro Tyr Pro Ile	Ser Glu Gly
1025	1030	1035
Leu Thr Met Thr Thr Gly Arg	Asn Ile Asn Ser Asn	Ser Leu Met
1040	1045	1050
Thr Asn Cys Leu Phe Ser Pro	Ile Phe Leu Cys His	His Ala Ile
1055	1060	1065
Met His Arg Lys Met Thr Ser	Pro His Phe Arg Leu	Phe Ser Ser
1070	1075	1080
Lys Ile Pro His Pro Gln Val	Pro Ser Val Val Ala	Leu Cys Lys
1085	1090	1095
Phe Leu Ala Asn Gly Leu Trp	Phe Asn Leu Ile Phe	Gln Lys Lys
1100	1105	1110
Gly His Met Ile Phe Ser Pro	Lys Phe Phe Leu Thr	Phe Ser Gln
1115	1120	1125
Arg Thr Leu Glu Ser Ala Gly	Leu Phe Pro Trp Leu	His Thr Gln
1130	1135	1140
Cys Arg Asn Lys Lys Thr Lys	Leu Trp Phe Ser Leu	Ile Asn Ile
1145	1150	1155
His His Arg Lys Asn Pro Leu	Leu Pro Met Arg Met	Ser Arg Thr
1160	1165	1170
Pro Pro Arg Arg Val Cys Gly	Ser Pro Pro Leu His	Leu Cys Gln
1175	1180	1185
Pro Leu Arg Gly Gly Lys Lys	Arg Ser Lys Phe Ala	Phe Trp Lys
1190	1195	1200
Pro Pro Ser Gln Gly Ile Ser	Ser Cys Leu Met Thr	Gly Cys Trp
1205	1210	1215
Gly Ser Cys Gly Arg Ala Cys	Ser Cys Gly Arg Gly	Cys Gly Thr

1220	1225	1230
Pro Arg Gly Asp Trp Lys Arg	His Pro Pro Arg Arg	Glu Leu Ser
1235	1240	1245
Leu Glu Pro Trp Ile Pro Tyr	Leu His Gln Gln Lys	Thr Gln Arg

1250	1255	1260
Lys Arg Met Lys Thr Gly Ala	Ile Gln Glu Lys Gly	Ala Ile Gln
1265	1270	1275
Glu Lys Gly Ala Met Thr Lys	Arg Ile Cys Val Val	Asn Phe Glu
1280	1285	1290
Ala Cys Arg Glu Met Glu Ser	Leu Ser Ala Pro Glu	Lys Ile Thr
1295	1300	1305
Leu Phe Glu Ala His Met Ala	Arg Cys Thr Ser Ile	Asn Val Leu

1310	1315	1320
Cys Val Arg Ala Ser Leu Ile	Glu Lys Leu Met Lys	Glu Lys Arg
1325	1330	1335
Lys Met Lys Arg Asn Gln Val	Ala Ser Pro Gln Ile	Met Gln Arg
1340	1345	1350
Leu Phe Ile Lys Gly Tyr Gln	Asn Asn His Phe Thr	Phe His Leu
1355	1360	1365
Gln Asn Phe Ala Phe Phe Ser	Ser Phe Gly Asn Asn	Lys Tyr Ile

1370	1375	1380
Asn Ile Leu Thr Arg Ala Phe	Ile His Thr Pro Arg	Ser Pro Gly
1385	1390	1395
Cys Ser Val Tyr Ala Asn Met	Cys Trp Arg Lys Met	Gln Ser Leu
1400	1405	1410
Asn His Pro Ser Arg Leu Thr	Asn Cys His Pro Ala	Trp Leu Ser
1415	1420	1425
Pro Ile Ser Ala Cys Pro Arg	Leu Leu Pro Tyr Pro	Phe His Val

1430	1435	1440
Leu Ala Leu Glu Val Thr Phe	Pro Pro Gly Thr Ala	Met Pro Gln
1445	1450	1455

Met Gln Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp Asp Lys
1460 1465 1470

Gln Glu Lys Lys Ser Arg Lys Leu Met Ser Ser Cys Leu Glu Lys
1475 1480 1485

Lys Ala Thr Trp Met Arg Arg Thr Pro Gly Thr Ser Leu Gln Cys

1490 1495 1500

Tyr Leu Asn Thr His Pro Cys Thr Met Leu Leu Pro Gln Gly Ile
1505 1510 1515

Pro Ser Leu Asn Ala Gln Trp Met Phe Leu Arg Ile Gly Tyr Pro
1520 1525 1530

Tyr Asp Val Pro Asp Tyr Ala Ser
1535 1540

<210> 1173

<211> 1546

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 3C

<400> 1173

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Pro Ile Pro

20 25 30

Pro His Leu Arg His Pro Leu Leu Leu Lys Asn Lys Lys Arg Arg Lys

35 40 45

Leu Arg Pro Lys Ser Arg Lys Lys Gly His Thr Lys Asn Arg Arg Lys

50 55 60

Ala Lys Arg Lys Pro Gln Ile Arg Asn Ser Arg Arg Ala Thr Pro Thr

65 70 75 80

Ser Lys Gly Ser Leu Arg Arg Lys Tyr Leu Arg Val Gly Ala Ala Ala

85 90 95

Ala Ser Cys Gln Ser Pro Pro Ser Pro Arg Glu Thr Thr Pro Ser Ser

100 105 110

Asp Ala Thr Arg Arg Thr Arg Pro Ile Ala Ala Gln Ser Lys Lys Thr
 115 120 125

Met Thr Ala Ala Gly Leu Thr Pro Ser Gln Lys Lys Asp Pro Ala Gly
 130 135 140

Lys Leu Lys Lys Gln Val Ser Val Tyr Ser Gly Asn Leu Leu Ser Phe
 145 150 155 160

Ser Arg Arg Gly Met Lys Ser Ser Val Arg Leu Lys Asn Cys Thr Asn
 165 170 175

Leu Ser Val Pro Met Met Leu Thr Ile Leu Ile Trp Lys Arg Val Phe
 180 185 190

Ile Leu Leu Leu Ser Asp Lys Lys Ser Ile Pro His Val Pro Lys Ala
 195 200 205

Thr Ala Ala His Ser Val Thr Val Lys Leu Gln Ser Arg Arg Asn Arg
 210 215 220

Arg Tyr Arg Lys Ile Tyr Gly Glu Leu Lys Met Ser Leu Gln Ala Ser
 225 230 235 240

Asn Gly Met Glu Ala Cys Gly Thr His Pro Thr Pro Arg Leu Ser Val
 245 250 255

Ser Val Ile Thr Met Lys Leu Trp Glu Lys His Phe Lys Gly Leu Asn
 260 265 270

Trp Asn Leu Val Val Trp Ile Leu Asn Leu Lys Met Met Leu Lys Lys
 275 280 285

Lys Tyr Leu Val Gln Arg Glu Trp Glu Lys Arg Lys Gln Ile Leu Gly
 290 295 300

Gly Gly Gly Lys Tyr Lys Glu Tyr Phe Leu Lys Arg Ile Leu Ile Arg
 305 310 315 320

Lys Ala Met Thr Val Leu Ala Gly Asp Lys Lys Gly Leu Gly Arg Phe
 325 330 335

Met Arg Cys Val Gln Ser Glu Thr Lys Ala Val Ser Leu Gln Leu Pro
 340 345 350

Leu Gly Arg Met Asp Leu Asp Gly Met Leu Thr Val Ile Gly Gln Gly

355	360	365	
Leu Val Gly Met Thr Pro Arg Asp Leu Gly Thr Val Ala Gly Ala Thr			
370	375	380	
Ala Gln Ile Gln Arg Pro Ile Gln Val Gln Thr Gly Gly Arg Leu Arg			
385	390	395	400
Gly Pro Arg Arg Lys Val Leu Met Val Leu Trp Leu Pro Ala Asn Gln			
405	410	415	
Ser Leu Gln Lys Ser Gln Val Phe Gln Trp Val Leu Arg Thr Glu Leu			
420	425	430	
Pro Leu Thr Phe Ser Thr Leu Leu Trp Asp Ser Arg His Asp Leu Pro			
435	440	445	
Arg Met Leu Pro Ile Ser Ser Pro Leu His Arg Pro Gln Met Pro Phe			
450	455	460	
Trp Thr Cys Thr Phe Pro Ala Thr Thr Trp Gly Thr Trp Glu Thr Pro			
465	470	475	480
Ser Thr Trp Gly Trp Arg Thr Phe Ala Arg Gln Pro Ser Arg Pro Thr			
485	490	495	
Gly Arg Thr Pro Thr Thr Arg Leu Met Ala Pro Val Gly Ser Val Met			
500	505	510	
Ser Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr Met			
515	520	525	
Pro Pro Leu Leu His Pro Gln Trp Ala Pro His Ser Ala Gly Leu Ser			
530	535	540	
Pro Gly Ala Cys Arg Pro Ala Cys Thr Cys Ile Ser Met Thr Thr Ile			
545	550	555	560
Ser Arg Ala Thr Trp Arg Arg Asn Leu Gln Arg Asn Leu Lys Val Leu			
565	570	575	
Arg Leu Arg Ile Pro Ser Leu Arg Lys Tyr Arg Gln Gln Asn Thr Arg			
580	585	590	
Ser Thr Asn Leu Glu Lys Asn Pro Ser Leu Lys Lys Gln Ser Gln Arg			
595	600	605	

Arg Gly Lys Leu Ser Leu Thr Thr Leu Ser Phe Val Leu Ile Glu Glu
610 615 620

Leu Leu Lys Lys Ser Ser Gln Leu Arg Arg Ser Trp Arg Asn Val Ser
625 630 635 640

Arg Ile Ser Asn Ile Arg Lys Leu Ile Trp Thr Lys Gln Arg Ser Phe
645 650 655

Leu Ser Leu Phe Pro Lys Leu Arg Ala Thr Glu Gln Met Thr Asn Val
660 665 670

Gly Cys Arg Leu Asp Phe His Pro Arg Ser Ser Ser Gly Asp Arg Val
675 680 685

Phe Leu Val Lys Ile Gln Ser Ser Pro Phe Leu Ala Arg Ser Trp Asn
690 695 700

Thr Met Gln Trp Asn Asn Lys Lys Met Ala Met Thr Val Ile Ala Gly
705 710 715 720

Ala His His Cys Gln Tyr Lys Leu Thr Tyr Thr Lys Val Trp Lys Met
725 730 735

Asn Trp Lys Lys Met Met Ile Gly Ser Gln His Leu Leu Phe Ser Pro
740 745 750

Leu Asp Ser Ser Pro Leu Gln Leu Leu Leu His Pro His Gly Lys Arg
755 760 765

Cys Asn Pro Cys Cys Arg Leu Thr Trp Met Ser His Leu Asn Arg Lys
770 775 780

Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu Thr Met Met Met Ser
785 790 795 800

Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile Pro Leu Pro Ser Pro
805 810 815

Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His Pro Pro Pro Pro Cys
820 825 830

Leu Leu Leu Leu His His Arg His His Leu Ala Phe Leu Glu Met Ala
835 840 845

Cys Ser Ser Gln His Thr His Ser Ile Lys Ile Trp Ile Ser Phe Ser

850	855	860	
His Glu Thr Met Ser Leu Ser Asn Ile Leu Met Lys Phe Arg Leu Thr			
865	870	875	880
Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg Ala Arg Gly			
	885	890	895
Gly Thr Thr Ile Gly Glu Val Thr Ser Ser Leu Phe Phe Ser His Cys			
	900	905	910
Leu Cys Val Ala Pro Arg Cys Pro Arg Ser Ala Val Asp Ile Ser Pro			
	915	920	925
Gly Pro Thr Ser Pro Ser Leu Ala Ser Cys Ala Ser Val Ala Ile Gly			
	930	935	940
Lys Leu Ala Leu Leu Gly Ala Ser Ala Pro Cys Gly Ala Ala Gly Ala			
945	950	955	960
Arg Glu Ala Gly Arg Phe Ala Val Leu Gly Thr Met Val Met Lys Asn			
	965	970	975
Met Glu His Arg Leu Thr Met Asp Ser Ala Leu Ser Leu Thr Lys Arg			
	980	985	990
Glu Gly Pro Glu Thr Gly Pro Val Tyr Tyr Val Cys Asn Arg Met Asn			
	995	1000	1005
Val Ser Ser Val Leu Lys Pro Phe Leu Phe Thr Val Pro Ile Glu			
1010	1015	1020	
Asp Met Arg Glu Cys Thr Leu Gly Arg Asn Arg Met Asn Val Ser			
1025	1030	1035	
Ser Val Leu Lys Pro Cys Leu Ile Pro Val Pro Ile Cys Lys Lys			
1040	1045	1050	
Lys Leu Leu Leu Lys Leu Leu Arg Gly Ala Ser Ser Ser Thr Ser			
1055	1060	1065	
Arg Asp Ser Arg Ser Phe Phe Thr Ser Ala His Pro Ser Arg Pro			
1070	1075	1080	
Cys Arg Met Arg Leu Tyr Gln Met Leu Gln Lys Gln Cys Cys Tyr			
1085	1090	1095	

Asn Leu Val Ile Lys His Pro	Leu Ile Phe Arg Ile	Asn Leu Arg
1100	1105	1110
Arg Gln Gly Lys Thr Lys Asp	Gly Val Val Gln Ser	Leu Gly Phe
1115	1120	1125
Leu Asn Gln Gln Ile Ile Leu	Gln Lys Glu Phe Phe	Ile Cys Leu
1130	1135	1140
Leu Met Phe Ile Lys Arg Trp	Lys Pro Ala Ala Thr	Lys Lys Gly
1145	1150	1155
Lys Asn Ser Pro Cys Cys Gln	Lys Lys Leu Arg Val	Gln Asn Gln
1160	1165	1170
Gly His Leu Leu Met Ile Leu	Leu His Asn Arg Gly	Pro Pro Leu
1175	1180	1185
His Thr Arg Phe Glu Lys Lys	Arg Pro Glu Trp Leu	Ser Arg Lys
1190	1195	1200
Ser Gly Val Met Lys Cys Trp	Asp Leu Cys Pro Ala	Phe Ser Gly
1205	1210	1215
Arg Ile Leu His Gln Pro Glu	Met Ala Ala Met Arg	Leu Met Pro
1220	1225	1230
Lys Phe Leu Asn Ser Thr Asn	Ser Trp Trp Thr Val	His Lys Lys
1235	1240	1245
Arg Gly Leu Phe His Gln Met	Lys Cys Leu Thr Ala	Val Asp Cys
1250	1255	1260
Leu Gln Ala Phe Trp Asp Met	Ser Glu Lys Lys Arg	Lys Leu Pro
1265	1270	1275
Met Ile Arg Lys Ile Gln Lys	Arg Arg Arg Thr Ala	Asn Arg Asn
1280	1285	1290
Ile Glu Ile Thr Pro Gln Arg	Ser Lys Ala His Leu	Lys Lys Thr
1295	1300	1305
Ser Ala Lys Gly Ala Lys Lys	Ile Thr Phe Leu Cys	Leu Arg Val
1310	1315	1320
Arg Cys Gly Gly Trp Leu Cys	Gly Trp Thr Pro Arg	Gly Trp Leu

1325	1330	1335
Lys Lys Ser Thr Lys Ser Arg Leu Cys Phe Phe Tyr Leu Leu Tyr		
1340	1345	1350
Tyr Leu Phe Phe Leu Thr Val Cys Gly Phe Thr Pro Pro Pro Leu		
1355	1360	1365
Ile Leu Trp Pro Gln Ala Ala Pro Gly Glu Lys Leu Lys His Cys		
1370	1375	1380
Phe Lys Ala Trp Gly Val Asp Pro Pro Gly Ser Val Trp Ile Leu		
1385	1390	1395
Pro Cys Phe Leu Ile His Leu Arg Lys Val Asp Thr His His Leu		
1400	1405	1410
Gln Val Val Thr Lys Thr Val Thr Ala Thr Thr Ala Asp Gly Gln		
1415	1420	1425
Arg Met Arg Arg Leu Lys Cys Lys Ala Cys Arg Leu Arg Trp Ala		
1430	1435	1440
Arg Pro Glu Pro Ala Ala Gln Ala Pro Pro Lys Ser His Phe Pro		
1445	1450	1455
Pro His Pro Ser Gly Pro Ser Arg Thr Ser Ser Leu Gln Leu Arg		
1460	1465	1470
Thr Tyr Met Glu Met His Tyr Gly His Gln Ala Pro Gln Val Ala		
1475	1480	1485
Met Leu Pro Lys Leu Leu Cys Arg Gln Met Leu Pro Thr Leu Ser		
1490	1495	1500
Thr Leu Gln Gln Arg His Pro Gln Gly Pro Cys Pro Pro Pro Val		
1505	1510	1515
Thr Pro Leu Arg Val Gln Ser Val Leu Leu Leu Gly Val Pro Gln		
1520	1525	1530
Thr Ala Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser		
1535	1540	1545
<210> 1174		
<211> 1547		
<212> PRT		

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 4C

<400> 1174

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Asp Ser Lys

20 25 30

Lys Met Thr Gln Lys Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys

35 40 45

His Arg Lys Thr Asp Asn Leu Asp Leu Gln His Gln Arg Arg Arg Lys

50 55 60

Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro Lys Ala Asn

65 70 75 80

Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln Asn Leu Leu Asn

85 90 95

Leu Val Gln Leu Asn Pro His Ser Pro His His Arg Lys Asp Glu Glu

100 105 110

Asp His Gln Lys Arg His His His His Asn Gln Lys Lys Met Ser Val

115 120 125

Asn Glu Gly Asn Asn His Trp Pro Arg Val Glu Met Pro Thr Gly Trp

130 135 140

Leu Leu Val Gly Tyr Asn Thr Arg Asn Thr Ala Gln Asn Pro Arg Leu

145 150 155 160

Gln Gln His Leu Lys His Trp Gln Gln Cys Thr Arg Ala Arg Trp Cys

165 170 175

Gln Glu Pro Cys Gln Thr Leu Thr Phe Phe His Phe Phe Phe Phe

180 185 190

Lys Thr Val Ser Leu Cys Cys Pro Gly Trp Ser Lys Gly Gln Pro Pro

195 200 205

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

210 215 220

Thr Gly Val Tyr Gln His Val Trp Leu Ile Cys Phe Val Phe Phe Val
 225 230 235 240
 Cys Val Glu Thr Gly Phe Cys His Val Ala Gln Val Gly Leu Glu Arg
 245 250 255

Leu Val Ser Leu Ser Gly Ile Thr Asp Val Asn His Trp Ala Gln Pro
 260 265 270
 Lys Pro Ser Pro Ser Lys Gly Thr Gly Met Asn Arg Pro Ile Gly Leu
 275 280 285
 Arg Val Gly Lys Gly Val Trp Ala Arg Leu Trp Leu Lys Asn Trp Lys
 290 295 300
 Arg Phe Lys Leu Lys Lys Lys Tyr Thr Gly Met Glu Ile Leu Leu Trp
 305 310 315 320

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

Cys Arg Pro Ser Pro Cys Leu Ser Trp Ser Ser Arg Ile Val Ala Pro
 385 390 395 400
 Gly His Ala Leu Ser Cys Arg Thr Arg Arg Arg Trp Ser Ser Lys Met
 405 410 415
 Ala Lys Lys Ser Gln Gln Pro Leu Cys Arg Gly Gly Pro Ser Ala Ser
 420 425 430
 Asp Arg Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly
 435 440 445

Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu
 450 455 460
 Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly

465 470 475 480
 Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro
 485 490 495
 Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Ala
 500 505 510

 Val Thr Val Met Ala Gly Ser Val Pro Ser Ala Gln Ser Val Asp Ala
 515 520 525
 Leu Glu Ser Pro Gly Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro Arg
 530 535 540
 Asn Leu Leu Trp Arg Glu Met Ser Ile Phe Leu Pro Gly Ile Phe Asn
 545 550 555 560
 Leu His Leu Cys Tyr Tyr His Ser Gln Ser Asn Arg Asn Lys Ser Arg
 565 570 575

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

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

 Ser Val Thr Leu Leu Ala Thr Ala Lys Lys Ser Pro Thr Ser Phe Cys
 705 710 715 720

Cys Gln Arg Pro Pro Leu Gln Pro Val Glu Glu Lys Lys Asn Gly Arg
 725 730 735
 Ile Ser Ser Val Pro Pro Ser Pro Pro Leu Ala Leu Gly Pro Arg Met
 740 745 750
 Gln Leu Cys Thr Gln Leu Ala Arg Phe Phe Pro Ile Thr Pro Pro Val
 755 760 765

 Trp His Ile Leu Gly Pro Gln Arg His Thr Pro Leu Leu Thr Pro Asp
 770 775 780
 Thr Arg Trp Ile Phe Ser Asn Gln Leu Gln Thr Val Gln Met Leu Cys
 785 790 795 800
 Leu Pro Pro Leu Lys Gln Gly Glu Arg Ile Ile Trp Pro Leu Gly Gly
 805 810 815
 Phe Gln Ile Pro Asn Phe Phe Trp Ser Leu Gly Ile Gly His Thr Gly
 820 825 830

 Ala Trp Trp His Thr Gly Arg Arg Arg Arg Glu Trp Gly Gly Ser Thr
 835 840 845
 Val Ser Arg Ser Pro Leu Trp Ile Ser Ser Met Ile Tyr Leu Arg Gly
 850 855 860
 Met Ala Phe Ala Ser Asp Ser Ser Ile Arg Thr Thr Arg Val Ser Trp
 865 870 875 880
 Cys Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala Ser Ser Asp Lys Lys
 885 890 895

 Lys Lys Ser Thr Glu Lys Thr Lys Asn Lys Ile Ile Cys Lys Gly His
 900 905 910
 Arg Ile Thr Gln Val Val Leu Arg Leu Gly Asn Leu Pro Pro Phe Phe
 915 920 925
 Arg Gly Ser Glu Val Pro Phe Pro Arg Pro Cys Arg Thr Lys Cys Gln
 930 935 940
 Lys Lys Val Pro Ser Ala Ser Pro Trp Gly Leu His Pro Arg Thr Ala
 945 950 955 960

 Ser Ile Thr Leu Pro Thr Thr Ser Leu Lys Gly Ser Arg Thr Ser Cys

965						970						975					
Cys	Pro	Arg	Ser	His	Pro	Arg	Leu	Pro	Arg	Thr	Lys	Trp	Pro	Leu	Gln		
980						985						990					
Cys	Leu	Leu	His	Ser	Leu	Gly	Thr	Thr	Gly	Thr	Leu	Val	Trp	Glu	Arg		
995						1000						1005					
Gly	Val	Leu	Gln	Met	Arg	Ser	Leu	Glu	Ala	His	Cys	Pro	Leu	Gln			
1010						1015						1020					
Thr	Phe	His	Leu	His	His	Cys	Arg	Thr	Gln	Pro	Ser	Ser	Cys	Pro			
1025						1030						1035					
Pro	Ala	Trp	Ile	Leu	Tyr	Gln	Gly	Gln	Trp	Ser	Gly	Ala	Val	Val			
1040						1045						1050					
Gly	Leu	Arg	Pro	Val	Ala	His	His	Leu	Pro	Arg	Pro	Ile	Gln	Gly			
1055						1060						1065					
Leu	His	Cys	Pro	Gln	Ala	Pro	His	Gln	Pro	Ala	Leu	Ser	Trp	Gly			
1070						1075						1080					
Lys	Trp	Pro	Val	Gly	Met	Thr	Gly	Pro	Ala	Arg	Cys	Cys	Arg	Trp			
1085						1090						1095					
Pro	Arg	Arg	Met	Cys	Ser	Ser	Leu	Ala	Leu	Pro	Thr	Gly	Leu	Thr			
1100						1105						1110					
Ser	Leu	Ile	Leu	Pro	Ser	Ser	Asp	Leu	Ala	Val	Leu	Ile	Ser	Ser			
1115						1120						1125					
Ser	Thr	Ser	His	Phe	Leu	Met	Arg	Ser	Pro	Val	Leu	Pro	Ser	Ser			
1130						1135						1140					
Arg	Leu	Thr	Cys	Ala	Ser	Pro	Gln	Leu	Pro	Arg	Met	Trp	Thr	Trp			
1145						1150						1155					
Ser	Ser	Trp	Leu	Lys	Glu	Trp	Gly	Gly	Gln	Ala	His	Arg	Gln	Arg			
1160						1165						1170					
Asn	Cys	Arg	Val	Asn	Ala	Val	Glu	Glu	Leu	His	Ser	Arg	Arg	Met			
1175						1180						1185					
Ser	Val	Arg	Ile	Val	Lys	Asn	Trp	Val	Ser	Cys	Cys	Tyr	Val	Arg			
1190						1195						1200					

Leu Ser	Ala Val Gly Leu Ser	Thr Trp Ser Ala Leu	Asp Ser Leu
1205	1210	1215	
Ile Leu	Ser Phe Gln Arg Val	Lys Thr Ser Arg Ile	Leu Asn Leu
1220	1225	1230	
Gln Val	Leu Lys Lys Ile Leu	Arg Ser Phe Met Lys	Leu Tyr His
1235	1240	1245	
Ser Leu	Val Met Cys Leu Arg	Leu Arg Thr Lys Leu	Glu Lys Ala
1250	1255	1260	
Leu Ser	Ala Leu Phe Ile Trp	Pro Gln His Ser Tyr	Lys Gly Gln
1265	1270	1275	
Ala Phe	Gly Ser Leu Cys Gln	Leu Val Ser Ala Asp	Phe Ser Ala
1280	1285	1290	
Pro Gln	Val Thr Arg Leu Arg	Ser Leu Asn His Leu	Leu Ile Arg
1295	1300	1305	
Trp Ile	Phe Ser Asn Gln Leu	Thr Val Gln Met Leu	Cys Leu Pro
1310	1315	1320	
Ile Ile	Lys Lys Met Lys Lys	Arg Ile Met Val His	Val Leu Lys
1325	1330	1335	
Lys Asn	Arg Lys Gln Ile Ile	Cys Ile Lys Asn Met	Phe Leu Gln
1340	1345	1350	
Arg Lys	Gly Phe Leu Asn Leu	Ser His Val Glu Lys	Phe Arg Glu
1355	1360	1365	
Ser Thr	Leu Gly Asn Phe Trp	Met Lys Leu Leu Gln	Leu Pro Pro
1370	1375	1380	
Ala Cys	Thr Ser Lys Ala Trp	Thr Pro Arg Lys Leu	Val Gly Arg
1385	1390	1395	
Ala Val	Arg Arg Lys Gly Val	Val Ile Asn Leu Lys	Arg Leu Gln
1400	1405	1410	
Lys Phe	Arg Ala Ser Val Ser	Phe Trp Thr Leu Leu	Pro Thr Thr
1415	1420	1425	
Gly Val	Arg Thr Arg Gly Ser	Pro Leu Arg Leu Thr	Leu Trp Pro

1430	1435	1440
Pro Arg Ser Gln Lys Ser Gln His His Cys Ala Leu Arg Lys Ile		
1445	1450	1455
Glu Trp Ala Thr Lys Leu Ser Leu Gly Gly Lys Ala Gly Pro Gln		
1460	1465	1470
Ala Gln Glu Lys Ala Asn Ile Leu Asn Ser Leu Pro Ser Ser Met		
1475	1480	1485
Glu Ile Ala Val Leu Gln Glu Met Leu Asn Gln Lys Cys Leu Ala		
1490	1495	1500
Pro Phe Glu Leu Lys Lys Asn Leu Leu Leu Pro Thr Tyr Thr Pro		
1505	1510	1515
His Ile Cys Arg His Thr Leu Lys Lys Lys Pro Arg Asp Ile Cys		
1520	1525	1530
Arg Ile Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser		
1535	1540	1545
<210> 1175		
<211> 1750		
<212> PRT		
<213> Artificial Sequence		
<220><223> hINV- and HA-extended poly-FSP polypeptide 1C		
<400> 1175		
Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val		
1 5 10 15		
Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met		
20 25 30		
Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala		
35 40 45		
Leu Tyr Thr Gly Phe Ser Ile Leu Val Thr Leu Leu Leu Ala Gly Gln		
50 55 60		
Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys		
65 70 75 80		

Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg Met Lys
 85 90 95
 Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala Thr Pro
 100 105 110
 Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met
 115 120 125

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

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

 Glu Val Lys Arg Ser Gln Ser Lys Leu Arg Leu Arg Asn Thr Ser Pro
 260 265 270
 Thr Glu Ile Gln Leu Thr Met Asn Asp Ser Lys His Lys Leu Glu Ser
 275 280 285
 Pro Ala Leu Lys Gln Val Ser Pro Ala Ser Pro Pro Thr Gln Gln Pro
 290 295 300
 Gln Thr Pro Gln Asp Ser Arg Gln Val Leu Ala Ala Ser Ser Pro Gly
 305 310 315 320

 His Pro Leu Gly Pro Gly Asp Cys Pro Arg Thr Met Ala Gly Pro Ser

	325		330		335										
Ala	Ser	Leu	His	Pro	Ala	Ser	Gly	Arg	Ala	Ser	Arg	Lys	Thr	Trp	Gln
	340		345		350										
Arg	Arg	Leu	Arg	Ala	Cys	Arg	Ala	Gly	Gly	Pro	Ala	Gly	Trp	Ala	Arg
	355		360		365										
Gln	Ala	Met	Thr	Leu	Lys	Ala	Leu	Val	Lys	Thr	Trp	Thr	Gln	Phe	Arg
	370		375		380										
Asn	Tyr	Pro	Arg	Val	Gly	Ala	Gly	Thr	Gly	Gly	Gly	Pro	Ala	Cys	Val
385			390		395		400								
Pro	Val	Ala	Glu	Ala	Ser	Thr	Gly	Ala	Trp	Thr	Ala	Glu	Gly	Ala	Ala
	405		410		415										
Gly	Thr	Arg	Cys	Arg	Ala	Ser	Arg	Ala	Pro	Cys	Arg	Gln	Leu	Pro	Ala
	420		425		430										
Ser	Ser	Pro	Thr	Lys	Cys	Glu	Ile	Cys	Val	Lys	Arg	Arg	Arg	Arg	Arg
	435		440		445										
Lys	Arg	Ser	Ser	Gln	Ser	Arg	Ser	Pro	Val	Pro	Lys	Lys	Arg	Glu	Arg
	450		455		460										
Met	Met	Leu	Pro	Val	Arg	Ala	Arg	Thr	Ala	Arg	Ser	Ala	Leu	Pro	Gln
465		470		475		480									
Gly	Arg	Ala	Pro	Leu	Glu	Gly	Met	Leu	Leu	Pro	Arg	Ala	Leu	Pro	Ser
	485		490		495										
Leu	Leu	Ser	Arg	Met	Pro	Ala	Arg	Arg	Glu	Ser	Arg	Phe	Trp	Leu	Ala
	500		505		510										
Leu	Gln	Ala	Leu	Gly	Leu	Arg	Pro	Pro	His	Leu	Pro	Ser	Cys	His	Pro
	515		520		525										
Leu	Pro	Gln	Leu	Leu	Gly	Pro	Pro	Pro	Pro	His	Gln	Ala	Pro	Phe	Asp
	530		535		540										
Lys	Lys	Gly	Phe	Val	Ile	Leu	Ser	Lys	Gly	Lys	Lys	Arg	Arg	Lys	Glu
545		550		555		560									
Ile	Arg	Arg	Met	Thr	Arg	Arg	Thr	Met	Thr	Thr	Thr	Lys	Met	Met	Met
	565		570		575										

Met Arg Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg Arg Met Thr Met
580 585 590

Met Thr Arg Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu Thr Pro Arg
595 600 605

Thr Ser Ala Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile Ser Gln Arg
610 615 620

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

Leu Pro Leu Arg Pro Gln Arg Gly Pro Arg Pro Leu His Arg Trp Leu
645 650 655

Gln Gln Thr Thr Gly Cys Ser Gln Arg Arg Ile Ala Lys Lys Arg Ile
660 665 670

Lys Leu Arg Arg Asn Thr Leu Ala Ile Arg Phe Ile Ser Ala Pro Gln
675 680 685

Pro Ser Ser Ser Thr Val Thr Ala Ala Pro Ser Gly Gln Tyr Phe Ser
690 695 700

Ser Phe Phe Tyr Thr Ser Asp Arg Thr Lys Cys Glu Ile Cys Val Lys
705 710 715 720

Asn Thr Ala Ile Leu Ala Ile Thr Leu Ile Thr Pro Gln Asp Pro His
725 730 735

Leu Asp Pro Val Cys His Pro His Arg Arg Pro Gly Trp Lys Gly His
740 745 750

His Arg Val Val Phe Ser His His Pro Ser Gly Ser Thr Lys Ser His
755 760 765

Trp Gln Gln Arg Glu Arg Gly Gly Gly Arg Arg Glu Lys Lys Gly Cys
770 775 780

Arg Glu Met Pro Ser Ser Trp Ser Ser Ser Gly Arg Thr Ala Asp Lys
785 790 795 800

Lys Asn Val Arg Ser Arg Thr Arg Leu Thr Leu Thr Gly Thr Arg Ser
805 810 815

Ser Gly Thr Arg Ala Ser Pro Ser Ala Val Cys Leu Cys Cys Trp Thr

820	825	830	
Cys Pro Ser Arg Ser Phe Pro Ala Ala Ser Pro Ser Gly Leu Arg Ala			
835	840	845	
Pro Val Gly Ala Gln Ala Pro Pro Glu Val Thr Leu Arg Ala Ser Cys			
850	855	860	
Ala Ser Ser Ala Ser Lys Ala Cys Ala Gly Leu Trp Pro Trp Gly Ala			
865	870	875	880
Gln Val Arg Asn Lys Val Arg Gln Asn Phe Lys Arg Asn Leu Ala Lys			
885	890	895	
Lys Thr Leu Thr Asn Ala Leu Arg Ser Met Pro Lys Ser Arg Asn Gln			
900	905	910	
Val Leu Phe Arg Arg Asn Leu Thr Pro Ser Gln Leu Arg Thr Leu Ala			
915	920	925	
Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser Arg			
930	935	940	
Lys Gln Ile Pro Ser Gln Ser Met Leu Val Thr Ala Phe Phe Leu Leu			
945	950	955	960
Asp Ile Ile Leu Arg Ser Leu Leu Tyr Ser Arg Met Cys Leu Val Gln			
965	970	975	
Ile Pro Thr His Thr Trp Glu Pro Asp Tyr Phe Val Ser Leu Pro Met			
980	985	990	
Met Phe Ser Trp Ala Thr Gln Ser Phe Pro Val Gly Ala Val Phe Leu			
995	1000	1005	
Thr Arg Pro Ala Ile Pro Cys Cys Ser Cys Thr Ser His Ser Asn			
1010	1015	1020	
Pro Trp Ser Gln Ser Phe Lys Lys Lys Lys Pro Leu Thr Phe Ser			
1025	1030	1035	
Pro Ser Val Pro Met Ser Leu Ala Cys Ser Ile Thr Val Ser Phe			
1040	1045	1050	
Val Gly Gln Ile Ser Thr Leu Val Leu Asp Val Ser Ser Ile Ser			
1055	1060	1065	

His Trp Arg Lys Arg Lys Arg Glu Lys Arg Ser Gln Lys Ser Arg
1070 1075 1080

Gln Asn His Leu Gln Leu Lys Ser Cys Arg Arg Lys Ile Ser Asn
1085 1090 1095

Trp Ser Lys Leu Arg Ser Pro Trp Ile Phe Tyr Pro Arg Leu Lys
1100 1105 1110

Thr Phe Gly Val Pro Leu Gly Ser Ile Leu Cys Leu Ala Gly Ser
1115 1120 1125

Leu Ser Thr Met Met Ile Ile Ser Thr Thr Arg Gln Glu Cys Gly
1130 1135 1140

Arg Arg Ala Ser Val Pro Cys Arg Pro Met Ile Gly Ser Ala Arg
1145 1150 1155

Pro Gly Pro Trp Arg Thr Ser Ala Met Pro Ser Ala Met Gly Val
1160 1165 1170

Ala Leu Pro Thr Ser Cys Glu Ser Gly Arg Ser Pro Pro Ala Thr
1175 1180 1185

Gly Gly Arg Met Pro Gly Ser Gln Ser Ile Met Met Ser Trp Met
1190 1195 1200

Pro Pro Leu Ala Pro Cys Ala Ala Cys Pro Cys Ser Pro Ala Pro
1205 1210 1215

Thr Leu Cys Pro Ala His Pro Ala Arg Ala Pro Thr Ala Val Pro
1220 1225 1230

Ala Phe Thr Pro Leu Ser Ala His Pro Val Pro Val Leu Ser Gly
1235 1240 1245

Cys His Leu Ala Val Arg Thr Ser Met Leu Thr Leu Leu Pro Met
1250 1255 1260

Arg His Pro His Arg Ser Pro Pro Thr Ser Cys Pro Pro Leu Leu
1265 1270 1275

Glu Ala Phe Pro Leu Pro Arg Ala Ser Leu Arg Ala Thr Val Pro
1280 1285 1290

Arg His Ser Ser Val Leu Ala Thr Gly Leu His Leu His Arg Gln

1295	1300	1305
Ile Ser Leu Pro Leu Arg Gly Phe Leu Leu His Gln Pro Leu Pro		
1310	1315	1320
Gly Gln His Leu Trp Leu Ser His Arg Leu Arg Leu Arg Leu Pro		
1325	1330	1335
Arg Thr Gly Glu Lys Asn Asp Leu Gln Leu Phe Val Met Ser Asp		
1340	1345	1350
Thr Thr Tyr Lys Ile Tyr Trp Thr Val Ile Leu Leu Asn Pro Cys		
1355	1360	1365
Gly Asn Leu His Leu Lys Thr Thr Ser Leu Arg Arg Ala Arg Pro		
1370	1375	1380
Thr Ser Cys Ser Thr Cys Arg Met Trp Trp Leu Lys Leu Ala Pro		
1385	1390	1395
Leu Gln Val Thr Thr Thr Leu Lys Leu Ile Leu Val Met Leu Glu		
1400	1405	1410
Ile Val Thr Glu Glu Ala Lys Lys Ser Met Lys Arg Ser Arg Arg		
1415	1420	1425
Ser Lys Ile Glu Ala Ser Pro Ile Gly Ser Ile Met Lys Lys Lys		
1430	1435	1440
Asp Ser Thr Ile Phe Ile Asn Gln Gln Leu Lys Trp Thr Pro His		
1445	1450	1455
Ile Leu Lys Ser Ala Ser Val Ser Lys Lys Arg Leu Pro Lys Leu		
1460	1465	1470
Asn Gly Ile Trp Glu Val Met Pro Arg Thr Leu Glu Gly Cys Ile		
1475	1480	1485
Ser Val Lys Asp His Arg Thr Ser Gln Asn His Ser Lys Cys Ile		
1490	1495	1500
Thr Glu Cys Val Arg Thr Ala Leu Asn Gln Arg Lys Val Val Lys		
1505	1510	1515
Asn Pro Ser Gln Pro Val Pro Leu Arg Asn Asp Gly Ile Thr Asn		
1520	1525	1530

Gly Asn Asp Ser Thr Arg Ser Cys Ser Ile Ser Leu Lys Lys Ser
1535 1540 1545

Leu Glu Lys Met Pro Leu Met Asn Ala Lys Lys Met Glu Asp Met
1550 1555 1560

Ile Trp Glu Ser Asn Met Gly Gly Asn Arg Ser Ile Cys Leu Thr
1565 1570 1575

Arg Leu Pro Cys Lys Val Thr Glu Ser Ser Gln Arg Pro Pro Arg
1580 1585 1590

Ser Ile Leu Ser Leu Ala Ser Arg Ala Gly Gln Phe Pro Val Trp
1595 1600 1605

Arg Arg Thr Ser Arg Gly Met Ser Leu Gln Trp Lys Ser Gly Asn
1610 1615 1620

Ala Cys Thr Pro Leu Arg Cys Pro Ser Arg Ser Pro Ala Thr Phe
1625 1630 1635

Leu Thr Ala Leu Asn Gly Trp His Arg Ser Gly Leu Arg Ala Gln
1640 1645 1650

Gln Pro Ser Leu Pro Gly Pro Cys Ala Ser Leu Leu Ser Thr Leu
1655 1660 1665

Ser Gln Pro Pro Pro Gln Ala Pro Ser Gln Val Trp Thr Ala Ala
1670 1675 1680

Thr Leu Arg Cys Pro Ala Val Pro Ala Ala Ala Cys Pro Pro Ile
1685 1690 1695

Val Phe Phe Leu Ala Pro Tyr Phe Pro Thr Pro Leu Ser Ile Ser
1700 1705 1710

Arg Pro Thr Ser Arg Ala Arg Gln Ser Cys Cys Leu Pro Gly Leu
1715 1720 1725

Thr His Pro Ala His Gln Pro Leu Gly Ser Met Gly Tyr Pro Tyr
1730 1735 1740

Asp Val Pro Asp Tyr Ala Ser
1745 1750

<210> 1176

<211> 1744

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 2C

<400> 1176

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu

180 185 190

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

195 200 205

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys

210 215 220
 Gln Asp Leu Gly Pro Val Pro Met Arg Gln Ile Asn Arg Arg Lys Leu

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

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

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

 420 425 430
 Leu Tyr His Arg Trp Ile Val Thr Ser Met Cys Gln Ser Gln Arg Trp
 435 440 445
 Leu Thr Ser Thr Thr Ser Arg Ser Ser Ala Leu Met Trp Thr Gln Trp
 450 455 460

Ser Ser Val Thr Ser Leu Glu Trp Thr Ala Gln Glu Arg Gly Cys Ser
 465 470 475 480
 Ser Trp Leu Met Lys Gln Thr Trp Met Lys Ser Trp Ser Leu Arg Asp
 485 490 495
 Pro Ser Tyr Arg Ser Ile Leu Glu Tyr Val Ser Thr Arg Val Leu Trp
 500 505 510
 Met Pro Thr Ser Thr Val Gly Ala Leu Arg Ala Thr Ala Pro Ala Thr
 515 520 525
 Ala Ala Pro Gln Ala Gln Thr Pro His Trp Arg Ala Ala Thr Thr Ser
 530 535 540
 Ser Met Ser Ser Ser Pro Arg Ala Glu Pro Thr Ser Ser Ser Ser Trp
 545 550 555 560
 Ala Thr Cys Trp Pro Arg Cys Cys Ser Ser Ser Cys Tyr Trp Ser Leu
 565 570 575
 Ser Ser Trp Pro Pro Ala Gly Ala Ala Glu Ala Thr Asn Thr Arg Thr
 580 585 590
 Arg Ser Arg Glu Ser Gln Arg Gly Arg Met Leu Thr Trp Arg Ser Ser
 595 600 605
 Leu Trp Leu Gln Gly Thr Arg Cys Phe Thr Gly Val Arg Thr Ser Ser
 610 615 620
 Arg His Pro Ser Trp Pro Trp Thr Arg Cys Leu Arg Met Arg Pro Pro
 625 630 635 640
 Arg Ser Asn Ser Arg Lys Lys Leu Leu Glu Asp Met Lys Gln Asn Gly
 645 650 655
 Phe Thr Arg Tyr Lys Lys Arg Gly Val Ile Ala Trp Arg Arg Ala Thr
 660 665 670
 Phe Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro Gln Ala Arg Leu Cys
 675 680 685
 Leu Ile Val Ser Arg Thr Leu Leu Leu Val Gln Ser Arg Cys Ser Leu
 690 695 700
 Met Glu Gln Ile Pro His Leu Lys Ser Trp Trp Cys Thr Arg Gly Gly

705 710 715 720
 Gly Lys Arg Lys Lys Lys Met Cys Lys Val Ser Gly Gly Cys Thr Ala
 725 730 735
 Cys Val Glu Arg Cys Pro Trp Lys Gly Ile Cys Trp Lys Trp Pro Val

 740 745 750
 Thr Val Ala Ala Leu Ile Leu Ile Gln His Gly Gly Ile Phe Thr Phe
 755 760 765
 Arg Phe Trp Val Glu Lys Leu Ser Trp Asn Ile Cys Lys Asn Leu Ser
 770 775 780
 Leu Tyr Leu Asp Lys Phe Val Gln Arg Leu Leu Tyr Val Tyr Ile Ile
 785 790 795 800
 Glu Thr Asn Val Phe Val Leu Asn Leu Phe His Val Pro Val Asn Gln

 805 810 815
 Ile Phe Met Met Ala Phe Tyr Leu Lys Tyr Thr Glu Lys Ala Trp Val
 820 825 830
 Met Glu Leu Glu Trp Leu Ile Gln Gln Gln Cys Tyr Gln Leu Leu Leu
 835 840 845
 Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr Gln Lys Gly Glu Cys
 850 855 860
 Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu Phe Ile Leu Lys Gln

 865 870 875 880
 Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met Ser Arg Ser His Leu
 885 890 895
 Asp Phe Ser Pro Tyr Trp Met Lys Lys Val Lys Ala Ser Pro Gln Ile
 900 905 910
 Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr Ile Arg Arg Lys Trp
 915 920 925
 Gln Ile Arg His Val Leu Lys Asn Leu Pro Leu Glu Asn Thr Gln Ile

 930 935 940
 Pro Arg Thr Ser Pro Leu Trp Lys Ile Thr Met Val Leu Thr Tyr Pro
 945 950 955 960

Asn Cys Val Val His Val Leu Met Phe Val Leu Phe Lys Ala Asp Gln
 965 970 975
 Ser Glu Ser Ser Leu Ser Ser Gly Ile Tyr Pro Pro Ser Thr Cys Ser
 980 985 990
 Leu Pro Cys Arg Gly Ile Arg Met Cys Ala Leu Ser His Pro Ser Phe

 995 1000 1005
 Tyr Ile Ser Ser Thr Val Cys Phe Leu Ser Lys His Cys Met Thr
 1010 1015 1020
 Ala Cys Thr Arg Glu Lys Ile Ile Asn Pro Thr Ile Ser Cys Pro
 1025 1030 1035
 Phe Gln Ser Pro Thr Lys Arg Leu Gly His Arg Glu Gly Ser Glu
 1040 1045 1050
 Ser Asp Asn Leu Gly Leu Leu Tyr Ser Phe Pro Pro Trp Leu Pro

 1055 1060 1065
 Met Arg Ser Leu Gly Glu Pro Trp Arg Ala Gly Phe Gln Trp Gly
 1070 1075 1080
 Glu Ser Pro Trp Gln Val Met Ala Ser Leu Thr Gly Asn Ser Val
 1085 1090 1095
 Ile Val His Lys Ile Val Leu Val Phe Leu Lys Ser Leu Ser Ser
 1100 1105 1110
 Tyr Asn Cys Glu Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile

 1115 1120 1125
 Glu Phe Ala Val Leu Lys Leu Leu Asn Met Asp Leu Ala Ser Pro
 1130 1135 1140
 Gln Ile Met Gln Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg
 1145 1150 1155
 Arg Met Gln Asn Leu Asp Asn Leu Gly Val Pro Trp Pro Leu Leu
 1160 1165 1170
 Pro Gly Ala Ala Pro Pro His Arg Leu Leu Gly Pro Ser Arg Trp

 1175 1180 1185
 Ile Leu Phe His Val Arg Asn Ile Val Tyr Gly Ile Gln Val Met

1190	1195	1200
Leu Cys Arg Arg Arg Asn Ser Arg Lys Gln Ser Gln Val Gln Leu		
1205	1210	1215
Ala Ile Gln Val Leu Leu Val Asp Lys His Lys Tyr Phe Leu Phe		
1220	1225	1230
Gly Pro Tyr Pro Ile Ser Glu Gly Leu Thr Met Thr Thr Gly Arg		

1235	1240	1245
Asn Ile Asn Ser Asn Ser Leu Met Thr Asn Cys Leu Phe Ser Pro		
1250	1255	1260
Ile Phe Leu Cys His His Ala Ile Met His Arg Lys Met Thr Ser		
1265	1270	1275
Pro His Phe Arg Leu Phe Ser Ser Lys Ile Pro His Pro Gln Val		
1280	1285	1290
Pro Ser Val Val Ala Leu Cys Lys Phe Leu Ala Asn Gly Leu Trp		

1295	1300	1305
Phe Asn Leu Ile Phe Gln Lys Lys Gly His Met Ile Phe Ser Pro		
1310	1315	1320
Lys Phe Phe Leu Thr Phe Ser Gln Arg Thr Leu Glu Ser Ala Gly		
1325	1330	1335
Leu Phe Pro Trp Leu His Thr Gln Cys Arg Asn Lys Lys Thr Lys		
1340	1345	1350
Leu Trp Phe Ser Leu Ile Asn Ile His His Arg Lys Asn Pro Leu		

1355	1360	1365
Leu Pro Met Arg Met Ser Arg Thr Pro Pro Arg Arg Val Cys Gly		
1370	1375	1380
Ser Pro Pro Leu His Leu Cys Gln Pro Leu Arg Gly Gly Lys Lys		
1385	1390	1395
Arg Ser Lys Phe Ala Phe Trp Lys Pro Pro Ser Gln Gly Ile Ser		
1400	1405	1410
Ser Cys Leu Met Thr Gly Cys Trp Gly Ser Cys Gly Arg Ala Cys		

1415	1420	1425

Ser Cys Gly Arg Gly Cys Gly Thr Pro Arg Gly Asp Trp Lys Arg		
1430	1435	1440
His Pro Pro Arg Arg Glu Leu Ser Leu Glu Pro Trp Ile Pro Tyr		
1445	1450	1455
Leu His Gln Gln Lys Thr Gln Arg Lys Arg Met Lys Thr Gly Ala		
1460	1465	1470
Ile Gln Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys		
1475	1480	1485
Arg Ile Cys Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser		
1490	1495	1500
Leu Ser Ala Pro Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala		
1505	1510	1515
Arg Cys Thr Ser Ile Asn Val Leu Cys Val Arg Ala Ser Leu Ile		
1520	1525	1530
Glu Lys Leu Met Lys Glu Lys Arg Lys Met Lys Arg Asn Gln Val		
1535	1540	1545
Ala Ser Pro Gln Ile Met Gln Arg Leu Phe Ile Lys Gly Tyr Gln		
1550	1555	1560
Asn Asn His Phe Thr Phe His Leu Gln Asn Phe Ala Phe Phe Ser		
1565	1570	1575
Ser Phe Gly Asn Asn Lys Tyr Ile Asn Ile Leu Thr Arg Ala Phe		
1580	1585	1590
Ile His Thr Pro Arg Ser Pro Gly Cys Ser Val Tyr Ala Asn Met		
1595	1600	1605
Cys Trp Arg Lys Met Gln Ser Leu Asn His Pro Ser Arg Leu Thr		
1610	1615	1620
Asn Cys His Pro Ala Trp Leu Ser Pro Ile Ser Ala Cys Pro Arg		
1625	1630	1635
Leu Leu Pro Tyr Pro Phe His Val Leu Ala Leu Glu Val Thr Phe		
1640	1645	1650
Pro Pro Gly Thr Ala Met Pro Gln Met Gln Leu Gln Ala Leu Ala		

1655 1660 1665
Met Trp Glu Lys Gly Trp Asp Lys Gln Glu Lys Lys Ser Arg Lys
1670 1675 1680
Leu Met Ser Ser Cys Leu Glu Lys Lys Ala Thr Trp Met Arg Arg
1685 1690 1695
Thr Pro Gly Thr Ser Leu Gln Cys Tyr Leu Asn Thr His Pro Cys
1700 1705 1710
Thr Met Leu Leu Pro Gln Gly Ile Pro Ser Leu Asn Ala Gln Trp

1715 1720 1725
Met Phe Leu Arg Ile Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1730 1735 1740
Ser

<210> 1177

<211> 1749

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 3C

<400> 1177

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
1 5 10 15
Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

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

85 90 95
Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala Thr Pro

100 105 110
 Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met
 115 120 125
 Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His
 130 135 140
 Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly

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

 210 215 220
 Gln Asp Leu Gly Pro Val Pro Met Pro Ile Pro Pro His Leu Arg His
 225 230 235 240
 Pro Leu Leu Leu Lys Asn Lys Lys Arg Arg Lys Leu Arg Pro Lys Ser
 245 250 255
 Arg Lys Lys Gly His Thr Lys Asn Arg Arg Lys Ala Lys Arg Lys Pro
 260 265 270
 Gln Ile Arg Asn Ser Arg Arg Ala Thr Pro Thr Ser Lys Gly Ser Leu

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

 340 345 350

Val Ser Val Tyr Ser Gly Asn Leu Leu Ser Phe Ser Arg Arg Gly Met
355 360 365

Lys Ser Ser Val Arg Leu Lys Asn Cys Thr Asn Leu Ser Val Pro Met
370 375 380

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

Asp Lys Lys Ser Ile Pro His Val Pro Lys Ala Thr Ala Ala His Ser
405 410 415

Val Thr Val Lys Leu Gln Ser Arg Arg Asn Arg Arg Tyr Arg Lys Ile
420 425 430

Tyr Gly Glu Leu Lys Met Ser Leu Gln Ala Ser Asn Gly Met Glu Ala
435 440 445

Cys Gly Thr His Pro Thr Pro Arg Leu Ser Val Ser Val Ile Thr Met
450 455 460

Lys Leu Trp Glu Lys His Phe Lys Gly Leu Asn Trp Asn Leu Val Val
465 470 475 480

Trp Ile Leu Asn Leu Lys Met Met Leu Lys Lys Lys Tyr Leu Val Gln
485 490 495

Arg Glu Trp Glu Lys Arg Lys Gln Ile Leu Gly Gly Gly Gly Lys Tyr
500 505 510

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

Leu Ala Gly Asp Lys Lys Gly Leu Gly Arg Phe Met Arg Cys Val Gln
530 535 540

Ser Glu Thr Lys Ala Val Ser Leu Gln Leu Pro Leu Gly Arg Met Asp
545 550 555 560

Leu Asp Gly Met Leu Thr Val Ile Gly Gln Gly Leu Val Gly Met Thr
565 570 575

Pro Arg Asp Leu Gly Thr Val Ala Gly Ala Thr Ala Gln Ile Gln Arg
580 585 590

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

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

 660 665 670
 Pro Ala Thr Thr Trp Gly Thr Trp Glu Thr Pro Ser Thr Trp Gly Trp
 675 680 685
 Arg Thr Phe Ala Arg Gln Pro Ser Arg Pro Thr Gly Arg Thr Pro Thr
 690 695 700
 Thr Arg Leu Met Ala Pro Val Gly Ser Val Met Ser Cys Ser Leu Leu
 705 710 715 720
 Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr Met Pro Pro Leu Leu His

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

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

Arg Lys Leu Ile Trp Thr Lys Gln Arg Ser Phe Leu Ser Leu Phe Pro

850

855

860

Lys Leu Arg Ala Thr Glu Gln Met Thr Asn Val Gly Cys Arg Leu Asp

865

870

875

880

Phe His Pro Arg Ser Ser Ser Gly Asp Arg Val Phe Leu Val Lys Ile

885

890

895

Gln Ser Ser Pro Phe Leu Ala Arg Ser Trp Asn Thr Met Gln Trp Asn

900

905

910

Asn Lys Lys Met Ala Met Thr Val Ile Ala Gly Ala His His Cys Gln

915

920

925

Tyr Lys Leu Thr Tyr Thr Lys Val Trp Lys Met Asn Trp Lys Lys Met

930

935

940

Met Ile Gly Ser Gln His Leu Leu Phe Ser Pro Leu Asp Ser Ser Pro

945

950

955

960

Leu Gln Leu Leu Leu His Pro His Gly Lys Arg Cys Asn Pro Cys Cys

965

970

975

Arg Leu Thr Trp Met Ser His Leu Asn Arg Lys Leu His Leu Thr Arg

980

985

990

Ser Cys Leu Ile Asp Leu Thr Met Met Met Ser Gln Lys Leu Trp Lys

995

1000

1005

Asn Gln Arg Lys Arg Ile Pro Leu Pro Ser Pro Arg Gln His Leu

1010

1015

1020

Leu Pro Gln Tyr Pro Leu His Pro Pro Pro Pro Cys Leu Leu Leu

1025

1030

1035

Leu His His Arg His His Leu Ala Phe Leu Glu Met Ala Cys Ser

1040

1045

1050

Ser Gln His Thr His Ser Ile Lys Ile Trp Ile Ser Phe Ser His

1055

1060

1065

Glu Thr Met Ser Leu Ser Asn Ile Leu Met Lys Phe Arg Leu Thr

1070

1075

1080

Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala Leu Arg Ala Arg

1085 1090 1095
Gly Gly Thr Thr Ile Gly Glu Val Thr Ser Ser Leu Phe Phe Ser

1100 1105 1110
His Cys Leu Cys Val Ala Pro Arg Cys Pro Arg Ser Ala Val Asp

1115 1120 1125
Ile Ser Pro Gly Pro Thr Ser Pro Ser Leu Ala Ser Cys Ala Ser

1130 1135 1140
Val Ala Ile Gly Lys Leu Ala Leu Leu Gly Ala Ser Ala Pro Cys

1145 1150 1155
Gly Ala Ala Gly Ala Arg Glu Ala Gly Arg Phe Ala Val Leu Gly

1160 1165 1170
Thr Met Val Met Lys Asn Met Glu His Arg Leu Thr Met Asp Ser

1175 1180 1185
Ala Leu Ser Leu Thr Lys Arg Glu Gly Pro Glu Thr Gly Pro Val

1190 1195 1200
Tyr Tyr Val Cys Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro

1205 1210 1215
Phe Leu Phe Thr Val Pro Ile Glu Asp Met Arg Glu Cys Thr Leu

1220 1225 1230
Gly Arg Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro Cys Leu

1235 1240 1245
Ile Pro Val Pro Ile Cys Lys Lys Lys Leu Leu Leu Lys Leu Leu

1250 1255 1260
Arg Gly Ala Ser Ser Ser Thr Ser Arg Asp Ser Arg Ser Phe Phe

1265 1270 1275
Thr Ser Ala His Pro Ser Arg Pro Cys Arg Met Arg Leu Tyr Gln

1280 1285 1290
Met Leu Gln Lys Gln Cys Cys Tyr Asn Leu Val Ile Lys His Pro

1295 1300 1305
Leu Ile Phe Arg Ile Asn Leu Arg Arg Gln Gly Lys Thr Lys Asp

1310 1315 1320

Gly Val	Val Gln Ser Leu Gly	Phe Leu Asn Gln Gln	Ile Ile Leu
1325	1330	1335	
Gln Lys	Glu Phe Phe Ile Cys	Leu Leu Met Phe Ile	Lys Arg Trp
1340	1345	1350	
Lys Pro	Ala Ala Thr Lys Lys	Gly Lys Asn Ser Pro	Cys Cys Gln
1355	1360	1365	
Lys Lys	Leu Arg Val Gln Asn	Gln Gly His Leu Leu	Met Ile Leu
1370	1375	1380	
Leu His	Asn Arg Gly Pro Pro	Leu His Thr Arg Phe	Glu Lys Lys
1385	1390	1395	
Arg Pro	Glu Trp Leu Ser Arg	Lys Ser Gly Val Met	Lys Cys Trp
1400	1405	1410	
Asp Leu	Cys Pro Ala Phe Ser	Gly Arg Ile Leu His	Gln Pro Glu
1415	1420	1425	
Met Ala	Ala Met Arg Leu Met	Pro Lys Phe Leu Asn	Ser Thr Asn
1430	1435	1440	
Ser Trp	Trp Thr Val His Lys	Lys Arg Gly Leu Phe	His Gln Met
1445	1450	1455	
Lys Cys	Leu Thr Ala Val Asp	Cys Leu Gln Ala Phe	Trp Asp Met
1460	1465	1470	
Ser Glu	Lys Lys Arg Lys Leu	Pro Met Ile Arg Lys	Ile Gln Lys
1475	1480	1485	
Arg Arg	Arg Thr Ala Asn Arg	Asn Ile Glu Ile Thr	Pro Gln Arg
1490	1495	1500	
Ser Lys	Ala His Leu Lys Lys	Thr Ser Ala Lys Gly	Ala Lys Lys
1505	1510	1515	
Ile Thr	Phe Leu Cys Leu Arg	Val Arg Cys Gly Gly	Trp Leu Cys
1520	1525	1530	
Gly Trp	Thr Pro Arg Gly Trp	Leu Lys Lys Ser Thr	Lys Ser Arg
1535	1540	1545	
Leu Cys	Phe Phe Tyr Leu Leu	Tyr Tyr Leu Phe Phe	Leu Thr Val

1550 1555 1560
 Cys Gly Phe Thr Pro Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala
 1565 1570 1575
 Pro Gly Glu Lys Leu Lys His Cys Phe Lys Ala Trp Gly Val Asp

1580 1585 1590
 Pro Pro Gly Ser Val Trp Ile Leu Pro Cys Phe Leu Ile His Leu
 1595 1600 1605
 Arg Lys Val Asp Thr His His Leu Gln Val Val Thr Lys Thr Val
 1610 1615 1620
 Thr Ala Thr Thr Ala Asp Gly Gln Arg Met Arg Arg Leu Lys Cys
 1625 1630 1635
 Lys Ala Cys Arg Leu Arg Trp Ala Arg Pro Glu Pro Ala Ala Gln

1640 1645 1650
 Ala Pro Pro Lys Ser His Phe Pro Pro His Pro Ser Gly Pro Ser
 1655 1660 1665
 Arg Thr Ser Ser Leu Gln Leu Arg Thr Tyr Met Glu Met His Tyr
 1670 1675 1680
 Gly His Gln Ala Pro Gln Val Ala Met Leu Pro Lys Leu Leu Cys
 1685 1690 1695
 Arg Gln Met Leu Pro Thr Leu Ser Thr Leu Gln Gln Arg His Pro

1700 1705 1710
 Gln Gly Pro Cys Pro Pro Pro Val Thr Pro Leu Arg Val Gln Ser
 1715 1720 1725
 Val Leu Leu Leu Gly Val Pro Gln Thr Ala Gly Tyr Pro Tyr Asp
 1730 1735 1740
 Val Pro Asp Tyr Ala Ser

1745

<210> 1178

<211> 1750

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 4C

<400> 1178

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu

180 185 190

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

195 200 205

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys

210 215 220

Gln Asp Leu Gly Pro Val Pro Met Asp Ser Lys Lys Met Thr Gln Lys

225 230 235 240
 Asn Arg Lys Thr Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr Asp
 245 250 255

 Asn Leu Asp Leu Gln His Gln Arg Arg Arg Lys Lys Lys Lys Asp Lys
 260 265 270
 Val Glu Ile Arg Asn Arg Ser Pro Lys Ala Asn Ser Thr Glu Cys Gln
 275 280 285
 Gly Glu His Ser Arg Glu Gln Asn Leu Leu Asn Leu Val Gln Leu Asn
 290 295 300
 Pro His Ser Pro His His Arg Lys Asp Glu Glu Asp His Gln Lys Arg
 305 310 315 320

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

 Thr Leu Thr Phe Phe His Phe Phe Phe Phe Phe Lys Thr Val Ser Leu
 385 390 395 400
 Cys Cys Pro Gly Trp Ser Lys Gly Gln Pro Pro Pro Pro Gly Leu Lys
 405 410 415
 Pro Ser Ser Leu Ala Ser Gln Val Ala Arg Thr Thr Gly Val Tyr Gln
 420 425 430
 His Val Trp Leu Ile Cys Phe Val Phe Phe Val Cys Val Glu Thr Gly
 435 440 445

 Phe Cys His Val Ala Gln Val Gly Leu Glu Arg Leu Val Ser Leu Ser
 450 455 460
 Gly Ile Thr Asp Val Asn His Trp Ala Gln Pro Lys Pro Ser Pro Ser
 465 470 475 480

Lys Gly Thr Gly Met Asn Arg Pro Ile Gly Leu Arg Val Gly Lys Gly
 485 490 495
 Val Trp Ala Arg Leu Trp Leu Lys Asn Trp Lys Arg Phe Lys Leu Lys
 500 505 510

 Lys Lys Tyr Thr Gly Met Glu Ile Leu Leu Trp Ile Leu Leu Lys Met
 515 520 525
 Glu Ile Gln Ile Phe Lys Ile Cys Leu Gly Glu Met Gln Leu Cys Leu
 530 535 540
 Lys Lys Lys Val Asn Ala Cys Ser Asn Ala Lys Lys Met Pro Phe Gln
 545 550 555 560
 Cys Arg Cys Arg Arg Glu Tyr Arg Val Thr Met Ile Gln Lys Lys Lys
 565 570 575

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

 Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly Arg Cys Pro Val Gln
 645 650 655
 Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu Arg Arg Trp Gly Pro
 660 665 670
 Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly Phe Gln Leu Leu Arg
 675 680 685
 Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro Arg Lys Gly Pro Phe
 690 695 700

 Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Ala Val Thr Val Met Ala
 705 710 715 720
 Gly Ser Val Pro Ser Ala Gln Ser Val Asp Ala Leu Glu Ser Pro Gly

725	730	735
Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro Arg Asn Leu Leu Trp Arg		
740	745	750
Glu Met Ser Ile Phe Leu Pro Gly Ile Phe Asn Leu His Leu Cys Tyr		
755	760	765
Tyr His Ser Gln Ser Asn Arg Asn Lys Ser Arg Gln Met Glu Ser Leu		
770	775	780
Gly Met Lys Leu Gln Ile Thr His Pro Phe Ala Ser Gln Pro Leu Gly		
785	790	795
Gln Glu Met Pro Asn Asn Thr Gln Ile Arg Leu Leu Lys Pro Gly Gln		
805	810	815
Ala Phe Gly Ser Phe Ser Ala Asp Phe Ser Ala Pro Gln Gln Ala Pro		
820	825	830
Leu Arg Leu Trp Ser Trp Cys Gly Thr Ser Gln Thr Tyr Phe Gly Ser		
835	840	845
Ile Glu Ala Leu Thr Ala Leu Phe Thr Cys Arg Thr Ala Ser Ile Ser		
850	855	860
Val Asn Ile Ser Thr Leu Met Ser Ile Leu Glu Ala Ile Leu Ala Met		
865	870	875
Thr Leu Thr Leu Asn Gly Ser Pro Leu Trp Asp Cys Ser Thr Thr Thr		
885	890	895
Gly Thr His His Gly Cys Leu Trp Glu Ile Pro Ser Val Thr Leu Leu		
900	905	910
Ala Thr Ala Lys Lys Ser Pro Thr Ser Phe Cys Cys Gln Arg Pro Pro		
915	920	925
Leu Gln Pro Val Glu Glu Lys Lys Asn Gly Arg Ile Ser Ser Val Pro		
930	935	940
Pro Ser Pro Pro Leu Ala Leu Gly Pro Arg Met Gln Leu Cys Thr Gln		
945	950	955
Leu Ala Arg Phe Phe Pro Ile Thr Pro Pro Val Trp His Ile Leu Gly		
965	970	975

1205	1210	1215
Leu Glu Ala His Cys Pro Leu	Gln Thr Phe His Leu	His His Cys
1220	1225	1230
Arg Thr Gln Pro Ser Ser Cys	Pro Pro Ala Trp Ile	Leu Tyr Gln
1235	1240	1245
Gly Gln Trp Ser Gly Ala Val	Val Gly Leu Arg Pro	Val Ala His
1250	1255	1260
His Leu Pro Arg Pro Ile Gln	Gly Leu His Cys Pro	Gln Ala Pro
1265	1270	1275
His Gln Pro Ala Leu Ser Trp	Gly Lys Trp Pro Val	Gly Met Thr
1280	1285	1290
Gly Pro Ala Arg Cys Cys Arg	Trp Pro Arg Arg Met	Cys Ser Ser
1295	1300	1305
Leu Ala Leu Pro Thr Gly Leu	Thr Ser Leu Ile Leu	Pro Ser Ser
1310	1315	1320
Asp Leu Ala Val Leu Ile Ser	Ser Ser Thr Ser His	Phe Leu Met
1325	1330	1335
Arg Ser Pro Val Leu Pro Ser	Ser Arg Leu Thr Cys	Ala Ser Pro
1340	1345	1350
Gln Leu Pro Arg Met Trp Thr	Trp Ser Ser Trp Leu	Lys Glu Trp
1355	1360	1365
Gly Gly Gln Ala His Arg Gln	Arg Asn Cys Arg Val	Asn Ala Val
1370	1375	1380
Glu Glu Leu His Ser Arg Arg	Met Ser Val Arg Ile	Val Lys Asn
1385	1390	1395
Trp Val Ser Cys Cys Tyr Val	Arg Leu Ser Ala Val	Gly Leu Ser
1400	1405	1410
Thr Trp Ser Ala Leu Asp Ser	Leu Ile Leu Ser Phe	Gln Arg Val
1415	1420	1425
Lys Thr Ser Arg Ile Leu Asn	Leu Gln Val Leu Lys	Lys Ile Leu
1430	1435	1440

Arg Ser Phe Met Lys Leu Tyr	His Ser Leu Val Met	Cys Leu Arg
1445	1450	1455
Leu Arg Thr Lys Leu Glu Lys	Ala Leu Ser Ala Leu	Phe Ile Trp
1460	1465	1470
Pro Gln His Ser Tyr Lys Gly	Gln Ala Phe Gly Ser	Leu Cys Gln
1475	1480	1485
Leu Val Ser Ala Asp Phe Ser	Ala Pro Gln Val Thr	Arg Leu Arg
1490	1495	1500
Ser Leu Asn His Leu Leu Ile	Arg Trp Ile Phe Ser	Asn Gln Leu
1505	1510	1515
Thr Val Gln Met Leu Cys Leu	Pro Ile Ile Lys Lys	Met Lys Lys
1520	1525	1530
Arg Ile Met Val His Val Leu	Lys Lys Asn Arg Lys	Gln Ile Ile
1535	1540	1545
Cys Ile Lys Asn Met Phe Leu	Gln Arg Lys Gly Phe	Leu Asn Leu
1550	1555	1560
Ser His Val Glu Lys Phe Arg	Glu Ser Thr Leu Gly	Asn Phe Trp
1565	1570	1575
Met Lys Leu Leu Gln Leu Pro	Pro Ala Cys Thr Ser	Lys Ala Trp
1580	1585	1590
Thr Pro Arg Lys Leu Val Gly	Arg Ala Val Arg Arg	Lys Gly Val
1595	1600	1605
Val Ile Asn Leu Lys Arg Leu	Gln Lys Phe Arg Ala	Ser Val Ser
1610	1615	1620
Phe Trp Thr Leu Leu Pro Thr	Thr Gly Val Arg Thr	Arg Gly Ser
1625	1630	1635
Pro Leu Arg Leu Thr Leu Trp	Pro Pro Arg Ser Gln	Lys Ser Gln
1640	1645	1650
His His Cys Ala Leu Arg Lys	Ile Glu Trp Ala Thr	Lys Leu Ser
1655	1660	1665
Leu Gly Gly Lys Ala Gly Pro	Gln Ala Gln Glu Lys	Ala Asn Ile

1670 1675 1680
 Leu Asn Ser Leu Pro Ser Ser Met Glu Ile Ala Val Leu Gln Glu
 1685 1690 1695
 Met Leu Asn Gln Lys Cys Leu Ala Pro Phe Glu Leu Lys Lys Asn
 1700 1705 1710
 Leu Leu Leu Pro Thr Tyr Thr Pro His Ile Cys Arg His Thr Leu
 1715 1720 1725
 Lys Lys Lys Pro Arg Asp Ile Cys Arg Ile Ser Gly Tyr Pro Tyr
 1730 1735 1740

 Asp Val Pro Asp Tyr Ala Ser
 1745 1750
 <210> 1179
 <211> 1547
 <212> PRT
 <213> Artificial Sequence
 <220><223> hTPA- and HA-extended poly-FSP polypeptide 1D
 <400> 1179
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Ala Asp Lys
 20 25 30
 Lys Asn Val Arg Ser Ala Ser Ser Pro Gly His Pro Leu Gly Pro Arg

 35 40 45
 Arg Met Thr Arg Arg Thr Met Thr Thr Thr Lys Met Met Met Met Arg
 50 55 60
 Arg Thr Lys Arg Arg Arg Arg Lys Arg Arg Arg Met Thr Met Met Thr
 65 70 75 80
 Arg Arg Thr Leu Leu Thr Lys Lys Thr Cys Leu Thr Pro Arg Thr Ser
 85 90 95
 Ala Ala Thr Lys Ala Leu Pro Arg Gln Thr Ile Ser Gln Arg Arg Pro

 100 105 110

Ile Gln Thr Pro Pro Gly Thr Ser Leu Ala Ile Trp Gly Arg Arg Ser
115 120 125

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

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

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

Gly Gly Pro Ala Cys Val Pro Val Ala Glu Ala Ser Thr Gly Ala Trp
180 185 190

Thr Ala Glu Gly Ala Ala Gly Thr Arg Cys Arg Ala Ser Arg Ala Pro
195 200 205

Cys Arg Gln Leu Pro Ala Ser Ser Pro Thr Lys Cys Glu Ile Cys Val
210 215 220

Lys Arg Arg Arg Arg Arg Lys Arg Ser Ser Gln Ser Arg Ser Pro Val
225 230 235 240

Pro Lys Lys Arg Glu Arg Met Met Leu Pro Val Arg Ala Arg Thr Ala
245 250 255

Arg Ser Ala Leu Pro Gln Gly Arg Ala Pro Leu Glu Gly Met Leu Leu
260 265 270

Pro Arg Ala Leu Pro Ser Leu Leu Ser Arg Met Pro Ala Arg Arg Glu
275 280 285

Ser Arg Phe Trp Leu Ala Leu Gln Ala Leu Gly Leu Arg Pro Pro His
290 295 300

Leu Pro Ser Cys His Pro Leu Pro Gln Leu Leu Gly Pro Pro Pro Pro
305 310 315 320

His Gln Ala Pro Gly Glu Lys Asn Asp Leu Gln Leu Phe Val Met Ser
325 330 335

Asp Thr Thr Tyr Lys Ile Tyr Trp Thr Val Ile Leu Leu Asn Pro Cys
340 345 350

Gly Asn Leu His Leu Lys Thr Thr Ser Leu Asn Ala Lys Lys Met Glu

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

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

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

 545 550 555 560
 Lys Arg Ser Gln Lys Ser Arg Gln Asn His Leu Gln Leu Lys Ser Cys
 565 570 575
 Arg Arg Lys Ile Ser Asn Trp Ser Lys Leu Arg Ser Pro Trp Ile Phe
 580 585 590
 Glu Ala Lys Lys Ser Met Lys Arg Ser Gln Arg Pro Pro Arg Ser Ile
 595 600 605

Leu Ser Leu Phe Lys Lys Lys Lys Pro Leu Thr Phe Ser Pro Ser Val

610

615

620

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

625

630

635

640

Ile Gln Arg Lys Val Val Lys Asn Pro Ser Gln Pro Val Pro Leu Arg

645

650

655

Asn Asp Gly Ile Thr Asn Gly Asn Asp Ser Thr Arg Ser Cys Ser Ile

660

665

670

Ser Leu Lys Lys Ser Leu Glu Lys Met Pro Leu Met Arg Ser Leu Leu

675

680

685

Tyr Ser Arg Met Cys Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro

690

695

700

Asp Tyr Phe Val Ser Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser

705

710

715

720

Phe Pro Val Gly Ala Val Phe Leu Thr Arg Pro Ala Ile Pro Cys Cys

725

730

735

Ser Cys Thr Ser His Ser Asn Pro Trp Ser Gln Ser Thr Leu Ala Ile

740

745

750

Arg Phe Ile Ser Ala Pro Gln Pro Ser Ser Ser Thr Val Thr Ala Ala

755

760

765

Pro Ser Gly Gln Tyr Phe Ala Leu Arg Ser Met Pro Lys Ser Arg Asn

770

775

780

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

785

790

795

800

Ala Pro Pro Tyr Met Leu Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser

805

810

815

Arg Lys Gln Ile Pro Ser Gln Ser Met Leu Val Arg Thr Arg Leu Thr

820

825

830

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

835

840

845

Cys Leu Cys Cys Trp Thr Cys Pro Ser Arg Ser Phe Pro Ala Ala Ser

850 855 860
 Pro Ser Gly Leu Arg Ala Pro Val Gly Ala Gln Ala Pro Pro Glu Val

 865 870 875 880
 Thr Leu Arg Ala Ser Cys Ala Ser Ser Ala Ser Lys Ala Cys Ala Gly

 885 890 895
 Leu Trp Pro Trp Gly Ala Gln Val Arg Met Lys Lys Lys Asp Ser Thr

 900 905 910
 Ile Phe Ile Tyr Pro Arg Leu Lys Thr Phe Gly Val Pro Leu Gly Ser

 915 920 925
 Ile Leu Cys Leu Ala Gly Ser Leu Ser Thr Met Met Ile Ile Ser Thr

 930 935 940
 Thr Arg Gln Glu Cys Gly Arg Arg Ala Ser Val Pro Cys Arg Pro Met

 945 950 955 960
 Ile Gly Ser Ala Arg Pro Gly Pro Trp Arg Thr Ser Ala Met Pro Ser

 965 970 975
 Ala Met Gly Val Ala Leu Pro Thr Ser Cys Glu Ser Gly Arg Ser Pro

 980 985 990
 Pro Ala Thr Gly Gly Arg Met Pro Gly Ser Gln Ser Ile Met Met Ser

 995 1000 1005
 Trp Met Pro Pro Leu Ala Pro Cys Ala Ala Cys Pro Cys Ser Pro

 1010 1015 1020
 Ala Pro Thr Leu Cys Pro Ala His Pro Ala Arg Ala Pro Thr Ala

 1025 1030 1035
 Val Pro Ala Phe Thr Pro Leu Ser Ala His Pro Val Pro Val Leu

 1040 1045 1050
 Ser Gly Cys His Leu Ala Val Arg Thr Ser Met Leu Thr Leu Leu

 1055 1060 1065
 Pro Met Met Thr Leu Lys Ala Leu Val Lys Thr Trp Thr Gln Phe

 1070 1075 1080
 Arg Asn Tyr Pro Arg Arg His Pro His Arg Ser Pro Pro Thr Ser

 1085 1090 1095

Cys Pro	Pro Leu Leu Glu Ala	Phe Pro Leu Pro Arg	Ala Ser Leu
1100	1105	1110	
Arg Ala	Thr Val Pro Arg His	Ser Ser Val Leu Ala	Thr Gly Leu
1115	1120	1125	
His Leu	His Arg Gln Ile Ser	Leu Pro Leu Arg Gly	Phe Leu Leu
1130	1135	1140	
His Gln	Pro Leu Pro Gly Gln	His Leu Trp Leu Ser	His Arg Leu
1145	1150	1155	
Arg Leu	Arg Leu Pro Arg Thr	Thr Glu Ile Gln Leu	Thr Met Asn
1160	1165	1170	
Asp Ser	Lys His Lys Leu Glu	Ser Pro Ala Leu Lys	Gln Val Ser
1175	1180	1185	
Pro Ala	Ser Pro Pro Thr Gln	Gln Pro Gln Thr Pro	Gln Asp Ser
1190	1195	1200	
Arg Gln	Val Leu Ala Val Pro	Met Ser Leu Ala Cys	Ser Ile Thr
1205	1210	1215	
Val Ser	Phe Val Gly Gln Ile	Ser Thr Leu Val Leu	Asp Val Ser
1220	1225	1230	
Ser Ile	Ser His Trp Asn Gly	Ile Trp Glu Val Met	Pro Arg Thr
1235	1240	1245	
Leu Glu	Gly Cys Ile Ser Val	Lys Asp His Arg Thr	Ser Gln Asn
1250	1255	1260	
His Ser	Lys Cys Ile Thr Glu	Cys Val Arg Thr Ala	Leu Asn Thr
1265	1270	1275	
Lys Cys	Glu Ile Cys Val Lys	Asn Thr Ala Ile Leu	Ala Ile Thr
1280	1285	1290	
Leu Ile	Thr Pro Gln Asp Pro	His Leu Asp Pro Val	Cys His Pro
1295	1300	1305	
His Arg	Arg Pro Gly Trp Lys	Gly His His Arg Val	Val Phe Ser
1310	1315	1320	
His His	Pro Ser Gly Ser Thr	Lys Ser His Trp Gln	Gln Arg Glu

1325 1330 1335
 Arg Gly Gly Gly Arg Arg Glu Lys Lys Gly Cys Arg Glu Ala Ser
 1340 1345 1350
 Arg Ala Gly Gln Phe Pro Val Trp Arg Arg Thr Ser Arg Gly Met

1355 1360 1365
 Ser Leu Gln Trp Lys Ser Gly Asn Ala Cys Thr Pro Leu Arg Cys
 1370 1375 1380
 Pro Ser Arg Ser Pro Ala Thr Phe Leu Thr Ala Leu Asn Gly Trp
 1385 1390 1395
 His Arg Ser Gly Leu Arg Ala Gln Thr Ala Phe Phe Leu Leu Asp
 1400 1405 1410
 Ile Ile Leu Arg Arg Ala Arg Pro Thr Ser Cys Ser Thr Cys Arg

1415 1420 1425
 Met Trp Trp Arg Leu Pro Cys Lys Val Thr Glu Ser Ser Leu Ala
 1430 1435 1440
 Lys Lys Thr Leu Thr Asn Gln Pro Ser Leu Pro Gly Pro Cys Ala
 1445 1450 1455
 Ser Leu Leu Ser Thr Leu Ser Gln Pro Pro Pro Gln Ala Pro Ser
 1460 1465 1470
 Gln Val Trp Thr Ala Ala Thr Leu Arg Cys Pro Ala Val Pro Ala

1475 1480 1485
 Ala Ala Cys Pro Pro Leu Lys Leu Ala Pro Leu Gln Val Thr Thr
 1490 1495 1500
 Thr Leu Lys Leu Ile Leu Val Met Leu Glu Ile Val Thr Glu Asn
 1505 1510 1515
 Lys Val Arg Gln Asn Phe Lys Arg Asn Ser Ser Phe Phe Tyr Thr
 1520 1525 1530
 Ser Asp Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser

1535 1540 1545
 <210> 1180
 <211> 1541

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 2D

<400> 1180

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Arg Lys Met

20 25 30

Gln Ser Leu Asn His Pro Ser Arg Leu Thr Asn Asn Pro Arg Arg Lys

35 40 45

Thr Trp Lys Met Arg Lys Lys Tyr Ala Gln Lys Pro Ser Gln Lys Asn

50 55 60

His Leu Tyr Arg Gln Ile Asn Arg Arg Lys Leu Gln Arg Lys Lys Ser

65 70 75 80

Arg Ser His Leu Asp Phe Ser Pro Tyr Trp Met Lys Lys Val Lys Arg

85 90 95

Ala Arg Asn Arg Asn Met Lys Lys Thr Met Ser His Leu Ile Ala His

100 105 110

Gln Ala Leu Lys Met Ser Gly Leu Arg Leu Phe His Pro Arg Leu Leu

115 120 125

Thr Arg Lys Lys Pro Gly Lys Gln Lys Lys Gly His Met Ile Phe Ser

130 135 140

Arg Arg Lys Trp Gln Ile Arg His Val Leu Lys Asn Leu Ile Pro Ser

145 150 155 160

Leu Asn Ala Gln Trp Met Phe Leu Arg Ile Ala Ser Pro Gln Ile Met

165 170 175

Gln Arg Thr Ser Ala Asp Arg Phe Arg Met Lys Arg Arg Met Gln Asn

180 185 190

Leu Asp Asn Leu Gly Val Pro Trp Pro Leu Leu Pro Gly Leu Leu Leu

195 200 205

Ala His Met Tyr Gly Phe Ser Thr Tyr Gly Thr Gln Lys Gly Glu Cys

210 215 220

Val Cys Leu Gln Cys Leu Ser Gly Ser Ser Leu Phe Ile Leu Lys Gln

225 230 235 240

Pro Leu Asp Leu Lys Ile Ser Lys Thr Phe Met Ala Ser Pro Gln Ile

245 250 255

Met Gln Arg Met Ser Ala Val Asn Phe Glu Thr Ile Leu Gln Ala His

260 265 270

Pro Gln Val Pro Ala Leu Ala Pro Gln Ala Trp Trp Pro Ala Arg Arg

275 280 285

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

290 295 300

Leu Glu Ser Ala Gly Leu Phe Pro Trp Leu His Thr Gln Cys Arg Ala

305 310 315 320

Phe Ile His Thr Pro Arg Ser Pro Gly Cys Ser Val Tyr Ala Asn Met

325 330 335

Cys Trp Arg Tyr Lys Lys Arg Gly Val Ile Ala Trp Arg Ile Tyr Pro

340 345 350

Pro Ser Thr Cys Ser Leu Pro Cys Arg Gly Leu Ile Leu Ile Gln His

355 360 365

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

370 375 380

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

385 390 395 400

Leu Tyr Val Tyr Ile Ile Glu Thr Asn Val Phe Val Leu Asn Leu Phe

405 410 415

His Val Pro Val Asn Gln Ile Phe Met Met Ala Phe Tyr Leu Lys Tyr

420 425 430

Thr Glu Lys Ala Trp Val Met Glu Leu Glu Trp Leu Ile Gln Gln Gln

435 440 445

Cys Tyr Gln Arg Lys Arg Met Lys Thr Gly Ala Ile Gln Glu Lys Gly

450 455 460

Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn

465 470 475 480
 Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro Glu Lys Ile

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

 545 550 555 560
 Ala Phe Phe Ser Ser Phe Gly Asn Asn Lys Tyr Ile Asn Ile Leu Thr
 565 570 575
 Phe Leu Pro Ser Arg Phe Pro Trp Gly Pro Pro Pro Leu Gly Ala Leu
 580 585 590
 Arg Ala Thr Ala Pro Ala Thr Ala Ala Pro Gln Ala Gln Thr Pro His
 595 600 605
 Trp Arg Ala Ala Thr Thr Ser Ser Met Ser Ser Ser Pro Arg Ala Glu

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

 675 680 685
 Thr Gly Val Arg Thr Ser Ser Arg Cys Ser Leu Met Glu Gln Ile Pro
 690 695 700
 His Leu Lys Ser Asn Ser Arg Lys Lys Leu Leu Glu Asp Met Lys Gln
 705 710 715 720

Asn Gly Phe Thr Arg Arg Arg Asn Ser Arg Lys Gln Ser Gln Val Gln
 725 730 735
 Leu Ala Ile Gln Val Leu Leu Val Asp Lys His Lys Tyr Phe Leu Phe
 740 745 750
 Gly Arg Ala Thr Phe Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro Gln
 755 760 765
 Ala Arg Leu Cys Leu Ile Val Ser Arg Thr Leu Leu Leu Val Gln Ser
 770 775 780
 Arg His Pro Ser Trp Pro Trp Thr Arg Cys Leu Arg Met Arg Pro Pro
 785 790 795 800
 Arg Ser His Trp Asn Ser Ala Tyr Leu Gly Arg Thr Leu Leu Val Thr
 805 810 815
 Cys Ile Leu Tyr His Arg Trp Ile Val Thr Ser Met Cys Gln Ser Gln
 820 825 830
 Arg Trp Leu Thr Ser Thr Thr Ser Arg Ser Ser Ala Leu Met Trp Thr
 835 840 845
 Trp Trp Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys Met Cys Lys
 850 855 860
 Val Ser Gly Gly Cys Thr Ala Cys Val Glu Arg Cys Pro Trp Lys Gly
 865 870 875 880
 Ile Cys Trp Lys Trp Pro Val Thr Val Ala Ala Met Ser Arg Thr Pro
 885 890 895
 Pro Arg Arg Val Cys Gly His Arg Glu Gly Ser Glu Ser Asp Asn Leu
 900 905 910
 Gly Leu Leu Tyr Ser Phe Pro Pro Val Leu Phe Lys Ala Asp Gln Ser
 915 920 925
 Glu Ser Ser Leu Ser Ser Gly Asn Ser Val Ile Val His Lys Ile Val
 930 935 940
 Leu Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn Cys Glu Arg Arg Ile
 945 950 955 960
 Ser Gly Ile Gln Lys Arg Ala Ile Glu Phe Ala Val Leu Lys Leu Leu

965					970					975					
Asn	Met	Asp	Leu	Gly	Lys	Gly	Leu	Thr	His	Pro	Val	Pro	Leu	Lys	Arg
980					985					990					
Thr	Leu	Gln	Asn	Lys	Arg	Asn	Lys	Asn	Ile	Lys	Arg	Val	Asn	Gln	Lys
995					1000					1005					
Lys	Gly	Asn	Ile	Lys	Arg	Lys	Ser	Ile	Leu	Leu	His	Leu	Ile	Val	
1010					1015					1020					
Leu	Asn	Ser	Pro	Glu	Ser	Asn	Arg	Glu	Lys	Ile	Ile	Asn	Pro	Thr	
1025					1030					1035					
Ile	Ser	Cys	Pro	Phe	Gln	Ser	Pro	Thr	Lys	Arg	Leu	Gly	Ser	Pro	
1040					1045					1050					
Pro	Leu	His	Leu	Cys	Gln	Pro	Leu	Arg	Pro	Tyr	Pro	Ile	Ser	Glu	
1055					1060					1065					
Gly	Leu	Thr	Met	Thr	Thr	Gly	Arg	Asn	Ile	Asn	Ser	Asn	Ser	Leu	
1070					1075					1080					
Met	Thr	Asn	Cys	Leu	Phe	Ser	Pro	Ile	Phe	Leu	Cys	His	His	Ala	
1085					1090					1095					
Ile	Met	His	Arg	Lys	Met	Thr	Ser	Pro	His	Phe	Arg	Leu	Phe	Ser	
1100					1105					1110					
Ser	Lys	Ile	Pro	His	Pro	Gln	Val	Pro	Ser	Val	Val	Ala	Leu	Cys	
1115					1120					1125					
Lys	Phe	Thr	His	Pro	Cys	Thr	Met	Leu	Leu	Pro	Gln	Gly	Ala	Phe	
1130					1135					1140					
Trp	Lys	Pro	Pro	Ser	Gln	Gly	Ile	Ser	Ser	Cys	Leu	Met	Thr	Gly	
1145					1150					1155					
Cys	Trp	Gln	Trp	Ser	Ser	Val	Thr	Ser	Leu	Glu	Trp	Thr	Ala	Gln	
1160					1165					1170					
Glu	Arg	Gly	Cys	Ser	Ser	Trp	Leu	Met	Lys	Gln	Thr	Trp	Met	Lys	
1175					1180					1185					
Ser	Trp	Ser	Leu	Arg	Asp	Pro	Ser	Tyr	Arg	Ser	Ile	Leu	Glu	Tyr	
1190					1195					1200					

Val Ser Thr Arg Val Leu Trp Met Pro Thr Ser Thr Val Pro Lys		
1205	1210	1215
Phe Phe Leu Thr Phe Ser Gln Ile Arg Met Cys Ala Leu Ser His		
1220	1225	1230
Pro Ser Phe Tyr Ile Ser Ser Thr Val Cys Phe Leu Ser Lys His		
1235	1240	1245
Cys Met Thr Ala Cys Thr Pro Gly Thr Ser Leu Gln Cys Tyr Leu		
1250	1255	1260
Asn Leu Ala Asn Gly Leu Trp Phe Asn Leu Ile Phe Arg Asn Lys		
1265	1270	1275
Lys Thr Lys Leu Trp Phe Ser Leu Ile Asn Ile His His Arg Lys		
1280	1285	1290
Asn Pro Leu Leu Pro Met Arg Leu Glu Lys Lys Ala Thr Trp Met		
1295	1300	1305
Arg Arg Thr Glu Leu Ser Leu Glu Pro Trp Ile Pro Tyr Leu His		
1310	1315	1320
Gln Gln Lys Thr Gln Trp Leu Pro Met Arg Ser Leu Gly Glu Pro		
1325	1330	1335
Trp Arg Ala Gly Phe Gln Trp Gly Glu Ser Pro Trp Gln Val Met		
1340	1345	1350
Ala Ser Leu Thr Gly Arg Arg Lys Lys Arg Glu Asp His Cys Gly		
1355	1360	1365
Leu Gln Glu Lys Lys Ser Arg Lys Leu Met Ser Ser Cys Ala Ala		
1370	1375	1380
Pro Pro His Arg Leu Leu Gly Pro Ser Arg Trp Gly Ser Cys Gly		
1385	1390	1395
Arg Ala Cys Ser Cys Gly Arg Gly Cys Gly Thr Pro Arg Gly Asp		
1400	1405	1410
Trp Lys Arg His Pro Pro Arg Arg Ile Leu Phe His Val Arg Asn		
1415	1420	1425
Ile Val Tyr Gly Ile Gln Val Met Leu Cys Cys His Pro Ala Trp		

1430 1435 1440
 Leu Ser Pro Ile Ser Ala Cys Pro Arg Leu Leu Pro Tyr Pro Phe
 1445 1450 1455
 His Val Leu Ala Leu Glu Val Thr Phe Pro Pro Gly Thr Ala Met
 1460 1465 1470
 Pro Gln Met Gln Leu Gln Ala Leu Ala Met Trp Glu Lys Gly Trp

1475 1480 1485
 Asp Lys Pro Leu Glu Asn Thr Gln Ile Pro Arg Thr Ser Pro Leu
 1490 1495 1500
 Trp Lys Ile Thr Met Val Leu Thr Tyr Pro Asn Cys Val Val His
 1505 1510 1515
 Val Leu Met Phe Gly Gly Lys Lys Arg Ser Lys Phe Gly Tyr Pro
 1520 1525 1530
 Tyr Asp Val Pro Asp Tyr Ala Ser
 1535 1540

<210> 1181

<211> 1546

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 3D

<400> 1181

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

 Arg Arg Gly Lys Leu Ser Ser Arg Lys Lys Gly His Thr Lys Asn Arg
 50 55 60
 Arg Lys Ala Lys Arg Lys Pro Gln Ile Ser Gln Lys Lys Asp Pro Ala
 65 70 75 80
 Gly Lys Leu Lys Lys His Leu Asn Arg Lys Leu His Leu Thr Arg Ser

	85	90	95
Cys	Leu	Ile	Asp
Leu	Thr	Met	Met
Ile	Met	Met	Ser
Asp	Gln	Lys	Leu
Leu	Trp	Lys	Asn
	100	105	110
Gln	Arg	Lys	Arg
Ile	Pro	Leu	Pro
Leu	Ser	Pro	Arg
Pro	Gln	His	Leu
Leu	Pro		
	115	120	125
Gln	Tyr	Pro	Leu
His	Pro	Pro	Pro
Pro	Cys	Leu	Leu
Leu	Leu	Leu	His
His			
	130	135	140
Arg	His	His	Leu
Ala	Phe	Leu	Glu
Met	Ala	Cys	Ser
Ser	Ser	Gln	His
Thr			
	145	150	155
160			
His	Ser	Ile	Lys
Ile	Trp	Ile	Ser
Phe	Ser	His	Glu
Asp	Leu	Pro	Arg
	165	170	175
Met	Leu	Pro	Ile
Ser	Ser	Pro	Leu
His	Arg	Pro	Gln
Met	Pro	Phe	Trp
	180	185	190
Thr	Cys	Thr	Phe
Pro	Ala	Thr	Thr
Trp	Gly	Thr	Trp
Glu	Thr	Pro	Ser
	195	200	205
Thr	Trp	Gly	Trp
Arg	Thr	Phe	Gly
Pro	Val	Tyr	Tyr
Val	Cys	Asn	Arg
	210	215	220
Met	Asn	Val	Ser
Ser	Val	Leu	Lys
Pro	Phe	Leu	Phe
Thr	Val	Pro	Ile
	225	230	235
240			
Glu	Asp	Met	Arg
Glu	Cys	Thr	Leu
Gly	Arg	Asn	Arg
Met	Asn	Val	Ser
	245	250	255
Ser	Val	Leu	Lys
Pro	Cys	Leu	Ile
Pro	Val	Pro	Ile
Leu	Thr	Thr	Leu
	260	265	270
Ser	Phe	Val	Leu
Ile	Glu	Glu	Ser
Arg	Arg	Asn	Arg
Arg	Tyr	Arg	Lys
	275	280	285
Ile	Tyr	Gly	Glu
Leu	Lys	Met	Ser
Leu	Gln	Ala	Leu
Pro	Leu	Thr	Phe
	290	295	300
Ser	Thr	Leu	Leu
Trp	Asp	Ser	Arg
His	Thr	Thr	Thr
Thr	Thr	Ser	Ser
Pro			
	305	310	315
320			
Arg	Arg	Ser	Pro
Ala	Leu	Arg	Ala
Arg	Gly	Gly	Thr
Thr	Thr	Ile	Gly
Glu			
	325	330	335

Val Thr Ser Arg Gly Ala Ser Ser Ser Thr Ser Arg Asp Ser Arg Ser
340 345 350

Phe Phe Thr Ser Ala His Pro Ser Arg Pro Cys Arg Met Arg Leu Tyr
355 360 365

Gln Ser Asn Gly Met Glu Ala Cys Gly Thr His Pro Thr Pro Arg Leu
370 375 380

Ser Arg Gly Pro Pro Leu His Thr Arg Thr Met Ser Leu Ser Asn Ile
385 390 395 400

Leu Met Lys Phe Arg Leu Met Leu Gln Lys Gln Cys Cys Tyr Asn Leu
405 410 415

Val Ile Lys His Pro Leu Ile Phe Arg Ile Asn Leu Arg Arg Gln Gly
420 425 430

Lys Thr Lys Asp Gly Val Val Gln Ser Leu Gly Phe Leu Asn Gln Gln
435 440 445

Ile Ile Leu Gln Lys Glu Phe Phe Ile Cys Leu Leu Met Phe Ile Lys
450 455 460

Arg Trp Lys Pro Ala Ala Thr Lys Thr Pro Pro Pro Leu Ile Leu Trp
465 470 475 480

Pro Gln Ala Ala Pro Val His Lys Lys Arg Gly Leu Phe Ser Leu Phe
485 490 495

Phe Ser His Cys Leu Cys His Gln Met Lys Cys Leu Thr Ala Val Asp
500 505 510

Cys Leu Gln Ala Phe Trp Asp Met Met Ile Arg Lys Ile Gln Lys Arg
515 520 525

Arg Arg Thr Ala Asn Arg Leu Lys Lys Lys Tyr Leu Val Gln Cys Thr
530 535 540

Asn Leu Ser Val Pro Met Met Leu Thr Ile Leu Ile Trp Lys Arg Val
545 550 555 560

Phe Ile Leu Leu Leu Ser Asp Lys Lys Cys Leu Arg Val Arg Cys Gly
565 570 575

Gly Trp Leu Cys Gly Trp Thr Pro Arg Gly Lys Asn Lys Lys Arg Arg

580 585 590
 Lys Leu Arg Pro Lys His Leu Lys Lys Thr Ser Ala Lys Val Ser Val
 595 600 605
 Ile Thr Met Lys Leu Trp Glu Lys His Phe Lys Gly Leu Asn Trp Asn
 610 615 620

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

 Trp Lys Lys Met Met Ile Gly Ser Gln His Leu Leu Phe Ser Pro Leu
 690 695 700
 Asp Ser Ser Pro Leu Gln Leu Leu Leu His Pro His Gly Lys Arg Cys
 705 710 715 720
 Asn Pro Cys Cys Arg Leu Thr Trp Met Ser Arg Glu Trp Glu Lys Arg
 725 730 735
 Lys Gln Ile Leu Gly Gly Gly Gly Lys Tyr Lys Glu Tyr Phe Leu Lys
 740 745 750

 Arg Ile Leu Ile Arg Lys Ala Met Thr Val Leu Ala Gly Asp Lys Lys
 755 760 765
 Gly Leu Gly Arg Phe Met Arg Cys Val Gln Ser Glu Thr Lys Ala Val
 770 775 780
 Ser Leu Gln Leu Pro Leu Gly Arg Arg Lys Ser Gly Val Met Lys Cys
 785 790 795 800
 Trp Asp Leu Cys Pro Arg Leu Asp Phe His Pro Arg Ser Ser Ser Gly
 805 810 815

 Gly Glu Lys Leu Lys His Cys Phe Lys Ala Trp Gly Leu Cys Phe Phe
 820 825 830

Tyr Leu Leu Tyr Phe Glu Lys Lys Arg Pro Glu Trp Leu Ser Val Asp

835 840 845

Pro Pro Gly Ser Val Trp Ile Leu Pro Cys Met Asp Leu Asp Gly Met

850 855 860

Leu Thr Val Ile Gly Gln Gly Leu Val Gly Met Thr Pro Arg Asp Leu

865 870 875 880

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

885 890 895

Gln Thr Gly Gly Arg Leu Phe Leu Ile His Leu Arg Lys Val Asp Thr

900 905 910

His His Leu Gln Val Val Thr Lys Thr Val Thr Ala Thr Thr Ala Asp

915 920 925

Gly Gln Arg Met Arg Arg Leu Lys Cys Lys Ala Cys Arg Leu Arg Trp

930 935 940

Ala Arg Pro Glu Pro Ala Ala Gln Ala Pro Pro Lys Ser His Phe Pro

945 950 955 960

Pro His Pro Ser Gly Pro Ser Arg Thr Ser Ser Leu Gln Leu Arg Pro

965 970 975

Ile Pro Pro His Leu Arg His Pro Leu Leu Leu Lys Gly Lys Asn Ser

980 985 990

Pro Cys Cys Gln Lys Lys Leu Arg Val Gln Asn Gln Gly His Leu Leu

995 1000 1005

Met Ile Leu Leu His Asn Ala Arg Gln Pro Ser Arg Pro Thr Gly

1010 1015 1020

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

1025 1030 1035

Ser Cys Ser Leu Leu Thr Gln Pro Ser Pro Ala Ser Ala Cys Thr

1040 1045 1050

Met Pro Pro Leu Leu His Pro Gln Trp Ala Pro His Ser Ala Gly

1055 1060 1065

Leu Ser Pro Gly Ala Cys Arg Pro Ala Cys Thr Cys Ile Ser Met

1070	1075	1080
Thr Thr Ile Ser Arg Ala Thr	Trp Arg Leu Arg Ile	Pro Ser Leu
1085	1090	1095
Arg Lys Tyr Arg Gln Asn Ile	Glu Ile Thr Pro Gln	Arg Ser Lys
1100	1105	1110
Ala Gln Val Ser Val Tyr Ser	Gly Asn Leu Leu Ser	Phe Ser Arg
1115	1120	1125
Arg Gly Met Lys Ser Ser Val	Arg Leu Lys Asn Ser	Ile Pro His
1130	1135	1140
Val Pro Lys Ala Thr Ala Ala	His Ser Val Thr Val	Lys Leu Gln
1145	1150	1155
Tyr Leu Phe Phe Leu Thr Val	Cys Gly Phe Asp Arg	Val Phe Leu
1160	1165	1170
Val Lys Ile Cys Lys Lys Lys	Leu Leu Leu Lys Leu	Leu Arg Gly
1175	1180	1185
Pro Arg Arg Lys Val Leu Met	Val Leu Trp Leu Pro	Ala Asn Gln
1190	1195	1200
Ser Leu Gln Lys Ser Gln Val	Phe Gln Trp Val Leu	Arg Thr Glu
1205	1210	1215
Thr Tyr Met Glu Met His Tyr	Gly His Gln Ala Pro	Gln Val Ala
1220	1225	1230
Met Leu Pro Lys Leu Leu Cys	Arg Gln Met Leu Pro	Thr Leu Ser
1235	1240	1245
Thr Leu Gln Gln Arg His Pro	Gln Gly Pro Cys Pro	Pro Pro Val
1250	1255	1260
Thr Pro Leu Arg Val Gln Ser	Val Leu Leu Leu Gly	Val Pro Gln
1265	1270	1275
Thr Ala Ala Phe Ser Gly Arg	Ile Leu His Gln Pro	Glu Met Ala
1280	1285	1290
Ala Met Arg Leu Met Pro Lys	Phe Leu Asn Ser Thr	Asn Ser Trp
1295	1300	1305

Trp Thr	Val Ala Pro Arg Cys	Pro Arg Ser Ala Val	Asp Ile Ser
1310	1315	1320	
Pro Gly	Pro Thr Ser Pro Ser	Leu Ala Ser Cys Ala	Ser Val Ala
1325	1330	1335	
Ile Gly	Lys Leu Ala Leu Leu	Gly Ala Ser Ala Pro	Cys Gly Ala
1340	1345	1350	
Ala Gly	Ala Arg Glu Ala Gly	Arg Phe Ala Val Leu	Gly Thr Met
1355	1360	1365	
Val Met	Lys Gly Ala Ala Ala	Ala Ser Cys Gln Ser	Pro Pro Ser
1370	1375	1380	
Pro Arg	Glu Thr Thr Pro Ser	Ser Asp Ala Thr Arg	Arg Thr Arg
1385	1390	1395	
Pro Ile	Ala Ala Gln Ser Lys	Lys Thr Met Thr Ala	Ala Gly Leu
1400	1405	1410	
Thr Pro	Arg Arg Asn Leu Gln	Arg Asn Leu Lys Val	Leu Gly Ala
1415	1420	1425	
Lys Lys	Ile Thr Phe Leu Arg	Asn Ser Arg Arg Ala	Thr Pro Thr
1430	1435	1440	
Ser Lys	Gly Ser Leu Arg Arg	Lys Tyr Leu Arg Val	Asn Ile Arg
1445	1450	1455	
Lys Leu	Ile Trp Thr Lys Gln	Arg Ser Phe Leu Ser	Leu Phe Pro
1460	1465	1470	
Lys Leu	Arg Ala Thr Glu Gln	Met Thr Asn Val Gly	Cys Leu Leu
1475	1480	1485	
Lys Lys	Ser Ser Gln Leu Arg	Arg Ser Trp Arg Asn	Val Ser Arg
1490	1495	1500	
Ile Ser	Asn Met Glu His Arg	Leu Thr Met Asp Ser	Ala Leu Ser
1505	1510	1515	
Leu Thr	Lys Arg Glu Gly Pro	Glu Thr Ser Glu Lys	Lys Arg Lys
1520	1525	1530	
Leu Pro	Gly Tyr Pro Tyr Asp	Val Pro Asp Tyr Ala	Ser
1535	1540	1545	

<210>

1182

<211> 1547

<212> PRT

<213> Artificial Sequence

<220><223> hTPA- and HA-extended poly-FSP polypeptide 4D

<400> 1182

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly

1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Asn Arg Lys

20 25 30

Thr Arg Lys Ala Ala Arg Glu Lys His Arg Lys Thr Asp Asp Lys Lys

35 40 45

Lys Lys Ser Thr Glu Lys Thr Lys Asn Ala Lys Lys Met Pro Phe Gln

50 55 60

Gln Arg Pro Pro Leu Gln Pro Val Asn Leu Asp Leu Gln His Gln Arg

65 70 75 80

Arg Arg Lys Lys Lys Lys Asp Lys Val Glu Ile Arg Asn Arg Ser Pro

85 90 95

Lys Ala Asn Ser Thr Glu Cys Gln Gly Glu His Ser Arg Glu Gln Asn

100 105 110

Leu Leu Asn Leu Val Gln Leu Asn Pro His Ser Pro His His Arg Lys

115 120 125

Asp Glu Glu Asp His Gln Lys Arg His His His His Asn Gln Lys Lys

130 135 140

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

145 150 155 160

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

165 170 175

Arg Val Pro Pro Ser Pro Pro Leu Ala Leu Gly Pro Arg Met Gln Leu

180 185 190

Cys Thr Gln Leu Ala Arg Phe Phe Pro Ile Thr Pro Pro Val Trp His

195 200 205
 Ile Leu Gly Pro Gln Arg His Thr Pro Gln Ala Pro Leu Arg Leu Trp
 210 215 220
 Ser Trp Cys Gly Thr Ser Gln Thr Tyr Phe Gly Ser Arg Pro Ser Pro
 225 230 235 240

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

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

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

 His Glu Leu Lys Lys Asn Leu Leu Leu Pro Met Cys Ser Ser Leu Ala
 435 440 445

Leu Pro Thr Gly Leu Thr Ser Leu Ile Leu Pro Ser Ser Asp Leu Ala
 450 455 460
 Val Leu Ile Ser Ser Ser Thr Ser His Phe Leu Met Arg Ser Pro Val
 465 470 475 480
 Leu Pro Ser Ser Arg Leu Thr Cys Ala Ser Pro Gln Leu Pro Arg Met
 485 490 495

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

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

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

 Ser Gln Gln Pro Leu Gln Val Val Leu Arg Leu Gly Asn Leu Pro Pro

690	695	700	
Phe Phe Arg Gly Ser Glu Val Pro Phe Pro Arg Pro Cys Arg Thr Lys			
705	710	715	720
Pro Ala Cys Thr Ser Lys Ala Trp Thr Pro Arg Lys Leu Val Gly Arg			
	725	730	735
Ala Val Arg Arg Lys Gly Ser Pro Leu Trp Asp Cys Ser Thr Thr Thr			
	740	745	750
Gly Thr His His Gly Cys Leu Trp Glu Ile Pro Ser Val Thr Leu Leu			
	755	760	765
Ala His Pro Arg Thr Ala Ser Ile Thr Leu Pro Thr Thr Ser Leu Lys			
	770	775	780
Gly Ser Arg Thr Ser Cys Cys Pro Arg Ser His Pro Arg Leu Pro Arg			
785	790	795	800
Thr Lys Trp Pro Leu Gln Cys Leu Leu His Ser Leu Gly Thr Thr Gly			
	805	810	815
Thr Leu Val Trp Glu Arg Gly Val Leu Gln Met Arg Ser Leu Glu Ala			
	820	825	830
His Cys Pro Leu Gln Thr Phe His Leu His His Cys Arg Thr Gln Pro			
	835	840	845
Ser Ser Cys Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln Trp Ser Gly			
	850	855	860
Ala Val Val Gly Leu Arg Pro Val Ala His His Leu Pro Arg Pro Ile			
865	870	875	880
Gln Gly Leu His Cys Pro Gln Ala Pro His Gln Pro Ala Leu Ser Trp			
	885	890	895
Gly Lys Trp Pro Val Gly Met Thr Gly Pro Ala Arg Cys Cys Arg Trp			
	900	905	910
Pro Arg Arg Cys Gln Lys Lys Val Pro Ser Ala Ser Pro Trp Gly Leu			
	915	920	925
Val Leu Lys Lys Asn Arg Lys Gln Met Leu Asn Gln Lys Cys Leu Ala			
	930	935	940

Pro Phe Arg Glu Ser Thr Leu Gly Asn Phe Trp Met Lys Leu Leu Gln
945 950 955 960
Leu Pro Val Val Ile Asn Leu Lys Arg Leu Gln Lys Phe Asn Leu His
965 970 975
Leu Cys Tyr Tyr His Ser Gln Ser Asn Arg Asn Lys Ser Arg Gln Met
980 985 990
Glu Ser Leu Gly Met Lys Leu Gln Ser Gln Lys Ser Gln His His Cys
995 1000 1005

Ala Leu Arg Lys Ile Glu Trp Ala Thr Lys Leu Ser Leu Gly Gly
1010 1015 1020
Lys Ala Gly Pro Gln Ala Gln Glu Lys Ala Thr Ser Arg Ile Leu
1025 1030 1035
Asn Leu Gln Val Leu Lys Lys Ile Leu Arg Ser Phe Met Lys Leu
1040 1045 1050
Tyr His Ser Leu Val Met Cys Leu Arg Leu Arg Thr Lys Leu Glu
1055 1060 1065

Lys Ala Leu Ser Ala Leu Phe Ile Trp Pro Gln His Ser Tyr Lys
1070 1075 1080
Pro Leu Phe Phe His Gly Asp Leu Cys Glu Trp Gly Gly Gln Ala
1085 1090 1095
His Arg Gln Arg Asn Trp Leu Lys Asn Trp Lys Arg Phe Lys Leu
1100 1105 1110
Lys Lys Lys Tyr Ile Gln Lys Lys Lys Gln Lys Ser Asn Lys Ile
1115 1120 1125

Ile Cys Lys Gly His Arg Ile Thr Ile Ile Cys Ile Lys Asn Met
1130 1135 1140
Phe Leu Gln Arg Lys Gly Phe Leu Asn Leu Ser His Val Glu Lys
1145 1150 1155
Phe Cys Arg Gly Gly Pro Ser Ala Ser Asp Arg Cys Cys Ser Cys
1160 1165 1170
Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly Arg Cys Pro Val Gln

1175	1180	1185
Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu Arg Arg Trp Gly		
1190	1195	1200
Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly Phe Gln Leu		
1205	1210	1215
Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro Arg Lys		
1220	1225	1230
Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Ala Val		
1235	1240	1245
Thr Val Met Ala Gly Ser Val Pro Ser Ala Gln Ser Val Asp Ala		
1250	1255	1260
Leu Glu Ser Pro Gly Pro Leu Ala Leu Glu Gly Pro Ser Ser Pro		
1265	1270	1275
Arg Asn Leu Leu Trp Arg Glu Met Ser Ile Phe Leu Pro Gly Ile		
1280	1285	1290
Phe Thr Ala Lys Lys Ser Pro Thr Ser Phe Cys Cys Asn Ile Leu		
1295	1300	1305
Asn Ser Leu Pro Ser Ser Met Glu Ile Ala Val Leu Gln Glu Asp		
1310	1315	1320
Ser Lys Lys Met Thr Gln Lys Gly Gln Ala Phe Gly Ser Leu Cys		
1325	1330	1335
Gln Leu Val Ser Ala Asp Phe Ser Ala Pro Gln Val Thr Arg Leu		
1340	1345	1350
Arg Ser Leu Asn His Leu Leu Ile Thr Tyr Thr Pro His Ile Cys		
1355	1360	1365
Arg His Thr Leu Leu Thr Pro Asp Thr Arg Trp Ile Phe Ser Asn		
1370	1375	1380
Gln Leu Gln Thr Val Gln Met Leu Cys Leu Pro Pro Leu Lys Gln		
1385	1390	1395
Gly Glu Arg Ile Ile Trp Pro Leu Gly Gly Phe Gln Ile Pro Asn		
1400	1405	1410

Phe Phe Trp Ser Leu Gly Ile Gly His Thr Gly Ala Trp Trp His
 1415 1420 1425

Thr Gly Arg Arg Arg Arg Glu Trp Gly Gly Ser Thr Val Ser Arg
 1430 1435 1440

Ser Pro Leu Trp Ile Ser Ser Met Ile Tyr Leu Arg Gly Met Ala
 1445 1450 1455

Phe Ala Ser Asp Ser Ser Ile Arg Thr Thr Arg Val Ser Trp Cys
 1460 1465 1470

Arg Arg Cys Gly Ala Lys Ser Ala Ala Ala Ser Ser Ile Glu Ala
 1475 1480 1485

Leu Thr Ala Leu Phe Thr Cys Arg Thr Ala Ser Ile Ser Val Asn
 1490 1495 1500

Ile Ser Thr Leu Met Ser Ile Leu Glu Ala Leu Lys Lys Lys Pro
 1505 1510 1515

Arg Asp Ile Cys Arg Ile Ser Cys Arg Cys Arg Arg Glu Tyr Arg
 1520 1525 1530

Val Thr Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1535 1540 1545

<210> 1183

<211> 1750

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 1D

<400> 1183

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val
 1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met
 20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala
 35 40 45

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

50	55	60	
Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys			
65	70	75	80
Leu Thr Val Thr Ser Gln Asn Leu Gln Leu Glu Asn Leu Arg Met Lys			
	85	90	95
Leu Pro Lys Pro Pro Lys Pro Val Ser Lys Met Arg Met Ala Thr Pro			
	100	105	110
Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met			
	115	120	125
Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His			
	130	135	140
Leu Leu Gln Asn Ala Asp Pro Leu Lys Val Tyr Pro Pro Leu Lys Gly			
145	150	155	160
Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile			
	165	170	175
Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu			
	180	185	190
Met Ser Arg His Ser Leu Glu Gln Lys Pro Thr Asp Ala Pro Pro Lys			
	195	200	205
Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys			
	210	215	220
Gln Asp Leu Gly Pro Val Pro Met Ala Asp Lys Lys Asn Val Arg Ser			
225	230	235	240
Ala Ser Ser Pro Gly His Pro Leu Gly Pro Arg Arg Met Thr Arg Arg			
	245	250	255
Thr Met Thr Thr Thr Lys Met Met Met Met Arg Arg Thr Lys Arg Arg			
	260	265	270
Arg Arg Lys Arg Arg Arg Met Thr Met Met Thr Arg Arg Thr Leu Leu			
	275	280	285
Thr Lys Lys Thr Cys Leu Thr Pro Arg Thr Ser Ala Ala Thr Lys Ala			
	290	295	300

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

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

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

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

545 550 555 560

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

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

 Leu Arg Pro Gln Arg Gly Pro Arg Pro Leu His Arg Trp Leu Gln Gln
 690 695 700
 Thr Thr Gly Cys Ser Gln Arg Arg Gly Asp Cys Pro Arg Thr Met Ala
 705 710 715 720
 Gly Pro Ser Ala Ser Leu His Pro Ala Ser Gly Arg Ala Ser Arg Lys
 725 730 735
 Thr Trp Gln Arg Arg Leu Arg Ala Cys Arg Ala Gly Gly Pro Ala Gly
 740 745 750

 Trp Ala Arg Gln Ala Arg Lys Arg Lys Arg Glu Lys Arg Ser Gln Lys
 755 760 765
 Ser Arg Gln Asn His Leu Gln Leu Lys Ser Cys Arg Arg Lys Ile Ser
 770 775 780
 Asn Trp Ser Lys Leu Arg Ser Pro Trp Ile Phe Glu Ala Lys Lys Ser
 785 790 795 800

Met Lys Arg Ser Gln Arg Pro Pro Arg Ser Ile Leu Ser Leu Phe Lys
805 810 815

Lys Lys Lys Pro Leu Thr Phe Ser Pro Ser Val Ser Lys Lys Arg Leu
820 825 830

Pro Lys Leu Lys Gly Lys Lys Arg Arg Lys Glu Ile Gln Arg Lys Val
835 840 845

Val Lys Asn Pro Ser Gln Pro Val Pro Leu Arg Asn Asp Gly Ile Thr
850 855 860

Asn Gly Asn Asp Ser Thr Arg Ser Cys Ser Ile Ser Leu Lys Lys Ser
865 870 875 880

Leu Glu Lys Met Pro Leu Met Arg Ser Leu Leu Tyr Ser Arg Met Cys
885 890 895

Leu Val Gln Ile Pro Thr His Thr Trp Glu Pro Asp Tyr Phe Val Ser
900 905 910

Leu Pro Met Met Phe Ser Trp Ala Thr Gln Ser Phe Pro Val Gly Ala
915 920 925

Val Phe Leu Thr Arg Pro Ala Ile Pro Cys Cys Ser Cys Thr Ser His
930 935 940

Ser Asn Pro Trp Ser Gln Ser Thr Leu Ala Ile Arg Phe Ile Ser Ala
945 950 955 960

Pro Gln Pro Ser Ser Ser Thr Val Thr Ala Ala Pro Ser Gly Gln Tyr
965 970 975

Phe Ala Leu Arg Ser Met Pro Lys Ser Arg Asn Gln Val Leu Phe Arg
980 985 990

Arg Asn Leu Thr Pro Ser Gln Leu Arg Thr Leu Ala Pro Pro Tyr Met
995 1000 1005

Leu Leu Pro Gln Ser Leu Ser Gln Ser Leu Ser Arg Lys Gln Ile
1010 1015 1020

Pro Ser Gln Ser Met Leu Val Arg Thr Arg Leu Thr Leu Thr Gly
1025 1030 1035

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

1040	1045	1050
Cys Cys Trp Thr Cys Pro Ser	Arg Ser Phe Pro Ala	Ala Ser Pro
1055	1060	1065
Ser Gly Leu Arg Ala Pro Val	Gly Ala Gln Ala Pro	Pro Glu Val
1070	1075	1080
Thr Leu Arg Ala Ser Cys Ala	Ser Ser Ala Ser Lys	Ala Cys Ala
1085	1090	1095
Gly Leu Trp Pro Trp Gly Ala	Gln Val Arg Met Lys	Lys Lys Asp
1100	1105	1110
Ser Thr Ile Phe Ile Tyr Pro	Arg Leu Lys Thr Phe	Gly Val Pro
1115	1120	1125
Leu Gly Ser Ile Leu Cys Leu	Ala Gly Ser Leu Ser	Thr Met Met
1130	1135	1140
Ile Ile Ser Thr Thr Arg Gln	Glu Cys Gly Arg Arg	Ala Ser Val
1145	1150	1155
Pro Cys Arg Pro Met Ile Gly	Ser Ala Arg Pro Gly	Pro Trp Arg
1160	1165	1170
Thr Ser Ala Met Pro Ser Ala	Met Gly Val Ala Leu	Pro Thr Ser
1175	1180	1185
Cys Glu Ser Gly Arg Ser Pro	Pro Ala Thr Gly Gly	Arg Met Pro
1190	1195	1200
Gly Ser Gln Ser Ile Met Met	Ser Trp Met Pro Pro	Leu Ala Pro
1205	1210	1215
Cys Ala Ala Cys Pro Cys Ser	Pro Ala Pro Thr Leu	Cys Pro Ala
1220	1225	1230
His Pro Ala Arg Ala Pro Thr	Ala Val Pro Ala Phe	Thr Pro Leu
1235	1240	1245
Ser Ala His Pro Val Pro Val	Leu Ser Gly Cys His	Leu Ala Val
1250	1255	1260
Arg Thr Ser Met Leu Thr Leu	Leu Pro Met Met Thr	Leu Lys Ala
1265	1270	1275

Leu Val	Lys Thr Trp Thr	Gln Phe Arg Asn Tyr	Pro Arg Arg His
1280		1285	1290
Pro His	Arg Ser Pro Pro Thr	Ser Cys Pro Pro Leu	Leu Glu Ala
1295		1300	1305
Phe Pro	Leu Pro Arg Ala Ser	Leu Arg Ala Thr Val	Pro Arg His
1310		1315	1320
Ser Ser	Val Leu Ala Thr Gly	Leu His Leu His Arg	Gln Ile Ser
1325		1330	1335
Leu Pro	Leu Arg Gly Phe Leu	Leu His Gln Pro Leu	Pro Gly Gln
1340		1345	1350
His Leu	Trp Leu Ser His Arg	Leu Arg Leu Arg Leu	Pro Arg Thr
1355		1360	1365
Thr Glu	Ile Gln Leu Thr Met	Asn Asp Ser Lys His	Lys Leu Glu
1370		1375	1380
Ser Pro	Ala Leu Lys Gln Val	Ser Pro Ala Ser Pro	Pro Thr Gln
1385		1390	1395
Gln Pro	Gln Thr Pro Gln Asp	Ser Arg Gln Val Leu	Ala Val Pro
1400		1405	1410
Met Ser	Leu Ala Cys Ser Ile	Thr Val Ser Phe Val	Gly Gln Ile
1415		1420	1425
Ser Thr	Leu Val Leu Asp Val	Ser Ser Ile Ser His	Trp Asn Gly
1430		1435	1440
Ile Trp	Glu Val Met Pro Arg	Thr Leu Glu Gly Cys	Ile Ser Val
1445		1450	1455
Lys Asp	His Arg Thr Ser Gln	Asn His Ser Lys Cys	Ile Thr Glu
1460		1465	1470
Cys Val	Arg Thr Ala Leu Asn	Thr Lys Cys Glu Ile	Cys Val Lys
1475		1480	1485
Asn Thr	Ala Ile Leu Ala Ile	Thr Leu Ile Thr Pro	Gln Asp Pro
1490		1495	1500
His Leu	Asp Pro Val Cys His	Pro His Arg Arg Pro	Gly Trp Lys

1505	1510	1515
Gly His His Arg Val Val Phe Ser His His Pro Ser Gly Ser Thr		
1520	1525	1530
Lys Ser His Trp Gln Gln Arg Glu Arg Gly Gly Gly Arg Arg Glu		
1535	1540	1545
Lys Lys Gly Cys Arg Glu Ala Ser Arg Ala Gly Gln Phe Pro Val		
1550	1555	1560
Trp Arg Arg Thr Ser Arg Gly Met Ser Leu Gln Trp Lys Ser Gly		
1565	1570	1575
Asn Ala Cys Thr Pro Leu Arg Cys Pro Ser Arg Ser Pro Ala Thr		
1580	1585	1590
Phe Leu Thr Ala Leu Asn Gly Trp His Arg Ser Gly Leu Arg Ala		
1595	1600	1605
Gln Thr Ala Phe Phe Leu Leu Asp Ile Ile Leu Arg Arg Ala Arg		
1610	1615	1620
Pro Thr Ser Cys Ser Thr Cys Arg Met Trp Trp Arg Leu Pro Cys		
1625	1630	1635
Lys Val Thr Glu Ser Ser Leu Ala Lys Lys Thr Leu Thr Asn Gln		
1640	1645	1650
Pro Ser Leu Pro Gly Pro Cys Ala Ser Leu Leu Ser Thr Leu Ser		
1655	1660	1665
Gln Pro Pro Pro Gln Ala Pro Ser Gln Val Trp Thr Ala Ala Thr		
1670	1675	1680
Leu Arg Cys Pro Ala Val Pro Ala Ala Ala Cys Pro Pro Leu Lys		
1685	1690	1695
Leu Ala Pro Leu Gln Val Thr Thr Thr Leu Lys Leu Ile Leu Val		
1700	1705	1710
Met Leu Glu Ile Val Thr Glu Asn Lys Val Arg Gln Asn Phe Lys		
1715	1720	1725
Arg Asn Ser Ser Phe Phe Tyr Thr Ser Asp Arg Gly Tyr Pro Tyr		
1730	1735	1740

Asp Val Pro Asp Tyr Ala Ser

1745 1750

<210> 1184

<211> 1744

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 2D

<400> 1184

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu

180 185 190

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

435 440 445
 Ile Ser Lys Thr Phe Met Ala Ser Pro Gln Ile Met Gln Arg Met Ser
 450 455 460
 Ala Val Asn Phe Glu Thr Ile Leu Gln Ala His Pro Gln Val Pro Ala

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

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

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

 660 665 670
 Gly Ala Met Thr Lys Arg Ile Cys Val Val Asn Phe Glu Ala Cys Arg
 675 680 685

Glu Met Glu Ser Leu Ser Ala Pro Glu Lys Ile Thr Leu Phe Glu Ala
 690 695 700
 His Met Ala Arg Cys Thr Ser Ile Asn Val Leu Cys Val Arg Ala Ser
 705 710 715 720
 Leu Ile Glu Lys Leu Met Lys Glu Lys Arg Lys Met Lys Arg Asn Gln
 725 730 735
 Val Ala Ser Pro Gln Ile Met Gln Arg Leu Phe Ile Lys Gly Tyr Gln
 740 745 750
 Asn Asn His Phe Thr Phe His Leu Gln Asn Phe Ala Phe Phe Ser Ser
 755 760 765
 Phe Gly Asn Asn Lys Tyr Ile Asn Ile Leu Thr Phe Leu Pro Ser Arg
 770 775 780
 Phe Pro Trp Gly Pro Pro Pro Leu Gly Ala Leu Arg Ala Thr Ala Pro
 785 790 795 800
 Ala Thr Ala Ala Pro Gln Ala Gln Thr Pro His Trp Arg Ala Ala Thr
 805 810 815
 Thr Ser Ser Met Ser Ser Ser Pro Arg Ala Glu Pro Thr Ser Ser Ser
 820 825 830
 Ser Trp Ala Thr Cys Trp Pro Arg Cys Cys Ser Ser Ser Cys Tyr Trp
 835 840 845
 Ser Leu Ser Ser Trp Pro Pro Ala Gly Ala Ala Glu Ala Thr Asn Thr
 850 855 860
 Arg Thr Arg Ser Arg Glu Ser Gln Arg Gly Arg Met Leu Thr Trp Arg
 865 870 875 880
 Ser Ser Leu Trp Leu Gln Gly Thr Arg Cys Phe Thr Gly Val Arg Thr
 885 890 895
 Ser Ser Arg Cys Ser Leu Met Glu Gln Ile Pro His Leu Lys Ser Asn
 900 905 910
 Ser Arg Lys Lys Leu Leu Glu Asp Met Lys Gln Asn Gly Phe Thr Arg
 915 920 925
 Arg Arg Asn Ser Arg Lys Gln Ser Gln Val Gln Leu Ala Ile Gln Val

930 935 940
 Leu Leu Val Asp Lys His Lys Tyr Phe Leu Phe Gly Arg Ala Thr Phe
 945 950 955 960
 Leu Leu Ala Leu Trp Glu Cys Ser Leu Pro Gln Ala Arg Leu Cys Leu
 965 970 975
 Ile Val Ser Arg Thr Leu Leu Leu Val Gln Ser Arg His Pro Ser Trp

 980 985 990
 Pro Trp Thr Arg Cys Leu Arg Met Arg Pro Pro Arg Ser His Trp Asn
 995 1000 1005
 Ser Ala Tyr Leu Gly Arg Thr Leu Leu Val Thr Cys Ile Leu Tyr
 1010 1015 1020
 His Arg Trp Ile Val Thr Ser Met Cys Gln Ser Gln Arg Trp Leu
 1025 1030 1035
 Thr Ser Thr Thr Ser Arg Ser Ser Ala Leu Met Trp Thr Trp Trp

 1040 1045 1050
 Cys Thr Arg Gly Gly Gly Lys Arg Lys Lys Lys Met Cys Lys Val
 1055 1060 1065
 Ser Gly Gly Cys Thr Ala Cys Val Glu Arg Cys Pro Trp Lys Gly
 1070 1075 1080
 Ile Cys Trp Lys Trp Pro Val Thr Val Ala Ala Met Ser Arg Thr
 1085 1090 1095
 Pro Pro Arg Arg Val Cys Gly His Arg Glu Gly Ser Glu Ser Asp

 1100 1105 1110
 Asn Leu Gly Leu Leu Tyr Ser Phe Pro Pro Val Leu Phe Lys Ala
 1115 1120 1125
 Asp Gln Ser Glu Ser Ser Leu Ser Ser Gly Asn Ser Val Ile Val
 1130 1135 1140
 His Lys Ile Val Leu Val Phe Leu Lys Ser Leu Ser Ser Tyr Asn
 1145 1150 1155
 Cys Glu Arg Arg Ile Ser Gly Ile Gln Lys Arg Ala Ile Glu Phe

1160 1165 1170

Ala Val	Leu Lys Leu Leu Asn	Met Asp Leu Gly Lys	Gly Leu Thr
1175	1180	1185	
His Pro	Val Pro Leu Lys Arg	Thr Leu Gln Asn Lys	Arg Asn Lys
1190	1195	1200	
Asn Ile	Lys Arg Val Asn Gln	Lys Lys Gly Asn Ile	Lys Arg Lys
1205	1210	1215	
Ser Ile	Leu Leu His Leu Ile	Val Leu Asn Ser Pro	Glu Ser Asn
1220	1225	1230	
Arg Glu	Lys Ile Ile Asn Pro	Thr Ile Ser Cys Pro	Phe Gln Ser
1235	1240	1245	
Pro Thr	Lys Arg Leu Gly Ser	Pro Pro Leu His Leu	Cys Gln Pro
1250	1255	1260	
Leu Arg	Pro Tyr Pro Ile Ser	Glu Gly Leu Thr Met	Thr Thr Gly
1265	1270	1275	
Arg Asn	Ile Asn Ser Asn Ser	Leu Met Thr Asn Cys	Leu Phe Ser
1280	1285	1290	
Pro Ile	Phe Leu Cys His His	Ala Ile Met His Arg	Lys Met Thr
1295	1300	1305	
Ser Pro	His Phe Arg Leu Phe	Ser Ser Lys Ile Pro	His Pro Gln
1310	1315	1320	
Val Pro	Ser Val Val Ala Leu	Cys Lys Phe Thr His	Pro Cys Thr
1325	1330	1335	
Met Leu	Leu Pro Gln Gly Ala	Phe Trp Lys Pro Pro	Ser Gln Gly
1340	1345	1350	
Ile Ser	Ser Cys Leu Met Thr	Gly Cys Trp Gln Trp	Ser Ser Val
1355	1360	1365	
Thr Ser	Leu Glu Trp Thr Ala	Gln Glu Arg Gly Cys	Ser Ser Trp
1370	1375	1380	
Leu Met	Lys Gln Thr Trp Met	Lys Ser Trp Ser Leu	Arg Asp Pro
1385	1390	1395	
Ser Tyr	Arg Ser Ile Leu Glu	Tyr Val Ser Thr Arg	Val Leu Trp

1400	1405	1410
Met Pro Thr Ser Thr Val	Pro Lys Phe Phe Leu Thr	Phe Ser Gln
1415	1420	1425
Ile Arg Met Cys Ala Leu Ser	His Pro Ser Phe Tyr	Ile Ser Ser
1430	1435	1440
Thr Val Cys Phe Leu Ser Lys	His Cys Met Thr Ala	Cys Thr Pro
1445	1450	1455
Gly Thr Ser Leu Gln Cys Tyr	Leu Asn Leu Ala Asn	Gly Leu Trp

1460	1465	1470
Phe Asn Leu Ile Phe Arg Asn	Lys Lys Thr Lys Leu	Trp Phe Ser
1475	1480	1485
Leu Ile Asn Ile His His Arg	Lys Asn Pro Leu Leu	Pro Met Arg
1490	1495	1500
Leu Glu Lys Lys Ala Thr Trp	Met Arg Arg Thr Glu	Leu Ser Leu
1505	1510	1515
Glu Pro Trp Ile Pro Tyr Leu	His Gln Gln Lys Thr	Gln Trp Leu

1520	1525	1530
Pro Met Arg Ser Leu Gly Glu	Pro Trp Arg Ala Gly	Phe Gln Trp
1535	1540	1545
Gly Glu Ser Pro Trp Gln Val	Met Ala Ser Leu Thr	Gly Arg Arg
1550	1555	1560
Lys Lys Arg Glu Asp His Cys	Gly Leu Gln Glu Lys	Lys Ser Arg
1565	1570	1575
Lys Leu Met Ser Ser Cys Ala	Ala Pro Pro His Arg	Leu Leu Gly

1580	1585	1590
Pro Ser Arg Trp Gly Ser Cys	Gly Arg Ala Cys Ser	Cys Gly Arg
1595	1600	1605
Gly Cys Gly Thr Pro Arg Gly	Asp Trp Lys Arg His	Pro Pro Arg
1610	1615	1620
Arg Ile Leu Phe His Val Arg	Asn Ile Val Tyr Gly	Ile Gln Val
1625	1630	1635

Met Leu Cys Cys His Pro Ala Trp Leu Ser Pro Ile Ser Ala Cys

1640 1645 1650
Pro Arg Leu Leu Pro Tyr Pro Phe His Val Leu Ala Leu Glu Val
1655 1660 1665
Thr Phe Pro Pro Gly Thr Ala Met Pro Gln Met Gln Leu Gln Ala
1670 1675 1680
Leu Ala Met Trp Glu Lys Gly Trp Asp Lys Pro Leu Glu Asn Thr
1685 1690 1695
Gln Ile Pro Arg Thr Ser Pro Leu Trp Lys Ile Thr Met Val Leu

1700 1705 1710
Thr Tyr Pro Asn Cys Val Val His Val Leu Met Phe Gly Gly Lys
1715 1720 1725
Lys Arg Ser Lys Phe Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1730 1735 1740

Ser

<210> 1185

<211> 1749

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 3D

<400> 1185

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

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

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

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

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

 260 265 270
 Lys Pro Gln Ile Ser Gln Lys Lys Asp Pro Ala Gly Lys Leu Lys Lys
 275 280 285
 His Leu Asn Arg Lys Leu His Leu Thr Arg Ser Cys Leu Ile Asp Leu
 290 295 300
 Thr Met Met Met Ser Gln Lys Leu Trp Lys Asn Gln Arg Lys Arg Ile
 305 310 315 320

Pro Leu Pro Ser Pro Arg Gln His Leu Leu Pro Gln Tyr Pro Leu His

325 330 335

Pro Pro Pro Pro Cys Leu Leu Leu Leu His His Arg His His Leu Ala

340 345 350

Phe Leu Glu Met Ala Cys Ser Ser Gln His Thr His Ser Ile Lys Ile

355 360 365

Trp Ile Ser Phe Ser His Glu Asp Leu Pro Arg Met Leu Pro Ile Ser

370 375 380

Ser Pro Leu His Arg Pro Gln Met Pro Phe Trp Thr Cys Thr Phe Pro

385 390 395 400

Ala Thr Thr Trp Gly Thr Trp Glu Thr Pro Ser Thr Trp Gly Trp Arg

405 410 415

Thr Phe Gly Pro Val Tyr Tyr Val Cys Asn Arg Met Asn Val Ser Ser

420 425 430

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

435 440 445

Cys Thr Leu Gly Arg Asn Arg Met Asn Val Ser Ser Val Leu Lys Pro

450 455 460

Cys Leu Ile Pro Val Pro Ile Leu Thr Thr Leu Ser Phe Val Leu Ile

465 470 475 480

Glu Glu Ser Arg Arg Asn Arg Arg Tyr Arg Lys Ile Tyr Gly Glu Leu

485 490 495

Lys Met Ser Leu Gln Ala Leu Pro Leu Thr Phe Ser Thr Leu Leu Trp

500 505 510

Asp Ser Arg His Thr Thr Thr Thr Ser Ser Pro Arg Arg Ser Pro Ala

515 520 525

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

530 535 540

Ala Ser Ser Ser Thr Ser Arg Asp Ser Arg Ser Phe Phe Thr Ser Ala

545 550 555 560

His Pro Ser Arg Pro Cys Arg Met Arg Leu Tyr Gln Ser Asn Gly Met

565 570 575
Glu Ala Cys Gly Thr His Pro Thr Pro Arg Leu Ser Arg Gly Pro Pro

580 585 590
Leu His Thr Arg Thr Met Ser Leu Ser Asn Ile Leu Met Lys Phe Arg

595 600 605
Leu Met Leu Gln Lys Gln Cys Cys Tyr Asn Leu Val Ile Lys His Pro

610 615 620
Leu Ile Phe Arg Ile Asn Leu Arg Arg Gln Gly Lys Thr Lys Asp Gly

625 630 635 640
Val Val Gln Ser Leu Gly Phe Leu Asn Gln Gln Ile Ile Leu Gln Lys

645 650 655
Glu Phe Phe Ile Cys Leu Leu Met Phe Ile Lys Arg Trp Lys Pro Ala

660 665 670
Ala Thr Lys Thr Pro Pro Pro Leu Ile Leu Trp Pro Gln Ala Ala Pro

675 680 685
Val His Lys Lys Arg Gly Leu Phe Ser Leu Phe Phe Ser His Cys Leu

690 695 700
Cys His Gln Met Lys Cys Leu Thr Ala Val Asp Cys Leu Gln Ala Phe

705 710 715 720
Trp Asp Met Met Ile Arg Lys Ile Gln Lys Arg Arg Arg Thr Ala Asn

725 730 735
Arg Leu Lys Lys Lys Tyr Leu Val Gln Cys Thr Asn Leu Ser Val Pro

740 745 750
Met Met Leu Thr Ile Leu Ile Trp Lys Arg Val Phe Ile Leu Leu Leu

755 760 765
Ser Asp Lys Lys Cys Leu Arg Val Arg Cys Gly Gly Trp Leu Cys Gly

770 775 780
Trp Thr Pro Arg Gly Lys Asn Lys Lys Arg Arg Lys Leu Arg Pro Lys

785 790 795 800
His Leu Lys Lys Thr Ser Ala Lys Val Ser Val Ile Thr Met Lys Leu

805 810 815

Trp Glu Lys His Phe Lys Gly Leu Asn Trp Asn Leu Val Val Trp Ile
 820 825 830
 Leu Asn Leu Lys Met Met Trp Leu Lys Lys Ser Thr Lys Ser Arg Gln
 835 840 845
 Ser Ser Pro Phe Leu Ala Arg Ser Trp Asn Thr Met Gln Trp Asn Asn
 850 855 860
 Lys Lys Met Ala Met Thr Val Ile Ala Gly Ala His His Cys Gln Tyr
 865 870 875 880
 Lys Leu Thr Tyr Thr Lys Val Trp Lys Met Asn Trp Lys Lys Met Met
 885 890 895
 Ile Gly Ser Gln His Leu Leu Phe Ser Pro Leu Asp Ser Ser Pro Leu
 900 905 910
 Gln Leu Leu Leu His Pro His Gly Lys Arg Cys Asn Pro Cys Cys Arg
 915 920 925
 Leu Thr Trp Met Ser Arg Glu Trp Glu Lys Arg Lys Gln Ile Leu Gly
 930 935 940
 Gly Gly Gly Lys Tyr Lys Glu Tyr Phe Leu Lys Arg Ile Leu Ile Arg
 945 950 955 960
 Lys Ala Met Thr Val Leu Ala Gly Asp Lys Lys Gly Leu Gly Arg Phe
 965 970 975
 Met Arg Cys Val Gln Ser Glu Thr Lys Ala Val Ser Leu Gln Leu Pro
 980 985 990
 Leu Gly Arg Arg Lys Ser Gly Val Met Lys Cys Trp Asp Leu Cys Pro
 995 1000 1005
 Arg Leu Asp Phe His Pro Arg Ser Ser Ser Gly Gly Glu Lys Leu
 1010 1015 1020
 Lys His Cys Phe Lys Ala Trp Gly Leu Cys Phe Phe Tyr Leu Leu
 1025 1030 1035
 Tyr Phe Glu Lys Lys Arg Pro Glu Trp Leu Ser Val Asp Pro Pro
 1040 1045 1050
 Gly Ser Val Trp Ile Leu Pro Cys Met Asp Leu Asp Gly Met Leu

1055	1060	1065
Thr Val Ile Gly Gln Gly Leu	Val Gly Met Thr Pro	Arg Asp Leu
1070	1075	1080
Gly Thr Val Ala Gly Ala Thr	Ala Gln Ile Gln Arg	Pro Ile Gln

1085	1090	1095
Val Gln Thr Gly Gly Arg Leu	Phe Leu Ile His Leu	Arg Lys Val
1100	1105	1110
Asp Thr His His Leu Gln Val	Val Thr Lys Thr Val	Thr Ala Thr
1115	1120	1125
Thr Ala Asp Gly Gln Arg Met	Arg Arg Leu Lys Cys	Lys Ala Cys
1130	1135	1140
Arg Leu Arg Trp Ala Arg Pro	Glu Pro Ala Ala Gln	Ala Pro Pro

1145	1150	1155
Lys Ser His Phe Pro Pro His	Pro Ser Gly Pro Ser	Arg Thr Ser
1160	1165	1170
Ser Leu Gln Leu Arg Pro Ile	Pro Pro His Leu Arg	His Pro Leu
1175	1180	1185
Leu Leu Lys Gly Lys Asn Ser	Pro Cys Cys Gln Lys	Lys Leu Arg
1190	1195	1200
Val Gln Asn Gln Gly His Leu	Leu Met Ile Leu Leu	His Asn Ala

1205	1210	1215
Arg Gln Pro Ser Arg Pro Thr	Gly Arg Thr Pro Thr	Thr Arg Leu
1220	1225	1230
Met Ala Pro Val Gly Ser Val	Met Ser Cys Ser Leu	Leu Thr Gln
1235	1240	1245
Pro Ser Pro Ala Ser Ala Cys	Thr Met Pro Pro Leu	Leu His Pro
1250	1255	1260
Gln Trp Ala Pro His Ser Ala	Gly Leu Ser Pro Gly	Ala Cys Arg

1265	1270	1275
Pro Ala Cys Thr Cys Ile Ser	Met Thr Thr Ile Ser	Arg Ala Thr
1280	1285	1290

Trp Arg	Leu Arg Ile Pro Ser	Leu Arg Lys Tyr Arg	Gln Asn Ile
1295	1300	1305	
Glu Ile	Thr Pro Gln Arg Ser	Lys Ala Gln Val Ser	Val Tyr Ser
1310	1315	1320	
Gly Asn	Leu Leu Ser Phe Ser	Arg Arg Gly Met Lys	Ser Ser Val
1325	1330	1335	
Arg Leu	Lys Asn Ser Ile Pro	His Val Pro Lys Ala	Thr Ala Ala
1340	1345	1350	
His Ser	Val Thr Val Lys Leu	Gln Tyr Leu Phe Phe	Leu Thr Val
1355	1360	1365	
Cys Gly	Phe Asp Arg Val Phe	Leu Val Lys Ile Cys	Lys Lys Lys
1370	1375	1380	
Leu Leu	Leu Lys Leu Leu Arg	Gly Pro Arg Arg Lys	Val Leu Met
1385	1390	1395	
Val Leu	Trp Leu Pro Ala Asn	Gln Ser Leu Gln Lys	Ser Gln Val
1400	1405	1410	
Phe Gln	Trp Val Leu Arg Thr	Glu Thr Tyr Met Glu	Met His Tyr
1415	1420	1425	
Gly His	Gln Ala Pro Gln Val	Ala Met Leu Pro Lys	Leu Leu Cys
1430	1435	1440	
Arg Gln	Met Leu Pro Thr Leu	Ser Thr Leu Gln Gln	Arg His Pro
1445	1450	1455	
Gln Gly	Pro Cys Pro Pro Pro	Val Thr Pro Leu Arg	Val Gln Ser
1460	1465	1470	
Val Leu	Leu Leu Gly Val Pro	Gln Thr Ala Ala Phe	Ser Gly Arg
1475	1480	1485	
Ile Leu	His Gln Pro Glu Met	Ala Ala Met Arg Leu	Met Pro Lys
1490	1495	1500	
Phe Leu	Asn Ser Thr Asn Ser	Trp Trp Thr Val Ala	Pro Arg Cys
1505	1510	1515	
Pro Arg	Ser Ala Val Asp Ile	Ser Pro Gly Pro Thr	Ser Pro Ser

1520	1525	1530
Leu Ala Ser Cys Ala Ser Val	Ala Ile Gly Lys Leu	Ala Leu Leu
1535	1540	1545
Gly Ala Ser Ala Pro Cys Gly	Ala Ala Gly Ala Arg	Glu Ala Gly
1550	1555	1560
Arg Phe Ala Val Leu Gly Thr	Met Val Met Lys Gly	Ala Ala Ala
1565	1570	1575
Ala Ser Cys Gln Ser Pro Pro	Ser Pro Arg Glu Thr	Thr Pro Ser
1580	1585	1590
Ser Asp Ala Thr Arg Arg Thr	Arg Pro Ile Ala Ala	Gln Ser Lys
1595	1600	1605
Lys Thr Met Thr Ala Ala Gly	Leu Thr Pro Arg Arg	Asn Leu Gln
1610	1615	1620
Arg Asn Leu Lys Val Leu Gly	Ala Lys Lys Ile Thr	Phe Leu Arg
1625	1630	1635
Asn Ser Arg Arg Ala Thr Pro	Thr Ser Lys Gly Ser	Leu Arg Arg
1640	1645	1650
Lys Tyr Leu Arg Val Asn Ile	Arg Lys Leu Ile Trp	Thr Lys Gln
1655	1660	1665
Arg Ser Phe Leu Ser Leu Phe	Pro Lys Leu Arg Ala	Thr Glu Gln
1670	1675	1680
Met Thr Asn Val Gly Cys Leu	Leu Lys Lys Ser Ser	Gln Leu Arg
1685	1690	1695
Arg Ser Trp Arg Asn Val Ser	Arg Ile Ser Asn Met	Glu His Arg
1700	1705	1710
Leu Thr Met Asp Ser Ala Leu	Ser Leu Thr Lys Arg	Glu Gly Pro
1715	1720	1725
Glu Thr Ser Glu Lys Lys Arg	Lys Leu Pro Gly Tyr	Pro Tyr Asp
1730	1735	1740
Val Pro Asp Tyr Ala Ser		
1745		

<210> 1186

<211> 1750

<212> PRT

<213> Artificial Sequence

<220><223> hINV- and HA-extended poly-FSP polypeptide 4D

<400> 1186

Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val

1 5 10 15

Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met

20 25 30

Leu Gly Arg Arg Pro Gly Ala Pro Glu Ser Lys Cys Ser Arg Gly Ala

35 40 45

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

50 55 60

Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys

65 70 75 80

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

85 90 95

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

100 105 110

Leu Leu Met Gln Ala Leu Pro Met Gly Ala Leu Pro Gln Gly Pro Met

115 120 125

Gln Asn Ala Thr Lys Tyr Gly Asn Met Thr Glu Asp His Val Met His

130 135 140

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

145 150 155 160

Ser Phe Pro Glu Asn Leu Arg His Leu Lys Asn Thr Met Glu Thr Ile

165 170 175

Asp Trp Lys Val Phe Glu Ser Trp Met His His Trp Leu Leu Phe Glu

180 185 190

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

195 200 205

Glu Ser Leu Glu Leu Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys
 210 215 220
 Gln Asp Leu Gly Pro Val Pro Met Asn Arg Lys Thr Arg Lys Ala Ala
 225 230 235 240

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

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

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

 Ser Gln Thr Tyr Phe Gly Ser Arg Pro Ser Pro Cys Leu Ser Trp Ser
 435 440 445
 Ser Arg Ile Val Ala Pro Gly His Ala Leu Ser Cys Arg Thr Arg Arg

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

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

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

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

 Leu Thr Cys Ala Ser Pro Gln Leu Pro Arg Met Trp Thr Trp Ser Ser
 690 695 700

Trp Leu Lys Asn Glu Gly Asn Asn His Trp Pro Arg Val Glu Met Pro
705 710 715 720

Thr Gly Trp Leu Leu Val Gly Tyr Asn Thr Arg Asn Thr Ala Gln Asn
725 730 735

Pro Arg Leu Gln Gln His Leu Lys His Trp Gln Gln Cys Thr Arg Ala
740 745 750

Arg Trp Cys Gln Glu Pro Cys Gln Thr Leu Thr Phe Phe His Phe Phe
755 760 765

Phe Phe Phe Lys Thr Val Ser Leu Cys Cys Pro Gly Trp Ser Lys Gly
770 775 780

Gln Pro Pro Pro Pro Gly Leu Lys Pro Ser Ser Leu Ala Ser Gln Val
785 790 795 800

Ala Arg Thr Thr Gly Val Tyr Gln His Val Trp Leu Ile Cys Phe Val
805 810 815

Phe Phe Val Cys Val Glu Thr Gly Phe Cys His Val Ala Gln Val Gly
820 825 830

Leu Glu Arg Leu Val Ser Leu Ser Gly Ile Thr Asp Val Asn His Trp
835 840 845

Ala Gln Pro Lys Pro Ser Pro Ser Lys Gly Thr Gly Met Asn Arg Pro
850 855 860

Ile Gly Leu Arg Val Gly Lys Gly Val Trp Ala Arg Leu Ile Leu Ala
865 870 875 880

Met Thr Leu Thr Leu Asn Gly Met Ala Lys Lys Ser Gln Gln Pro Leu
885 890 895

Gln Val Val Leu Arg Leu Gly Asn Leu Pro Pro Phe Phe Arg Gly Ser
900 905 910

Glu Val Pro Phe Pro Arg Pro Cys Arg Thr Lys Pro Ala Cys Thr Ser
915 920 925

Lys Ala Trp Thr Pro Arg Lys Leu Val Gly Arg Ala Val Arg Arg Lys
930 935 940

Gly Ser Pro Leu Trp Asp Cys Ser Thr Thr Thr Gly Thr His His Gly

945 950 955 960
 Cys Leu Trp Glu Ile Pro Ser Val Thr Leu Leu Ala His Pro Arg Thr
 965 970 975
 Ala Ser Ile Thr Leu Pro Thr Thr Ser Leu Lys Gly Ser Arg Thr Ser
 980 985 990
 Cys Cys Pro Arg Ser His Pro Arg Leu Pro Arg Thr Lys Trp Pro Leu
 995 1000 1005

Gln Cys Leu Leu His Ser Leu Gly Thr Thr Gly Thr Leu Val Trp
 1010 1015 1020
 Glu Arg Gly Val Leu Gln Met Arg Ser Leu Glu Ala His Cys Pro
 1025 1030 1035
 Leu Gln Thr Phe His Leu His His Cys Arg Thr Gln Pro Ser Ser
 1040 1045 1050
 Cys Pro Pro Ala Trp Ile Leu Tyr Gln Gly Gln Trp Ser Gly Ala
 1055 1060 1065

Val Val Gly Leu Arg Pro Val Ala His His Leu Pro Arg Pro Ile
 1070 1075 1080
 Gln Gly Leu His Cys Pro Gln Ala Pro His Gln Pro Ala Leu Ser
 1085 1090 1095
 Trp Gly Lys Trp Pro Val Gly Met Thr Gly Pro Ala Arg Cys Cys
 1100 1105 1110
 Arg Trp Pro Arg Arg Cys Gln Lys Lys Val Pro Ser Ala Ser Pro
 1115 1120 1125

Trp Gly Leu Val Leu Lys Lys Asn Arg Lys Gln Met Leu Asn Gln
 1130 1135 1140
 Lys Cys Leu Ala Pro Phe Arg Glu Ser Thr Leu Gly Asn Phe Trp
 1145 1150 1155
 Met Lys Leu Leu Gln Leu Pro Val Val Ile Asn Leu Lys Arg Leu
 1160 1165 1170
 Gln Lys Phe Asn Leu His Leu Cys Tyr Tyr His Ser Gln Ser Asn
 1175 1180 1185

Arg Asn	Lys Ser	Arg Gln	Met	Glu Ser	Leu Gly	Met	Lys Leu	Gln
1190		1195		1200				
Ser Gln	Lys Ser	Gln His	His	Cys Ala	Leu Arg	Lys	Ile Glu	Trp
1205		1210		1215				
Ala Thr	Lys Leu	Ser Leu	Gly	Gly Lys	Ala Gly	Pro	Gln Ala	Gln
1220		1225		1230				
Glu Lys	Ala Thr	Ser Arg	Ile	Leu Asn	Leu Gln	Val	Leu Lys	Lys
1235		1240		1245				
Ile Leu	Arg Ser	Phe Met	Lys	Leu Tyr	His Ser	Leu	Val Met	Cys
1250		1255		1260				
Leu Arg	Leu Arg	Thr Lys	Leu	Glu Lys	Ala Leu	Ser	Ala Leu	Phe
1265		1270		1275				
Ile Trp	Pro Gln	His Ser	Tyr	Lys Pro	Leu Phe	Phe	His Gly	Asp
1280		1285		1290				
Leu Cys	Glu Trp	Gly Gly	Gln	Ala His	Arg Gln	Arg	Asn Trp	Leu
1295		1300		1305				
Lys Asn	Trp Lys	Arg Phe	Lys	Leu Lys	Lys Lys	Tyr	Ile Gln	Lys
1310		1315		1320				
Lys Lys	Gln Lys	Ser Asn	Lys	Ile Ile	Cys Lys	Gly	His Arg	Ile
1325		1330		1335				
Thr Ile	Ile Cys	Ile Lys	Asn	Met Phe	Leu Gln	Arg	Lys Gly	Phe
1340		1345		1350				
Leu Asn	Leu Ser	His Val	Glu	Lys Phe	Cys Arg	Gly	Gly Pro	Ser
1355		1360		1365				
Ala Ser	Asp Arg	Cys Cys	Ser	Cys Ser	Pro Ser	Gly	Phe Ser	Ala
1370		1375		1380				
Gly Arg	Gly Arg	Cys Pro	Val	Gln Gly	Cys Leu	Arg	Pro His	Arg
1385		1390		1395				
Val Gln	Leu Leu	Arg Arg	Trp	Gly Pro	Gly Ser	Pro	Ala Gly	Gln
1400		1405		1410				
Arg Leu	Ser Lys	Gly Phe	Gln	Leu Leu	Arg Trp	Trp	Gly Pro	Gly

1415	1420	1425
Ser Pro Ala Pro Glu Pro Arg Lys Gly Pro Phe Pro Pro Pro Asp		
1430	1435	1440
Pro Pro Trp Pro Val Thr Ala Val Thr Val Met Ala Gly Ser Val		
1445	1450	1455
Pro Ser Ala Gln Ser Val Asp Ala Leu Glu Ser Pro Gly Pro Leu		
1460	1465	1470
Ala Leu Glu Gly Pro Ser Ser Pro Arg Asn Leu Leu Trp Arg Glu		
1475	1480	1485
Met Ser Ile Phe Leu Pro Gly Ile Phe Thr Ala Lys Lys Ser Pro		
1490	1495	1500
Thr Ser Phe Cys Cys Asn Ile Leu Asn Ser Leu Pro Ser Ser Met		
1505	1510	1515
Glu Ile Ala Val Leu Gln Glu Asp Ser Lys Lys Met Thr Gln Lys		
1520	1525	1530
Gly Gln Ala Phe Gly Ser Leu Cys Gln Leu Val Ser Ala Asp Phe		
1535	1540	1545
Ser Ala Pro Gln Val Thr Arg Leu Arg Ser Leu Asn His Leu Leu		
1550	1555	1560
Ile Thr Tyr Thr Pro His Ile Cys Arg His Thr Leu Leu Thr Pro		
1565	1570	1575
Asp Thr Arg Trp Ile Phe Ser Asn Gln Leu Gln Thr Val Gln Met		
1580	1585	1590
Leu Cys Leu Pro Pro Leu Lys Gln Gly Glu Arg Ile Ile Trp Pro		
1595	1600	1605
Leu Gly Gly Phe Gln Ile Pro Asn Phe Phe Trp Ser Leu Gly Ile		
1610	1615	1620
Gly His Thr Gly Ala Trp Trp His Thr Gly Arg Arg Arg Arg Glu		
1625	1630	1635
Trp Gly Gly Ser Thr Val Ser Arg Ser Pro Leu Trp Ile Ser Ser		
1640	1645	1650

Met Ile Tyr Leu Arg Gly Met Ala Phe Ala Ser Asp Ser Ser Ile
1655 1660 1665

Arg Thr Thr Arg Val Ser Trp Cys Arg Arg Cys Gly Ala Lys Ser
1670 1675 1680

Ala Ala Ala Ser Ser Ile Glu Ala Leu Thr Ala Leu Phe Thr Cys
1685 1690 1695

Arg Thr Ala Ser Ile Ser Val Asn Ile Ser Thr Leu Met Ser Ile
1700 1705 1710

Leu Glu Ala Leu Lys Lys Lys Pro Arg Asp Ile Cys Arg Ile Ser
1715 1720 1725

Cys Arg Cys Arg Arg Glu Tyr Arg Val Thr Met Gly Tyr Pro Tyr
1730 1735 1740

Asp Val Pro Asp Tyr Ala Ser
1745 1750

<210> 1187

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA⁻ and HA-extended poly-FSP
polypeptide 1C

<400> 1187

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60
tcgcccagcc aggaaatcca tgcccgaagc accagacggg aaatgccttc tcaggccaca 120

ccttctccac ctggaccttg gagagccgct ctgggcaaag aagtgaagcg gagccagagc 180
aagctgcggc tgagaaacac aagccccacc gagatccaat tgaccatgaa cgacagcaag 240
cacaagctgg aaagccccgc tctgaacag gtgtccctg cctctccacc tacacagcag 300
cctcagacac cccagatag cagacaggtg ctggccgctt cttctcctgg acatcctctt 360
ggccctggcg actgccctag aacaatggct ggaccttctg cctctctgca ccagcatct 420
ggcagagcca gcagaaagac ctggcagaga aggctgagag cctgtagagc tgggtggacct 480
gtcggatggg ctagacaggc catgacactg aaggccctgg tcaagacctg gacacagttc 540

agaaactacc ccagagtcgg agccggaaca ggcggaggac ctgcttgtgt tcctgtggcc 600

gaagcttcta ctggcgctg gacagctgaa ggcgctgccg gaacaagatg cagagcttct 660
agagccctt gcagacagct gcctgccagc tctcctacca agtgcgagat ctgcgtgaag 720
agaagcggc ggagaaagcg gagcagccag tctagatctc ccgtgcctaa gaaacgcgag 780
cggatgatgc tgctgtgcg ggccagaaca gctagatctg ctctgccaca aggcagagcc 840
cctctggaag gaatgcttct gcctagagca ctgccagcc tgctgagcag aatgccagcc 900
agaagagaga gccggttttg gctggcactg caggctctgg gactcagacc tcctcatctg 960

cctagctgtc accctctgcc tcaactgctt ggacctctc cacctcatca ggccctttc 1020
gacaagaaag gcttcgtgat cctgagcaag ggcaagaagc gccggaaga aatccggcgg 1080
atgaccagac ggacatgac caccacaaa atgatgatga tgcggcggac caagcggcgg 1140
aggcgaaaac gtagaagaat gaccatgatg acccgcagaa ccctgctgac caagaaaacc 1200
tgtctgacct ctagaaccag cgccgccaca aaagctctgc ccagacagac aatcagccag 1260
cggaggccta tccagacacc tcctggaaca agcctggcca tctggggcag actgcctctc 1320
agaccacaga gaggacctcg gcctctgcat agatggctgc agcagacaac aggtctctcc 1380

cagagaagaa tcgccaagaa gcggatcaag ctgaggcgga acacactggc catccggttt 1440
atctctgccc ctcagcctag cagcagcacc gttacagctg ctcttagcgg ccagtacttc 1500
agcagcttct tctacaccag cgaccggacc aagtgtgaaa tctgtgtcaa gaacaccgcc 1560
atcctggcta tcacctgat caccctcag gacctcacc tggacctgt gtgtcacca 1620
catagaaggc ctggctggaa gggccaccac agagtgggtg ttagccacca tccaagcggc 1680
tccaccaaga gccattggca gcagagagaa agaggcggag gccgcagaga aaaaaagggc 1740
tgcagagaga tgcccagcag ctggtctagc tctggcagaa ccgccgacaa aaagaacgtg 1800

cggagcagaa ccagactgac cctgacaggc acaagaagca gcgcacaaag agcctctcca 1860
agcgccgtgt gtctgtgctg ttggacatgc cctccagaa gcttccctgc cgcacttcca 1920
tctggactga gagcacctgt tggagcccag gctcctctg aagtgacct gagagccagc 1980
tgtgcctcta gcgctctaa agcctgtgct ggactttggc cttggggagc ccaagtgcgg 2040
aacaagtgc ggcagaactt caagcggaac ctggcctaaa agacctgac taacgcctg 2100
cggagtatgc ccaagagcag aaaccagggtg ctgttcagac ggaatctgac ccaagccag 2160
ctgagaactc tggccctcc ttacatgctg ctgccccagt ctctgtctca gagcctgtcc 2220

agaaagcaga tccccagca atcaatgctc gtgaccgct tcttctgct cgacatcatc 2280
ctgagaagcc tgctgtactc ccggatgtgc ctggtgcaga tccctacaca cacctgggag 2340
cccactact tctgtccct gcctatgatg ttcagctggg ccaactagag ctttccagtg 2400
ggagccgtgt tctgaccag acctgccatt ccttgtgca gctgtaccag ccacagcaac 2460

ccttggagcc agtccttcaa gaagaagaag ccctgacat tcagcccag cgtgccaatg	2520
tctctggcct gtagcatcac cgtgtccttc gtgggccaga tcagcacact ggtgtctggac	2580
gtgtcctcca tctctactg gcgcaagcgc aagagagaga agcggtecca gaagtcccgg	2640
cagaacctatc tgcagctgaa gtcctgcaga cggaagatca gcaactggtc caagctgaga	2700
tccccgtgga tcttctaccc tcggctgaaa accttcggcg tgccactggg ctctatcctg	2760
tgtctggcag gtcacctgag cacgatgatg atcattagca ccaccagaca agagtgtggc	2820
agacgggcct ccgtgccttg tagacctatg atcggcagcg ctagaccggg accttggcgg	2880
acatctgcta tgccatctgc catgggagtc gccctgccta ccagctgtga aagcggaaga	2940
tctctcctg ccaccggcgg aagaatgcct ggatctcagt ctatcatgat gagctggatg	3000
cctccactgg ctccctgtgc cgcttgtcct tgttctcctg ctctacact gtgccctgct	3060
catcctgcaa gagcccctac agccgtgcct gcctttacac ctctgtctgc tcacctgtg	3120
ccagtctgt ctggatgtca cctggccgtg cgcacctcta tgctgacact gctgcccattg	3180
agacacctc acagaagccc acctacaagc tgccctccac tgctggaagc tttccactg	3240
ccaagggcca gctgagagc taccgtgcct agacacagct ctgtgctggc cactggactg	3300
catctgcac ggagattag cctgcctctg aggggcttcc tgctgcatca acctctgcct	3360
ggacaacacc tgtggctgtc ccacagactg aggctgagac tgccaagaac aggcgagaag	3420
aacgacctc agctgttcgt gatgagcgac accacataca agatctactg gacagtgatc	3480
ctgtgaacc cctgcggcaa cctgcacctg aaaaccacat ctctgcggag agccagacct	3540
acctctgca gcacatgcag aatgtggtgg ctgaagctgg cccactgca agtgaccaca	3600
acactgaagc tgatcctggt catgtctgaa atcgtgaccg aagaggccaa gaaatccatg	3660
aagagatccc ggcggagcaa gatcgaggcc tctctatcg gctccatcat gaagaagaaa	3720
gacagacca tcttcatcaa ccagcagctc aagtggaccc ctacatcct gaagtctgcc	3780
agcgtgtcca agaagagact gccaagctg aacggcatct gggaagtgat gccccggaca	3840
ctggaaggct gcatcagct gaaggaccac cggacaagcc agaaccacag caagtgcac	3900
accgagtgtg tgcggacagc cctgaaccag agaaaggtgg tcaagaacct cagccagcca	3960
gtgccactga gaaacgacgg catcaccaac ggcaacgact ccaccagatc ctgctccatc	4020
agcctgaaga aaagcctgga aaagatgccc ctgatgaacg ccaagaaaat ggaagatatg	4080
atctgggaga gcaacatggg cggcaaccgg tccatctgcc tgacaagact gccctgcaaa	4140
gtgaccgagt ccagccaaag accacctcgg agcattctgt ccctggcctc tagagccgga	4200
cagtttcccg tttggcggag aaccagcaga ggcatgtccc tgcaagtggaa gtccggcaat	4260

gcctgcacac ctctgaggtg ccctagcaga agccctgccca catttctgac cgcactgaac 4320

ggctggcaca gatctggact tagggctcag caacctagcc tgccaggacc ttgtgctagc 4380

ctgctgtcta cactgagcca gcctccacca caggctccaa gccaaagttg gacagccgcc 4440

acactgagat gtcccgtgt tctgcagct gcttgccctc ctatcgtgtt ctttctggcc 4500

ccatacttcc ccacaccact gagcatcagc agaccacact ctggggccag acagtcttgt 4560

tgtctccccg gactgacaca ccctgctcac cagcctcttg gctctatggg ctaccctac 4620

gatgtccctg actatgcgtc c 4641

<210> 1188

<211> 4623

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 2C

<400> 1188

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgccagcc aggaaatcca tgcccgacgg cagatcaaca gacggaagct gcagagaaag 120

aagcgccgga agaagagaga ggaccactgc ggactgcggg ccagaaaccg gaacatgaag 180

aaaaccatga gccacctgat cgcccatcag gccctgaaga tgtctggcct gagactgttt 240

cacccagac tgttgacacg gaagaagcct ggcaagaacc ctggagaaa gacctggaag 300

atgcggaaga agtacgcca gaagcctagc cagaagaacc acctgtacgg caagggcctg 360

acacaccctg tgcctctgaa gagaaccctg cagaacaagc ggaacaagaa catcaagcgc 420

gtgaaccaga agaagggcaa catcaagaga aagagcatcc tgtgcacct catcgtgctg 480

aacagccccg agagcaacct gcaggctcat cctcaagttc cagcactggc tctcaggct 540

tggtagcctg ctagaagagg ccctctgaca agcgtccat ctgctcagca gacgtgacc 600

ttctgccta gcagatttcc ttggggcct cctccactgc actggaactc tgcctacctg 660

ggcagaacac tgctcgtgac ctgcatcctg taccacagat ggatcgtgac cagcatgtgc 720

cagagccaga gatggctgac cagcaccacc tctagaagca gcgcctgat gtggaccag 780

tggtagcgtg tgacaagcct ggaatggaca gcccaagaga ggggctgtag cagctggctg 840

atgaagcaga cctggatgaa gtcttgagc ctgcgggacc ccagctacag atccatcctg 900

gaatacgtgt ccaccagagt gctgtggatg cccacatcta cagtgggagc cctgagagcc 960

acagctcctg caacagctgc tccacaggct cagaccctc attggagagc cgccacaaca 1020

agcagcatga gcagcagccc tagagccgag cctacaagct ctagctcttg ggccacctgt 1080
 tggcccagat gttgcagctc cagctgttac tggtcctgt cctcttgcc tctgctggt 1140
 gctgccgagg ccacaaatac caggaccaga agcagagagt cccagcgggg cagaatgctg 1200

 acttggagaa gcagcctgtg gctgcagggc accagatgtt ttacaggcgt gcggacctcc 1260
 agcagacacc cttcttgcc ttggaccaga tgcctgagaa tgcggcctcc tagaagcaac 1320
 agccggaaaa agctgctcga ggacatgaag caaatggct tcacccggt caagaaacgg 1380
 ggcgtgatag cctggcggag agccactttc ctgctggccc tttgggagt cagtctgccc 1440
 caagctagac tgtcctgat cgtgtctagg accctgctgc tggccagag cagatgcagc 1500
 ctgatggaac agatccctca cctgaagtcc tgggtgtgta caagaggcgg cggaaagcgg 1560
 aagaaaaaga tgtgcaaggt gtccggcggc tgcaccgcct gtgttgaaag atgtccttgg 1620

 aaggcatct gctggaagtg gcctgtgaca gtggccgctc tgatcctgat tcagcacggc 1680
 ggcatcttca ccttccggt ctgggtcgag aagctgtcct ggaacatctg caagaatctg 1740
 tccctgtacc tggacaagtt cgtgcagcgg ctgctgtacg tgtacatcat cgagacaaac 1800
 gtgttcgtcc tgaacctgtt ccacgtgcca gtgaatcaga tcttcatgat ggccttctac 1860
 ctgaagtaca ccgagaaggc ctgggtcatg gaactggaat ggctcattca gcagcagtgc 1920
 taccagttgc tgcgtgctca tatgtacggc ttcagcacct acggcaccca gaaaggcgag 1980
 tgcgtgtgtc tgcagtgtct gagcggcagc tcctgttca tctgaagca gccactggac 2040

 ctgaagatca gcaagacctt catgagcaga tcccacctgg atttcagccc ctattggatg 2100
 aagaaagtga aggcctctcc acagatcatg cagcggatga gcgccgtgaa cttcgagaca 2160
 atcaggcgga agtggcagat ccggcacgtg ctgaagaacc tgcctctgga aaacacacag 2220
 atccccagga caagccctct gtggaagatc acaatggtgc tgacataccc caactgcgtg 2280
 gtgcatgtgc tgatgttctg gctgttcaag gccgaccaga gcgagtctag cctgagcagc 2340
 ggaatctacc ctctagcac ctgtagcctg ccttgccggg gcattagaat gtgcgcctg 2400
 tctcaccta gttctacat cagcagcacc gtgtgctttc tgagcaagca ctgcatgacc 2460

 gcctgcacca gagagaagat catcaacccc accatcagct gcccttttca gagccccaca 2520
 aagagactgg gccacagaga gggcagcgag agcgataatc tgggcctgct gtactccttt 2580
 cctccttgcc tgcctatgag atccctgggc gaaccttga gagctggctt tcagtgggga 2640
 gagtccctt ggcaagtgat ggctagcctg accggcaaca gcgtgatcgt gcacaagatc 2700
 gtgctggtgt ttctgaagtc tctgagcagc tacaactgcg agcggcggat ctctggcatc 2760
 cagaagagag ccatcgagtt cgccgtcctg aagctgtga acatggacct ggctagccct 2820

cagattatgc agagaaccag cgccgaccgg ttccggatga agcggagaat gcagaacctg 2880

gataacctgg gcgtgccctg gccattgctt ccaggtgctg ctctccaca tagactgctg 2940

ggccctcta gatggattct gtttcatgtg cggaacatcg tgtacggcat ccaagtgatg 3000

ctgtgccggc ggagaaacag cagaaagcag agtcaggtgc agctggccat tcaggtcctg 3060

ctcgtggaca agcacaagta ctttctgttc ggccctatc ctatcagca gggactgacc 3120

atgaccaccg gccggaacat caacagcaac tccctgatga ccaactgcct gttcagcccc 3180

atcttctgt gccaccacgc catcatgcac cggaagatga caagcccaca cttcagactg 3240

ttctccagca agatcccaca tctcaggtg ccaagtgtgg tggccctgtg caagttcctg 3300

gccaatggcc tigtgttcaa cctgatcttt cagaaaaagg gccacatgat ctttagcccc 3360

aagtcttcc tgaccttag ccagcggacc ctggaatccg ccgactgtt tccatggctg 3420

cacaccagt gccggaacaa aaagaccaag ctgtggtttt cctgatcaa catccaccac 3480

cgcaagaatc ctctgctgcc tatgagaatg agcagaacac ctctcggag agtgtgcgga 3540

tctccacctc tgcatctgtg ccaacctctg agaggcggca agaagagaag caagttcgcc 3600

ttctggaagc ctctagcca gggcatcagc tcttgtctga tgacaggctg ttggggctcc 3660

tgtggcagag ctgttcttg cggaagaggc tgcggtacac ccagaggcga ctggaaaaga 3720

caccacctc gcagagagct gagcctggaa ccatggattc cttatctgca ccagcaaaag 3780

accagcgga agcggatgaa gaccggcgcc attcaagaga agggcgctat ccaagaaaaa 3840

ggcgcaatga ccaagcggat ctgcgtggtc aatttcgagg cctgcagaga gatggaaagc 3900

ctgagcgccc ctgagaagat taccctgttc gaagcccaca tggcccggtg cacctccatc 3960

aatgtgctgt gtgtccgggc cagcctgatt gagaagctga tgaagaaaa gcgcaaatg 4020

aagcgcaacc aggtggcatc cctcaaatc atgcaacggc tgttcatcaa gggctaccag 4080

aacaaccact tcacgttcca cctccaaaac ttgcttct tcagctcctt cggcaacaac 4140

aagtatatca acattctcac ccgggccttc atccacacac ctagaagccc tggctgttcc 4200

gtgtaccca atatgtgctg gcggaagatg cagtcctga atcaccacag cagactgacc 4260

aactgtcacc ccgttggct gagccccatt agtcttctg ctaggctgct gccctatcct 4320

tttcactgac tggcactgga agtgaccttt ccacctggca cagccatgcc tcagatgcaa 4380

ttgcaggcac tggctatgtg ggagaaaggc tgggacaagc aagagaagaa atcccgaag 4440

ctgatgtcct cctgcctgga aaaaaaggct acctggatgc ggagaacccc tggcacaagc 4500

ctgcagtgtt acctgaacac acaccctgc accatgtgc tgcctcaggg aatcccatct 4560

ctgaacgccc agtggatgtt cctgcggatc ggctaccctt acgatgtccc tgactatgcg 4620
tcc 4623

<210> 1189
<211> 4638
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 3C
<400> 1189

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60
tcgccagacc aggaatcca tgcccgacct attcctccac acctgagaca ccctctgctg 120
ctgaagaaca agaagcggag aaagctgcgg cccaagagca gaaagaaggg ccacaccaag 180

aaccggcgga aggccaagag aaagccccag atcagaaaca gccgcagagc cacacctacc 240
agcaagggca gcctgagaag aaagtacctg agagtgggag ccgccgctgc tagctgtcaa 300
tctcctccat ctcttagaga gacaaccctt agcagcgacg ccaccagaag aaccagacct 360
atcgccgctc agagcaagaa aacctgaca gccgccggac tgacccttag ccagaagaaa 420
gatctgccc gcaagctgaa gaaacaggtg tccgtgtaca gcggcaacct gctgagcttc 480
tctcggagag gcatgaagtc tagcgtgcgc ctgaagaact gcaccaacct gagcgtgccc 540
atgatgctga ccatcctgat ctggaagcgg gtgttcatcc tgctgctgtc cgacaagaaa 600

tctatccctc acgtgcccaa ggccaccgcc gctcattctg tgacagtga gctgcagagc 660
cggcggaaca gacggtacag aaagatctat ggcgagctga agatgtccct gcaggccagc 720
aatggcatgg aagcctgtgg cacacacccc acacctagac tgtccgtgtc cgtgatcacc 780
atgaagctgt gggagaagca cttcaagggc ctgaactgga acctggctgt gtggattctg 840
aacctgaaga tgatgtcaa gaagaagtat ctggtccagc gcgagtggga gaaacggaag 900
cagattcttg gcggcggagg caagtacaaa gactacttcc tgaagagaat cctcatccgc 960
aaggccatga cagtgtggc cggcgataag aaagcctgg gcagattcat gagatgcgtg 1020

cagagcgaga caaaggccgt cagtctgcag ctgcctctgg gcagaatgga cctggatgga 1080
atgctgaccg tgatcgcca gggactctg ggcatgacac ctagagatct gggaacagtg 1140
gctggcgcca ccgcacagat tcagaggcct attcaggtgc agacaggcgg cagactgaga 1200
ggccctagaa gaaagtgct gatgtgtctg tgctgtccc ccaatcagag cctgcagaaa 1260
agccaggtgt tccagtgggt gctgagaacc gagctgcccc tgaccttag caccctgctg 1320
tgggacagca gacacgacct gcctagaatg ctgccatca gcagccctct gcacagacct 1380

cagatgcctt tctggacctg cacctttcct gccaccacat ggggcacatg ggagacacct 1440

tctacatggg gctggcggac ctttgccaga cagccttcta gaccacacgg cagaaccctt 1500

accaccagac tgatggctcc agtgggcagc gtgatgagct gtagcctgct gacacagcca 1560

tctccagcca gcgcctgtac aatgcctcca ctgctgcatc ctgagtgggc ccttcattct 1620

gctggacttt ctccaggcgc ttgcagacct gcctgtacct gcatcagcat gaccacaatc 1680

agcagggcca cctggcgcag aaacctgcag agaaacctga aagtgtgcg gctgagaatc 1740

cccagcctgc ggaagtacag acagcagaac acccggcca ccaacctga gaagaacca 1800

tctctgaaga agcagagcca gaggcggggc aagctgtctc tgaccacact gagcttcgtg 1860

ctgatcgagg aactgctgaa aaagagcagc cagctgcgga gaagctggcg gaacgtgtcc 1920

agaatcagca acatccggaa gctgatttgg accaagcagc ggagcttcct gtctctgttc 1980

cccaagctga gagccaccga gcagatgacc aatgtgggct gtagactgga ttttcacccc 2040

agaagcagct ccggcgacag agtgttcttg gtcaagatcc agagcagccc attcctggcc 2100

agatcctgga ataccatgca gtggaacaac aagaaaatgg ccatgactgt gatcgctggc 2160

gcccaccact gtcagtacaa gctgacctac accaaagtgt ggaagatgaa ttggaagaaa 2220

atgatgatcg gcagccagca cctcctgttc tccccactgg atagctctcc actccagctg 2280

ctgctgcacc cacacggcaa gagatgcaac cctgttgtc ggctgacatg gatgagccac 2340

ctgaatcgga agctgcacct caccaggtcc tgctgatcg acctgacct gatgatgagc 2400

cagaaactgt ggaagaatca gcggaagcgc atccctctgc cttctccaag acagcatctg 2460

ctgcctcagt atcctctgca ccctcctcca ccttgtctgc tgccttctca ccatagacac 2520

cacctggcat tctcagatg ggcctgtagc tctcagcaca cccacagcat caagatctgg 2580

atcagcttca gccacgagac aatgagcctg tccaacatcc tgatgaagtt ccggtgacc 2640

accaccacaa gcagccccag aagaagcctt gctctgcgag ctgagggcgg cacaacaatc 2700

ggcgaagtga ccagcagcct gttcttttagc cactgcctgt gcgtggcccc tagatgtcct 2760

agatctgccg tggacatcag ccccgacct acatctcctt ctctggctc ttgtgcctct 2820

gtggccattg gaaagctggc actgcttggc gcctctgctc cttgtggtgc tgctggcgct 2880

agagaggcgg gaagatttgc tgtgctgggc accatggtca tgaagaacat ggaacacaga 2940

ctgacctagg acagcgccct gagcctgaca aagagagagg gccctgaaac aggccccgtg 3000

tactacgtgt gcaaccggat gaatgtgtcc agcgtgctga agcctttcct gttcacctg 3060

cctatcgagg acatgagaga gtgcaccctg ggacgcaaca gaatgaatgt ctcttcctg 3120

ctgaaaccct gtctgatccc cgtgccaatc tgcaagaaga aactgctgct caagctgctg 3180
 aggggcgccct ccagctctac cagcagagat agcagaagct ttttcaccag cgctcaccct 3240
 agcagaccct gcaggatgag actgtaccag atgtctgcaga agcagtgtg ctacaacctc 3300
 gtgatcaagc accctctgat cttccggatc aacctgcgga gacagggcaa gaccaaagac 3360
 ggcggtgtgc agagcctggg cttcctgaac cagcagatca tcctccagaa agagtcttc 3420
 atctgcctgc tgatgttcat caagcgggtg aagccagccg ccaccaagaa gggcaagaac 3480
 agcccctgct gccagaaaaa actgcgggtg cagaaccagg gccatctgct gatgattctg 3540

ctgcacaaca gaggcccacc tctgcatacc agattcgaga aaaagcggcc cgagtggctg 3600
 agcagaaaaat ccggcgtgat gaagtgtggt gatctgtgcc ctgccttcag cggcaggatt 3660
 ctgcaccagc cagaaatggc cgccatgaga ctgatgcca agttcctgaa ctccaccaac 3720
 agctgggtga cagtgcacaa gaagagaggc ctgttccacc agatgaagt tctgaccgcc 3780
 gtggactgtc tgcaggcctt ctgggatatg agcgagaaga aacgcaagct gcctatgatt 3840
 cgcaaaatcc agaagcggcg gagaaccgcc aaccggaaca tcgagatcac ccctcagaga 3900
 agcaaagccc acctgaagaa aacctcgcc aaggcgcca agaaaatcac ctctctgtgc 3960

ctgagagtca gatcggagg ctggctgtgt ggctggacac caagaggatg gctgaagaag 4020
 tccaccaagt ccagactgtg cttctcttac ctgtgtact acctgtttt cctgaccgtg 4080
 tgcggcttca cccctccacc acttattctg tggcctcagg cagccctgg cgagaagctg 4140
 aagcactgtt ttaaagcctg gggcgctgac cctcctggca gcgtttggat tctgccctgc 4200
 ttctgtattc acctgagaaa ggtggacacc caccacctcc aggtggtcac caaacagtg 4260
 accgccacaa cagccgacgg ccagaggatg agaaggctga agtgcaaggc ctgccggctg 4320
 agatgggcta gacctgaacc tgcagctcag gccctccta agagccactt tccacctcat 4380

cctagcggcc cctccagaac cagctctctg caattgagaa cctacatgga aatgcactac 4440
 ggccatcagg cccacaggt ggcaatgtg cctaaactgc tgtgtcggca gatgtcccc 4500
 actctgtcta cctgcagca gagacatcct cagggcccat gtcctctcc agtgacacct 4560
 ctgagagtgc agtctgtgct gctgtcggga gtgcctcaaa cagctggcta ccctacgat 4620
 gtccctgact atgcgtcc 4638

<210> 1190

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP

polypeptide 4C

<400> 1190

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt	60
tcgcccagcc aggaaatcca tgcccagac agcaagaaga tgaccagaa gaaccgcaag	120
acccggaagg ccgcccagaga gaagcacaga aagaccgaca acctggacct gcagcaccag	180
cgcagacgca aaaagaagaa ggacaaggtc gagatccgga atcggagccc taaggccaat	240
agcaccgagt gtcaggcgca gcacagcaga gaggagaacc tgctgaacct ggtgcaattg	300
aacctcaca gccctcacca ccggaaggac gaggaagatc accagaagag acaccaccac	360
cacaatcaaa agaagatgtc cgtcaacgag ggcaacaacc actggcctag agtggaaatg	420
cctaccggct ggctgctcgt gggctacaac accagaaaca cagcccagaa tctcggctg	480
cagcagcacc tgaaacactg gcagcagtgc accagagcca gatggtgtca agagccctgt	540
cagaccctga cttcttcca cttcttcttc tttttcaaaa cgggtgccct gtgctgcccc	600
ggctggctca aaggacaacc tctccacct ggctgaagc cttctagcct ggcttctcag	660
gtggccagaa ccacaggcgt gtaccagcac gtgtggctga tctgcttcgt gttttctgtg	720
tgctggaaa ccggcttctg tcacgtggcc caagtgggac tcgagagact cgttagcctg	780
agcggcatca ccgacgtgaa ccattgggcc cagcctaagc catctcctag caaaggcacc	840
ggcatgaaca gaccatcgg cctgagagtt ggcaaaggcg tgtgggctag actgtggctg	900
aagaactgga agcggttcaa gctcaaaaag aaatacacag gcatggaaat cctgctgtgg	960
attctgctga agatggaaat tcagatcttc aagatttgcc tgggcgagat gcagctgtgc	1020
ctcaagaaga aagtcaacgc ctgcagcaac gccaaagaaa tgcccttcca gtgccggtgc	1080
agacgcgagt acagagtgc catgattcag aagaagaaac agaagtcccc gctgttcttc	1140
cacggcgacc tgtgcagacc ttctccttgc ctgtcttga gcagcaggat cgtggctcct	1200
ggacacgccc tgagctgtcg gactcgtaga agatggcca gcaagatggc caagaagtcc	1260
cagcagcctc tgtgtagagg cgcccttct gccagcgata gatgctgtag ctgtagcccc	1320
agcggcttta gcctggaag aggcagatgt cctgtgcagg gatgtctgag gccacacaga	1380
gttcagctgc tgagaagatg gggccctgga tctcctgctg gccagagact gtctaagggc	1440
ttccaactgc tgcgttggtg gggaccagga tctccagctc ctgagcctag aaagggccca	1500
tttccaccac ctgatectcc atggcctgtg accgctgtga cagtgatggc tggctctgtg	1560
cctagcgtc agtctgtgga tgctctggaa tcccctggac ctctggctct cgaaggccct	1620
agcagcccta gaaacctgct ctggcgggaa atgagcatct tctgcctgg catcttcaac	1680
ctgcacctgt gtiactacca cagccagagc aaccggaaca agagccggca gatggaatcc	1740

ctgggcatga agctgcagat cacacaccca ttcgccagcc agccactggg ccaagagatg 1800

cccaacaaca cccagatcag actgctgaag cccggccagg cctttggcag cttttccgcc 1860

gatttttcag cccctcagca ggccctcttg agactgtggt cttgggtcgg cacaagccag 1920

acctacttcg gctctatcga agccctgaca gccctgttca cctgtagaac cgccagcatc 1980

agcgtgaaca tcagcacctt gatgagcatc ctggaagcca tcctggccat gacactgacc 2040

ctgaatggca gccctctgtg ggactgcagc acaacaacag gcacacacca cggctgcctg 2100

tgggagatcc ctctgttac cctgctggct accgcaaaa agagccctac cagcttctgc 2160

tgtcagcggc ctctctgca gccagtggaa gagaagaaga acggccggat cagcagcgtg 2220

ccaccttctc cactcttgc tctgggccct agaatgcagc tctgcacca gctggcccg 2280

ttcttccta ttacacctcc tgtgtggcac atcctgggac ctgagagaca caccctctg 2340

ctgacccctg acaccagatg gatcttctcc aaccagctgc agaccgtgca gatgctgtgt 2400

ctgcctccac tgaagcaggc cgagagaatc atctggcctc tcggcggctt tcagatcccc 2460

aacttctttt ggagcctcgg catcggacac actggcgcct ggtggcatat tggaaggcgg 2520

agaagagaat ggggcggcag caccgtgtct agaagccac tgtggatcag ctccatgac 2580

tacctgagag gcatggcctt cgctccgac agcagcatca gaaccaccag agtgtcctgg 2640

tgtcggagat gtggcgccaa aagcgccga gccagcagcg acaagaagaa gaaaagcacc 2700

gaaaagacca agaacaagat catctgcaag ggccacagaa tcaccaggt ggtgctgaga 2760

ctgggcaacc tgctccatt cttcagaggc agcgaggtgc ctttcttag accttgccgg 2820

accaagtgcc agaagaaggt tccaagcgc tctccttggg gactgcaccc aagaacagcc 2880

tccatcacac tgctaccac cagcctgaag ggagcagaa caagctgctg cccagatct 2940

cacccagac tgccagaac aaagtggcct ctgcagtgcc tgctgcacag cctgggaaca 3000

actggaacac tcgtgtggga aagggcgctg ctgcagatga gaagtctgga agctcactgc 3060

cctctgcaga cattccact ccaccactgc agaaccagc ctactcttg tctccagcc 3120

tggattctgt accaaggaca gtggagcgga gccgtcgtgg gacttagacc tgtggctcac 3180

catctgcaa gacctatcca ggggtgcac tgcctcagg ctctcatca accagctctg 3240

tcttgggaa agtggccgt gggaatgaca ggaccgcca gatgtgccg gtggcctaga 3300

agaatgtgta gctctctggc cctgccaacc ggctgacat ctctgacct gcctagcagt 3360

gatctggcgg tgctgactc tagctccacc agccactttc tgatgcggag cccagtgtg 3420

ccaagcagca gactgacatg tgcctctcca cagctgcctc ggatgtggac atggtctagc 3480

tggctgaaag agtggggagg acaggccac agacagcgga actgtagagt gaacgccgtt 3540

gaggaactgc acagcaggcg gatgtctgtg cggatcgtga agaattgggt gtcctgctgt 3600

tacgtgcggc tgagtgcagt gggactgtct acttggagcg ccctggattc cctgatcctg 3660
tccttccaga gagtgaatac cagccggata ctgaacctcc aggtgctgaa gaagatcctg 3720
cggagcttta tgaagctgta ccactctctc gtgatgtgcc tgcggctgcg gaccaagctg 3780

gaaaaagctc tgagcgctct gtttatcttg ccccagcaca gctacaaagg ccaggcattc 3840
ggaagcctgt gccagctggt gtctgccgat ttcagcgcgc ctcaagtgc cagactgcgg 3900
agcctgaacc atctgctgat tcggtggatc tttagcaatc agctgacagt ccaaagtctc 3960
tgcttccga tcatcaagaa aatgaagaaa cggatcatgg tgcacgtctt gaagaagaat 4020
cggaaagcaga ttatctgtat caagaatatg ttcctgcagc ggaagggatt cctgaacctg 4080
agccacgtgg aaaagttcag agagagcacc ctgggcaatt tctggatgaa gctcctgcag 4140
ctgccaccag ctgacacctc taaggcctgg acaccagaa agcttgtggg gagagccgtg 4200

cggagaaagg gcgtcgtgat caacctgaag agactgcaga aattccgggc tagcgtgtcc 4260
ttctggactc tgctgcctac aacaggcgtg cggacaagag gctctccact gagactgact 4320
ctgtggcctc caagaagcca gaaaagccag caccactgcg ccctgagaaa gatcgagtgg 4380
gccacaaagc tgctccctcg cggcaaagca ggaccacagg ctcaagagaa ggccaacatc 4440
ctgaacagcc tgccttctc tatggaaatc gccgtgctgc aagaaatgct gaaccagaag 4500
tgtctggccc ctctcgagct taagaagaac ctctgtctgc caacctacac accccacatc 4560
tgtcggcaca cccttaaaaa gaagcccaga gacatctgca gaatcagcgg ctaccctac 4620

gatgtccctg actatgcgtc c 4641

<210> 1191
<211> 4641
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 1D
<400> 1191

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60
tcgccagcc aggaatcca tgcccagcc gacaagaaaa acgtcggag cgctagtctt 120
cctggacatc ctcttggccc cagaagaatg accagacgga ccatgaccac caccaaatg 180
atgatgatgc ggcggaccaa gcggcggaga agaaaaagac gccggatgac catgatgacc 240

agaagaaccc tgcagacaa gaaaacctgt ctgacccta gaaccagcgc cgccacaaaa 300
gctctgccc gagagacaat cagccagcgg aggcctatcc agacacctcc tggaacaagc 360

ctggccatct ggggcagaag aagcaagatc gaggcctctc ctatcggcag catcacccct 420

ctgagcatca gcagacctac cagcagagcc agacagagct gttgcctgcc tggactgaca 480

cacctgctc atcagcctct gggctctatg gttggagctg gaacaggcgg aggacctgct 540

tgtgtgcctg tggccgaagc ttctacaggc gcttggacag ctgaaggcgc tgccggcaca 600

agatgtagag ccagcagagc cccttcgaga cagctgcctg cttctagccc taccaagtgc 660

gagatctgcg tgaagagaag aaggcggcgc aagcggagca gccagtctag atctccctg 720

cctaagaaac gcgagcggat gatgtccct gtgcgggcca gaacagctag atctgctctg 780

ccacaaggca gggctcctct ggaaggaatg cttctgccta gagcactgcc cagcctgctg 840

agcagaatgc ctgccagaag agagagcaga ttctggctgg ccctgcaggc ccttggactc 900

agacctctc atctgcctag ctgtcacct ctgcctcaac tgcttggacc tctccacct 960

catcaggccc ctggcgagaa aaacgacctg cagctgttcg tgatgagcga caccacctac 1020

aagatctact ggaccgtgat cctgctgaac ccctgcggca acctgcacct gaaaaccacc 1080

agcctgaacg ccaagaaaat ggaagatatg atctgggaga gcaaccagca gctgaagtgg 1140

acccctcaca tctgaagtc cgcctctatc gccagaagc ggatcaagct gcggcggaac 1200

agcaccagac gggaaatgcc ttctcaggcc acacctctc cacctggacc ttggagagcc 1260

gctctgggca aagaagtga gcgagccag agcaagctga gactgagaaa cacaagcccc 1320

ttcgacaaaa agggctttgt gatcctgagc aacatgggcg gcaaccggtc tatctgcctg 1380

accatcgtgt tctttctggc cccttacttc cccatgccta gcagctggtc tagcagcggc 1440

agaaccagac tgcctctgag gccacagaga ggccctagac ctctgcatag atggctgcag 1500

cagaccaccg gctgctctca gagaagaggc gactgcccaa gaacctggc cggacctct 1560

gcttctctgc accctgcac tggcagagcc tccagaaaga cctggcagag aaggctgaga 1620

gcctgtagag caggcggacc tgctggatgg gctagacagg ccagaaaacg caagagagag 1680

aagcggctcc agaagtccag acagaacct ctgcagctga aaagctgcag acggaagatc 1740

agcaactggt ctaagctgcg gagcccttg atcttcgagg ccaaaaagag catgaagaga 1800

tcccagcggc ctctcggag catcctgagc ctgttcaaga agaagaagcc cctgacattc 1860

agccccagcg tgtccaagaa gaggtgcct aagctgaagg gcaagaaacg ccggaagaa 1920

atccagcgga agtggtcaa gaaccccagc cagcctgtgc cactgagaaa tgacggcatc 1980

accaacggca acgacagcac ccggtcttgc agcatcagcc tgaagaaaag cctggaaaag 2040

atgccctga tgcggagcct gctgtactcc agaattgtcc ttggtgcagat cccacacac 2100

acctgggagc ccgactactt tgttccctg cctatgatgt tcagctgggc cacacagagc 2160

tttcagtggt gcgccgtgtt tctgaccaga cctgccattc cttgtgtag ctgtaccagc 2220

cactccaatc ctiggagcca gtccacactg gccatccggt ttatctctgc ccctcagcca	2280
agcagcagca ccgttacagc tgctcctagc ggccagtatt ttgccctgcg gagtatgccc	2340
aagagccgga accaggtgct gtttcggaga aatctgaccc caagccagct gcggacactg	2400
gcccctccat atatgctgct gcctcagtct ctgtcccaga gccgtgtctg gaagcagatc	2460
ccatctcagt ccatgctcgt gcggaccagg ctgacactga caggcactag aagctccggc	2520
accagagcct ctccatctgc cgtgtgtctg tctgtctgga catgccccag cagaagcttt	2580
cctgccgcct ctccaagcgg actgagagca cctgttggag cacaggctcc tccagaagtg	2640
acactgagag ccagctgtgc cagctccgcc agcaaagctt gtgcaggact ttggccttgg	2700
ggagcccaag tgcggatgaa gaagaaggac agcaccatct tcatctaccc caggctgaaa	2760
accttcggcg tgccactggg cagcattctg tgtctggctg gaagcctgag cacgatgatg	2820
atcattagca ccaccagaca agagtgcggc agacgggcca gcgtgccctg tagacctatg	2880
atcggaagcg ccagacctgg accatggcgg acaagtgcta tgccttctgc catgggagtc	2940
gcccctgcta ccagctgtga aagcgggaaga tctctctctg ccaccggcgg aagaatgcca	3000
ggatctcagt ctatcatgat gagctggatg cctccactgg ctcctgcgc tgcttgtcct	3060
tgttctctg ctctacact gtgccctgct caccctgcta gagcaccaac agccgtgcct	3120
gcctttacac cctgtctgc tcatcctgtg ccagtgtgt ctggatgtca cctggctgtg	3180
cggacctcca tgcttacctt gctgccaatg atgacctga aggccttgg caagacatgg	3240
accagtcca gaaactacc cagacggcac cctcacagaa gccaccaac aagctgtcct	3300
ccactgctcg aggcctttcc actgccaaga gccagcctga gagctaccgt gcctagacac	3360
tctagcgtgc tggccacagg actgcatctg cataggcaga ttagcctgcc tctgcggggc	3420
ttcctgctgc atcaaccact gccaggacaa cactgtggc tgtccacag actgagactg	3480
cggctgccta gaacaaccga gatccagctg accatgaacg actccaagca caagctggaa	3540
agccccgctc tgaaacaggt gtccccagct agtctccta cacagcagcc tcagacaccc	3600
caggattcta gacaggtgct ggccgtgcct atgagcctgg cctgtagcat caccgtgtcc	3660
ttcgtgggcc agatctctac cctggtgctg gacgtgtcct ccatcagcca ctggaacggc	3720
atctgggaag tgatgccag aacactggaa ggctgcatct ccgtgaagga ccaccggaca	3780
tccagaacc acagcaagtg catcaccgag tgtgtgcgga cagccctgaa caccaagtgt	3840
gaaatttgtg tgaagaacac cgccatcctg gctatcacc tgatcaccac acaggaccct	3900
cacctggacc ctgtgtgtca tccccataga aggcccggt ggaagggaca ccacagagtg	3960

gtgttttagcc accatccttc cggcagcacc aagtctcact ggcagcagag agaaagaggc 4020

ggagggccgca gagaaaagaa gggctgtaga gaggcaagca gagccggcca gtttcctgtg 4080

tggcggagaa catctagagg catgtccctg cagtggaaat ccggcaatgc ctgcacacct 4140

ctgagatgtc ccagcagatc tccagccacc ttcttgactg cctgaacgg ctggcataga 4200

tctggactga gggcccagac cgccttcttt ctgctggaca tcatcctgcg gagagcccgg 4260

cctacaagct gcagcacatg tagaatgtgg tggcggctgc cctgcaaagt gaccgaaagc 4320

tccttgccca agaaaacct gaccaatcag cctagcttgc ccggaccttg tgctagcctg 4380

ctgtctacac tgagccagcc accacctcag gctcctagcc aagtttgac agccgctaca 4440

ctgcggtgtc ctgctgtgcc tgctgtgca tgtccacctc tgaagctggc tccactgcaa 4500

gtgaccacaa cactgaagct gatcctggtc atgctggaaa tcgtgaccga gaacaaagtt 4560

cggcagaact tcaagcgga cttcagcttc ttctacacca gcgacagagg ctaccctac 4620

gatgtccctg actatgcgtc c 4641

<210> 1192

<211> 4623

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 2D

<400> 1192

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60

tcgcccagcc aggaaatcca tgcccagcgg aagatgcaga gcctgaatca ccccagcaga 120

ctgaccaaca atcctcggag aaagacctgg aagatgcgga agaagtacgc ccagaagcct 180

agccagaaga accacctgta ccggcagatc aaccggcgca agctgcagag aaagaagtcc 240

agaagccacc tggacttcag cccctactgg atgaagaaag tgaagcgggc cagaaaccgg 300

aacatgaaga aaacatgag ccacctgac gcccatcagg ccctgaagat gtctggcctg 360

agactgtttc accccagact gctgaccaga aagaagcccg gcaagcagaa aaagggccac 420

atgatcttca gccggcgga gtggcagatc cggcacgtgc tgaagaatct gatccccagc 480

ctgaacgccc agtggatgtt cctgagaatc gctagccac agatcatgca gagaaccagc 540

gccgaccggt tccggatgaa gcggagaatg cagaacctgg acaatctggg cgtgccctgg 600

cctctgttgc ctggattgct gctggcccat atgtacggct tcagcaccta cggcaccag 660

aaaggcgagt gcgtgtgtct gcagtgtctg agcggcagca gcctgttcat cctgaagcag 720

cccctggacc tgaagatctc caagaccttc atggccagcc ctacagattat gcagcggatg	780
agcgccgtga acttcgagac aatcctgcag gcccatcctc aggtgccagc tcttgctcct	840
caagcttggg gggccgctag aagaggccct ctgacatctg ctccaagcgc acagcagtcc	900
ctgacacgga cactggaaag cgccggactg tttccttggc tgcacacca gtgccgggccc	960
ttcattcaca cacctagaag ccttggctgc agcgtgtacg ccaacatgtg ctggcggtac	1020
aagaaacggg gagtgatcgc ctggcggtac taccctccta gcacatgcag cctgccttgc	1080
agaggcctga tcttgattca gcacggcggc atcttcacct tccggttctg ggtcgagaag	1140
ctgagctgga acatctgcaa gaacctgagc ctgtacctgg ataagtctgt gcagcggctg	1200
ctgtacgtgt acatcatcga gacaaacgtg ttcgtgctga acctgttcca cgtgccagtg	1260
aaccagatct tcatgatggc cttctacctg aagtacaccg agaaggcctg ggtcatggaa	1320
ctggaatggc tgatccagca gcagtgtctac cagcgggaaga gaatgaagac cggcgccatc	1380
caagagaagg gcgctattca agagaaaggg gccatgacca agcggatctg cgtgggtcaat	1440
ttcgaggcct gcagagagat ggaaagcctg agcgccccctg agaagatcac cctgtttgaa	1500
gcccacatgg cccggtgcac cagcatcaat gtgctgtgtg tcagggccag cctgatcgag	1560
aaactgatga aagaaaagcg caagatgaag cgcaaccagg tggcatcccc tcaaatcatg	1620
caacggctgt tcatcaaggg ctaccagaac aaccacttca cgttccacct ccaaaacttc	1680
gcctttctta gctccttcgg caacaacaag tatatcaaca tctgacctt tctgeccagc	1740
agattccctt ggggacctcc tccactggga gcccttagag ctacagctcc tgctacagct	1800
gctccccagg cacagacacc tcattggaga gccgccacca caagcagcat gagcagctct	1860
ccaagagccg agcctaccag ctctagctct tggggcactt gctggcctag atgctgcagc	1920
tccagctgct attggagcct gtctagctgg cctcctgctg gcgctgccga agccacaaat	1980
accagaacca gaagccgcga gagccagcgg ggaagaatgc tgaactggag aagctccctg	2040
tggctgcagg gcaccagatg ttttacaggc gtgcggacca gctccagtg cagcctgatg	2100
gaacagatcc ctacctgaa gtctaacagc cggaagaaac tgctcgagga catgaagcag	2160
aacggcttca ccagacggcg gaacagcaga aagcagagcc aagtgcagct ggccatccag	2220
gtgctgctgg tggacaagca caagtacttt ctgttcggca gagccacatt tctgctggct	2280
ctgtgggagt gtagcctgcc tcaggctaga ctgtgcctga tcgtgtctag aacctgctg	2340
ctcgtgcagt ctagacacce aagctggcct tggaccagat gcctgagaat gcggcctcca	2400
cgcagccact ggaactctgc ctacctgggg agaacactgc tcgtgacctg catcctgtac	2460
cacagatgga tcgtgaccag catgtgccag agccagagat ggctgacctc caccacctct	2520

agaagctctg ccctgatgtg gacctggtgg tgtacaagag gtggcggcaa gcggaagaaa 2580

aagatgtgca aggtgtccgg cggctgcacc gcctgtgttg aaagatgtcc ttggaagggc 2640

atctgttga agtggcctgt gacagtggcc gccatgagca gaacacctcc aagacgcgtg 2700

tgcggccaca gagaggcgag cgagtcgat aatctgggcc tgctgtactc ctttcacct 2760

gtgctgttca aggccgacca gagcgaaagc tctctgagca gcggcaacag cgtgatcgtg 2820

cacaagatcg tgctggtgtt cctgaagtcc ctgagcagct acaactgcga gagaagaatc 2880

agcggcatcc agaagagagc catcgagttc gccgtcctga agctgctgaa catggacctc 2940

ggcaaggagc tgacacaccc cgtgcctctg aagaggaccc tgcagaacaa gcggaacaag 3000

aacatcaagc gggtaacca gaagaagggc aacatcaaga ggaagtccat cctgctgcat 3060

ctgattgtgc tgaacagccc cgagagcaac cgggaaaaga tcatcaaccc caccatcagc 3120

tgcccttttc agagccccac aaagagactg ggaagccctc ctctgcacct gtgtcagcct 3180

ctgaggccct atcctatcag cgaggccctg accatgacca ccggcagaaa catcaacagc 3240

aactccctga tgaccaactg cctgttcagc cccatcttcc tgtgccacca cgccatcatg 3300

caccggaaga tgacaagccc tcaattcaga ctgtttctcca gcaagatccc acatccacag 3360

gtcccaagtg tggtagccct gtgcaagttt acacaccct gcaccatgct gctgcccaca 3420

ggcgcttttt ggaagccctc tagccagggc atctccagct gtctgatgac aggctgttgg 3480

cagtgttcca gcgtgacaag cctggaatgg acagcccaag agagaggctg ttcctcctgg 3540

ctgatgaagc aaacatggat gaagtcttgg tccttgcggg accccagcta cagatccatc 3600

ctggaatacg tgtccacacg ggtgctgttg atgcccacct ctaccgtgcc taagtctttt 3660

ctgaccttca gccagatccg gatgtgcgcc ctgtctcacc ctactttcta catcagctcc 3720

accgtgtgct ttctgagcaa gcactgcatg accgcctgca caccatggaac cagcctgcag 3780

tgttacctga acctggccaa cggcctgttg ttcaacctga tcttccggaa caaaaagacc 3840

aagctgtggt tctccctgat taacatccac caccgcaaga acccactgct gcccatgcgg 3900

ctggaaaaaa aggccacttg gatgcggcgg accgagctgt ctctggaacc ttggattcct 3960

tacctgcatc agcagaaaaac ccagtggctc cccatgagaa gcctgggcga gccttggcga 4020

gctggatttc agtggggaga gtctccctgg caagtgatgg cctctctgac aggcagacgc 4080

aagaaaaagag aggatcactg cggactgcaa gagaaaaaaa gccggaagct gatgtccagc 4140

tgcgccgctc ctccacatag actgtctggga cctagcagat ggggaagctg tgggagagcc 4200

tgttcttgtg gcagaggctg ttgaaccctt agaggcgact ggaagagaca cccacctcgg 4260

cggattctgt ttcacgtgcg gaacatcgtg tacggaatcc aagtgatgct gtgctgtcac 4320
cccgcctggc tgtctccaat cagecgttgt cctcgctgc tgccttatcc attccacgtt 4380
ctggccctgg aagtgcatt cctccaggc actgcatgc ctcagatgca attgcaggca 4440
ctggcaatgt gggagaaagg ctgggacaag cctctggaaa acacacagat ccccaggaca 4500
agcccactgt ggaagatcac aatggtgctg acatacccca actgcgtggt gcacgtcctg 4560
atgttcggcg gcaagaagcg gagcaagttc ggctaccct acgatgtccc tgactatgcg 4620
tcc 4623

<210> 1193

<211> 4638

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 3D

<400> 1193

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt 60
tcgccagcc aggaaatcca tgcccgacag aacaccagaa gcaccaacct ggaaaagaac 120
cccagcctga agaagcagag ccagcggaga ggaaagctga gcagcagaaa gaagggccac 180
accaagaacc ggcggaaggc caagagaaag cccagatca gccagaagaa ggacctgcc 240
ggcaagctga agaaacacct gaaccggaag ctgcacctga ccagatcctg cctgatcgac 300

ctgacctga tgatgagcca gaagctgtgg aagaaccagc gcaagagaat ccctctgcct 360
tctccagggc agcatctgct gcctcagat ccaactgcat cccacctcc atgctgctg 420
ctgctccacc acagacacca tctggccttt ctcgagatgg cctgcagcag ccagcacacc 480
cacagcatca agatctggat cagcttcagc cagaggacc tgcctagaat gctgcccac 540
agcagccctc tgcagacacc ccagatgcct ttctggacct gcacctttcc tgccaccaca 600
tggggcacat gggagacacc ttctacatgg ggtggcgga cattcgcccc tgtgtactac 660
gtgtgcaacc ggatgaacgt gtccagcgtg ctgaagcctt tcctgttcac cgtgcctatc 720

gaggacatga gagagtgcac cctgggcaga aacagaatga atgtgtctc tgtgtgaaa 780
ccctgtctga tccccgtgcc aatcctgacc aactgagct tcgtgctgat cgaggaaagc 840
cggcggaaca gacggtacag aaagatctac ggggagctga agatgtccct gcaggccctg 900
cctctgacct ttagcacact gctgtgggac agcagacaca ccaccaccac aagcagcccc 960
agaagatccc ctgctctgag agctagaggc ggcaccacaa tcggcgaagt gacaagcaga 1020
ggcgccagca gctctaccag cagagacagc agaagctttt tcaccagcgc tcacccagc 1080

agacctgca gaatgagact gtaccagagc aacggcatgg aagcctgcgg cacacacct 1140

acacctagac tgtctagagg cctccactg cacaccagaa ccatgagcct gagcaacatc 1200

ctgatgaagt tccggtgat gctgcagaag cagtgtgtct acaacctcgt gatcaagcac 1260

cctctgatct tccggatcaa cctgcggaga cagggaaga ccaaagacgg cgttgtgcag 1320

agcctgggct tctgaacca gcagatcatc ctgcagaaag agtttctcat ctgcctgtg 1380

atgttcatca agcgggtgaa gccagccgcc acaaagacac ctcaccact gattctgtgg 1440

cctcaggcgg ctctgtgca caagaagaga ggctgttca gcctgttctt ctccactgc 1500

ctgtgccacc agatgaagtg cctgaccgcc gtggattgtc tgcaggcctt ctgggacatg 1560

atgattcgca agatccagaa gcggcggaga accgccaacc ggctgaaaaa gaaataacctg 1620

gtgcagtgtg ccaacctgag cgtgcccatt atgtgacca tctgatctg gaagcgggtg 1680

ttcatcctcc tctgagcga caagaagtgt ctgagagtca gatgcggcgg atggctgtgt 1740

ggctggacac ctaggagcaa gaacaagaag cggagaaagc tgcggcccaa gcacctgaag 1800

aaaaccagcg ccaagggtgc cgtgatcacc atgaagctct gggagaagca cttcaagggc 1860

ctgaactgga acctggtcgt gtggattctg aacctgaaga tgatgtggct caagaagtec 1920

accaagagca gacagagcag cccattcctg gctcggagct ggaataccat gcaatggaac 1980

aacaagaaaa tggccatgac cgtgatcgtt ggcccccacc actgtcagta caagctgacc 2040

tacaccaaag tgtggaagat gaattggaag aaaatgatga tcggctccca gcacctcctg 2100

tttagccac tggattcaag cccactgcag ttgtgtgtgc accctcacgg caagagatgc 2160

aaccttgct gcagactgac ctggatgagc agagagtggg aaaagcggaa gcagatcctc 2220

ggcggaggcg gcaagtacaa agagtacttc ctgaagcgga ttctcatccg gaaggctatg 2280

acagtgtgg ccggcgataa gaaaggcctg ggaagattca tgatgtcgt gcagagcgag 2340

acaaaggcgg tgtctctgca gctgcctctc ggccgaagaa agtccggcgt gatgaagtgt 2400

tgggatctgt gccccagact ggactttcac ccagatcta gctctggcgg cgagaagctg 2460

aagcactgtt tcaaagcctg gggcctgtgc ttcttctacc tctgtactt cgagaagaaa 2520

cggcccagat ggctgagcgt tgacctcct ggatctgtct ggattctgcc ctgcatggac 2580

ctggacggaa tctgacagt gatcgccag ggactcgtgg gcatgacccc tagagatctg 2640

ggaacagtgg ctggcgccac cgcacagatt cagaggccta tccaggtgca gacaggcggc 2700

agactgttcc tgattcacct gagaagggtg gacaccacc atctgcaggt cgtgaccaag 2760

accgtgacag ccacaacagc tgacggccag aggatgcgga gactgaagt caaggcctgt 2820

cggctgagat gggccagacc tgaacctgct gcacaggctc ctccaaagag ccactttcca 2880
 cctcatccta gggcccccctc cagaacctct agcctgcagc tcagacccat tctccacac 2940
 ctgagacacc cactgctgct gaagggaag aacagcccct gctgccaaaa gaaactgcgg 3000
 gtgcagaacc agggccatct gctgatgac ctgctgcata acgccagaca gcccagcagg 3060
 cctaccggaa gaacccttac cacaagactg atggcccctg tgggcagcgt gatgtctgt 3120
 agcctgctga ccagccatc tctgccagc gcatgtacaa tgccaccact cctgcatcca 3180
 cagtggggcc cacatagtgc tggactgtct ccaggcgctt gcagacctgc ctgtacctgc 3240

 atcagcatga ccaccatctc cagagccaca tggcggtga gaatccaag cctgaggaag 3300
 taccggcaga acatcgagat caccctcag cggcttaagg cccaggtttc cgtgtacagc 3360
 ggcaatctgc tgagcttctc cagacggggc atgaagagta gcgtgcggct gaagaacagc 3420
 atccctcacg tgccaaaagc caccgccgt cactctgtga cagtgaagct gcagtacctg 3480
 tttttcctga ccgtgtgcgg cttcgaccgg gtgttcttgg ttaagatctg caagaagaag 3540
 ctgctcctca agctgctgag agggcccaga cggaaagtgc tgatggtgct ttggctgccc 3600
 gccaacaga gtctgcagaa aagccaggtg ttccagtggg tgctgcggac cgaaacctac 3660

 atggaaatgc actacggcca tcaggcccct cagggtggcca tgctgcctaa actgctgtgt 3720
 agacagatgc tccccactct gtccacactc cagcagaggc atctcaggg accttgtct 3780
 cctcctgtga cactctgag agtgcagtct gtgctgtctc tgggagtgcc tcagacagcc 3840
 gcttttagcg gccgattct gcaccagcca gaaatggccg ccatgagact gatgcccaag 3900
 ttctgaact ccaccaacag ctggtggaca gtggccccta gatgtcctag aagcgccgtg 3960
 gacattagcc ccggacctac atctcctagc ctggcctctt gtgcctctgt ggccattgga 4020
 aaactggcac tgctgggcgc atctgcccct tgtggcgcag ctggtgctag agaggctgga 4080

 agatttgccg tgctgggcac catggttatg aagggtgctg ccgcagcctc ctgtcagtct 4140
 cctccatctc caagagagac aaccctagc agcgacgcca ccagacggac aagacctatt 4200
 gccgctcaga gcaaaaagac catgactgcc gccggactga cccctcgag aaacctgcag 4260
 agaaatctga aggtcctggg cgccaagaag atcaccttcc tgagaaacag cagacgcgc 4320
 acacctacct ctaagggcag cctgagaaga aagtacctga gagtgaacat ccgaagctc 4380
 atctggacca agcagcgag cttctgtct ctgttccca agctgagagc caccgagcag 4440
 atgaccaatg tgggatgct gctcaagaaa agcagccaat tgcggcgag ctggcgcaat 4500

 gtgtcccga tcagcaacat ggaacacagg ctgaccatgg acagcgcct gagcctgaca 4560
 aagagagagg gccctgagac aagcgagaag aagaggaagt tgctggcta cccctacgat 4620
 gtccctgact atgcgtcc 4638

<210> 1194

<211> 4641

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hTPA- and HA-extended poly-FSP
polypeptide 4D

<400> 1194

```

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt      60
tcgcccagcc aggaaatcca tgcccgaac agaaagacca gaaaggccgc cagagagaag      120

caccgaaga ccgacgacaa gaagaagaag tccaccgaaa agaccaagaa cgccaagaag      180
atgcccttcc agcagcggcc tctctgctgc cctgttaacc tggatctgca gcaccagcgc      240
agacgcaaaa agaagaaaga caaggtcgaa atccggaatc ggagccctaa ggccaatagc      300
accgagtgtc agggcgagca cagcagagag cagaacctgc tgaatctggt gcagctgaac      360
cctcacagcc ctaccacag aaaggacgaa gaggaccacc agaagcggca ccaccaccac      420
aatcaaaaga aaatgagcgt gcgggctagc gtgtccttct ggacactttt gccaacaacc      480
ggcgtgcgga caagaggctc tccactgaga ctgacactgt ggcctccacg ggttccacct      540

tctccacctc ttgctctggg ccccagaatg cagctgtgta cccagctcgc ccggtttctc      600
cctatcacac ctctgtgtg gcacatcctg ggacctcaga gacacacacc tcaggctcct      660
ctgaggctgt ggtcttggtg cggcacaagc cagacctact tcggcagcag accatctcct      720
tgcttgagct ggtccagcag aattgtggcc cctggacacg ccctgagctg tcggactaga      780
agaagatggt ctagcaagcg gtggatcttc tccaaccagc tgaccgtgca gatgctgtgc      840
ctgccaatca cacaccatt cgctctcag cctctgggac aagagatgcc caacaacacc      900
cagatccggc tgctgaagcc ctgcagagtg aacgccgtgg aagaactgca cagcaggcgg      960

atgtctgtgc ggatcgtgaa gaactgggtg tctgtctgtt acgtcggct gtctgtgtg      1020
ggcctgtcta cttggagtgc cctggacgag gaaaagaaga acggccggat cagcagcctg      1080
aaaaaagaag tgaatgcctg cagctccctg atcctgagct tccagcgcgt gaaaaccggc      1140
atggaaatcc tgctgtggat tctgtgaag atggaaattc agatcttcaa gatttgctg      1200
ggcgagatgc agctctgcgg ccaggccttt ggaagcttta gcgccgattt cagcgcctt      1260
cagatcatta agaagatgaa gaaacggatc atggtgcacg agctgaagaa gaatctgctg      1320
ctgcctatgt gctccagcct ggctctgcca acaggcctga catctctgat cctgcctagc      1380

agcgatctgg ccgtgctgat ctctagctcc accagccact ttctgatgcg gagccctgtg      1440

```

ctgccaagca gcagactgac ttgtgcctct ccacagctgc cccggatgtg gacttggtct 1500
 agctggctga agaacgaggg caacaaccac tggcctagag tggaaatgcc taccggctgg 1560
 ctgctcgtcg gctacaacac cagaaacaca gcccagaatc ctcggctgca gcagcacctg 1620
 aaacactggc agcagtgcac cagagccaga tgggtgtcaag agccctgtca gaccctgacc 1680
 ttcttccatt tcttcttctt ttcaaaacg gtgtccctgt gttgccccgg ctggtctaaa 1740
 ggacaacctc ctccacctgg cctgaagcct tctagcctgg cttctcaggt ggccagaacc 1800

 acaggcgtgt accagcacgt gtggctgac tgtttcgtgt ttttcgtgtg tgtggaaacc 1860
 ggcttctgtc acgtggccca agtgggactc gagagactgg tgtctctgtc cggcatcacc 1920
 gacgtgaacc attgggcccc gcctaagcca tctcctagca aaggcaccgg catgaacaga 1980
 cccatcgccc tgagagtgg caaaggcgtg tgggccagac tgatcctggc catgacactg 2040
 accctgaacg gcatggccaa gaagtcccag cagcctctgc aggtcgtgct gagactggga 2100
 aacctgcctc cattcttcag aggcagcgag gtgccctttc ctagaccttg tcggaccaag 2160
 cctgcctgca caagcaaggc ctggactccc agaaaactcg tggggagagc cgtgcggaga 2220

 aagggatctc cactctggga ttgtccacc acaacaggca cacaccacgg atgcctgtgg 2280
 gagatcccat ctgtgacct gctggcccat cctagaaccg cctctatcac cctgcctacc 2340
 acaagcctga agggctccag aaccagctgc tgccctagat ctcaccccag actgcctagg 2400
 accaaatggc cctgcagtg tctgtgcac agcctgggaa caaccggaac actcgtttgg 2460
 gaaaggggcg tctgcagat gagatccctc gaagccatt gtccactgca gaccttccat 2520
 ctgcaccact gcaggaccca gcctagctct tgtcctcctg cctggattct gtaccaagga 2580
 cagtggagcg gagccgtcgt gggacttaga cctgtggctc accatctgcc tagacctatc 2640

 cagggcctgc actgtccaca ggcacctcat caacctgctc tgagctgggg aaaatggccc 2700
 gtgggaatga caggccctgc cagatgttgc agatggccca gacggtgcca gaagaaggtt 2760
 ccatcagcct ctccatgggg cctcgtgctc aaaaagaacc ggaaacagat gctgaaccag 2820
 aagtgtctgg ccccttttag agagagcacc ctgggcaatt tctggatgaa gctgctccag 2880
 ctgcctgtcg tgatcaacct gaagagactg cagaagtcca acctgcacct gtgctactac 2940
 cacagccaga gcaacagaaa caagagccgc cagatggaat ccctgggcat gaagttgcag 3000
 tcccagaaat cccagacca ctgtgccctg cggaagatcg agtgggccac aaagttgtct 3060

 ctcggcggaa aagccggacc acaggctcaa gagaaggcca cctctcgat tctgaacctg 3120
 caagtgtca agaagatcct gcggagcttt atgaagctgt accactctct ggtcatgtgc 3180
 ctgcggtgta ggaccaagct ggaaaaggct ctgagcgccc tgttcactcg gccccagcac 3240
 agctacaagc ccctgttctt tcacggcgac ctgtgcgagt ggggaggcca ggctcataga 3300

cagcggaaact ggctgaaaaa ctggaagcgg ttcaagctta aaaagaagta catccagaag 3360
aagaagcaga agtctaaca gatcatctgc aagggccacc gcatcaccat catctgtatc 3420
aagaatatgt tctgcagcg caagggttc ctgaacctga gccacgtgga aaagttctgt 3480

agaggcggcc ctacgccag cgatagatgc tgttcttgta gcccagcgg cttcagtgcc 3540
ggcagaggaa gatgtctgt tcaaggctgt ctgaggcccc acagagttca actgctgaga 3600
agatggggcc ctggctctcc tgctggacag aggtgtctta agggctttca gctgctccgt 3660
tggtggggac caggatctcc tgctcctgag cctagaaagg gccatttcc accacctgat 3720
cctccatggc ctgtgaccgc tgtgacagt atggttgat ctgtgcctag tgctcagtct 3780
gtggacgccc tggaatctcc tggacctctg gctctgaag gacctagcag ccctagaaac 3840
ctgctttgga gagagatgag catctttctg cccggcatct tcaccgcaa gaaaagcccc 3900

accagctttt gctgcaatat cctgaacagc ctgccaagct ctatggaaat cgccgtgctg 3960
caaggaggaca gaaaaagat gaccagaag ggccaagcct tcggctccct gtgtcagctt 4020
gtgtccgctg acttctctgc cctcaagtg acccggtgc ggagcctgaa tcattctgtg 4080
atcacctaca caccacat ctgcagacac accctgtga ccctgacac cagatggatc 4140
tttagcaatc agctgcagac agtccagatg ctctgtctgc ctccactgaa gcaggcgag 4200
agaatcattt ggccctcgg cggtttcag atccccaact tcttttgag cctcgcatc 4260
ggacacactg gcgctggtg gcatactgga aggcggagaa gagaatgggg cggcagcacc 4320

gigtctagaa gccctctgtg gatcagctcc atgatctacc tgagaggcat ggccttcgcc 4380
agcgacagca gcatcagaac caccagagtg tcttggtgca gaagatgcgg cgccaaaagc 4440
gctgccgcca gctctattga agctctgacc gctctgttta cctgccggac cgccagcatc 4500
agcgtgaaca tcagcaccct gatgtccatc ctggaagcac ttaagaagaa acccagagac 4560
atctgccga tcagctgccg gtgtagacgc gactacagag tgactatggg ctaccctac 4620
gatgtccctg actatgcgtc c 4641

<210> 1195

<211> 5250

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 1C

<400> 1195

atgcatcgac ggcgctcacg gagttgccgg gaagacaaa agcctgtgat ggacgatcag 60

cgggacctta ttictaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
 gagtccaagt gtcttagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
 ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
 cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
 ccaaagcccc tctccaaaat gaggatggcg acaccgctcc ttatgcaagc ccttcccatg 360

 ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
 catgtcatgc atttgcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480
 agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaagggtg 540
 tttagagact ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
 aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
 ggcgtcacaa agcaagacct gggaccctg ccgatgagca ccagacggga aatgccttct 720
 caggccacac ctctccacc tggaccttgg agagccgctc tgggcaaaga agtgaagcgg 780

 agccagagca agctgcggct gagaacaca agccccaccg agatccaatt gaccatgaac 840
 gacagcaagc acaagctgga aagccccgt ctgaaacagg tgtccctgc ctctccacct 900
 acacagcagc ctacagacc ccaggatagc agacaggtgc tggccgcttc ttctcctgga 960
 catectcttg gccctggcga ctgccctaga acaatggctg gaccttctgc ctctctgcac 1020
 ccagcatctg gcagagccag cagaaagacc tggcagagaa ggctgagagc ctgtagagct 1080
 ggtggacctg ctggatgggc tagacaggcc atgacactga aggccttggt caagacctgg 1140
 acacagttca gaaactacc cagagtcgga gccggaacag gcggaggacc tgcttgtgtt 1200

 cctgtggcgg aagcttctac tggcgcttgg acagctgaag gcgctgccgg aacaagatgc 1260
 agagcttcta gagccccctg cagacagctg cctgccagct ctctaccaa gtgcgagatc 1320
 tgcgtgaaga gaaggcggcg gaaaaagcgg agcagccagt ctagatctcc cgtgcctaag 1380
 aaacgcgagc ggatgatgct gcctgtgcgg gccagaacag ctagatctgc tctgccacaa 1440
 ggcagagccc ctctggaagg aatgcttctg cctagagcac tgccagcct gctgagcaga 1500
 atgccagcca gaagagagag ccggttttgg ctggcactgc aggtcttggg actcagacct 1560
 cctcatctgc ctagctgtca ccctctgcct caactgcttg gacctctcc acctcatcag 1620

 gcccttttcg acaagaaagg cttcgtgatc ctgagcaagg gcaagaagcg ccgaaagaa 1680
 atccggcgga tgaccagacg gaccatgacc accacaaaa tgatgatgat gcggcggacc 1740
 aagcggcgga ggcgaaaacg tagaagaatg accatgatga cccgcagaac cctgctgacc 1800
 aagaaaaact gtctgacccc tagaaccagc gccgccacaa aagctctgcc cagacagaca 1860
 atcagccagc ggaggcctat ccagacacct cctggaacaa gcctggccat ctggggcaga 1920

ctgcctctca gaccacagag aggacctcgg cctctgcata gatggctgca gcagacaaca	1980
ggctgctccc agagaagaat cgccaagaag cggatcaagc tgaggcggaa cacactggcc	2040
atccggttta tctctgcccc tcagcctagc agcagcacccg ttacagctgc tcctagcggc	2100
cagtacttca gcagcttctt ctacaccagc gaccggacca agtgtgaaat ctgtgtcaag	2160
aacaccgcca tcttggtat caccctgac acccctcagg accctcacct ggaccctgtg	2220
tgtcacccac atagaaggcc tggctggaag ggccaccaca gagtgggtgt tagccaccat	2280
ccaagcggct ccaccaagag ccattggcag cagagagaaa gaggcggagg ccgcagagaa	2340
aaaaagggt gcagagagat gccagcagc tggcttagct ctggcagaac cgccgacaaa	2400
aagaacgtgc ggagcagaac cagactgacc ctgacaggca caagaagcag cggcacaaga	2460
gcctctccaa gcgccgtgtg tctgtgctgt tggacatgcc cctccagaag cttccctgcc	2520
gcctctccat ctggactgag agcacctgtt ggagcccagg ctctctctga agtgacactg	2580
agagccagct gtgcctctag cgctctaaa gcctgtgctg gactttggcc ttggggagcc	2640
caagtgcgga acaaagtgcg gcagaacttc aagcgggaacc tggccaaaaa gaccctgact	2700
aacgccctgc ggagtatgcc caagagcaga aaccaggtgc tgttcagacg gaatctgacc	2760
ccaagccagc tgagaactct ggccctcct tacatgtgc tgccccagtc tctgtctcag	2820
agcctgtcca gaaagcagat cccagccaa tcaatgtcgc tgaccgcctt cttctgtctc	2880
gacatcatcc tgagaagcct gctgtactcc cggatgtgcc tggcagat ccctacacac	2940
acctgggagc ccgactactt cgtgtccctg cctatgatgt tcagctgggc cactcagagc	3000
tttccagtgg gagccgtgtt cctgaccaga cctgccattc cttgtctcag ctgtaccagc	3060
cacagcaacc ctiggagcca gtccttcaag aagaagaagc cctgacatt cagccccagc	3120
gtgccaatgt ctctggcctg tagcatcacc gtgtccttcg tgggccagat cagcacactg	3180
gtgtcggacg tgtcctccat ctctcactgg cgcaagcgca agagagagaa gcggtcccag	3240
aagtcccgcg agaaccatct gcagctgaag tctgcagac ggaagatcag caactggtcc	3300
aagctgagat ccccgctggat cttctaccct cggtgaaaa ccttcggcgt gccactgggc	3360
tctatcctgt gtctggcagg ctccctgagc acgatgatga tcattagcac caccagacaa	3420
gagtgtggca gacgggcctc cgtgccttgt agacctatga tcggcagcgc tagaccgga	3480
ccttggcgga catctgctat gccatctgcc atgggagtcg cctgcctac cagctgtgaa	3540
agcgggaagat ctctctctgc caccggcgga agaatgcctg gatctcagtc tatcatgatg	3600
agctggatgc ctccactggc tccctgtgcc gcttgcctt gttctctgc tcctacactg	3660

tgccctgctc atcctgcaag agcccctaca gccgtgcctg cctttacacc tctgtctgct 3720

caccctgtgc cagtgctgtc tggatgtcac ctggccgtgc gcacctctat gctgacactg 3780

ctgccatga gacacctca cagaagccca cctacaagct gccctccact getggaagct 3840

ttcccactgc caagggccag cctgagagct accgtgccta gacacagctc tgtgctggcc 3900

actggactgc atctgcatcg gcagattagc ctgcctctga ggggttcct gctgcatcaa 3960

cctctgcctg gacaacacct gtggtgtcc cacagactga ggctgagact gccaagaaca 4020

ggcgagaaga acgacctca gctgttcgtg atgagcgaca ccacataca gatctactgg 4080

acagtgatec tgttgaaccc ctgcggcaac ctgcacctga aaaccacatc tctgcggaga 4140

gccagacctc cctcctgcag cacatgcaga atgtggtggc tgaagctggc cccactgcaa 4200

gtgaccacaa cactgaagct gatcctggtc atgctggaaa tcgtgaccga agaggccaag 4260

aatccatga agagatcccg gcggagcaag atcgaggcct ctctatcgg ctccatcatg 4320

aagaagaaag acagcacat cttcatcaac cagcagctca agtggacccc tcacatcctg 4380

aagtctgcca gcgtgtccaa gaagagactg cccaagctga acggcatctg ggaagtgatg 4440

ccccggacac tggaaggtg catcagcgtg aaggaccacc ggacaagcca gaaccacagc 4500

aagtgcata ccgagtgtgt gcggacagcc ctgaaccaga gaaaggtggt caagaacccc 4560

agccagccag tgccactgag aaacgacggc atcaccaacg gcaacgactc caccagatcc 4620

tgctccatca gcctgaagaa aagcctggaa aagatgcccc tgatgaacgc caagaaaatg 4680

gaagatatga tctgggagag caacatgggc ggcaaccggt ccatctgcct gacaagactg 4740

ccctgcaaag tgaccgagtc cagccaaaga ccacctcgga gcattctgtc cctggcctct 4800

agagccggac agtttccgt ttggcggaga accagcagag gcatgtccct gcagtggaag 4860

tccggcaatg cctgcacacc tctgaggtgc cctagcagaa gccctgccac atttctgacc 4920

gcactgaacg gctggcacag atctggactt agggctcagc aacctagcct gccaggacct 4980

tgtgctagcc tgctgtctac actgagccag cctccaccac aggtctcaag ccaagtttgg 5040

acagccgcca cactgagatg tcccgtgtt cctgcagctg cttgccctcc tategtgttc 5100

tttctggccc catacttccc cacaccactg agcatcagca gaccacctc tcgggccaga 5160

cagtcttgtt gtctccccgg actgacacac cctgtcacc agcctcttgg ctctatgggc 5220

taccctacg atgtccctga ctatgcgtcc 5250

<210> 1196

<211> 5232

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV - and HA-extended poly-FSP

polypeptide 2C

<400> 1196

atgcatcgac ggcgctcacg gagttgccgg gaagaccaa agcctgtgat ggacgatcag	60
cgggacctta tttctaaca tgaacaactt ccgatgcttg gtaggcggcc tggagcacca	120
gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg	180
ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag	240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc	300
ccaaagcccc tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg	360
ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat	420
catgtcatgc atttgcctca aaacgtgat ccccttaaag tttaccctcc tctgaagggg	480
agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg	540
tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa	600
aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggaccgag tagtgggctg	660
ggcgtcacia agcaagacct gggacccgtg ccgatgcggc agatcaacag acggaagctg	720
cagagaaaga agcgccggaa gaagagagag gaccactgcg gactgcgggc cagaaaccgg	780
aacatgaaga aaacatgag ccacctgatc gcccatcagg cctgaagat gtctggcctg	840
agactgtttc accccagact gctgacacgg aagaagcctg gcaagaacct tcggagaaag	900
acctggaaga tgcggaagaa gtaccccag aagcctagcc agaagaacca cctgtacggc	960
aagggcctga cacacctgt gcctctgaag agaaccctgc agaacaagcg gaacaagaac	1020
atcaagcgcg tgaaccagaa gaagggaac atcaagagaa agagcatcct gctgcacctc	1080
atcgtgctga acagccccga gagcaacctg caggctcctc ctcaagttcc agcactggt	1140
cctcaggctt ggtggcctgc tagaagaggc cctctgacaa gcgctccatc tgctcagcag	1200
agcctgacct tctgcctag cagatttct tggggccctc ctccactgca ctggaactct	1260
gcctacctgg gcagaacct gctcgtgacc tgcctcctgt accacagatg gatcgtgacc	1320
agcatgtgcc agagccagag atggctgacc agcaccacct ctagaagcag cgccctgatg	1380
tggaccacgt ggtctagcgt gacaagcctg gaatggacag cccaagagag gggctgtagc	1440
agctggctga tgaagcagac ctggatgaag tcttggagcc tgcgggacct cagctacaga	1500
tccatcctgg aatacgtgtc caccagagtg ctgtggatgc ccacatctac agtgggagcc	1560
ctgagagcca cagctcctgc aacagctgct ccacaggctc agaccctca ttggagagcc	1620

gccacaacaa gcagcatgag cagcagccct agagccgagc ctacaagctc tagctcttgg 1680

gccacctgtt ggcccagatg ttgcagctcc agctgttact ggtccctgtc ctcttggcct 1740

cctgctggtg ctgccgaggc cacaataacc aggaccagaa gcagagagtc ccagcggggc 1800

agaatgctga ctiggagaag cagcctgttg ctgcagggca ccagatgttt tacaggcgtg 1860

cggacctcca gcagacaccc ttcttggcct tggaccagat gcctgagaat gcggcctcct 1920

agaagcaaca gccggaaaaa gctgctcgag gacatgaagc aaaatggctt cacccggtac 1980

aagaaacggg gcgtgatagc ctggcggaga gccactttcc tgctggccct ttgggagtgc 2040

agtctgcccc aagctagact gtgcctgac gtgtctagga ccctgctgct ggtccagagc 2100

agatgcagcc tgatggaaca gatccctcac ctgaagtcct ggtggtgtac aagaggcggc 2160

ggaaagcggg agaaaaagat gtgcaagggt tccggcggct gcaccgcctg tgttgaaaga 2220

tgtccttggg agggcatctg ctggaagtgg cctgtgacag tggccgctct gatcctgatt 2280

cagcacggcg gcatcttcac ctcccggttc tgggtcgaga agctgtcctg gaacatctgc 2340

aagaatctgt cctgtacct ggacaagttc gtgcagcggc tgctgtacgt gtacatcatc 2400

gagacaaacg tttctgctt gaacctgttc cactgtccag tgaatcagat cttcatgatg 2460

gccttctacc tgaagtacac cgagaaggcc tgggtcatgg aactggaatg gtcattcag 2520

cagcagtgt accagttgt gctggctcat atgtacggct tcagcaccta cggcacccag 2580

aaaggcgagt gcgtgtgtct gcagtgtctg agcggcagct ccctgttcat cctgaagcag 2640

ccactggacc tgaagatcag caagaccttc atgacagat cccacctgga tttagcccc 2700

tattggatga agaaagtga ggccctctca cagatcatgc agcggatgag cgccgtgaac 2760

ttcgagacaa tcaggcgga gtggcagatc cggcacgtgc tgaagaacct gcctctggaa 2820

aacacacaga tccccaggac aagccctctg tggaagatca caatggtgct gacatacccc 2880

aactgcgtgg tgcatgtgct gatgttctg ctgttcaagg ccgaccagag cgagtctagc 2940

ctgagcagcg gaatctacc tcttagcacc tgtagcctgc cttgccgggg cattagaatg 3000

tgcgccctgt ctaccctag cttctacatc agcagcaccg tgtgctttct gagcaagcac 3060

tgcatgaccg cctgcaccag agagaagatc atcaacccca ccatcagctg cccctttcag 3120

agccccacaa agagactggg ccacagagag ggcagcgaga gcgataatct gggcctgctg 3180

tactcctttc ctcttggct gcccatgaga tccttgggag aaccttggag agctggcttt 3240

cagtggggag agtccccttg gcaagtgatg gctagcctga ccggcaacag cgtgatcgtg 3300

cacaagatcg tgctggtgtt tctgaagtct ctgagcagct acaactgcga gcggcggatc 3360

tctggcatcc agaagagagc catcgagttc gccgtcctga agctgctgaa catggacctg	3420
gctagccctc agattatgca gagaaccagc gccgaccggt tccggatgaa gcggagaatg	3480
cagaacctgg ataacctggg cgtgccctgg ccattgcttc caggtgctgc tcctccacat	3540
agactgctgg gccctctag atggattctg tttcatgtgc ggaacatcgt gtacggcatc	3600
caagtgatgc tgtgccggcg gagaacagc agaaagcaga gtcaggtgca gctggccatt	3660
caggtcctgc tcgtggacaa gcacaagtac tttctgttcg gccctatcc tatcagcgag	3720
ggactgacca tgaccaccgg ccggaacatc aacagcaact cctgatgac caactgcctg	3780
ttcagcccca tcttctgtg ccaccacgcc atcatgcacc ggaagatgac aagcccacac	3840
ttcagactgt tctccagaa gatccacat cctcaggtgc caagtgtggt ggccctgtgc	3900
aagttcctgg ccaatggcct gtggttcaac ctgatctttc agaaaaaggg ccacatgatc	3960
tttagcccca agttcttctt gacctttagc cagcggaccc tggaatccgc cggactgttt	4020
ccatggctgc acaccagtg ccggaacaaa aagaccaagc tgtggttttc cctgatcaac	4080
atccaccacc gcaagaatcc tctgtgcct atgagaatga gcagaacacc tcctcggaga	4140
gtgtgcggat ctccacctct gcactgtgc caacctctga gaggcggcaa gaagagaagc	4200
aagttgcct tctggaagcc tcctagccag ggcatcagct cttgtctgat gacaggctgt	4260
tggggctcct gtggcagagc ttgttcttgc ggaagaggct gcggtacacc cagaggcgac	4320
tggaaaaagc acccacctcg cagagagctg agcctggaac catggattcc ttatctgcac	4380
cagcaaaaga ccagcggaa gcggatgaag accggcgcca ttcaagagaa gggcgctatc	4440
caagaaaaag gcgcaatgac caagcggatc tgcgtggtca atttcgaggc ctgcagagag	4500
atggaaagcc tgagcgcccc tgagaagatt accctgttcg aagcccacat ggcccgtgc	4560
acctcatca atgtgctgtg tgtccgggcc agcctgattg agaagctgat gaaagaaaag	4620
cgcaagatga agcgcaacca ggtggcatcc cctcaaatca tgcaacggct gttcatcaag	4680
ggctaccaga acaaccactt cacgttcac ctccaaaact ttgccttctt cagctccttc	4740
ggcaacaaca agtatatcaa cattctcacc cgggccttca tccacacacc tagaagccct	4800
ggctgttccg tgtacgcaa tatgtgctgg cggaagatgc agtccctgaa tcacccagc	4860
agactgacca actgtcacc cgcttggctg agccccatta gtgcttgcc taggctgctg	4920
ccctatcctt ttacgtgct ggcactggaa gtgaccttcc cactggcac agccatgcct	4980
cagatgcaat tgcaggcact ggctatgtgg gagaaaggct gggacaagca agagaagaaa	5040
tcccgaagc tgatgtctc ctgcctggaa aaaaaggcta cctggatgcg gagaaccct	5100
ggcacaagcc tgcagtgtta cctgaacaca caccctgca ccatgctgct gcctcaggga	5160
atcccatctc tgaacgcccc gtggatgttc ctgcggatcg gctacccta cgatgtcct	5220

gactatgcgt cc 5232

<210> 1197

<211> 5247

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV - and HA-extended poly-FSP
polypeptide 3C

<400> 1197

atgcatcgac ggcgctcacg gagttgccgg gaagaccaa agcctgtgat ggacgatcag 60

cgggacctta ttctaacaa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120

gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180

ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300

ccaaagcccg tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360

ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420

catgtcatgc atttgcttca aaacgtgat cccttaaag tttaccctcc tctgaagggg 480

agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540

tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600

aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660

ggcgtcacia agcaagacct gggacccgtg ccgatgccta ttcctccaca cctgagacac 720

cctctgctgc tgaagaacia gaagcggaga aagctgcggc ccaagagcag aaagaagggc 780

cacaccaaga accggcggaa ggccaagaga aagccccaga tcagaaacag ccgcagagcc 840

acacctacca gcaagggcag cctgagaaga aagtacctga gagtgggagc cgccgctgct 900

agctgtcaat ctctccatc tcttagagag acaacccta gcagcgacgc caccagaaga 960

accagacctc tcgccgtca gagcaagaaa accatgacag ccgccggact gaccctagc 1020

cagaagaaag atcttgccgg caagctgaag aaacaggtgt ccgtgtacag cggcaacctg 1080

ctgagcttct ctcggaagg catgaagtct agcgtgcgcc tgaagaactg caccaacctg 1140

agcgtgcccc tgatgtgac catctgatc tggaagcggg tgttcacct gctgctgtcc 1200

gacaagaaat ctatccctca cgtgccaag gccaccgccg ctcatctgtg gacagtgaag 1260

ctgcagagcc ggcggaacag acggtacaga aagatctatg gcgagctgaa gatgtccctg 1320

caggccagca atggcatgga agcctgtggc acacaccca cacctagact gtccgtgtcc 1380

gtgatcacca tgaagctgtg ggagaagcac ttcaagggcc tgaactggaa cctggctgtg 1440
 tggattctga acctgaagat gatgctcaag aagaagtatc tggccagcg cgagtgggag 1500
 aaacggaagc agattcttgg cggcggaggc aagtacaaag agtacttcct gaagagaatc 1560
 ctcatccgca aggccatgac agtgcctggc ggcgataaga aaggcctggg cagattcatg 1620
 agatgcgtgc agagcgagac aaagccgtc agtctgcagc tgcctctggg cagaatggac 1680
 ctggatggaa tgctgaccgt gatcgccag ggactcgtgg gcatgacacc tagagatctg 1740

ggaacagtgg ctggcgccac cgcacagatt cagaggccta ttcaggtgca gacaggcggc 1800
 agactgagag gccctagaag aaagtgctg atggtgctgt ggctccccgc caatcagagc 1860
 ctgcagaaaa gccagggtgt ccagtgggtg ctgagaaccg agctgccct gacctttagc 1920
 accctgctgt gggacagcag acacgacctg cctagaatgc tgcccatcag cagccctctg 1980
 cacagacccc agatgccttt ctggacctgc acctttctg ccaccacatg gggcacatgg 2040
 gagacacctt ctacatgggg ctggcgacc ttgcccagac agccttctag acccaccggc 2100
 agaacccta ccaccagact gatggctcca gtgggcagcg tgatgagctg tagcctgctg 2160

acacagccat ctccagccag cgctgtaca atgcctcac tgcgcatcc tcagtgggccc 2220
 cctattctg ctggactttc tccaggcgct tgcagacctg cctglacctg catcagcatg 2280
 accacaatca gcagggccac ctggcgaga aacctgcaga gaaacctgaa agtgctgcgg 2340
 ctgagaatcc ccagcctgag gaagtacaga cagcagaaca cccggtccac caacctcag 2400
 aagaacccat ctctgaagaa gcagagccag aggcggggca agctgtctct gaccacactg 2460
 agcttctgct tgatcgagga actgctgaaa aagagcagcc agctgcggag aagctggcgg 2520
 aacgtgtcca gaatcagcaa catccggaag ctgatttga ccaagcagcg gagcttctg 2580

tctctgttcc ccaagctgag agccaccgag cagatgacca atgtgggctg tagactggat 2640
 ttaccacca gaagcagctc cggcgacaga gtgttcttgg tcaagatcca gagcagccca 2700
 ttcctggcca gatcctggaa taccatgcag tggaacaaca agaaaatggc catgactgtg 2760
 atcgtggcg cccaccactg tcagtacaag ctgacctaca ccaaagtgtg gaagatgaat 2820
 tggaagaaaa tgatgatcgg cagccagcac ctctgttct cccactgga tagcttcca 2880
 ctccagctgc tgctgaccc acacggcaag agatgcaacc cctgttgtc gctgacatgg 2940
 atgagccacc tgaatcgga gctgcacctc accaggtcct gctgatcga cctgaccatg 3000

atgatgagcc agaaactgtg gaagaatcag cggaagcgca tccctctgcc ttctcaaga 3060
 cagcatctgc tgcctcagta tctctgcac cctctccac cttgtctgct gcttctccac 3120
 catagacacc acctggcatt cctcgagatg gctgttagct ctcagcacac ccacagcatc 3180
 aagatctgga tcagcttcag ccacagagaca atgagcctgt ccaacatcct gatgaagttc 3240

cggctgacca ccaccacaag cagccccaga agaagccctg ctctgcgagc tagaggcggc	3300
acaacaatcg gcgaagtgac cagcagcctg ttcttttagcc actgcctgtg cgtggccctt	3360
agatgtccta gatctgccgt ggacatcagc cccggaccta catctccttc tctggcctct	3420
tgtgcctctg tggccattgg aaagctggca ctgcttggcg cctctgctcc ttgtggtgct	3480
gctggcgcta gagaggccgg aagatttgct gtgctgggca ccatggtcat gaagaacatg	3540
gaacacagac tgaccatgga cagcgccctg agcctgacaa agagagaggg ccctgaaaca	3600
ggccccgtgt actacgtgtg caaccggatg aatgtgtcca gcgtgctgaa gcctttcctg	3660
ttcaccgtgc ctatcgagga catgagagag tgcaccctgg gacgcaacag aatgaatgtc	3720
tcttcctgtc tgaaacctg tctgatcccc gtgccaatct gcaagaagaa actgctgctc	3780
aagctgctga ggggcgcctc cagctctacc agcagagata gcagaagctt tttcaccagc	3840
gctcacccca gcagaccctg caggatgaga ctgtaccaga tgctgcagaa gcagtgtgctc	3900
tacaacctcg tgatcaagca ccctctgata ttccggatca acctgcggag acagggcaag	3960
accaaagacg gcgttgtgca gagcctgggc ttcttgaacc agcagatcat cctccagaaa	4020
gagtttctta tctgcctgct gatgttcata aagcgggtgga agccagccgc caccaagaag	4080
ggcaagaaca gcccctgctc ccagaaaaaa ctgcgggtgc agaaccaggg ccatctgctg	4140
atgattctgc tgcacaacag agggccacct ctgcatacca gattcgagaa aaagcggccc	4200
gagtggctga gcagaaaatc cggcgtgatg aagtgtggg atctgtgccc tgccttcagc	4260
ggcaggattc tgcaccagcc agaaatggcc gccatgagac tgatgcccaa gttcctgaac	4320
tccaccaaca gctggtggac agtgcacaag aagagaggcc tgttcacca gatgaagtgt	4380
ctgaccgccg tggactgtct gcaggccttc tgggatatga gcgagaagaa acgcaagctg	4440
cctatgattc gcaaaatcca gaagcggcgg agaaccgcca accggaacat cgagatcacc	4500
cctcagagaa gcaaagccca cctgaagaaa acctccgcca agggcgccaa gaaaatcacc	4560
ttcctgtgcc tgagagtcag atgcggaggc tggctgtgtg gctggacacc aagaggatgg	4620
ctgaagaagt ccaccaagtc cagactgtgc ttctttctacc tgetgtacta cctgtttttc	4680
ctgaccgtgt gcggcttcac ccctccacca cttattctgt ggcctcaggc agcccctggc	4740
gagaagctga agcactgttt taaagcctgg ggcgtcgacc ctctggcag cgtttggatt	4800
ctgcctgtct tctgattca cctgagaaaag gtggacaccc accacctcca ggtggtcacc	4860
aaaacagtga ccgccacaac agccgacggc cagaggatga gaaggctgaa gtgcaaggcc	4920
tgccggctga gatgggctag acctgaacct gcagctcagg cccctcctaa gagccacttt	4980
ccacctcacc ctagcgcccc ctccagaacc agctctctgc aattgagaac ctacatggaa	5040

atgcactacg gccatcaggc cccacagggtg gcaatgctgc ctaaactgct gtgtcggcag 5100

atgtcctcca ctctgtctac cctgcagcag agacatcctc agggcccatg tcctcctcca 5160

gtgacacctc tgagagtga gtctgtgtg ctgctcggag tgcctcaaac agctggctac 5220

ccctacgatg tcctgacta tgcgtcc 5247

<210> 1198

<211> 5250

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV - and HA-extended poly-FSP
polypeptide 4C

<400> 1198

atgcatcgac ggcgctcacg gagttgccgg gaagacaaa agcctgtgat ggacgatcag 60

cgggacctta ttctaacaa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120

gagtccaagt gttctagggg cgccctgtac actggtttct ccctcctcgt gacactgttg 180

ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300

ccaaagcccg tctccaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360

ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420

catgtcatgc atttcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480

agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaagggtg 540

tttgagagct ggatgcacca ttggtcctg ttcgagatgt cccggcattc tctggagcaa 600

aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggaccgag tagtgggctg 660

ggcgtcaca agcaagacct gggacccgtg ccgatggaca gcaagaagat gaccagaag 720

aaccgcaaga cccggaaggc cgccagagag aagcacagaa agaccgacaa cctggacctg 780

cagcaccagc gcagacgcaa aaagaagaag gacaaggctc agatccggaa tccgagccct 840

aaggccaata gcaccgagtg tcaggcgag cacagcagag agcagaacct gctgaacctg 900

gtgcaattga accctcacag cctcaccac cggaaggacg aggaagatca ccagaagaga 960

caccaccacc acaatcaaaa gaagatgtcc gtcaacgagg gcaacaacca ctggcctaga 1020

gtggaaatgc ctaccggctg gctgctcgtg ggctacaaca ccagaaacac agcccagaat 1080

cctcggctgc agcagacct gaaacactgg cagcagtga ccagagccag atggtgtcaa 1140

gagccctgtc agaccctgac cttcttccac ttctttctt ttttcaaac ggtgtccctg 1200

tgctgccccg gctgggtctaa aggacaacct cctccacctg gcctgaagcc ttctagcctg	1260
gctttctcagg tggccagaac cacaggcgtg taccagcacg tgtggctgat ctgcttcgtg	1320
tttttcgtgt gcgtggaaac cggcttctgt cacgtggccc aagtgggact cgagagactc	1380
gttagcctga gcggcatcac cgacgtgaac cattggggccc agcctaagcc atctcctagc	1440
aaaggcaccg gcatgaacag acccatcggc ctgagagtgt gcaaaggcgt gtgggctaga	1500
ctgtggctga agaactggaa gcggttcaag ctcaaaaaga aatacacagg catggaaatc	1560
ctgctgtgga ttctgtgaa gatggaaatt cagatcttca agatttgcct gggcgagatg	1620
cagctgtgcc tcaagaaga agtcaacgcc tgcagcaacg ccaagaaaat gcccttccag	1680
tgccggtgca gacgcgagta cagagtgacc atgattcaga agaagaaaca gaagtccccg	1740
ctgttcttcc acggcgacct gtgcagacct tctccttgcc tgtcttggag cagcaggatc	1800
gtggctcctg gacacgccct gagctgtcgg actcgtagaa gatggtcag caagatggcc	1860
aagaagtccc agcagcctct gtgtagaggc ggcccttctg ccagcgatag atgctgtagc	1920
tgtagcccca gcggctttag cgctggaaga ggcagatgtc ctgtgcaggg atgtctgagg	1980
ccacacagag ttacgtgtct gagaagatgg ggccctggat ctctgtctgg ccagagactg	2040
tctaagggtt tccaactgct gcgttgggtg ggaccaggat ctccagctcc tgagcctaga	2100
aagggcccat ttccaccacc tgatcctcca tggcctgtga ccgctgtgac agtgatggct	2160
ggctctgtgc ctacgcgtca gtctgtggat gctctggaat cccctggacc tctggctctc	2220
gaaggcccta gcagccctag aaacctgtct tggcgggaaa tgagcatctt cctgcctggc	2280
atcttcaacc tgcacctgtg ctactaccac agccagagca accggaacaa gagccggcag	2340
atggaatccc tgggcatgaa gctgcagatc acacacccat tcgccagcca gccactgggc	2400
caagagatgc ccaacaacac ccagatcaga ctgctgaagc ccggccaggc ctttggcagc	2460
ttttcgcggc atttttcagc ccctcagcag gcccctctga gactgtggtc ttggtgcggc	2520
acaagccaga cctacttcgg ctctatcgaa gccctgacag cctgtttcac ctgtagaacc	2580
gccagcatca gcgtgaacat cagcaccctg atgagcatcc tggaagccat cctggccatg	2640
acactgacct tgaatggcag ccctctgtgg gactgcagca caacaacagg cacacaccac	2700
ggctgcctgt gggagatccc ttctgttacc ctgctggcta ccgcaaaaa gagccctacc	2760
agcttctgct gtcagcggcc tcctctgcag ccagtggaag agaagaagaa cggccggatc	2820
agcagcgtgc cacccttctc acctcttgct ctgggcctta gaatgcagct ctgcacccag	2880
ctggccccgt tcttcctat tacacctct gtgtggcaca tcctgggacc tcagagacac	2940
acctctctgc tgacctctga caccagatgg atcttctcca accagctgca gaccgtgcag	3000

atgctgtgtc tgcctccact gaagcagggc gagagaatca tctggcctct cggcggcttt 3060

cagatcccca acttcttttg gagcctcggc atcggacaca ctggcgcctg gtggcatact 3120

ggaaggcgga gaagagaatg gggcggcagc accgtgtcta gaagcccact gtggatcagc 3180

tccatgatct acctgagagg catggccttc gcctccgaca gcagcatcag aaccaccaga 3240

gtgtcctggt gtcgagatg tggcgccaaa agcgccgcag ccagcagcga caagaagaag 3300

aaaagcaccg aaaagaccaa gaacaagatc atctgcaagg gccacagaat caccaggtg 3360

gtgtgagac tgggcaacct gcctccattc ttcagaggca gcgagggtgc ctttcctaga 3420

ccttgccgga ccaagtgcc gaagaaggtt ccaagcgct ctccttgggg actgcacca 3480

agaacagcct ccatcacact gcctaccacc agcctgaagg gcagcagaac aagctgctgc 3540

cccagatctc accccagact gcccagaaca aagtggcctc tgcagtgcct gctgcacagc 3600

ctgggaacaa ctggaacact cgtgtgggaa aggggcgtgc tgcagatgag aagtctggaa 3660

gctcactgcc ctctgcagac attccacctc caccactgca gaaccagcc tagctcttgt 3720

cctccagcct ggattctgta ccaaggacag tggagcggag ccgtcgtggg acttagacct 3780

gtggctcacc atctgccaag acctatccag gggctgcact gtectcaggc tectcatcaa 3840

ccagctctgt cctggggaaa gtggcccggt ggaatgacag gaccgccag atgttgccgg 3900

tggcctagaa gaatgtgtag ctctctggcc ctgccaaccg gcctgacatc tctgatcctg 3960

cctagcagtg atctggccgt gctgatctct agctccacca gccactttct gatgcggagc 4020

ccagtgtgc caagcagcag actgacatgt gcctctccac agctgcctcg gatgtggaca 4080

tggcttagct ggcgtaaaaga gtggggagga caggcccaca gacagcggaa ctgtagagtg 4140

aacgccgttg aggaactgca cagcaggcgg atgtctgtgc ggatcgtgaa gaattgggtg 4200

tcctgtctgt acgtgcggct gagtgcagtg ggactgtcta cttggagcgc cctggattcc 4260

ctgatcctgt ccttccagag agtgaaaacc agccggatac tgaacctcca ggtgctgaag 4320

aagatcctgc ggagctttat gaagctgtac cactctctcg tgatgtgcct gcggctgcgg 4380

accaagctgg aaaaagctct gagcgtcttg tttatctggc ccagcacag ctacaaaggc 4440

caggcattcg gaagcctgtg ccagctgggt tctgccgatt tcagcgcgcc tcaagtgacc 4500

agactgcgga gcctgaacca tctgtgatt cgggtggatct ttagcaatca gctgacagtc 4560

caaatgtctt gcctgccgat catcaagaaa atgaagaaac ggatcatggt gcacgtcttg 4620

aagaagaatc ggaagcagat tatctgtatc aagaatatgt tcctgcagcg gaagggattc 4680

ctgaacctga gccacgtgga aaagttcaga gagagcacc tgggcaattt ctggatgaag 4740

ctcctgcagc tgccaccagc ttgcacctct aaggcctgga caccagaaa gcttgtgggg 4800
agagccgtgc ggagaaaggg cgtcgtgatc aacctgaaga gactgcagaa attccgggct 4860
agcgtgtcct tctggactct gctgcctaca acaggcgtgc ggacaagagg ctctccactg 4920
agactgactc tgtggcctcc aagaagccag aaaagccagc accactgcgc cctgagaaag 4980
atcgagtggg ccacaaagct gtccctcggc ggcaaagcag gaccacaggc tcaagagaag 5040
gccaacatcc tgaacagcct gccttcctct atggaaatcg ccgtgctgca agaaatgctg 5100
aaccagaagt gtctggcccc ttctgagctt aagaagaacc tcctgctgcc aacctacaca 5160

ccccacatct gtcggcacac ccttaaaaag aagcccagag acatctgcag aatcagcggc 5220
taccctacg atgtccctga ctatgcgtcc 5250

<210> 1199
<211> 5250
<212> DNA
<213> Artificial Sequence
<220><223> Polynucleotide encoding the hINV- and HA-extended poly-FSP
polypeptide 1D
<400> 1199

atgcatgcag ggcgtcacg gagttgccgg gaagaccaa agcctgtgat ggacgatcag 60
cgggacctta ttcttaacaa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180

ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
ccaaagcccc tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360
ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
catgtcatgc atttgcttca aaacgtgat cccttaaag ttaccctcc tctgaagggg 480
agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540
tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600

aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
ggcgtcacia agcaagacct gggacccgtg ccgatggccg acaagaaaaa cgtgcggagc 720
gctagtcttc ctggacatcc tcttggtccc agaagaatga ccagacggac catgaccacc 780
accaaaatga tgatgatgcg gcggaccaag cggcggagaa gaaaaagacg ccgatgacc 840
atgatgacca gaagaacct gctgaccaag aaaacctgtc tgacccttag aaccagcgcc 900
gccacaaaag ctctgcccag acagacaatc agccagcgga ggcctatcca gacacctcct 960

ggaacaagcc tggccatctg gggcagaaga agcaagatcg aggcctctcc tatcggcagc 1020

atcacccctc tgagcatcag cagacctacc agcagagcca gacagagctg ttgcctgcct 1080

ggactgacac accctgctca tcagcctctg ggctctatgg ttggagctgg aacaggcgga 1140

ggacctgctt gtgtgcctgt ggccgaagct tctacaggcg cttggacagc tgaaggcgct 1200

gccggcacia gatgtagagc cagcagagcc ccttcagac agctgcctgc ttctagccct 1260

accaagtgcg agatctgcgt gaagagaaga aggcggcgca agcggagcag ccagtctaga 1320

tctcccgctg ctaagaaacg cgagcggatg atgctccctg tgcgggccag aacagctaga 1380

tctgctctgc cacaaggcag ggctcctctg gaaggaatgc ttctgcctag agcactgccc 1440

agcctgctga gcagaatgcc tgccagaaga gagagcagat tctggctggc cctgcaggcc 1500

cttggactca gacctctca tctgcctagc tgtcacctc tgcctcaact gcttggacct 1560

cctccacctc atcaggcccc tggcgagaaa aacgacctgc agctgttctg gatgagcgac 1620

accacctaca agatctactg gaccgtgatc ctgctgaacc cctgcggcaa cctgcacctg 1680

aaaaccacca gcctgaacgc caagaaaatg gaagatatga tctgggagag caaccagcag 1740

ctgaagtgga cccctcacat cctgaagtcc gcctctatcg ccaagaagcg gatcaagctg 1800

cggcggaaca gcaccagacg ggaaatgcct tctcaggcca caccttctcc acctggacct 1860

tggagagccg ctctgggcaa agaagtgaag cgagaccaga gcaagctgag actgagaaac 1920

acaagcccct tcgacaaaaa gggctttgtg atcctgagca acatgggcgg caaccgtct 1980

atctgcctga ccatcgtgtt ctttctggcc ctttacttcc ccatgcctag cagctggtct 2040

agcagcgga gaaccagact gcctctgagg ccacagagag gccttagacc tctgcataga 2100

tggctgcagc agaccaccgg ctgctctcag agaagaggcg actgccaag aacctaggcc 2160

ggaccatctg cttctctgca ccctgcatct ggacagaccc ccagaaagac ctggcagaga 2220

aggctgagag cctgtagagc aggcggacct gctggatggg ctagacaggc cagaaaacgc 2280

aagagagaga agcgggtccc gaagtccaga cagaaccatc tgcagctgaa aagctgcaga 2340

cgaagatca gcaactggtc taagctgcgg agccccgga tcttcagagc caaaaagagc 2400

atgaagagat cccagcggcc tcctcggagc atcctgagcc tgttcaagaa gaagaagccc 2460

ctgacattca gccccagcgt gtccaagaag aggctgccta agctgaaggg caagaaacgc 2520

cggaaagaaa tccagcggaa ggtgttcaag aacccagcc agcctgtgcc actgagaaat 2580

gacggcatca ccaacggcaa cgacagcacc cggctcttga gcatcagcct gaagaaaagc 2640

ctggaaaaga tgcccctgat gcggagcctg ctgtactcca gaatgtgcct ggtgcagatc 2700

cccacacaca cctgggagcc cgactacttt gtgtccctgc ctatgatgtt cagctgggcc 2760
 acacagagct ttccagtggg cgccgtgttt ctgaccagac ctgccattcc ttgctgtagc 2820
 tgtaccagcc actccaatcc ttggagccag tccacactgg ccatccggtt tatctctgcc 2880
 cctcagccaa gcagcagcac cgttacagct gtccttagcg gccagtatit tgccctgcgg 2940
 agtatgcccc agagccggaa ccaggtgctg tticggagaa atctgacccc aagccagctg 3000
 cggacactgg cccctccata tatgtctgtg cctcagcttc tgtcccagag cctgtctcgg 3060
 aagcagatcc catctcagtc catgtctgtg cggaccaggc tgacactgac aggcactaga 3120

 agctccggca ccagagcctc tccatctgcc gtgtgtctgt gctgctggac atgccccagc 3180
 agaagctttc ctgccgcctc tccaagcgga ctgagagcac ctgttgagc acaggtcct 3240
 ccagaagtga cactgagagc cagctgtgcc agtccgcca gcaaagcttg tgcaggactt 3300
 tggccttggg gagcccaagt gcggatgaag aagaaggaca gcaccatctt catctacccc 3360
 aggctgaaaa ccttcggcgt gccactgggc agcattctgt gtctggctgg aagcctgagc 3420
 acgatgatga tcattagcac caccagacaa gagtgcggca gacgggccag cgtgccctgt 3480
 agacctatga tcggaagcgc cagacctgga ccatggcgga caagtgtat gccttctgcc 3540

 atgggagtcg cctgcctac cagctgtgaa agcgggaagat ctctcctgc caccggcgga 3600
 agaatgccag gatctcagtc tatcatgatg agctggatgc ctccactggc tccctgcgt 3660
 gcttgcctt gtctcctgc tctacactg tgccctgctc acctgctag agcaccaaca 3720
 gccgtgcctg cctttacacc cctgtctgtc catcctgtgc cagtgtgtc tggatgtcac 3780
 ctggctgtgc ggacctccat gcttaccttg ctccaatga tgacctgaa ggccctggtc 3840
 aagacatgga ccagttcag aaactacccc agacggcacc ctacagaag cccaccaaca 3900
 agctgtcctc cactgtcga ggctttcca ctgccaagag ccagcctgag agctaccgtg 3960

 cctagacact ctacgtgtg ggccacagga ctgcatctgc ataggcagat tagcctgcct 4020
 ctgcggggct tctgtctga tcaaccactg ccaggacaac acctgtggct gtccacaga 4080
 ctgagactgc ggctgcctag aacaaccgag atccagctga ccatgaacga ctccaagcac 4140
 aagctggaaa gccccgtct gaaacaggtg tccccagcta gtctcctac acagcagcct 4200
 cagacacccc aggattctag acaggtgtg gccgtgccta tgagcctggc ctgtagcatc 4260
 accgtgtcct tcgtgggcca gatctctacc ctggtgtggt acgtgtcctc catcagccac 4320
 tggaacggca tctgggaagt gatgccaga aactggaag gctgcatctc cgtgaaggac 4380

 caccggacat ccagaacca cagcaagtgc atcaccgagt gtgtgcggac agccctgaac 4440
 accaagtgtg aaatttgtgt gaagaacacc gccatcctgg ctatcaccct gatcacccca 4500
 caggaccctc acctggaccc tgttgtcat ccccatagaa ggcccggtg gaaggacac 4560

cacagagtgg tgttttagcca ccatccttcc ggccagcacca agtctcactg gcagcagaga 4620
 gaaagaggcg gagggccgag agaaaagaag ggctgtagag aggcaagcag agccggccag 4680
 tttcctgtgt ggccggagaac atctagaggc atgtccctgc agtgggaagtc cggcaatgcc 4740
 tgcacacctc tgagatgtcc cagcagatct ccagccacct tcctgactgc cctgaacggc 4800

 tggcatagat ctggactgag ggcccagacc gccttctttc tgctggacat catcctgcgg 4860
 agagcccggc ctacaagctg cagcacatgt agaattgtgt ggccggctgcc ctgcaaagtg 4920
 accgaaagct ccttggccaa gaaaacctg accaatcagc ctagcttgcc cggaccttgt 4980
 gctagcctgc tgtctacact gagccagcca ccacctcagg ctctagcca agtttggaca 5040
 gccgctacac tgcggtgtcc tgctgtgcct gctgtgcat gtccacctct gaagctggct 5100
 ccaactgaag tgaccacaac actgaagctg atcctgggtca tgctggaaat cgtgaccgag 5160
 aacaaagttc ggcagaactt caagcggaac tccagcttct tctacaccag cgacagaggc 5220

 taccctacg atgtccctga ctatgcgtcc 5250
 <210> 1200
 <211> 5232
 <212> DNA
 <213> Artificial Sequence
 <220><223> Polynucleotide encoding the hINV - and HA-extended poly-FSP
 polypeptide 2D
 <400> 1200
 atgcatcgac ggcgctcacg gaggttgccg gaagacaaa agcctgtgat ggacgatcag 60
 cgggacctta ttcttaacaa tgaacaactt ccgatgcttg taggcggcc tggagcacca 120
 gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180
 ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

 cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300
 ccaaagcccg tctccaaaat gaggatggcg acaccgtcc ttatgcaagc ctttcccatg 360
 ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
 catgtcatgc atttgcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480
 agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaagggtg 540
 tttagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
 aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660

 ggcgtcacia agcaagacct gggacccgtg ccgatgcgga agatgcagag cctgaatcac 720

cccagcagac tgaccaacaa tcctcggaga aagacctgga agatgcggaa gaagtacgcc 780
 cagaagccta gccagaagaa ccacctgtac cggcagatca accggcgcaa gctgcagaga 840
 aagaagtcca gaagccacct ggacttcagc ccctactgga tgaagaaagt gaagcggggc 900
 agaaaccgga acatgaagaa aaccatgagc cacctgatcg cccatcaggc cctgaagatg 960
 tctggcctga gactgtttca cccagactg ctgaccagaa agaagcccgg caagcagaaa 1020
 aagggccaca tgatcttcag cggcggaag tggcagatcc ggcacgtgct gaagaatctg 1080

 atccccagcc tgaacgcca gtggatgttc ctgagaatcg ctagccaca gatcatgcag 1140
 agaaccagcg ccgaccggtt cgggatgaag cggagaatgc agaacctgga caatctgggc 1200
 gtgccctggc ctctgttgcc tggattgtcg ctggccata tgtacggctt cagcacctac 1260
 ggcaccaga aaggcgagtg cgtgtgtctg cagtgtctga gcggcagcag cctgttcac 1320
 ctgaagcagc cctggacct gaagatctcc aagaccttca tggccagccc tcagattatg 1380
 cagcggatga gcgccgtgaa cttcgagaca atcctgcagg cccatcctca ggtgccagct 1440
 cttgtctctc aagcttgggtg gcccgctaga agaggccctc tgacatctgc tccaagcgca 1500

 cagcagtcctc tgacacggac actggaaagc gccggactgt ttcttggct gcacaccag 1560
 tgccggcctc tcattcacac acctagaagc cctggctgca gcgtgtacgc caacatgtgc 1620
 tggcgttaca agaaacgggg agtgatcgcc tggcggatct accctcctag cacatgcagc 1680
 ctgccttgca gaggcctgat cctgattcag caggcggca tcttcacctt ccggttctgg 1740
 gtcgagaagc tgagctggaa catctgcaag aacctgagcc tgtacctgga taagtctgtg 1800
 cagcggctgc tgtacgtgta catcatcgag acaaactgtt tcgtgctgaa cctgttccac 1860
 gtgccagtga accagatctt catgatggcc ttctacctga agtacaccga gaaggcctgg 1920

 gtcattggaac tggaatggct gatccagcag cagtgtctacc agcgaagag aatgaagacc 1980
 ggcgccatcc aagagaaggg cgctattcaa gagaaagggg ccatgaccaa gcgcatctgc 2040
 gtggtcaatt tcgaggcctg cagagagatg gaaagcctga gcgcccctga gaagatcacc 2100
 ctgtttgaag cccacatggc ccggtgcacc agcatcaatg tgtgtgtgt caggccagc 2160
 ctgatcgaga aactgatgaa agaaaagcgc aagatgaagc gcaaccaggt ggcacccct 2220
 caaatcatgc aacggctgtt catcaagggc taccagaaca accacttcac gttccacctc 2280
 caaaacttcg cttcttcag ctcttcggc aacaacaagt atatcaacat cctgaccttt 2340

 ctgccagca gattcccttg gggacctcct ccaactgggag cccttagagc tacagtcct 2400
 gctacagctg ctccccagc acagacacct cattggagag ccgccaccac aagcagcatg 2460
 agcagctctc caagagccga gcctaccagc tctagctctt gggccacttg ctggcctaga 2520
 tgctgcagct ccagctgcta ttggagcctg tctagctggc ctctgctgg cgctgccgaa 2580

gccacaaata ccagaaccag aagccgcgag agccagcggg gaagaatgct gacttggaga	2640
agctccctgt ggctgcaggg caccagatgt ttacaggcg tgcggaccag ctccaggtgc	2700
agcctgatgg aacagatccc tcacctgaag tctaacagcc ggaagaaact gctcaggac	2760
atgaagcaga acggcttcac cagacggcgg aacagcagaa agcagagcca agtgcagctg	2820
gccatccagg tgcctgtggt ggacaagcac aagtactttc tgttcggcag agccacattt	2880
ctgctggctc tgtgggagtg tagcctgcct caggctagac tgtgcctgat cgtgtctaga	2940
accctgctgc tcgtgcagtc tagacacca agctggcctt ggaccagatg cctgagaatg	3000
cggcctccac gcagccactg gaactctgcc tacctgggga gaacactgct cgtgacctgc	3060
atcctgtacc acagatggat cgtgaccagc atgtgccaga gccagagatg gctgacctcc	3120
accacctcta gaagctctgc cctgatgtgg acctggtggt gtacaagagg tggcggcaag	3180
cggaagaaaa agatgtgcaa ggtgtccggc ggctgcaccg cctgtgttga aagatgtcct	3240
tggaagggca tctgttgaa gtggcctgtg acagtggccg ccatgagcag aacacctcca	3300
agacgcgtgt gcggccacag agagggcagc gactctgata atctgggcct gctgtactcc	3360
tttccacctg tgcgtttcaa ggccgaccag agcgaaagct ctctgagcag cggcaacagc	3420
gtgatcgtgc acaagatcgt gctggtgttc ctgaagtcct tgagcagcta caactgcgag	3480
agaagaatca gcggcatcca gaagagagcc atcgagtctg ccgtcctgaa gctgctgaac	3540
atggacctcg gcaagggact gacacacccc gtgcctctga agaggacct gcagaacaag	3600
cggaacaaga acatcaagcg ggtcaaccag aagaagggca acatcaagag gaagtccatc	3660
ctgctgcatc tgatttgtct gaacagcccc gagagcaacc gggaaaagat catcaacccc	3720
accatcagct gcccttttca gagccccaca aagagactgg gaagccctcc tctgcacctg	3780
tgtcagctc tgaggcccta tctatcagc gagggcctga ccatgaccac cggcagaaac	3840
atcaacagca actccctgat gaccaactgc ctgttcagcc ccatcttctt gtgccaccac	3900
gccatcatgc accggaagat gacaagccct cacttcagac tgttctccag caagatccca	3960
catccacagg tccaagtgt ggtggccctg tgcaagtta cacaccctg caccatgctg	4020
ctgccccaaag gcgttttttg gaagcctcct agccagggca tctccagctg tctgatgaca	4080
ggctgttggc agtgggtccag cgtgacaagc ctggaatgga cagcccaaga gagagctgt	4140
tctctctggc tgatgaagca aacatggatg aagtcttggc cctgcggga cccagctac	4200
agatccatcc tggaatacgt gtccacacgg gtgctgtgga tgcccacctc taccgtgcct	4260
aagtcttttc tgaccttcag ccagatccgg atgtgcgcc tgtctcacc tagcttctac	4320
atcagctcca ccgtgtgctt tctgagcaag cactgcatga ccgctgcac acctggaacc	4380

agcctgcagt gttacctgaa cctggccaac ggcctgtggt tcaacctgat ctccggaac 4440

aaaaagacca agctgtggtt ctccctgatt aacatccacc accgcaagaa cccactgctg 4500

cccatgcggc tggaaaaaaa ggccacttgg atcgggcgga ccgagctgtc tctggaacct 4560

tggattcctt acctgcatca gcagaaaacc cagtggctcc ccatgagaag cctgggcgag 4620

ccttggcgag ctggatttca gtggggagag tctccctggc aagtgatggc ctctctgaca 4680

ggcagacgca agaaaagaga ggatcactgc ggactgcaag agaaaaaag ccggaagctg 4740

atgtccagct gcgccgctcc tccacataga ctgctgggac ctagcagatg gggaagctgt 4800

gggagagcct gttcttgtgg cagaggctgt ggaacccta gaggcgactg gaagagacac 4860

ccacctcggc ggattctgtt tcacgtgcgg aacatcgtgt acggaatcca agtgaatgctg 4920

tgctgtcacc ccgcttggt gtctccaatc agcgcttgtc ctgcctgct gccttatcca 4980

ttccacgttc tggccctgga agtgacattc cctccaggca ctgccatgcc tcagatgcaa 5040

ttgcaggcac tggcaatgtg ggagaaaggc tgggacaagc ctctggaaaa cacacagatc 5100

cccaggacaa gccactgtg gaagatcaca atggtgctga catacccaa ctgcgtggtg 5160

cacgtcctga tgttcggcgg caagaagcgg agcaagttcg gctacccta cgatgtccct 5220

gactatgcgt cc 5232

<210> 1201

<211> 5247

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV - and HA-extended poly-FSP
polypeptide 3D

<400> 1201

atgcatcgac ggcgctcacg gattgcccgg gaagacaaa agcctgtgat ggacgatcag 60

cgggacctta ttctaaca tgaacaactt ccgatgcttg gtaggcgcc tggagcacca 120

gagtccaagt gttctagggg cgccctgtac actggtttct ccatcctcgt gacactgttg 180

ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240

cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300

ccaaagcccg tctccaaaat gaggatggcg acaccgctcc ttatgcaagc ctttcccatg 360

ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420

catgtcatgc atttcttca aaacgtgat ccccttaaag ttaccctcc tctgaagggg 480

agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaaggtg 540

tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa	600
aagccgacgg acgcacctcc caagaaagc ctggaattgg aggacccgag tagtgggctg	660
ggcgtcacia agcaagacct gggacccgtg ccgatgcaga acaccagaag caccaacctg	720
gaaaagaacc ccagcctgaa gaagcagagc cagcggagag gaaagctgag cagcagaaag	780
aagggccaca ccaagaaccg gcggaaggcc aagagaaagc cccagatcag ccagaagaag	840
gaccctgccg gcaagctgaa gaaacacctg aaccggaagc tgcacctgac cagatcctgc	900
ctgatcgacc tgacctgat gatgagccag aagctgtgga agaaccagcg caagagaatc	960
cctctgcctt ctccacggca gcatctgtg cctcagtatc cactgcatcc tccacctcca	1020
tgcttctgc tgetccacca cagacacct ctggcctttc tcgagatggc ctgcagcagc	1080
cagcacacc acagcatcaa gatctggatc agcttcagcc acgaggacct gcctagaatg	1140
ctgcccata gcagcctct gcacagacc cagatgcctt tctggacctg cacctttcct	1200
gccaccacat ggggcacatg ggagacacct tctacatggg gctggcggac attcggccct	1260
gtgtactacg tgtgcaaccg gatgaacgtg tccagcgtgc tgaagccttt cctgttcacc	1320
gtgcctatcg aggacatgag agagtgcacc ctgggcagaa acagaatgaa tgtgtcctct	1380
gtgtgaaac cctgtctgat ccccgctgca atcctgacca cactgagctt cgtgtctgac	1440
gaggaaagcc ggcggaacag acggtacaga aagatctacg gggagctgaa gatgtccctg	1500
caggccctgc ctctgacct tagcacactg ctgtgggaca gcagacacac caccaccaca	1560
agcagcccca gaagatcccc tgctctgaga gctagaggcg gcaccacaat cggcgaagtg	1620
acaagcagag gcgccagcag ctctaccagc agagacagca gaagcttttt caccagcgt	1680
cacccagca gaccctgcag aatgagactg taccagagca acggcatgga agcctgcggc	1740
acacacccta cacctagact gtctagaggc cctccactgc acaccagaac catgagcctg	1800
agcaacatcc tgatgaagtt ccggtgatg ctgcagaagc agtgtctgta caacctcgtg	1860
atcaagcacc ctctgatctt ccggatcaac ctgcggagac agggcaagac caaagacggc	1920
gttgtgcaga gcctgggctt cctgaaccag cagatcatcc tgcagaaaga gttcttcac	1980
tgcttctga tgttcatcaa gcggtggaag ccagccgcca caaagacacc tccaccactg	2040
attctgtggc ctgagccgc tcctgtgcac aagaagagag gcctgttcag cctgttcttc	2100
tccactgcc tgtgccacca gatgaagtgc ctgaccgccg tggattgtct gcaggccttc	2160
tgggacatga tgattcgaa gatccagaag cggcggagaa ccgccaaccg gctgaaaaag	2220
aaataacctg tgcagtgtac caacctgagc gtgccatga tgctgacct cctgatctgg	2280
aagcgggtgt tcatcctcct gctgagcgac aagaagtgtc tgagagtcag atgcggcgga	2340

tggtgtgtg gctggacacc tagaggcaag aacaagaagc ggagaaagct gcggcccaag	2400
cacctgaaga aaaccagcgc caaggtgtcc gtgatcacca tgaagctctg ggagaagcac	2460
ttcaagggcc tgaactggaa cctggtcgtg tggattctga acctgaagat gatgtggctc	2520
aagaagtcca ccaagagcag acagagcagc ccattcctgg ctcgagctg gaataccatg	2580
caatggaaca acaagaaaaat ggccatgacc gtgatcgtg gcgcccacca ctgtcagtac	2640
aagctgacct acaccaaagt gtggaagatg aattggaaga aaatgatgat cggctcccag	2700
cacctcctgt ttagcccaact ggattcaagc ccactgcagt tgctgctgca ccctcacggc	2760
aagagatgca acccttgctg cagactgacc tggatgagca gagagtggga aaagcggaag	2820
cagatcctcg gcggaggcgg caagtacaaa gactacttcc tgaagcggat tctcatccgg	2880
aaggctatga cagtgtggc cggcgataag aaaggcctgg gaagattcat gagatgcgtg	2940
cagagcgaga caaaggccgt gtctctgcag ctgcctctcg gccgaagaaa gtccggcgtg	3000
atgaagtgtt gggatctgtg cccagactg gactttcacc ccagatctag ctctggcggc	3060
gagaagctga agcactgttt caaagcctgg ggctgtgct tcttctacct gctgtacttc	3120
gagaagaaac ggcccgagtg gctgagcgtt gacctcctg gatctgtctg gattctgccc	3180
tgcattggacc tggacggaat gctgacagt atcggccagg gactcgtggg catgaccct	3240
agagatctgg gaacagtggc tggcgccacc gcacagattc agaggcctat ccaggtgcag	3300
acaggcggca gactgttctt gattcacctg agaaaggtgg acaccacca tctgcaggtc	3360
gtgaccaaga ccgtgacagc cacaacagct gacggccaga ggatgcggag actgaagtgc	3420
aaggcctgtc ggtgagatg ggccagacct gaacctgctg cacaggctcc tccaaagagc	3480
cactttccac ctcatcctag cgccccctcc agaacctcta gcctgcagct cagaccatt	3540
cctccacacc tgagacacc actgtctgtg aagggaaga acagcccctg ctgcaaaaag	3600
aaactcgggg tgcagaacca gggccatctg ctgatgatcc tgctgcataa cgccagacag	3660
cccagcaggc ctaccggaag aaccttacc acaagactga tggcccctgt gggcagcgtg	3720
atgtcttgta gctgtctgac ccagccatct cctgccagcg catgtacaat gccaccactc	3780
ctgcatccac agtgggcccc acatagtgtt ggactgtctc caggcgttg cagacctgcc	3840
tgtacctgca tcagcatgac caccatctcc agagccacat ggcggctgag aatccaagc	3900
ctgaggaagt accggcagaa catcgagatc acccctcagc ggtctaaggc ccaggtttcc	3960
gtgtacagcg gcaatctgtt gagcttctcc agacggggca tgaagagtag cgtgcggctg	4020
aagaacagca tccctcacgt gccaaaagcc accgccctc actctgtgac agtgaagctg	4080

cagtacctgt ttttcctgac cgtgtgcggc ttcgaccggg tgttcctggt taagatctgc 4140
aagaagaagc tgctcctcaa gctgctgaga ggccccagac ggaaagtgt gatggtgctt 4200
tggtgcccc ccaaccagag tctgcagaaa agccaggtgt tccagtgggt gctgcggacc 4260
gaaacctaca tggaatgca ctacggccat caggccctc aggtggccat gctgcctaaa 4320
ctgctgtgta gacagatgct cccactctg tccacactcc agcagaggca tcctcagga 4380
ccttgctc ctcctgtgac acctctgaga gtgcagtctg tgctgctcct gggagtgcct 4440
cagacagccg cttttagcgg ccggattctg caccagccag aaatggccgc catgagactg 4500

atgcccaagt tctgaactc caccaacagc tggtaggacag tggccctag atgtcctaga 4560
agcgccgtgg acattagccc cggacctaca tctcctagcc tggcctcttg tgcctctgtg 4620
gccattggaa aactggcact gctgggcgca tctgccctt gtggcgagc tggtagctaga 4680
gaggctggaa gatttgcgt gctgggcacc atggttatga aggtgtgtgc cgcagcctcc 4740
tgtcagtctc ctccatctcc aagagagaca acccctagca gcgacgccac cagacggaca 4800
agacctattg ccgtcagag caaaaagacc atgactgccg ccggactgac ccctcggaga 4860
aacctgcaga gaaatctgaa ggtcctgggc gccagaaga tcaccttctt gagaaacagc 4920

agacgcgcca cacctacctc taaggcgagc ctgagaagaa agtacctgag agtgaacatc 4980
cgcaagctca tctggaccaa gcagcggagc ttcctgtctc tgttcccaa gctgagagcc 5040
accgagcaga tgaccaatgt gggatgcctg ctcaagaaaa gcagccaatt gcggcggagc 5100
tggcgcaatg tgtcccgat cagcaacatg gaacacaggc tgaccatgga cagcgccctg 5160
agcctgacaa agagagaggg ccctgagaca agcgagaaga agaggaagtt gcctggctac 5220
ccctacgatg tccctgacta tgcgtcc 5247

<210> 1202

<211> 5250

<212> DNA

<213> Artificial Sequence

<220><223> Polynucleotide encoding the hINV - and HA-extended poly-FSP
polypeptide 4D

<400> 1202

atgcatcgac ggcgctcacg gagttgccgg gaagacaaa agcctgtgat ggacgatcag 60
cgggacctta ttctaacaa tgaacaactt ccgatgcttg gtaggcggcc tggagcacca 120
gagtccaagt gttctagggg gcacctgtac actggtttct ccatcctcgt gacactgttg 180
ctggcgggac aggcaacaac tgcgtatttc ttgtatcagc agcaaggaag actggataag 240
cttacagtta catcccagaa tctccaactt gaaaacctca gaatgaagct tccgaagccc 300

ccaaagcccg tctccaaaat gaggatggcg acaccgctcc ttatgcaagc ccttcccatg 360

 ggggctctgc cccaagggcc aatgcagaac gctacaaagt atggaaatat gacagaggat 420
 catgtcatgc atttgcctca aaacgctgat ccccttaaag tttaccctcc tctgaagggg 480
 agctttccag aaaatcttcg acatctcaag aacacgatgg aaacgattga ctggaagggtg 540
 tttgagagct ggatgcacca ttggctcctg ttcgagatgt cccggcattc tctggagcaa 600
 aagccgacgg acgcacctcc caaggaaagc ctggaattgg aggacccgag tagtgggctg 660
 ggcgtcacia agcaagacct gggacccgtg ccgatgaaca gaaagaccag aaaggccgcc 720
 agagagaagc accgcaagac cgacgacaag aagaagaagt ccaccgaaaa gaccaagaac 780

 gccaaagaaga tgcccttcca gcagcggcct cctctgcagc ctgttaacct ggatctgcag 840
 caccagcgca gacgcaaaaa gaagaaagac aaggctgaaa tccggaatcg gagccctaag 900
 gccaatgca ccgagtgtca gggcgagcac agcagagagc agaacctgct gaatctgggtg 960
 cagctgaacc ctacagccc tcaccacaga aaggacgaag aggaccacca gaagcggcac 1020
 caccaccaca atcaaaagaa aatgagcgtg cgggctagcg tgtccttctg gacacttttg 1080
 ccaacaaccg gcgtgcggac aagaggctct cactgagac tgacactgtg gcctccacgg 1140
 gtccacctt ctccacctt tgctctgggc ccagaaatgc agctgtgtac ccagctcgcc 1200

 cggttcttcc ctatcacacc tctgtgtgg cacatcctgg gacctagag acacacacct 1260
 caggctcttc tgaggctgtg gtcttgggtc ggcacaagcc agacctactt cggcagcaga 1320
 ccatctctt gcctgagctg gtccagcaga attgtgcccc ctggacacgc cctgagctgt 1380
 cggactagaa gaagatggtc tagcaagcgg tggatcttct ccaaccagct gaccgtgcag 1440
 atgtgtgtcc tgccaatcac acaccattc gcctctcagc ctctgggaca agagatgccc 1500
 aacaacaccc agatccggct gctgaagccc tgcagagtga acgccgtgga agaactgcac 1560
 agcaggcgga tgtctgtcgc gatcgtgaag aactgggtgt cctgtgttta cgtgcggctg 1620

 tctgtgtgg gcctgtctac ttggagtgcc ctggacgagg aaaagaagaa cgcccgatc 1680
 agcagcctga aaaagaaagt gaatgcctgc agctccctga tctgagctt ccagcgcgtg 1740
 aaaaccggca tggaatcct gctgtggatt ctgctgaaga tggaaattca gatcttcaag 1800
 atttgcttg gcgagatgca gctctgcggc caggcctttg gaagctttag cgccgatttc 1860
 agcgccttc agatcattaa gaagatgaag aaacggatca tgggtcacga gctgaagaag 1920
 aatctgctgc tgcctatgtg ctccagcctg gctctgcaa caggcctgac atctctgac 1980
 ctgcctagca gcgatctggc cgtgtgtatc tctagctcca ccagccactt tctgatgcgg 2040

agccctgtgc tgccaagcag cagactgact tgtgcctctc cacagctgcc ccgcatgtgg 2100

acttggtcta gctggctgaa gaacgagggc aacaaccact ggcctagagt ggaaatgcct 2160

accggtgtgc tgctctcgg ctacaacacc agaaacacag cccagaatcc tcggctgcag 2220

cagcacctga aacactggca gcagtgcacc agagccagat ggtgtcaaga gccctgtcag 2280

accctgacct tcttccatctt cttcttcttt ttcaaaacgg tgtccctgtg ttgccccggc 2340

tggtctaaag gacaacctcc tccacctggc ctgaagcctt ctagcctggc ttctcaggtg 2400

gccagaacca caggcgtgta ccagcacgtg tggctgatct gtctcgtgtt ttctcgtgtg 2460

gtggaaaccg gcttctgtca cgtggcccaa gtgggactcg agagactggt gtctctgtcc 2520

ggcatcaccg acgtgaacca ttgggcccag cctaagccat ctcttagcaa aggcaccggc 2580

atgaacagac ccatcggcct gagagtggc aaaggcgtgt gggccagact gatcctggcc 2640

atgacactga cctgaacgg catggccaag aagtccagc agcctctgca ggtcgtgtg 2700

agactgggaa acctgcctcc attcttcaga ggcagcgagg tgccttttcc tagacctgt 2760

cggaccaagc ctgcctgcac aagcaaggcc tggactcca gaaaactcgt ggggagagcc 2820

gtgcggagaa agggatctcc actctgggat tgcctccaca caacaggcac acaccacgga 2880

tgctgtggg agatcccatc tgtgacctg ctggcccatc ctagaaccgc ctctatcacc 2940

ctgcctacca caagcctgaa gggctccaga accagctgct gccctagatc tcacccca 3000

ctgcctagga ccaaatggcc cctgcagtgt ctgctgcaca gcctgggaac aaccggaaca 3060

ctcgtttggg aaaggggct cctgcagatg agatccctcg aagccattg tccactgcag 3120

accttccatc tgcaccactg caggaccag cctagctctt gtctctctgc ctggattctg 3180

taccaaggac agtggagcgg agccgtctg ggacttagac ctgtggctca ccatctgcct 3240

agacctatcc agggcctgca ctgtccacag gcacctcatc aacctgctct gagctgggga 3300

aatggcccc tggaatgac aggcctgcc agatgttgca gatggcccag acggtgccag 3360

aagaaggttc catcagctc tccatggggc ctctgtctca aaaagaaccg gaaacagatg 3420

ctgaaccaga agtgtctggc cctttttaga gagagcacc tgggcaattt ctggatgaag 3480

ctgctccagc tgctgtctg gatcaacctg aagagactgc agaagttaa cctgcacctg 3540

tgctactacc acagccagag caacagaaac aagagccgcc agatggaatc cctgggcatg 3600

aagttgcagt cccagaaatc ccagcaccac tgtgcctgc ggaagatcga gtgggccaca 3660

aagttgtctc tcggcgaaa agccggacca caggctcaag agaaggccac ctctcgatt 3720

ctgaacctgc aagtgtcaa gaagatcctg cggagcttta tgaagctgta ccactctctg 3780

gtcatgtgcc tgcggctgag gaccaagctg gaaaaggctc tgagcgccct gttcatctgg 3840

ccccagcaca gctacaagcc cctgttcttt cacggcgacc tgtgcgagtg gggaggccag 3900

gctcatagac agcggaactg gctgaaaaac tggaagcggg tcaagcttaa aaagaagtac 3960
atccagaaga agaagcagaa gtctaacaag atcatctgca agggccaccg catcaccatc 4020
atctgtatca agaatatgtt cctgcagcgc aagggtctcc tgaacctgag ccacgtggaa 4080
aagttctgta gaggcggccc tagcgccagc gatagatgct gttctttag cccagcggc 4140

ttcagtgccg gcagaggaag atgtcctgtt cagggtctgc tgaggccca cagagttcaa 4200
ctgctgagaa gatggggccc tggctctcct gctggacaga ggctgtctaa gggctttcag 4260
ctgctccgtt ggtggggacc aggatctcct gctcctgagc ctagaaagg cccatttcca 4320
ccacctgac ctccatgcc tgtgaccgct gtgacagtga tggctggatc tgtgcctagt 4380
gctcagtctg tggacgcctt ggaatctcct ggacctctgg ctctcgaagg acctagcagc 4440
cctagaaacc tgctttggag agagatgagc atctttctgc ccggcatctt caccgccaag 4500
aaaagcccca ccagcttttg ctgcaatatc ctgaacagcc tgccaagctc tatggaaatc 4560

gccgtgctgc aagaggacag caaaaagatg acccagaagg gccaaagcctt cggtccctg 4620
tgtcagcttg tgtccgtga cttctctgcc cctcaagtga cccggctgcg gacgtgaat 4680
catctgtga tcacctacac accccacatc tgcagacaca cctgtgtgac cctgacacc 4740
agatggatct ttagcaatca gctgcagaca gtccagatgc tctgtctgcc tccactgaag 4800
cagggcgaga gaatcatttg gccctcggc ggctttcaga tcccaactt cttttggagc 4860
ctcggcatcg gacacactgg cgctgtgtgg catactggaa ggcgagagaag agaatggggc 4920
ggcagcaccg tgtctagaag ccctctgttg atcagctcca tgatctacct gagaggcatg 4980

gccttcgcca gcgacagcag catcagaacc accagagtgt cctggtgcag aagatcgggc 5040
gccaaaagcg ctgccgccag ctctattgaa gctctgaccg ctctgtttac ctgccggacc 5100
gccagcatca gcgtgaacat cagcaccctg atgtccatcc tggaagcact taagaagaaa 5160
cccagagaca tctgccgcat cagctgccgg ttagacgagc agtacagagt gactatgggc 5220
taccctacg atgtccctga ctatgcgtcc 5280

<210> 1203
<211> 4690
<212> DNA
<213> Artificial Sequence
<220><223> Cloning cassette hTPA 1C
<400> 1203

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg 60

ctgctgctgt gtggagcagt cttcgtttcg cccagccagg aaatccatgc ccgaagcacc 120

agacgggaaa tgcctttctca ggccacacct tctccacctg gaccttggag agccgctctg 180
 ggcaaagaag tgaagcggag ccagagcaag ctgcggctga gaaacacaag cccaccgag 240
 atccaattga ccatgaacga cagcaagcac aagctggaaa gccccgctct gaaacaggtg 300
 tccccctgct ctccacctac acagcagcct cagacacccc aggatagcag acagggtgctg 360
 gccgctttctt ctcttgaca tctcttggc cctggcgact gccctagaac aatggctgga 420
 ctttctgctt ctctgcacc agcatctggc agagccagca gaaagacctg gcagagaagg 480

 ctgagagcct gtagagctgg tggacctgct ggatgggcta gacaggccat gacctgaag 540
 gccctggta agacctggac acagtgcaga aactaccca ggtcggagc cggaacaggc 600
 ggaggacctg ctgtgttcc tgtggccgaa gcttctactg gcgcctggac agctgaaggc 660
 gctgccgga caagatgcag agcttctaga gcccttgca gacagctgcc tgccagctct 720
 cctaccaagt gcgagatctg cgtgaagaga aggcggcgga gaaagcggag cagccagctt 780
 agatctcccc tgcctaagaa acgcgagcgg atgatgctgc ctgtgcgggc cagaacagct 840
 agatctgctc tgccacaagg cagagcccct ctggaaggaa tgcttctgcc tagagcactg 900

 cccagcctgc tgagcagaat gccagccaga agagagagcc ggttttggct ggcaactgcag 960
 gctctgggac tcagacctcc tcatctgcct agctgtcacc ctctgcctca actgcttgga 1020
 cctctccac ctcatcaggc ccttttcgac aaaaaaggct tcgtgatcct gagcaagggc 1080
 aagaagcgcc ggaaagaaat ccggcggatg accagacgga ccatgaccac caccaaaatg 1140
 atgatgatgc ggcggacca ggcggcggagg cgaaaacgta gaagaatgac catgatgacc 1200
 cgcaaaccc tctgaccaa gaaaacctgt ctgacccta gaaccagcgc cgccacaaaa 1260
 gctctgccc gacagacaat cagccagcgg aggcctatcc agacacctcc tggaacaagc 1320

 ctggccatct ggggcagact gcctctcaga ccacagagag gacctcggcc tctgcataga 1380
 tggctgcagc agacaacagg ctgctcccag agaagaatcg ccaagaagcg gatcaagctg 1440
 aggcggaaca cactggccat ccggtttatc tctgcccctc agcctagcag cagcacggtt 1500
 acagctgctc ctacggcca gtacttcagc agcttcttct acaccagcga ccggaccaag 1560
 tgtgaaatct gtgtcaagaa caccgccatc ctggctatca cctgatcac cctcaggac 1620
 cctcacctgg acctgtgtg taccacatc agaaggcctg gctggaaggg ccaccacaga 1680
 gtggtgttta gccaccatcc aagcggtcc accaagagcc attggcagca gagagaaaga 1740

 ggcggaggcc gcagagaaaa aaaggctgc agagagatgc ccagcagctg gtctagctct 1800
 ggcagaaccg ccgacaaaaa gaacgtgcgg agcagaacca gactgacct gacaggcaca 1860
 agaagcagcg gcacaagagc ctctccaagc gccgtgtgtc tgtgtgttg gacatgcccc 1920
 tccagaagct tcctgcccgc atctccatct ggactgagag cacctgttgg agcccaggct 1980

cctcctgaag tgacactgag agccagctgt gcctctagcg cctctaaagc ctgtgctgga	2040
ctttggcctt ggggagccca agtgcggaac aaagtgcggc agaacttcaa gcggaacctg	2100
gccaaaaaga ccttgactaa cgccctgcgg agtatgccca agagcagaaa ccaggtgctg	2160
ttcagacgga atctgacccc aagccagctg agaactctgg cccctcctta catgctgctg	2220
ccccagtctc tgtctcagag cctgtccaga aagcagatcc ccagccaatc aatgctcgtg	2280
accgccttct tectgctcga catcatcctg agaagcctgc tgtactcccg gatgtgcctg	2340
gtgcagatcc ctacacacac ctgggagccc gactacttcg tgtccctgcc tatgatgttc	2400
agctgggcca ctgagagctt tccagtggga gccgtgttcc tgaccagacc tgccattcct	2460
tgctgcagct gtaccagcca cagcaaccct tggagccagt ccttcaagaa gaagaagccc	2520
ctgacattca gccccagcgt gccaatgtct ctggcctgta gcatcacctg gtccttcgtg	2580
ggccagatca gcacactggt gctggacgtg tcttccatct ctcactggcg caagcgcaag	2640
agagagaagc ggtcccagaa gtcccggcag aaccatctgc agctgaagtc ctgcagacgg	2700
aagatcagca actggtccaa gctgagatcc cctgggatct tctaccctcg gctgaaaacc	2760
ttcggcgctg cactgggctc tatctgtgt ctggcaggct cctgagcac gatgatgac	2820
attagacca ccagacaaga gtgtggcaga cgggcctccg tgcctttag acctatgac	2880
ggcagcgcta gaccggacc ttggcggaca tctgctatgc catctgcat gggagtcgcc	2940
ctgcctacca gctgtgaaag cggaagatct cctcctgcca ccggcggaag aatgcctgga	3000
tctcagtcta tcatgatgag ctggatgcct cactggctc cctgtgccgc ttgtccttgt	3060
tctcctgctc ctacactgtg ccctgctcat cctgcaagag ccctacagc cgtgcctgcc	3120
tttacacctc tgtctgctca ccctgtgcca gtgctgtctg gatgtcacct ggccgtgcgc	3180
acctctatgc tgacactgct gcccatgaga caccctcaca gaagcccacc tacaagctgc	3240
cctccactgc tggaagcttt cccactgcca agggccagcc tgagagctac cgtgcctaga	3300
cacagctctg tgctggccac tggactgcat ctgcatcggc agattagcct gcctctgagg	3360
ggcttctgc tgcatcaacc tctgcctgga caacacctgt ggctgtccca cagactgagg	3420
ctgagactgc caagaacagg cgagaagaac gacctccagc tgttcgtgat gagcgacacc	3480
acatacaaga tctactggac agtgatcctg ctgaaccct gcggcaacct gcacctgaaa	3540
accacatctc tcgggagagc cagacctacc tctgcagca catgcagaat gtggtggctg	3600
aagctggccc cactgcaagt gaccacaaca ctgaagctga tccgtgtcat gctggaaatc	3660
gtgaccgaag aggccaagaa atccatgaag agatccggc ggagcaagat cgaggcctct	3720
cctatcggt ccatcatgaa gaagaaagac agcacctct tcatcaacca gcagctcaag	3780

tggacccctc acatcctgaa gtctgccagc gtgtccaaga agagactgcc caagctgaac 3840

ggcatctggg aagtgatgcc ccggacactg gaaggctgca tcagcgtgaa ggaccaccgg 3900

acaagccaga accacagcaa gtgcatcacc gagtgtgtgc ggacagccct gaaccagaga 3960

aaggtggtca agaaccaccg ccagccagtg ccaactgagaa acgacggcat caccaacggc 4020

aacgactcca ccagatcctg ctccatcagc ctgaagaaaa gcctggaaaa gatgcccttg 4080

atgaacgcca agaaaatgga agatatgatc tgggagagca acatgggcgg caaccggtcc 4140

atctgctga caagactgcc ctgcaaagt accgagtcca gccaaagacc acctcggagc 4200

attctgtccc tggcctctag agccggacag ttccccgttt ggccggagaac cagcagaggc 4260

atgtccctgc agtggaaagtc cggcaatgcc tgcacacctc tgaggtgccc tagcagaagc 4320

cctgccacat ttctgaccgc actgaacggc tggcacagat ctggacttag ggctcagcaa 4380

cctagcctgc caggaccttg tgctagcctg ctgtctacac tgagccagcc tccaccacag 4440

gctccaagcc aagtttggac agccgccaca ctgagatgtc ccgtgttcc tgcagctgct 4500

tgccctccta tcgtgttctt tctggcccca tacttcccca caccactgag catcagcaga 4560

cccactctc gggccagaca gtcttgttgt cccccggac tgacacaccc tgctcaccag 4620

cctcttggct ctatgggcta cccctacgat gtccctgact atgcgtccta aaggcgcgcc 4680

tagcggccgc 4690

<210> 1204

<211> 4672

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 2C

<400> 1204

gaattcggat cccgcgactt cgccgcatg gatgcaatga agagagggt ctgctgtgtg 60

ctgctgtgt gtggagcagt ctctgtttcg ccagccagg aatccatgc ccgacggcag 120

atcaacagac ggaagctgca gagaaagaag cgccggaaga agagagagga ccaactcggg 180

ctgcgggcca gaaaccggaa catgaagaaa accatgagcc acctgatcgc ccatcaggcc 240

ctgaagatgt ctggcctgag actgtttcac ccagactgc tgacacggaa gaagcctggc 300

aagaaccctc ggagaaagac ctggaagatg cggaagaagt acgcccagaa gcctagccag 360

aagaaccacc tgtacggcaa gggcctgaca caccctgtgc ctctgaagag aaccctgcag 420

aacaagcgga acaagaacat caagcgcgtg aaccagaaga agggcaacat caagagaaag 480

agcatcctgc tgcacctcat cgtgtgaac agccccgaga gcaacctgca ggctcatcct 540

caagttccag cactggctcc tcaggcttgg tggcctgcta gaagaggccc tctgacaagc	600
gctccatctg ctcagcagag cctgaccttc ctgcctagca gatttccttg gggccctcct	660
ccactgcact ggaactctgc ctacctgggc agaacactgc tcgtgacctg catcctgtac	720
cacagatgga tcgtgaccag catgtgccag agccagagat ggctgaccag caccacctct	780
agaagcagcg ccctgatgtg gacctagtgg tctagcgtga caagcctgga atggacagcc	840
caagagaggg gctgtagcag ctggctgatg aagcagacct ggatgaagtc ttggagcctg	900
cgggacccca gctacagatc catcctggaa tacgtgtcca ccagagtgtc gtggatgccc	960
acatctacag tgggagccct gagagccaca gctcctgcaa cagctgtccc acaggctcag	1020
acccctcatt ggagagccgc cacaacaagc agcatgagca gcagccctag agccgagcct	1080
acaagctcta gctcttgggc cacctgttgg ccagatgtt gcagctccag ctgttactgg	1140
tcctgtcct cttggcctcc tgctgggtgt ggcgaggcca caaataccag gaccagaagc	1200
agagagtccc agcggggcag aatgtgtact tggagaagca gcctgtggct gcagggcacc	1260
agatgtttta caggcgtgcg gacctccagc agacaccctt cttggccttg gaccagatgc	1320
ctgagaatgc ggctcctag aagcaacagc cggaaaaagc tgctcgagga catgaagcaa	1380
aatggcttca cccggtacaa gaaacggggc gtgatatcct ggccgagagc cactttcctg	1440
ctggcccttt gggagtgcag tctgccccaa gctagactgt gcctgatcgt gtctaggacc	1500
ctgctgctgg tcagagcag atgcagcctg atggaacaga tcctcacct gaagtcctgg	1560
tggtgtacaa gaggcggcgg aaagcgggaag aaaaagatgt gcaaggtgtc cggcggtgc	1620
accgcctgtg ttgaaagatg tccttggaag ggcatctgct ggaagtggcc tgtgacagtg	1680
gccgctctga tctgattca gcacggcggc atcttcacct tccggttctg ggtcgagaag	1740
ctgtcctgga acatctgcaa gaatctgtcc ctgtacctgg acaagtctgt gcagcggctg	1800
ctgtactgtg acatcatga gacaaactg ttcgtctga acctgttcca cgtgccagtg	1860
aatcagatct tcatgatggc cttctacctg aagtacaccg agaaggcctg ggtcatggaa	1920
ctggaatggc tcattcagca gcagtgtac cagttgtgc tggtcatat gtacggcttc	1980
agcacctacg gcacccagaa aggcgagtgc gtgtgtctgc agtgtctgag cggcagctcc	2040
ctgttcaccc tgaagcagcc actggacctg aagatcagca agaccttcac gagcagatcc	2100
cacctggatt tcagccccta ttggatgaag aaagtgaagg cctctccaca gatcatgcag	2160
cggatgagcg ccgtgaactt cgagacaatc aggcggaagt ggcagatccg gcacgtgctg	2220
aagaacctgc ctctggaaaa cacacagatc ccaggacaa gccctctgtg gaagatcaca	2280
atggtgctga catacccaa ctgcgtgggtg catgtgtga tgttcgtgtg gttcaaggcc	2340

gaccagagcg agtctagcct gagcagcgga atctaccctc ctagcacctg tagcctgcct	2400
tgccggggca ttagaatgtg cgccctgtct caccctagct tctacatcag cagcaccgtg	2460
tgctttctga gcaagcactg catgaccgcc tgcaccagag agaagatcat caaccccacc	2520
atcagctgcc cctttcagag cccacaaaag agactgggcc acagagaggg cagcgagagc	2580
gataatctgg gcctgctgta ctcttttct ccttggctgc ccatgagatc cctgggcgaa	2640
ccttggagag ctggctttca gtggggagag tccccttggc aagtgatggc tagcctgacc	2700
ggcaacacgc tgatcgtgca caagatcgtg ctggtgtttc tgaagtctct gagcagctac	2760
aactgcgagc ggcggtatctc tggcatccag aagagagcca tcgagttcgc cgtcctgaag	2820
ctgctgaaca tggacctggc tagccctcag attatgcaga gaaccagcgc cgaccggttc	2880
cggatgaagc ggagaatgca gaacctggat aacctgggcg tgccctggcc attgcttcca	2940
ggtgctgctc ctccacatag actgctgggc cctcttagat ggattctgtt tcatgtgcgg	3000
aacatcgtgt acggcatcca agtgatgctg tgccggcgga gaaacagcag aaagcagagt	3060
caggtgcagc tggccattca ggtcctgctc gtggacaagc acaagtactt tctgttcggc	3120
ccctatccta tcagcgaggg actgacctg accaccggcc ggaacatcaa cagcaactcc	3180
ctgatgacca actgcctgtt cagcccatc ttctgtgcc accacgcat catgcaccgg	3240
aagatgacaa gcccacactt cagactgttc tccagcaaga tcccacatcc tcaggtgcca	3300
agtgtggtgg cctgtgcaa gttcctggcc aatggcctgt ggttcaacct gatctttcag	3360
aaaaagggcc acatgatctt tagccccaag ttcttctga cctttagcca gcggaccctg	3420
gaatccgccg gactgtttcc atggctgcac acccagtgcc ggaacaaaaa gaccaagctg	3480
tggttttccc tgatcaacat ccaccaccgc aagaatctc tgctgcctat gagaatgagc	3540
agaacacctc ctcgagagt gtgcggatct ccacctctgc atctgtgcca acctctgaga	3600
ggcggcaaga agagaagcaa gttcgccttc tggaagcctc ctagccaggg catcagctct	3660
tgtctgatga caggctgttg gggctcctgt ggacagactt gttcttgccg aagaggctgc	3720
ggtacacca gaggcgactg gaaaagacac ccacctcgca gagagctgag cctggaacca	3780
tggattcctt atctgcacca gcaaaagacc cagcggagc ggatgaagac cggcgccatt	3840
caagagaagg gcgctatcca agaaaaaggc gcaatgacca agcggatctg cgtggtcaat	3900
ttcgaggcct gcagagagat ggaaagcctg agcgccctg agaagattac cctgttcgaa	3960
gcccacatgg cccggtgcac ctccatcaat gtgctgtgtg tccgggccag cctgattgag	4020
aagctgatga aagaaaagcg caagatgaag cgcaaccagg tggcatcccc tcaaatcatg	4080

caacggctgt tcatcaaggg ctaccagaac aaccacttca cgttccacct ccaaaacttt 4140
gccttcttca gtccttccg caacaacaag tatatcaaca ttctcaccg gcccttcac 4200
cacacaccta gaagccctgg ctgttccgtg tacgccaata tgtgctggcg gaagatgcag 4260
tccctgaatc accccagcag actgaccaac tgtcaccccg cttggctgag cccattagt 4320
gcttgctcta ggctgctgcc ctatcctttt cacgtgctgg cactggaagt gacctttcca 4380
cctggcacag ccatgcctca gatgcaattg caggcactgg ctatgtggga gaaaggctgg 4440
gacaagcaag agaagaaatc ccgcaagctg atgtcctcct gccctggaaaa aaaggctacc 4500

tggatgcgga gaaccctgg cacaagcctg cagtgttacc tgaacacaca cccctgcacc 4560
atgctgctgc ctcagggaat cccatctctg aacgccaggt ggatgttcct gcggatcggc 4620
taccctacg atgtccctga ctatgcgtcc taaaggcgcg cctagcggcc gc 4672

<210> 1205

<211> 4687

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 3C

<400> 1205

gaattcggat ccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg 60
ctgctgctgt gtggagcagt cttcgtttcg ccagccagg aaatccatgc ccgacctatt 120
cctccacacc tgagacacc tctgctgctg aagaacaaga agcggagaaa gctgcggccc 180

aagagcagaa agaagggcc caaccaaac cgcggaagg ccaagagaaa gcccagatc 240
agaaacagcc gcagagccac acctaccagc aagggcagcc tgagaagaaa gtacctgaga 300
gtgggagccg ccgctgctag ctgtcaatct cctccatctc ctagagagac aaccctagc 360
agcgagccca ccagaagaac cagacctatc gccgctcaga gcaagaaaac catgacagcc 420
gccggactga cccctagcca gaagaaagat cctgccggca agctgaagaa acaggtgtcc 480
gtgtacagcg gcaacctgct gagcttctct cggagaggca tgaagtctag cgtgcgcctg 540
aagaactgca ccaacctgag cgtgcccatg atgctgacca tcctgatctg gaagcgggtg 600

ttcatcctgc tgcgtgccg caagaaatct atccctcacg tgcccaaggc caccgccgt 660
cattctgtga cagtgaagct gcagagccgg cggaacagac ggtacagaaa gatctatggc 720
gagctgaaga tgtccctgca ggccagcaat ggcatggaag cctgtggcac acaccacaca 780
cctagactgt ccgtgtccgt gatcaccatg aagctgtggg agaagcactt caaggcctg 840
aactggaacc tggctgtgtg gattctgaac ctgaagatga tgctcaagaa gaagtatctg 900
gtccagcgcg agtgggagaa acggaagcag attcttggcg gcggaggcaa gtacaaagag 960

tacttcctga agagaatcct catccgcaag gccatgacag tgctggccgg cgataagaaa	1020
ggcctgggca gattcatgag atgcgtgcag agcgagacaa aggccgtcag tctgcagctg	1080
cctctgggca gaatggacct ggatggaatg ctgaccgtga tcggccaggg actcgtgggc	1140
atgacaccta gagatctggg aacagtggct ggccgccaccg cacagattca gaggcctatt	1200
caggtgcaga caggcggcag actgagaggc cctagaagaa aggtgctgat ggtgctgtgg	1260
ctgcccgcca atcagagcct gcagaaaagc caggtgttcc agtgggtgct gagaaccgag	1320
ctgccccctga cctttagcac cctgctgtgg gacagcagac acgacctgcc tagaatgctg	1380
cccatcagca gccctctgca cagaccccag atgcctttct ggacctgcac ctttctgcc	1440
accacatggg gcacatggga gacaccttct acatggggct ggccggacctt tgccagacag	1500
ccttctagac ccaccggcag aaccctacc accagactga tggctccagt gggcagcgtg	1560
atgagctgta gcctgtgac acagccatct ccagccagcg cctgtacaat gcctccactg	1620
ctgcatcctc agtgggcccc tcattctgct ggactttctc caggcgttg cagacctgcc	1680
tgtacctgca tcagcatgac cacaatcagc agggccacct ggccgagaaa cctgcagaga	1740
aacctgaaag tgctgcggct gagaatcccc agcctgcgga agtacagaca gcagaacacc	1800
cgggtccacca acctcgagaa gaacccatct ctgaagaagc agagccagag gcggggcaag	1860
ctgtctctga ccacactgag cttcgtgctg atcgaggaac tgctgaaaaa gagcagccag	1920
ctgcggagaa gctggcgga cgtgtccaga atcagcaaca tccggaagct gattttgacc	1980
aagcagcggga gtttctgtc tctgttcccc aagctgagag ccaccgagca gatgaccaat	2040
gtgggctgta gactggattt tcaccccaga agcagctccg gcgacagagt gttcctggtc	2100
aagatccaga gcagcccatt cctggccaga tcttggata ccatgcagtg gaacaacaag	2160
aaaatggcca tgactgtgat cgctggcgcc caccactgtc agtacaagct gacctacacc	2220
aaagtgtgga agatgaattg gaagaaaatg atgatcggca gccagcacct cctgttctec	2280
ccactggata gctctccact ccagctgctg ctgcacccac acggcaagag atgcaacccc	2340
tgttgtcggc tgacatggat gagccacctg aatcggaagc tgcacctcac caggtcctgc	2400
ctgatcgacc tgacatgat gatgagccag aaactgtgga agaatacagc gaagcgcac	2460
cctctgcctt ctccaagaca gcactgtgtg cctcagtatc ctctgcaccc tctccacct	2520
tgtctgtgc ttctccacca tagacaccac ctggcattcc tcgagatggc ctgtagctct	2580
cagcacaccc acagcatcaa gatctggatc agcttcagcc acgagacaat gagcctgtcc	2640
aacatcctga tgaagtccg gctgaccacc accacaagca gcccagaag aagccctgct	2700

ctgcgagcta gaggcggcac aacaatcggc gaagtgacca gcagcctgtt ctttagccac	2760
tgcctgtgcg tggcccttag atgtcctaga tctgccgtgg acatcagccc cggacctaca	2820
tctccttctc tggcctcttg tgcctctgtg gccattggaa agctggcact gcttggcgcc	2880
tctgtctctt gtgggtgtgc tggcgctaga gaggcggaa gatttgctgt gctgggcacc	2940
atggtcatga agaacatgga acacagactg accatggaca gcgcctgag cctgacaaag	3000
agagagggcc ctgaaacagg ccccggttac tacgtgtgca accgcatgaa tgtgtccagc	3060
gtgctgaagc ctttctgtt caccgtgcct atcgaggaca tgagagagtg caccctggga	3120
cgcaacagaa tgaatgtctc ttccgtgctg aaaccctgtc tgatccccgt gccaatctgc	3180
aagaagaaac tgctgtctaa gctgtctgagg ggcgccctcca gctctaccag cagagatagc	3240
agaagctttt tcaccagcgc tcaccccagc agaccctgca ggatgagact gtaccagatg	3300
ctgcagaagc agtgtctgta caacctctg atcaagcacc ctctgatctt ccgcatcaac	3360
ctgcggagac agggcaagac caaagacggc gttgtgcaga gcctgggctt cctgaaccag	3420
cagatcatcc tccagaaaga gttcttcatc tgctgtgta tgttcatcaa gcggtggaag	3480
ccagccgcca ccaagaaggg caagaacagc cctgtgtgcc agaaaaaact gcgggtgcag	3540
aaccagggcc atctgtgat gattctgtct cacaacagag gccacctct gcataccaga	3600
ttcgagaaaa agcgggccga gtggctgagc agaaaatccg gcgtgatgaa gtgtgggat	3660
ctgtgccctg ccttcagcgg caggattctg caccagccag aaatggccgc catgagactg	3720
atgccaagt tctgaactc caccaacagc tgggtggacag tgcacaagaa gagaggcctg	3780
ttccaccaga tgaagtgtct gaccgccgtg gactgtctgc aggccttctg ggatatgagc	3840
gagaagaaac gcaagctgcc tatgattcgc aaaatccaga agcggcggag aaccgccaac	3900
cggaacatcg agatcacccc tcagagaagc aaagcccacc tgaagaaaac ctccgccaag	3960
ggcgccaaga aaatcacctt cctgtgcctg agagtcagat gcggaggctg gctgtgtggc	4020
tggacaccaa gaggatggct gaagaagtcc accaagtcca gactgtgctt cttctacctg	4080
ctgtactacc tgtttttctt gaccgtgtgc ggcttcaccc ctccaccact tattctgttg	4140
cctcaggcag ccctggcga gaagctgaag cactgtttta aagcctgggg cgtcgacctt	4200
cctggcagcg ttiggaattct gccctgcttc ctgattcacc tgagaaaggt ggacaccac	4260
cacctccagg tggtcaccaa aacagtgacc gccacaacag ccgacggcca gaggatgaga	4320
aggctgaagt gcaaggcctg ccggtgaga tgggctagac ctgaacctgc agctcaggcc	4380
cctcctaaga gccactttcc acctcatcct agcggcccct ccagaaccag ctctctgcaa	4440
ttgagaacct acatggaat gcactacggc catcaggccc cacaggtggc aatgctgcct	4500
aaactgctgt gtcggcagat gctccccact ctgtctaccc tgcagcagag acatcctcag	4560

ggcccatgtc ctctccagt gacacctctg agagtgcagt ctgtgctgct gctcggagtg 4620

cctcaaacag ctggctaccc ctacgatgtc cctgactatg cgtcctaaag gcgcgcctag 4680

cggccgc 4687

<210> 1206

<211> 4690

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 4C

<400> 1206

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg 60

ctgctgtgtg gtggagcagt cttcgtttcg ccagccagg aatccatgc ccgagacagc 120

aagaagatga ccagaagaa ccgcaagacc cggaaggccg ccagagagaa gcacagaaag 180

accgacaacc tggacctgca gcaccagcgc agacgcaaaa agaagaagga caaggtcgag 240

atccggaatc ggagccctaa ggccaatagc accgagtgtc agggcgagca cagcagagag 300

cagaacctgc tgaacctggt gcaattgaac ctcacagcc ctcaccaccg gaaggacgag 360

gaagatcacc agaagagaca ccaccaccac aatcaaaaga agatgtccgt caacgagggc 420

aacaaccact ggcttagagt ggaaatgcct accggctggc tgctcgtggg ctacaacacc 480

agaaacacag ccagaatcc tcggctgcag cagcacctga aacctggca gcagtgcacc 540

agagccagat ggtgtcaaga gccctgtcag accctgacct tcttccactt cttcttcttt 600

ttcaaacagg tgcctctgtg ctgccccggc tggctctaaag gacaacctcc tccacctggc 660

ctgaagcctt ctacacctggc ttctcaggtg gccagaacca caggcgtgta ccagcacgtg 720

tggctgatct gcttcgtgtt ttctgtgtgc gtggaaaccg gcttctgtca cgtggcccaa 780

gtgggactcg agagactcgt tagcctgagc ggcatcaccg acgtgaacca ttgggcccag 840

cctaagccat ctcttagcaa aggcaccggc atgaacagac ccctcggcct gagagttggc 900

aaaggcgtgt gggctagact gtggctgaag aactggaagc ggttcaagct caaaaagaaa 960

tacacaggca tggaaatcct gctgtggatt ctgctgaaga tggaaattca gatcttcaag 1020

atttgctgg gcgagatgca gctgtgcctc aagaagaaag tcaacgcctg cagcaacgcc 1080

aagaaaatgc cttccagtgc ccggtgcaga cgcgagtaca gagtgacat gattcagaag 1140

aagaacaga agtccccgct gttcttccac ggcgacctgt gcagaccttc tccttgctg 1200

tcttgagca gcaggatcgt ggctcctgga cagccctga gctgtcggac tcgtagaaga 1260

tgggtccagca agatggccaa gaagtcccag cagcctctgt gtagaggcgg cccttctgcc 1320

agcgatagat gctgtagctg tagccccagc ggcttttagcg ctggaagagg cagatgtcct 1380
 gtgcagggat gtctgaggcc acacagagtt cagctgctga gaagatgggg ccctggatct 1440
 cctgtctggc agagactgtc taagggttc caactgtgc gttggtggg accaggatct 1500
 ccagtcctg agcctagaaa gggccattt ccaccactg atcctccatg gcctgtgacc 1560
 gctgtgacag tgatggctgg ctctgtgcct agcgtcagt ctgtggatgc tctggaatcc 1620

 cctggacctc tggtctcga aggccttagc agccctagaa acctgctctg gcgggaaatg 1680
 agcatcttcc tgctggcat cttcaacctg cacctgtgct actaccacag ccagagcaac 1740
 cggaacaaga gccggcagat ggaatccctg ggcatgaagc tgcagatcac acaccattc 1800
 gccagccagc cactgggcca agagatgccc aacaacacc agatcagact gctgaagccc 1860
 ggccaggcct ttggcagctt ttccgccgat ttttcagccc ctgagcaggc ccctctgaga 1920
 ctgtggtctt ggtgcggcac aagccagacc tacttcggct ctatcgaagc cctgacagcc 1980
 ctgttcacct gtagaacgc cagcatcagc gtgaacatca gcaccctgat gagcatcctg 2040

 gaagccatcc tggccatgac actgacctg aatggcagcc ctctgtgga ctgcagcaca 2100
 acaacaggca cacaccagg ctgctgtgg gagatccctt ctgttacct getggetacc 2160
 gccaaaaaga gccctaccg cttctgctgt cagcggcctc ctctgcagcc agtggagag 2220
 aagaagaacg gccggatcag cagcgtgcc cttctccac ctctgtctt gggccctaga 2280
 atgcagctct geacccagct ggcccggctt ttccctatta cacctcctgt gtggcacatc 2340
 ctgggacctc agagacacac ccctctgtg acccctgaca ccagatggat cttctccaac 2400
 cagctgcaga ccgtgcagat gctgtgtctg cctccactga agcagggcga gagaatcatc 2460

 tggcctctcg gcggctttca gatcccaac ttcttttga gcctcgcat cggacacact 2520
 ggcgctgtgt ggcatactgg aaggcggaga agagaatggg gcggcagcac cgtgtctaga 2580
 agccactgt ggatcagctc catgatctac ctgagaggca tggccttcgc ctccgacagc 2640
 agcatcagaa ccaccagagt gtcctggtgt cggagatgtg gcgcaaaag gccgcagcc 2700
 agcagcgaca agaagaagaa aagcaccgaa aagaccaaga acaagatcat ctgcaagggc 2760
 cacagaatca ccaggtggt gctgagactg ggcaacctgc ctccattctt cagaggcagc 2820
 gaggtgccct ttctagacc ttgccggacc aagtgccaga agaaggttcc aagcgctct 2880

 ccttggggac tgcaccaag aacagcctcc atcacactgc ctaccaccag cctgaagggc 2940
 agcagaacaa gctgctgccc cagatctcac ccagactgc ccagaacaaa gtggcctctg 3000
 cagtgcctgc tgcacagcct gggaacaact ggaacactcg tgtgggaaag gggcgtgctg 3060
 cagatgagaa gtctggaagc tcactgcct ctgcagacat tccacctca cactgcaga 3120
 accagccta gctctgtcc tccagcctgg attctgtacc aaggacagt gagcggagcc 3180

gtcgtgggac ttagacctgt ggctcaccat ctgccaagac ctatccaggg gctgcactgt 3240
 cctcaggctc ctcatcaacc agctctgtcc tggggaaagt ggcccgtggg aatgacagga 3300

cccgccagat gttgccggtg gcctagaaga atgtgtagct ctctggccct gccaacccgc 3360
 ctgacatctc tgatcctgcc tagcagtgat ctggccgtgc tgatctctag ctccaccagc 3420
 cactttctga tgcggagccc agtgtctgca agcagcagac tgacatgtgc ctctccacag 3480
 ctgcctcgga tgtggacatg gtctagctgg ctgaaagagt ggggaggaca ggcccacaga 3540
 cagcggaact gtagagtga cgccgttgag gaactgcaca gcaggcggat gtctgtgcgg 3600
 atcgtgaaga attgggtgtc ctgctgttac gtgcggctga gtgcagtggg actgtctact 3660
 tggagcgccc tggattccct gatcctgtcc ttccagagag tgaaaaccag ccggatactg 3720

aacctccagg tgctgaagaa gatcctgcgg agctttatga agctgtacca ctctctcgtg 3780
 atgtgcctgc ggctgcccga caagctggaa aaagctctga gcgtctgtt tatctggccc 3840
 cagcacagct acaaaggcca ggcatcggga agcctgtgcc agctgggtgc tgccgatttc 3900
 agcggccctc aagtgaccag actgcggagc ctgaaccatc tgctgattcg gtggatcttt 3960
 agcaatcagc tgacagtcca aatgtctgtc ctgccgatca tcaagaaaat gaagaaacgg 4020
 atcatgggtgc acgtcttgaa gaagaatcgg aagcagatta tctgtatcaa gaatatgttc 4080
 ctgcagcggga agggattcct gaacctgagc cacgtggaaa agttcagaga gagcacctg 4140

ggcaatttct ggatgaagct cctgcagctg ccaccagctt gcacctctaa ggccctggaca 4200
 cccagaaagc ttgtggggag agccgtgcgg agaaagggcg tcgtgatcaa cctgaagaga 4260
 ctgcagaaat tccgggctag cgtgtccttc tggactctgc tgctacaac aggcgtgcgg 4320
 acaagaggct ctccactgag actgactctg tggcctccaa gaagccagaa aagccagcac 4380
 cactgcgccc tgagaaagat cgagtgggcc acaaagctgt ccctcggcgg caaagcagga 4440
 ccacaggctc aagagaaggc caacatcctg aacagcctgc cttcctctat ggaaatcgcc 4500
 gtgctgaag aaatgtgaa ccagaagtgt ctggccctt tcgagcttaa gaagaacctc 4560

ctgctgcca cctacacacc ccacatctgt cggcacaccc ttaaaaagaa gcccagagac 4620
 atctgcagaa tcagcggtc cccctacgat gtccctgact atgcgtccta aaggcgcgcc 4680
 tagcgccgc 4690

<210> 1207
 <211> 4690
 <212> DNA
 <213> Artificial Sequence
 <220><223> Cloning cassette hTPA 1D

<400> 1207

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggt ctgctgtgtg	60
ctgctgtgt gtggagcagt cttcgtttcg ccagccagg aaatccatgc ccgagccgac	120
aagaaaaacg tgcggagcgc tagttctcct ggacatcctc ttggccccag aagaatgacc	180
agacggacca tgaccaccac caaatgatg atgatgcggc ggaccaagcg gcggagaaga	240
aaaagacgcc ggatgacat gatgaccaga agaacctgc tgaccaagaa aacctgtctg	300
accctagaa ccagcgccgc caaaaagct ctcccagac agacaatcag ccagcggagg	360
cctatccaga cacctcctgg aacaagcctg gccatctggg gcagaagaag caagatcgag	420
gcctctccta tcggcagcat caccctctg agcatcagca gacctaccag cagagccaga	480
cagagctgtt gcctgcctgg actgacacac cctgctcctc agcctctggg ctctatggtt	540
ggagctggaa caggcggagg acctgcttgt gtgcctgtgg ccgaagcttc tacaggcgt	600
tggacagctg aaggcgctgc cggcacaaga ttagagcca gcagagcccc ttgcagacag	660
ctgcctgctt ctagccctac caagtgcgag atctgcgtga agagaagaag gcggcgcaag	720
cggagcagcc agtctagatc tcccgctgct aagaaacgag agcggatgat gctccctgtg	780
cgggccagaa cagctagatc tgctctgcca caaggcaggg ctccctctgga aggaatgctt	840
ctgcctagag cactgccag cctgctgagc agaatgcctg ccagaagaga gagcagattc	900
tggttgccc tcaggccct tggactcaga cctcctcctc tgctagctg tcacctctg	960
cctcaactgc ttggacctcc tccacctcat caggccctg gcgagaaaaa cgacctgcag	1020
ctgttcgtga tgagcgacac cacctacaag atctactgga ccgtgatcct gctgaacccc	1080
tgcggcaacc tgcacctgaa aaccaccagc ctgaaccca agaaaatgga agatatgac	1140
tgggagagca accagcagct gaagtggacc cctcacatcc tgaagtccgc ctctatcgcc	1200
aagaagcgga tcaagctgag gcggaacagc accagacggg aaatgccttc tcaggccaca	1260
ccttctccac ctggacctg gagagccgct ctgggcaaag aagtgaagcg gagccagagc	1320
aagctgagac tgagaaacac aagcccttc gacaaaaagg gctttgtgat cctgagcaac	1380
atgggctgca accggtctat ctgctgacc atcgtgttct ttctggcccc ttacttcccc	1440
atgcctagca gctggtctag cagcggcaga accagactgc ctctgaggcc acagagaggc	1500
cctagacctc tgcatagatg gctgcagcag accaccggct gctctcagag aagaggcgac	1560
tgccaagaa ccatggccgg accatctgct tctctgcacc ctgcatctgg cagagcctcc	1620
agaaagacct ggcagagaag gctgagagcc ttagagcag gcggacctgc tggatgggct	1680
agacaggcca gaaaacgcaa gagagagaag cgtcccaga agtccagaca gaacctctg	1740
cagctgaaaa gctgcagacg gaagatcagc aactggtcta agctgcggag ccctggatc	1800

ttcagggccca aaaagagcat gaagagatcc cagcggcctc ctcgagcat cctgagcctg	1860
ttcaagaaga agaagcccct gacattcagc ccagcgtgt ccaagaagag gctgcctaag	1920
ctgaaggcca agaaacgccg gaaagaaatc cagcggaagg tggtaagaa cccagccag	1980
cctgtgccac tgagaaatga cggcatcacc aacggcaacg acagcaccg gtcttcagc	2040
atcagcctga agaaaagcct ggaaaagatg cccctgatgc ggagcctgct gtactccaga	2100
atgtgcctgg tgcagatccc cacacacacc tgggagcccg actactttgt gtccctgcct	2160
atgatgttca gctgggccac acagagcttt ccagtggcg cegtgtttct gaccagacct	2220
gccattcctt gctgtagctg taccagccac tccaatcctt ggagccagtc cacactggcc	2280
atccggttta tctctgcccc tcagccaagc agcagcaccg ttacagctgc tcctagcggc	2340
cagtattttg cctctcggag tatgcccaag agccggaacc aggtgctgtt tcggagaaat	2400
ctgaccccaa gccagctcgg gacactggcc cctccatata tgcctgctgcc tcagtctctg	2460
tcccagagcc tgcctcgaa gcagatccca tctcagtcga tgcctgctgc gaccaggctg	2520
acactgacag gactagaag ctccggcacc agagcctctc catctgccgt gtgtctgtgc	2580
tgtggacat gccccagcag aagctttcct gccgcctctc caagcggact gagagcacct	2640
gttggagcac aggtctctcc agaagtgaca ctgagagcca gctgtgccag ctccgccagc	2700
aaagcttgtg caggactttg gccttgggga gccaagtgc ggatgaagaa gaaggacagc	2760
accatcttca tctaccccag gctgaaaacc ttcggcgtgc cactgggcag cattctgtgt	2820
ctggctggaa gcctgagcac gatgatgatc attagacca ccagacaaga gtgcggcaga	2880
cgggccagcg tgccctgtag acctatgatc ggaagcgcca gacctggacc atggcggaca	2940
agtgtctatgc ctctgccaat gggagtcgcc ctgcctacca gctgtgaaag cggaagatct	3000
cctctgccca cggcggaag aatgccagga tctcagtcga tcatgatgag ctggatgcct	3060
ccactggctc cctgcgtgc ttgtccttgt tctctgctc ctacactgtg cctgtctac	3120
cctgctagag caccaacagc cgtgcctgcc ttacacccc tgtctgtca tctgtgcc	3180
gtgtgtctg gatgtcacct ggctgtgcgg acctccatgc ttaccttget gccaatgatg	3240
acctgaagg ccttggtaaa gacatggacc cagttcagaa actaccccag acggcacctt	3300
cacagaagcc caccaacaag ctgtcctcca ctgctcagg cttttccact gccaaagacc	3360
agcctgagag ctaccgtgcc tagacactct agcgtgtggt ccacaggact gcattgcat	3420
aggcagatta gcctgcctct gcggggcttc ctgctgcatc aacctgccc aggacaacac	3480
ctgtggctgt cccacagact gagactgcgg ctgcctagaa caaccgagat ccagctgacc	3540

atgaacgact ccaagcacia gctggaaagc cccgctctga aacagggtgc cccagctagt 3600
 cctcctacac agcagcctca gacaccccag gattctagac aggtgctggc cgtgcctatg 3660
 agcctggcct gtagcatcac cgtgtccttc gtgggccaga tctctaccct ggtgctggac 3720
 gtgtcctcca tcagccactg gaacggcatc tgggaagtga tgcccagaac actggaaggc 3780
 tgcattctccg tgaaggacca ccgacatcc cagaaccaca gcaagtgcac caccgagtgt 3840
 gtgcggacag cctgaacac caagtgtgaa atttgtgtga agaaccaccg catcctggct 3900
 atcacctga tcacccaca ggaccctcac ctggaccctg tgtgtcatcc ccatagaagg 3960

cccggctgga agggacacca cagagtgtg tttagccacc atccttcgg cagcaccaag 4020
 tctcactggc agcagagaga aagaggcgga ggccgcagag aaaagaaggg ctgtagagag 4080
 gcaagcagag ccggccagtt tctgtgtgg cggagaacat ctagaggcat gtccctgcag 4140
 tggaaagtccg gcaatgcctg cacacctctg agatgtccca gcagatctcc agccaccttc 4200
 ctgactgccc tgaacggctg gcatagatct ggactgaggg cccagaccgc ctctttctg 4260
 ctggacatca tctgcgag agcccgccct acaagctgca gcacatgtag aatgtggtgg 4320
 cggctgccc gcaaagtgc cgaaagctcc ctggccaaga aaacctgac caatcagcct 4380

agcttgcccc gacctgtgc tagcctgtg tctacactga gccagccacc acctcaggct 4440
 cctagccaag tttggacagc cgctacactg cgggtgtctg ctgtgcctgc tgctgcatgt 4500
 ccaccttga agctggctcc actgcaagt accacaacac tgaagctgat cctggctcatg 4560
 ctggaaatcg tgaccgagaa caaagtccg cagaactca agcggaactc cagcttcttc 4620
 tacaccagcg acagaggcta cccctacgat gtccctgact atgcgtcta aaggcgcgcc 4680
 tagcgccgc 4690

<210> 1208

<211> 4672

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 2D

<400> 1208

gaattcggat cccgcgactt cgccgcatg gatgcaatga agagagggt ctgctgtgtg 60
 ctgctgctgt gtggagcagt ctctgttctg cccagccagg aaatccatgc ccgacggaag 120
 atgcagagcc tgaatcacc cagcagactg accaacaatc ctccgagaaa gacctggaag 180
 atgcggaaga agtacgccc gaagcctagc cagaagaacc acctgtaccg gcagatcaac 240
 cgcgcaagc tgcagagaaa gaagtcaga agccacctgg acttcagccc ctactggatg 300

aagaaagtga agcgggccag aaaccggaac atgaagaaaa ccatgagcca cctgatcgcc 360

catcaggccc tgaagatgtc tggcctgaga ctgtttcacc ccagactgct gaccagaaag 420

aagcccgga agcagaaaaa gggccacatg atcttcagcc ggcggaagtg gcagatccgg 480

cacgtgctga agaattgat cccagccctg aacgcccagt ggatgttcct gagaatcgct 540

agccacaga tcatgcagag aaccagcgcc gaccgggtcc ggatgaagcg gagaatgcag 600

aacctggaca atctgggcgt gccctggcct ctgttgccctg gattgctgct ggcccatatg 660

tacggcttca gcacctacgg caccagaaa ggcgagtgcg tgtgtctgca gtgtctgagc 720

ggcagcagcc tgttcacct gaagcagccc ctggacctga agatctccaa gaccttcattg 780

gccagccctc agattatgca gcggatgagc gccgtgaact tcgagacaat cctgcaggcc 840

catcctcagg tgccagctct tgcctctcaa gcttgggtggc ccgctagaag aggccctctg 900

acatctgctc caagcgaca gcagtcctg acacggacac tggaaagcgc cggactgttt 960

ccttggtctg acaccagtg ccgggccttc attcacacac ctagaagccc tggtgcagc 1020

gtgtaccca acatgtgctg gcggtacaag aaacggggag tgatcgctg gcggatctac 1080

cctctagca catgcagcct gccttgca gaagcctgatcc tgattcagca cggcggcac 1140

ttcaccttc ggttctgggt cgagaagctg agctggaaca tctgcaagaa cctgagcctg 1200

tacctggata agttcgtgca gcggctgctg tacgtgtaca tcatcgagac aaacgtgttc 1260

gtgtgaacc tgttcacgt gccagtgaac cagatcttca tgatggcctt ctacctgaag 1320

tacaccgaga aggcctgggt catggaactg gaatggctga tccagcagca gtgtaccag 1380

cggaagagaa tgaagaccgg cgccatccaa gagaagggcg ctattcaaga gaaaggggcc 1440

atgaccaagc ggatctgctg ggtcaatttc gaggcctgca gagagatgga aagcctgagc 1500

gccccgaga agatcacct gtttgaagcc cacatggccc ggtgcaccag catcaatgtg 1560

ctgtgtgtca gggccagcct gatcgagaaa ctgatgaaag aaaagcgcaa gatgaagcgc 1620

aaccaggtgg catccctca aatcatgcaa cggtgttca tcaagggcta ccagaacaac 1680

catttcagct tccacctca aaacttcgcc ttcttcagct ccttcggcaa caacaagtat 1740

atcaacatcc tgacctttct gccagcaga ttcccttggg gacctcctcc actgggagcc 1800

cttagagcta cagctcctgc tacagctgct cccaggcac agacacctca ttggagagcc 1860

gccaccacaa gcagcatgag cagctctcca agagccgagc ctaccagctc tagctcttgg 1920

gccacttgct ggcttagatg ctgcagctcc agctgctatt ggagcctgtc tagctggcct 1980

cctgctggcg ctgccgaagc cacaataacc agaaccagaa gccgcgagag ccagcgggga 2040

agaatgctga ctiggagaag ctccctgtgg ctgcaggga ccagatgttt tacaggcgtg 2100
 cggaccagct ccaggtgcag cctgatggaa cagatccctc acctgaagtc taacagccgg 2160
 aagaaactgc tcgaggacat gaagcagaac ggcttcacca gacggcggaa cagcagaaag 2220
 cagagccaag tgcagctggc catccagggt ctgctgggtg acaagcacia gtactttctg 2280
 ttcggcagag ccacatttct gctggctctg tgggagtgtg gcctgcctca ggctagactg 2340
 tgctgatcg tgtctagaac cctgctgctc gtgcagtcta gacaccaag ctggccttgg 2400
 accagatgcc tgagaatgcg gcctccacgc agccactgga actctgccta cctggggaga 2460

 acactgctcg tgacctgcat cctgtaccac agatggatcg tgaccagcat gtgccagagc 2520
 cagagatggc tgacctccac cacctctaga agctctgccc tgatgtggac ctgggtgtgt 2580
 acaagagggtg gcggcaagcg gaagaaaaag atgtgcaagg tgtccggcgg ctgcaccgcc 2640
 tgtgttgaaa gatgtccttg gaagggcatc tgttggaagt ggctgtgac agtggccgcc 2700
 atgagcagaa cacctccaag acgctgtgtc ggccacagag agggcagcga gtctgataat 2760
 ctgggcctgc tgtactcctt tccacctgtg ctgttcaagg ccgaccagag cgaaagctct 2820
 ctgagcagcg gcaacagcgt gatcgtgcac aagatcgtgc tgggtttcct gaagtccttg 2880

 agcagctaca actgcgagag aagaatcagc ggcatccaga agagagccat cgagttcgcc 2940
 gtctgaagc tgcigaacat ggacctcggc aagggaactga cacaccccg gcctctgaag 3000
 aggacctgc agaacaagg gaacaagaac atcaagcggg tcaaccagaa gaagggaac 3060
 atcaagagga agtccatct gctgcatctg attgtgtgta acagccccga gagcaaccgg 3120
 gaaaagatca tcaacccac catcagctgc ccttttcaga gcccacaaa gagactggga 3180
 agccctctc tgcacctgtg tcagcctctg aggccctatc ctatcagcga gggcctgacc 3240
 atgaccaccg gcagaaacat caacagcaac tcctgatga ccaactgcct gttcagcccc 3300

 atcttctgt gccaccacgc catcatgcac cggaagatga caagccctca cttcagactg 3360
 ttctccagca agatcccaca tccacaggtc ccaagtgtgg tggcctgtg caagtttaca 3420
 caccctgca ccatgctgct gcccgaaggc gctttttgga agcctctag ccagggcac 3480
 tccagctgtc tgatgacagg ctgttggcag tggccagcg tgacaagcct ggaatggaca 3540
 gcccagaga gaggtgttc ctctggctg atgaagcaaa catggatgaa gtcttggacc 3600
 ctgcgggacc ccagctacag atccatctg gaatacgtgt ccacacgggt gctgtggatg 3660
 cccacctcta ccgtgcctaa gttctttctg accttcagcc agatccggat gtgcgcctg 3720

 tctcaccta gttctacat cagctccacc gtgtgctttc tgagcaagca ctgcatgacc 3780
 gcctgcacac ctggaaccag cctgcagtgt tactgaacc tggccaacgg cctgtggttc 3840
 aacctgatct tccggaacaa aaagaccaag ctgtggttct cctgattaa catccaccac 3900

cgcaagaacc cactgctgcc catgcggctg gaaaaaaagg ccacttggat gcggcggacc 3960
gagctgtctc tggaaccttg gattccttac ctgcatcagc agaaaaccca gtggctcccc 4020
atgagaagcc tgggcgagcc ttggcgagct ggatttcagt ggggagagtc tccctggcaa 4080
gtgatggcct ctctgacagg cagacgcaag aaaagagagg atcactgcgg actgcaagag 4140

aaaaaaagcc ggaagctgat gtccagctgc gccgctcctc cacatagact gctgggacct 4200
agcagatggg gaagctgtgg gagagcctgt tcttgtggca gaggtgtgg aaccctaga 4260
ggcgactgga agagacaccc acctcggcgg attctgtttc acgtgcggaa catcgtgtac 4320
ggaatccaag tgatgctgtg ctgtcacccc gcctggctgt ctccaatcag cgcttgtcct 4380
cgctgctgc ctatccatt ccacgttctg gccctggaag tgacattccc tccaggcact 4440
gccatgcctc agatgcaatt gcaggcactg gcaatgtggg agaaaggctg ggacaagcct 4500
ctggaaaaca cacagatccc caggacaagc ccactgtgga agatcacaat ggtgctgaca 4560

tacccaact gcgtggtgca cgtcctgatg ttcggcggca agaagcggag caagttcggc 4620
taccctacg atgtccctga ctatgcgtcc taaaggcgcg cctagcggcc gc 4672

<210> 1209
<211> 4687
<212> DNA
<213> Artificial Sequence
<220><223> Cloning cassette hTPA 3D
<400> 1209

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggtc ctgctgtgtg 60
ctgctgtgtg gtggagcagt cttcgtttcg ccagccagg aatccatgc ccgacagaac 120
accagaagca ccaacctgga aaagaacccc agcctgaaga agcagagcca gcggagagga 180
aagctgagca gcagaaagaa gggccacacc aagaaccggc ggaaggccaa gagaaagccc 240

cagatcagcc agaagaagga ccctgccggc aagctgaaga aacacctgaa ccggaagctg 300
cacctgacca gatcctgcct gatcgacctg accatgatga tgagccagaa gctgtggaag 360
aaccagcgca agagaatccc tctgccttct ccacggcagc atctgctgcc tcagtatcca 420
ctgcatectc cacctccatg cctgtgtgtg ctccaccaca gacaccatct ggcctttctc 480
gagatggcct gcagcagcca gcacaccac agcatcaaga tctggatcag cttcagccac 540
gaggacctgc ctagaatgct gcccatcagc agccctctgc acagaccca gatgcctttc 600
tggacctgca cttttctgc caccacatgg ggcacatggg agacaccttc tacatggggc 660

tggcggacat tcggccctgt gtactacgtg tgcaaccgga tgaacgtgtc cagcgtgctg 720

aagcctttcc tgttcaccgt gcctatcgag gacatgagag agtgcaccct gggcagaaac 780
agaatgaatg tgtcctctgt gctgaaaccc tgtctgatcc ccgtgccaat cctgaccaca 840
ctgagcttcg tgtctgatcg ggaaagccgg cggaacagac ggtacagaaa gatctacggg 900
gagctgaaga tgtccctgca ggccctgcct ctgaccttta gcacactgct gtgggacagc 960
agacacacca ccaccacaag cagccccaga agatccctg ctctgagagc tagaggcggc 1020
accacaatcg gcgaagtgac aagcagaggc gccagcagct ctaccagcag agacagcaga 1080

agctttttca ccagcgtca cccagcaga cctgcagaa tgagactgta ccagagcaac 1140
ggcatggaag cctgcggcac acacctaca cctagactgt ctagaggccc tccactgcac 1200
accagaacca tgagcctgag caacatcctg atgaagtcc ggctgatgct gcagaagcag 1260
tgctgtaca acctcgtgat caagcacct ctgatcttcc ggatcaacct gcggagacag 1320
ggcaagacca aagacggcgt tgtgcagagc ctgggcttcc tgaaccagca gatcatcctg 1380
cagaaagagt tcttcatctg cctgctgatg ttcataaagc ggtggaagcc agccgccaca 1440
aagacacctc caccactgat tctgtggcct caggccgctc ctgtgcaca gaagagaggc 1500

ctgttcagcc tgttcttctc ccactgcctg tgccaccaga tgaagtgcct gaccgccgtg 1560
gattgtctgc aggccttctg ggacatgatg attcgcaaga tccagaagcg gcggagaacc 1620
gccaaccggc taaaaagaa atacctggtg cagtgtacca acctgagcgt gcccatgatg 1680
ctgaccatcc tgatctggaa gcgggtgttc atcctctgc tgagcgacaa gaagtgtctg 1740
agagtcagat gcggcggatg gctgtgtggc tggacaccta gaggcaagaa caagaagcgg 1800
agaaagctgc ggccaagca cctgaagaaa accagcgcca aggtgtccgt gatcaccatg 1860
aagctctggg agaagcactt caaggccctg aactggaacc tggctgtgtg gattctgaac 1920

ctgaagatga tgtggctcaa gaagtcacc aagagcagac agagcagccc attcctggct 1980
cggagctgga ataccatgca atggaacaac aagaaaatgg ccatgaccgt gatcgtggc 2040
gcccaccact gtcagtacaa gctgacctac accaaagtgt ggaagatgaa ttggaagaaa 2100
atgatgatcg gctcccaga cctctgttt agccactgg attcaagccc actgcagttg 2160
ctgctgcacc ctcacggcaa gagatgcaac ccttgctgca gactgacctg gatgagcaga 2220
gagtgggaaa agcggaagca gatcctcggc ggaggcggca agtacaagaa gtacttctg 2280
aagcggattc tcatccggaa ggctatgaca gtgctggccg gcgataagaa aggcctggga 2340

agattcatga gatgcgtgca gagcgagaca aaggccgtgt ctctgcagct gcctctcggc 2400
cgaagaaagt ccggcgtgat gaagtgttg gatctgtgcc ccagactgga ctttcacccc 2460
agatctagct ctggcgga gaagctgaag cactgtttca aagcctgggg cctgtgcttc 2520
ttctacctgc tglacttca gaagaaacgg cccgagtggc tgagcgttga cctcctgga 2580

tctgtctgga ttctgccctg catggacctg gacggaatgc tgacagtgat cggccaggga	2640
ctcgtgggca tgacccctag agatctggga acagtggctg gcgccaccgc acagattcag	2700
aggcctatcc aggtgcagac aggcggcaga ctgttcctga ttcacctgag aaaggtggac	2760
accaccatc tgagggtcgt gaccaagacc gtgacagcca caacagtga cggccagagg	2820
atgcggagac tgaagtgcaa ggcctgtcgg ctgagatggg ccagacctga acctgtctga	2880
caggctcctc caaagagcca ctttcacct catcctagcg gccctccag aacctctagc	2940
ctgcagctca gacctattcc tccacacctg agacaccac tgctgtgaa gggaaagaac	3000
agccctgtct gcaaaaagaa actgcgggtg cagaaccagg gccatctgt gatgatcctg	3060
ctgcataacg ccagacagcc cagcaggcct accggaagaa cccctaccac aagactgatg	3120
gcccctgtgg gcagcgtgat gtctttagc ctgtgaccc agccatctcc tgccagcgca	3180
tgtacaatgc caccactcct gcattccacag tgggccccac atagtgtgg actgtctcca	3240
ggcgcttgca gacctgcctg tacctgcac agcatgacca ccattccag agcccatgg	3300
cggctgagaa tccaagcct gaggaagtac cggcagaaca tcgagatcac ccctcagcgg	3360
tctaaggccc aggtttccgt gtacagcggc aatctgtga gcttctccag acggggcatg	3420
aagagtagcg tgcggctgaa gaacagcatc cctcacgtgc caaaagccac cgccgtcac	3480
tctgtgacag tgaagctgca gtacctgtt ttcctgaccg tgtgcggctt cgaccgggtg	3540
ttcctggta agatctgcaa gaagaagctg ctctcaage tgctgagagg cccagacgg	3600
aaagtgtga tgggtctttg gctgcccccc aaccagagtc tgcagaaaag ccaggtgttc	3660
cagtgggtgc tgcggaccga aacctacatg gaaatgcact acggccatca ggccctcag	3720
gtggccatgc tgcctaaact gctgtgtaga cagatgtcc ccactctgtc cacactccag	3780
cagaggcatc ctgaggacc ttgtctcct cctgtgacac ctctgagagt gcagtctgtg	3840
ctgtcctgg gagtgcctca gacagccgt tttagcggcc ggattctgca ccagccagaa	3900
atggccgcca tgagactgat gccaagtgc ctgaactcca ccaacagctg gtggacagtg	3960
gcccctagat gtctagaag gcgcgtggac attagccccg gacctacac tcctagcctg	4020
gcctcttgtg cctctgtggc cattggaaaa ctggcactgc tgggcgcac tgccccttgt	4080
ggcgcagctg gtgctagaga ggctggaaga tttgccgtgc tgggcacat ggttatgaag	4140
ggtgtgccg cagcctcctg tcagtctcct ccattctcaa gagagacaac ccctagcagc	4200
gacgccacca gacggacaag acctattgcc gctcagagca aaaagacat gactgccgcc	4260
ggactgaccc ctcgagaaaa cctgcagaga aatctgaagg tcctgggcgc caagaagatc	4320
accttctga gaaacagcag acgcgccaca cctacctta agggcagcct gagaagaaag	4380

tacctgagag tgaacatccg caagctcatc tggaccaagc agcggagctt cctgtctctg 4440

ttccccaagc tgagagccac cgagcagatg accaatgtgg gatgcctgct caagaaaagc 4500

agccaattgc ggcggagctg gcgcaatgtg tcccggatca gcaacatgga acacaggctg 4560

accatggaca gcgccctgag cctgacaaag agagagggcc ctgagacaag cgagaagaag 4620

aggaagtgtc ctggctaccc ctacgatgtc cctgactatg cgtcctaaag gcgcgcctag 4680

cggccgc 4687

<210> 1210

<211> 4690

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hTPA 4D

<400> 1210

gaattcggat cccgcgactt cgccgccatg gatgcaatga agagagggtc ctgctgtgtg 60

ctgctgtgtg gtggagcagt ctctgtttcg cccagccagg aaatccatgc ccgaaacaga 120

aagaccagaa aggccgccag agagaagcac cgcaagaccg acgacaagaa gaagaagtcc 180

accgaaaaga ccaagaacgc caagaagatg cccttccagc agcggcctcc tctgcagcct 240

gttaacctgg atctgcagca ccagcgcaga cgcaaaaaga agaaagacaa ggtcgaaatc 300

cggaatcgga gccctaaggc caatagcacc gagtgtcagg gcgagcacag cagagagcag 360

aacctgctga atctggtgca gctgaacctc cacagccctc accacagaaa ggacgaagag 420

gaccaccaga agcggcacca ccaccacaat caaaagaaaa tgagcgtgcg ggctagcgtg 480

tccttctgga cacttttggc aacaaccggc gtgcggacaa gaggtctctc actgagactg 540

acactgtggc ctccacgggt tccaccttct ccacctcttg ctctgggccc cagaatgcag 600

ctgtgtacc agctcgcccg gttcttccct atcacacctc ctgtgtggca catcctggga 660

cctcagagac acacacctca ggctcctctg aggtctgtgt cttggtgcgg cacaagccag 720

acctacttcg gcagcagacc atctccttgc ctgagctggt ccagcagaat tgtggccct 780

ggacacgccc tgagctgtcg gactagaaga agatggtcta gcaagcgggt gatcttctcc 840

aaccagctga ccgtgcagat gctgtgcctg ccaatcacac accatttcgc ctctcagcct 900

ctgggacaag agatgcccaa caacaccag atccggctgc tgaagccctg cagagtgaac 960

gccgtggaag aactgcacag caggcggatg tctgtgcgga tcgtgaagaa ctgggtgtcc 1020

tgctgttacg tcgggtgtc tgctgtgggc ctgtctactt ggagtgcct ggacaggaa 1080

aagaagaacg gccggatcag cagcctgaaa aagaaagtga atgcctgcag ctccctgatc 1140

ctgagcttcc agcgcgtaga aaccggcatg gaaatcctgc tgtggattct gctgaagatg	1200
gaaattcaga ttttcaagat ttgcctgggc gagatgcagc tctgcggcca ggccttttga	1260
agcttttagcg ccgatttcag cgccttcag atcattaaga agatgaagaa acggatcatg	1320
gtgcacgagc tgaagaagaa tctgtctgtg cctatgtgct ccagcctggc tctgccaaca	1380
ggcctgacat ctctgatcct gcctagcagc gatctggccg tctgatctc tagctccacc	1440
agccactttc tgatgcggag ccctgtgtgt ccaagcagca gactgacttg tgcctctcca	1500
cagctgcccc ggatgtggac ttggtctagc tggtgaaga acgagggcaa caaccactgg	1560
cctagagtgg aaatgcctac cggctggctg ctctgctggc acaacaccag aaacacagcc	1620
cagaatcctc ggctgcagca gcacctgaaa cactggcagc agtgaccag agccagatgg	1680
tgtcaagagc cctgtcagac cctgacctc ttccatttct tcttctttt caaacgggtg	1740
tcctgtgtt gccccggctg gtctaaagga caacctctc cactggcct gaagccttct	1800
agcctggctt ctcagggtgc cagaaccaca ggcgtgtacc agcacgtgtg gctgatctgt	1860
ttcgtgtttt tctgtgtgt ggaaaccggc ttctgtcacg tggcccaagt gggactcgag	1920
agactgggtg ctctgtccgg catcaccgac gtgaaccatt gggcccagcc taagccatct	1980
cctagcaaag gcaccggcat gaacagacc atcgccctga gagtggcaa aggcgtgtgg	2040
gccagactga tcttgccat gacactgacc ctgaacggca tggccaagaa gtcccagcag	2100
cctctgcagg tctgtctgag actgggaaac ctgcctccat tcttcagagg cagcaggtg	2160
ccctttccta gacctgtcg gaccaagcct gcctgcacaa gcaaggcctg gactcccaga	2220
aaactcgtgg ggagagccgt gcggagaaaag ggatctccac tctgggattg ctccaccaca	2280
acaggcacac accacggatg cctgtgggag atcccatctg tgacctgct ggcccatcct	2340
agaaccgct ctatcacct gcctaccaca agcctgaagg gctccagaac cagctgctgc	2400
cctagatctc accccagact gcctaggacc aaatggcccc tgcagtgtct gctgcacagc	2460
ctgggaacaa ccggaacact cgtttgggaa aggggcgtcc tgcagatgag atccctcgaa	2520
gcccattgtc cactgcagac ctccatctg caccactgca ggaccagcc tagctcttgt	2580
cctcctgcct ggattctgta ccaaggacag tggagcggag ccgtcgtggg acttagacct	2640
gtggctcacc atctgcctag acctatccag ggctgcact gtccacagcc acctcatcaa	2700
cctgtcttga gctggggaaa atggccctg ggaatgacag gccctgccag atgttgacaa	2760
tggcccagac ggtgccagaa gaagttcca tcagcctctc catggggcct cgtgctcaaa	2820
aagaaccgga aacagatgct gaaccagaag tctctgccc cttttagaga gagaccctg	2880
ggcaatttct ggatgaagct gctccagctg cctgtctga tcaacctgaa gagactgcag	2940

aagttcaacc tgcacctgtg ctactaccac agccagagca acagaaacaa gagccgccag 3000

atggaatccc tgggcatgaa gttgcagtcc cagaaatccc agcaccactg tgcctgcgg 3060
aagatcgagt gggccacaaa gttgtctctc ggcggaag cgggaccaca ggctcaagag 3120
aaggccacct ctcgattct gaacctgcaa gtgctcaaga agatcctgcg gagctttatg 3180
aagctgtacc actctctggt catgtgcctg cggtgagga ccaagctgga aaaggctctg 3240
agcgccctgt tcactgtgcc ccagcacagc tacaagcccc tgttctttca cggcgacctg 3300
tgcgagtggg gaggccaggc tcatagacag cggaactggc tgaaaaactg gaagcggttc 3360
aagcttaaaa agaagtacat ccagaagaag aagcagaagt ctaacaagat catctgcaag 3420

ggccaccgca tcaccatcat ctgtatcaag aatatgttcc tgcagcgcaa gggttctctg 3480
aacctgagcc acgtggaaaa gttctgtaga ggcgcccta gcgcagcga tagatgctgt 3540
tcttgtagcc ccagcggtt cagtgcggc agaggaagat gtctgttca gggtgtctg 3600
aggccccaca gattcaact gctgagaaga tggggccctg gctctcctgc tggacagagg 3660
ctgtctaagg gctttcagct gctccgttgg tggggaccag gatctcctgc tctgagcct 3720
agaaagggcc catttcacc acctgacct ccatggcctg tgaccgctgt gacagtgatg 3780
gctggatctg tgctagtgc tcagtctgtg gacgccctgg aatctcctgg acctctggct 3840

ctgaaggac ctacgagccc tagaaacctg ctttgagag agatgagcat ctttctgccc 3900
ggcatcttca ccgccaagaa aagccccacc agcttttct gcaatctct gaacagcctg 3960
ccaagctcta tggaatcgc cgtgtgcaa gaggacagca aaaagatgac ccagaagggc 4020
caagccttcg gctccctgtg tcagcttgtg tccgtgact tctctgccc tcaagtgacc 4080
cggctgcgga gcctgaatca tctgtgatc acctacacac ccacatctg cagacacacc 4140
ctgtgagcc ctgacaccag atggatcttt agcaatcagc tgcagacagt ccagatgctc 4200
tgtctgcctc cactgaagca gggcgagaga atcatttggc cctcggcgg ctttcagatc 4260

cccaacttct ttggagcct cggcatcgga cactggcg cctggtggca tactggaagg 4320
cggagaagag aatggggcgg cagcaccgtg tctagaagcc ctctgtgat cagctccatg 4380
atctacctga gaggcattggc cttcgccagc gacagcagca tcagaaccac cagagtgtcc 4440
tggtgcagaa gatgcggcgc caaaagcgt gccgccagct ctattgaagc tctgaccgt 4500
ctgtttacct gccggaccgc cagcatcagc gtgaacatca gcacctgat gtccatcctg 4560
gaagcactta agaagaacc cagagacatc tgccgcatca gctgccggtg tagacgcgag 4620
tacagagtga ctatgggcta cccctacgat gtccctgact atgcgtccta aaggcgcgcc 4680

tagcgccgc 4690

<210> 1211

<211> 5299

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 1C

<400> 1211

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60

gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120

atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggagc cctgtacact 180

ggtttctcca tctctgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg 240

tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300

aaactcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360

ccgctcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt 420

acaaagtatg gaaatatgac agaggatcat gtcattgatt tgcttcaaaa cgctgatccc 480

cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540

acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600

gagatgtccc ggcatctctt ggagcaaaag ccgacggacg cacctccaa ggaaagcctg 660

gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720

atgagcacca gacgggaaat gccttctcag gccacacctt ctccacctgg accttgaga 780

gccgctctgg gcaaagaagt gaagcggagc cagagcaagc tgcggctgag aaacacaagc 840

cccaccgaga tccaattgac catgaacgac agcaagcaca agctggaaag ccccgctctg 900

aaacaggtgt cccctgcctc tccacctaca cagcagcctc agacaccca ggatagcaga 960

caggtgctgg ccgcttcttc tcttgacat cctcttgccc ctggcgactg ccctagaaca 1020

atggctggac cttctgcctc tctgcacca gcatctggca gagccagcag aaagacctgg 1080

cagagaaggc tgagagcctg tagagctggt ggacctgctg gatgggctag acaggccatg 1140

acactgaagg ccttggtcaa gacctggaca cagttcagaa actaccccag agtcggagcc 1200

ggaacaggcg gaggacctgc ttgtgttctt gtggccgaag cttctactgg cgcctggaca 1260

gctgaaggcg ctgccgaac aagatgcaga gcttctagag ccccttgag acagctgcct 1320

gccagctctc ctaccaagtg cgagatctgc gtgaagagaa ggcgccggag aaagcggagc 1380

agccagtcta gatctccgt gcctaagaaa cgcgagcgga tgatgctgcc tgtgcgggcc 1440

agaacagcta gatctgctct gccacaaggc agagccctc tggaaggaat gcttctgcct 1500

agagcactgc ccagcctgct gagcagaatg ccagccagaa gagagagccg gttttggctg 1560

gcactgcagg ctctgggact cagacctcct catctgccta gctgtcaccc tctgcctcaa 1620

ctgcttggac ctctccacc tcatcaggcc cctttcgaca agaaaggctt cgtgatcctg 1680

agcaagggca agaagcgccg gaaagaaatc cggcggatga ccagacggac catgaccacc 1740

accaaataga tgatgatgcg gcggaccaag cggcggaggc gaaaacgtag aagaatgacc 1800

atgatgaccc gcagaacctt gctgaccaag aaaacctgtc tgacccttag aaccagcgcc 1860

gccacaaaag ctctgccag acagacaatc agccagcgga ggcctatcca gacacctcct 1920

ggaacaagcc tggccatctg gggcagactg cctctcagac cacagagagg acctcggcct 1980

ctgcatagat ggctgcagca gacaacaggc tgctcccaga gaagaatcgc caagaagcgg 2040

atcaagctga ggcggaacac actggccatc cggtttatct ctgccctca gcctagcagc 2100

agcaccttta cagctgtcc tagcggccag tacttcagca gcttcttcta caccagcgac 2160

cggaccaagt gtgaaatctg tgtcaagaac accgcatcc tggctatcac cctgatcacc 2220

cctcaggacc ctccctgga cctgtgtgt caccacata gaaggcctgg ctggaagggc 2280

caccacagag tgggtgttag ccaccatcca agcggctcca ccaagagcca ttggcagcag 2340

agagaaagag gcggaggccg cagagaaaaa aagggtgca gagagatgcc cagcagctgg 2400

tctagctctg gcagaaccgc cgacaaaaag aacgtgcgga gcagaaccag actgacctg 2460

acaggcacia gaagcagcgg cacaagagcc tctccaagcg ccgtgtgtct gtgctgttgg 2520

acatgccct ccagaagctt cctgccgca tctccatctg gactgagagc acctgttga 2580

gcccaggctc ctctgaagt gacactgaga gccagctgtg cctctagcgc ctctaaagcc 2640

tgtgctggac ttiggccttg gggagcccaa gtgcggaaca aagtgcgga gaacticaag 2700

cggaacctgg caaaaagac cctgactaac gcctgcgga gtatgccaa gagcagaaac 2760

caggtgctgt tcagacggaa tctgaccca agccagctga gaactctggc cctccttac 2820

atgtctgtgc ccagctctt gtctcagagc ctgtccagaa agcagatccc cagccaatca 2880

atgtcgtga ccgcttctt cctgtcgac atcatctga gaagcctgct gtactccgg 2940

atgtgcctgg tgcagatccc tacacacacc tgggagcccg actacttctg gtccctgcct 3000

atgatgttca gctgggccac tcagagcttt ccagtgggag ccgtgttctt gaccagacct 3060

gccattcctt gctgcagctg taccagccac agcaacctt ggagccagtc cttaagaag 3120

aagaagcccc tgacattcag cccagcgtg ccaatgtctc tggcctgtag catcacctg 3180

tccttcgtgg gccagatcag cacactggtg ctggacgtgt cctccatctc tcaactggcg 3240

aagcgcaaga gagagaagcg gtcccagaag tcccggcaga accatctgca gctgaagtcc 3300
tgcagacgga agatcagcaa ctggtccaag ctgagatccc cgtggatctt ctaccctcgg 3360
ctgaaaacct tcggcgtgcc actgggctct atcctgtgtc tggcaggctc cctgagcacg 3420
atgatgatca ttagcaccac cagacaagag tgtggcagac gggcctccgt gcctttaga 3480
cctatgatcg gcagcgctag acccggacct tggcggacat ctgctatgcc atctgccatg 3540
ggagtgcgcc tgcctaccag ctgtgaaagc ggaagatctc ctctgccac cggcgggaaga 3600
atgcctggat ctcagtctat catgatgagc tggatgcctc cactggctcc ctgtgccgct 3660

tgtccttggt ctctgtctc tacactgtgc cctgtctatc ctgcaagagc ccctacagcc 3720
gtgcctgcct ttacacctct gtctgtctac cctgtgccag tgcgtcttgg atgtcacctg 3780
gccgtgcgca cctctatgct gacactgtct cccatgagac accctcacag aagccacct 3840
acaagctgcc ctccactgct ggaagctttc cactgccaa gggccagcct gagagctacc 3900
gtgcctagac acagctctgt gctggccact ggactgcac tgcatcgga gattagcctg 3960
cctctgaggg gcttctgtct gcatcaacct ctgcctggac aacacctgtg gctgtccac 4020
agactgaggc tgagactgcc aagaacaggc gagaagaacg acctccagct gtctgtgatg 4080

agcgacacca catacaagat ctactggaca gtgatcctgc tgaaccctg cggcaacctg 4140
cacctgaaaa ccacatctct gcggagagcc agacctacct cctgcagcac atgcagaatg 4200
tgggtggctga agctggcccc actgcaagtg accacaacac tgaagctgat cctggctcatg 4260
ctggaatcgc tgaccgaaga ggccaagaaa tccatgaaga gatcccgcg gagcaagatc 4320
gaggcctctc ctatcggtc catcatgaag aaaaaagaca gcaccatctt catcaaccag 4380
cagctcaagt ggacccctca catctgaag tctgccagcg tgtccaagaa gagactgccc 4440
aagctgaacg gcatctggga agtgatgccc cggacactgg aaggctgcat cagcgtgaag 4500

gaccaccgga caagccagaa ccacagcaag tgcatcaccg agtgtgtgcg gacagccctg 4560
aaccagagaa aggtggtcaa gaacccagc cagccagtgc cactgagaaa cgacggcatc 4620
accaacggca acgactccac cagatcctgc tccatcagcc tgaagaaaag cctggaagaa 4680
atgccctga tgaacgcaa gaaaatggaa gatatgatct gggagagcaa catggcggc 4740
aaccggtcca tctgcctgac aagactgccc tgcaaagtga ccgagtccag ccaaagacca 4800
cctcggagca ttctgtccct ggctctaga gccggacagt ttcccgttg gcggagaacc 4860
agcagaggca tctccctgca gtggaagtcc ggcaatgcct gcacacctct gaggtgccct 4920

agcagaagcc ctgccacatt tctgaccgca ctgaacggct ggcacagatc tggacttagg 4980
gtcagcaac ctacgtgcc aggccttgt gctagcctgc tgtctacct gagccagcct 5040
ccaccacagg ctccaagcca agtttggaca gccgccacac tgagatgtcc cgctgttctt 5100

gcagctgctt gccctcttat cgtgttcttt ctggcccat acttccccac accactgagc 5160
atcagcagac ccacctctcg ggccagacag tcttgttgtc tccccggact gacacacct 5220
gtcaccagc ctcttgctc tatgggctac ccctacgatg tccctgacta tgcgtcctaa 5280
aggcgcgcct agcgccgc 5299

<210> 1212

<211> 5281

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 2C

<400> 1212

gaattcggt cccgcgactt cgccccatg catcgacggc gtcacggag ttgccgggaa 60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
atgcttggtta ggccgctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
ggtttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg 240
tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300
aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360

ccgtcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt 420
acaaagtatg gaaatatgac agaggatcat gtcattgatt tgcttcaaaa cgctgatccc 480
cttaaagttt accctctctt gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gtcctgttc 600
gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacttccaa ggaaagcctg 660
gaattggagg acccgagtag tgggctgggc gtcacaaaag aagacctggg acccgtgccg 720
atgcggcaga tcaacagacg gaagctgcag agaaagaagc gccggaagaa gagagaggac 780

cactgcggac tgcgggccag aaaccggaac atgaagaaaa ccatgagcca cctgatgcc 840
catcaggccc tgaagatgct tggcctgaga ctgtttcacc ccagactgct gacacggaag 900
aagcctggca agaaccctcg gagaaagacc tggaagatgc ggaagaagta cggccagaag 960
cctagccaga agaaccacct gtacggcaag ggctgacac accctgtgcc tctgaagaga 1020
accctgcaga acaagcggaa caagaacatc aagcgcgtga accagaagaa gggcaacatc 1080
aagagaaaga gcatcctgct gcacctcatc gtgctgaaca gccccgagag caacctgcag 1140
gtcctcctc aagttccagc actggctcct caggcttggg ggctgctag aagaggccct 1200

ctgacaagcg ctccatctgc tcagcagagc ctgaccttcc tgcctagcag atttcttgg 1260

ggccctcctc cactgactg gaactctgcc tacctgggca gaacactgct cgtgacctgc 1320
 atcctgtacc acagatggat cgtgaccagc atgtgccaga gccagagatg gctgaccagc 1380
 accacctcta gaagcagcgc cctgatgtgg acccagtggc ctagcgtgac aagcctggaa 1440
 tggacagccc aagagagggg ctgtagcagc tggctgatga agcagacctg gatgaagtct 1500
 tggagcctgc gggaccccag ctacagatcc atcctggaat acgtgtccac cagagtgtctg 1560
 tggatgcccc catctacagt gggagccctg agagccacag ctctgcaac agctgtctca 1620

 caggctcaga cccctcattg gagagccgcc acaacaagca gcatgagcag cagccctaga 1680
 gccgagccta caagctctag ctcttgggcc acctgttggc ccagatgttg cagctccagc 1740
 tgttactggt cctgtcctc ttggcctcct gctggtgctg ccgaggccac aaataccagg 1800
 accagaagca gagagtccca gcggggcaga atgctgactt ggagaagcag cctgtggctg 1860
 cagggcacca gatgttttac aggcgtgcgg acctccagca gacacccttc ttggccttgg 1920
 accagatgcc tgagaatgcg gcctcctaga agcaacagcc ggaaaaagct gctcgaggac 1980
 atgaagcaaa atggcttcac ccgttacaag aaacggggcg tgatagcctg gcggagagcc 2040

 actttcctgc tggccctttg ggagtgcagt ctgccccaa gctagactgtg cctgatcgtg 2100
 tctaggacct tgcctgctgt ccagagcaga tgcagcctga tggaaacagat cctcacctg 2160
 aagtcctggt ggtgtacaag aggcggcgga aagcggaaga aaaagatgtg caaggtgtcc 2220
 ggccgctgca ccgcctgtgt tgaaagatgt ccttgggaagg gcatctgctg gaagtggcct 2280
 gtgacagtgg ccgctctgat cctgattcag cacggcggca tcttcacctt ccggttcttg 2340
 gtcgagaagc tgtcctggaa catctgcaag aatctgtccc tgtacctgga caagttcgtg 2400
 cagcggctgc tgiactgtg catcatcgag acaaacgtgt tcgtcctgaa cctgttccac 2460

 gtgccagtga atcagatctt catgatggcc ttctacctga agtacaccga gaaggcctgg 2520
 gtcattggaac tggaatggct cattcagcag cagtgtctacc agttgtctgt ggctcatatg 2580
 tacggcttca gcacctacgg caccagaaa ggcgagtgcg tgtgtctgca gtgtctgagc 2640
 ggcagctccc ttttcatctt gaagcagcca ctggacctga agatcagcaa gaccttcattg 2700
 agcagatccc acctggattt cagcccctat tggatgaaga aagtgaaggc ctctccacag 2760
 atcatgcagc ggatgagcgc cgtgaacttc gagacaatca ggcggaagtg gcagatccgg 2820
 cacgtgtgta agaacctgcc tctggaaaac acacagatcc ccaggacaag ccctctgttg 2880

 aagatcaciaa tgggtgctgac atacccaac tgcgtggtgc atgtgctgat gttcgtgctg 2940
 ttcaaggccg accagagcga gtctagcctg agcagcggaa tctacctcc tagcacctgt 3000
 agcctgcctt gccggggcat tagaatgtgc gcctgtctc acctagctt ctacatcagc 3060
 agcaccgtgt gctttctgag caagcactgc atgaccgcct gcaccagaga gaagatcatc 3120

aacccccacca tcagctgccc ctttcagagc cccacaaaga gactgggcca cagagagggc	3180
agcgagagcg ataatctggg cctgtgttac tcctttcttc cttggctgcc catgagatcc	3240
ctgggcgaac cttggagagc tggctttcag tggggagagt ccccttgca agtgatggct	3300
agcctgaccg gcaacagcgt gatcgtgcac aagatcgtgc tgggttttct gaagtctctg	3360
agcagctaca actgcgagcg gcggatctct ggcatccaga agagagccat cgagttcgcc	3420
gtcctgaagc tgctgaacat ggacctggct agccctcaga ttatgcagag aaccagcgcc	3480
gaccggttcc ggatgaagcg gagaatgcag aacctggata acctgggcgt gccctggcca	3540
ttgcttcag gtgctgtcc tccacataga ctgctgggcc cctctagatg gattctgttt	3600
catgtgcgga acatcgtgta cggcatccaa gtgatgctgt gccggcggag aaacagcaga	3660
aagcagagtc aggtgcagct ggccattcag gtctgtctcg tggacaagca caagtacttt	3720
ctgttcggcc cctatcctat cagcgaggga ctgacatga ccaccggccg gaacatcaac	3780
agcaactccc tgatgaccaa ctgcctgttc agcccatct tctgtgccca ccacgccatc	3840
atgcaccgga agatgacaag cccacacttc agactgttct ccagcaagat cccacatcct	3900
caggtgccaa gtgtggtggc cctgtgcaag ttcttgccca atggcctgtg gttcaacctg	3960
atctttcaga aaaagggcca catgatcttt agccccaagt tcttctgac ctttagccag	4020
cggaccctgg aatccgccgg actgtttcca tggtgcaca cccagtgccg gaacaaaaag	4080
accaagctgt ggttttcct gatcaacatc caccaccgca agaactctct gctgcctatg	4140
agaatgagca gaacacctcc tcggagagtg tgcggatctc cactctgca tctgtgccaa	4200
cctctgagag gcggcaagaa gagaagcaag ttgccttctt ggaagcctcc tagccagggc	4260
atcagctctt gtctgatgac aggcgtgttg ggctcctgtg gcagagcttg ttcttgcgga	4320
agaggctcgc gtacaccag aggcgactgg aaaagacacc cactctgcag agagctgagc	4380
ctggaacat ggattcctta tctgcaccag caaaagaccc agcgggaagcg gatgaagacc	4440
ggcgccattc aagagaaggc cgctatccaa gaaaaaggcg caatgaccaa gcggatctgc	4500
gtggtcaatt tcgaggcctg cagagagatg gaaagcctga gcgccctga gaagattacc	4560
ctgttcgaag cccacatggc ccggtgcacc tccatcaatg tgctgtgtgt ccgggccagc	4620
ctgattgaga agctgatgaa agaaaagcgc aagatgaagc gcaaccaggt ggcattccct	4680
caaatcatgc aacggctgtt catcaagggc taccagaaca accacttcac gttccacctc	4740
caaaactttg ccttcttcag ctcttcggc aacaacaagt atatcaacat tctcaccgg	4800
gccttcaccc acacacctag aagccctggc tgttccgtgt acgccaatat gtgctggcgg	4860
aagatgcagt cctgaatca cccagcaga ctgaccaact gtcacccgc ttggctgagc	4920

cccattagtg ctgtcctag gctgctgccc tatccttttc acgtgctggc actggaagtg 4980

acctttccac ctggcacagc catgcctcag atgcaattgc aggcactggc tatgtgggag 5040

aaaggtctggg acaagcaaga gaagaaatcc cgcaagctga tgtcctcctg cctggaaaaa 5100

aaggctacct ggatgcggag aacctctggc acaagcctgc agtgttacct gaacacacac 5160

ccctgcacca tgtctgtgcc tcagggaatc ccatctctga acgcccagtg gatgttcctg 5220

cggatcggct acccctacga tgctcctgac tatgcgtcct aaaggcgcgc ctagcggcgc 5280

c 5281

<210> 1213

<211> 5296

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 3C

<400> 1213

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60

gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120

atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180

ggttttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtattttctg 240

tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300

aacctcagaa tgaagcttcc gaagcccca aagcccgtct ccaaaatgag gatggcgaca 360

ccgctcctta tgcaagccct tcccatgggg gctctgcccc aagggccaat gcagaacgct 420

acaaagtatg gaaatatgac agaggatcat gtcattgatt tgcttcaaaa cgctgatccc 480

cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540

acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gtcctgttc 600

gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctccaa ggaaagcctg 660

gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720

atgcctattc ctccacacct gagacacct ctgctgctga agaacaagaa gcggagaaag 780

ctgcggccca agagcagaaa gaagggccac accaagaacc ggcggaaggc caagagaaag 840

ccccagatca gaaacagccg cagagccaca cctaccagca agggcagcct gagaagaaag 900

tacctgagag tgggagccgc cgctgctagc tgtcaatctc ctccatctcc tagagagaca 960

accctagca gcgacgccac cagaagaacc agacctatcg ccgtcagag caagaaaacc 1020

atgacagccg ccggactgac ccctagccag aagaaagatc ctgccggcaa gctgaagaaa 1080

caggtgtccg tgiacagcgg caacctgctg agctttcttc ggagaggcat gaagtctagc	1140
gtgcgcctga agaactgcac caacctgagc gtgcccata tgcctgacct cctgatctgg	1200
aagcgggtgt tcatcctgct gctgtccgac aagaaatcta tccctcacgt gcccagggc	1260
accgccctc attctgtgac agtgaagctg cagagccggc ggaacagacg gtacagaaag	1320
atctatggcg agctgaagat gtccctgcag gccagcaatg gcatggaagc ctgtggcaca	1380
cacccacac ctagactgtc cgtgtccgtg atcacatga agctgtggga gaagcattc	1440
aagggcctga actggaacct ggtcgtgtgg attctgaacc tgaagatgat gctcaagaag	1500
aagtatctgg tccagcgca gtgggagaaa cggaagcaga ttcttggcgg cggaggcaag	1560
tacaaagagt acttctgaa gagaatctc atccgcaagg ccatgacagt gctggccggc	1620
gataagaaag gcctgggcag attcatgaga tgcgtgcaga gcgagacaaa ggccgtcagt	1680
ctgcagctgc ctctgggcag aatggacctg gatggaatgc tgacctgat cggccaggga	1740
ctcgtgggca tgacacctag agatctggga acagtggctg gcgccaccgc acagattcag	1800
aggcctattc aggtgcagac aggcggcaga ctgagaggcc ctagaagaaa ggtgctgatg	1860
gtgctgtggc tgcccgccaa tcagagcctg cagaaaagcc aggtgttcca gtgggtgctg	1920
agaaccgagc tgccctgac ctttagcacc ctgctgtggg acagcagaca cgacctgcct	1980
agaatgctgc ccatcagcag cctctgcac agacccaga tgcctttctg gacctgcacc	2040
tttctgcca ccacatgggg cacatgggag acaccttcta catggggctg gcggaccttt	2100
gccagacagc cttctagacc caccggcaga acccctacca ccagactgat ggctccagt	2160
ggcagcgtga tgagctgtag cctgtgaca cagccatctc cagccagcgc ctgtacaatg	2220
cctccactgc tgcatcctca gtgggcccct cattctgctg gactttctcc aggcgcttgc	2280
agacctgcct gtacctgcat cagcatgacc acaatcagca gggccacctg gcgcagaaac	2340
ctgcagagaa acctgaaagt gctgcggctg agaatcccca gcctgcggaa gtacagacag	2400
cagaacaccc ggtccaccaa cctcgagaag aacctatctc tgaagaagca gagccagagg	2460
cggggcaagc tgtctctgac cacactgagc ttcgtgctga tcaggaact gctgaaaaag	2520
agcagccagc tgcggagaag ctggcggaac gtgtccagaa tcagcaacat ccggaagctg	2580
atttgacca agcagcggag cttcctgtct ctgttcccca agctgagagc caccgagcag	2640
atgaccaatg tgggctgtag actggatttt caccacagaa gcagctccgg cgacagagt	2700
ttcctggtca agatccagag cagccatttc ctggccagat cctggaatac catgcagtgg	2760
aacaacaaga aaatggccat gactgtgatc gctggcgccc accactgtca gtacaagctg	2820

acctacacca aagtgtggaa gatgaattgg aagaaaatga tgatcggcag ccagcacctc 2880

ctgtttctccc cactggatag ctctccactc cagctgctgc tgcacccaca cggcaagaga 2940

tgcaaccctt gttgtcggct gacatggatg agccacctga atcggaagct gcacctcacc 3000

aggtcctgcc tgatcgacct gaccatgatg atgagccaga aactgtggaa gaatcagcgg 3060

aagcgcaccc ctctgccttc tccaagacag catctgctgc ctgagtatcc tctgcacctt 3120

cctccacctt gtctgctgct tctccacat agacaccacc tggcattcct cgagatggcc 3180

tgtagctctc agcacacca cagcatcaag atctggatca gcttcagcca cgagacaatg 3240

agcctgtcca acatcctgat gaagtccgg ctgaccacca ccacaagcag cccagaaga 3300

agccctgctc tgcgagctag aggcggcaca acaatcggcg aagtgaccag cagcctgttc 3360

tttagccact gcctgtgcgt ggcccctaga tgccttagat ctgccgtgga catcagcccc 3420

ggacctacat ctctttctct ggccctttgt gcctctgtgg ccattggaaa gctggcactg 3480

cttggcgctt ctgctccttg tggctgctgt ggcgctagag aggcgggaag atttgctgtg 3540

ctgggcacca tggcatgaa gaacatggaa cacagactga ccatggacag cgccttgagc 3600

ctgacaaaga gagaggcccc tgaaacaggc ccggtgtact acgtgtgcaa ccgatgaat 3660

gtgtccagcg tgtgaagcc tttctgttc accgtgccta tcgaggacat gagagagtgc 3720

accctgggac gcaacagaat gaatgtctct tccgtgctga aacctgtct gatccccgtg 3780

ccaatctgca agaagaaact gctgctcaag ctgctgaggg gcgcctccag ctctaccagc 3840

agagatagca gaagcttttt caccagcgt caccacagca gacctgcag gatgagactg 3900

taccagatgc tgcagaagca gtgctgtac aacctcgtga tcaagcacc tctgatcttc 3960

cggatcaacc tgcggagaca gggcaagacc aaagacggcg ttgtgcagag cctgggcctc 4020

ctgaaccagc agatcatct ccagaaagag ttcttcatct gcctgctgat gttcatcaag 4080

cgggtggaagc cagccgccac caagaagggc aagaacagcc cctgctgcca gaaaaaactg 4140

cgggtgcaga accagggccca tctgctgatg attctgctgc acaacagagg cccacctctg 4200

cataccagat tcgagaaaaa gcggccccgag tggctgagca gaaaatccgg cgtgatgaag 4260

tgtctgggac tgtgccctgc cttcagcggc aggattctgc accagccaga aatggccgcc 4320

atgagactga tgcccaagtt cctgaactcc accaacagct ggtggacagt gcacaagaag 4380

agaggcctgt tccaccagat gaagtgtctg accgccgtgg actgtctgca ggcccttctg 4440

gatatgagcg agaagaaacg caagctgcct atgattcgca aaatccagaa gcggcggaga 4500

accgccaacc ggaacatcga gatcaccct cagagaagca aagcccacct gaagaaaacc 4560

tccgccaagg gcgccaagaa aatcaccttc ctgtgcctga gattcagatg cggaggctgg 4620
ctgtgtggct ggacaccaag aggatggctg aagaagtcca ccaagtccag actgtgcttc 4680
ttctacctgc tgtactacct gtttttctg accgtgtgcg gcttcacccc tccaccactt 4740
attctgtggc ctacggcagc ccctggcgag aagctgaagc actgttttaa agcctggggc 4800
gtcgaccctc ctggcagcgt ttggattctg ccctgcttcc tgattcacct gagaaagggtg 4860
gacaccacc accctcaggt ggtcacaaa acagtgaccg ccacaacagc cgacggccag 4920
aggatgagaa ggctgaagtg caaggcctgc cggctgagat gggctagacc tgaacctgca 4980

gctcagggccc ctctaagag ccactttcca cctcactcta gcggccctc cagaaccagc 5040
tctctgcaat tgagaaccta catggaaatg cactacggcc atcagggccc acaggtggca 5100
atgtgccta aactgctgtg tcggcagatg ctcccactc tgtctaccct gcagcagaga 5160
cactctcagg gcccatgtcc tctccagtg acacctctga gattgcagtc tgtgtgtgtg 5220
ctcggagtgc ctcaaacagc tggctacccc tacgatgtcc ctgactatgc gtcctaaagg 5280
cgcgctagc ggccgc 5296

<210> 1214

<211> 5299

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 4C

<220><221> Cloning cassette hINV 4C

<222> (1)..(5299)

<400> 1214

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
atgtttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
ggttttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtattttctg 240
tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300
aacctcagaa tgaagcttcc gaagccccc aagcccgctt ccaaaatgag gatggcgaca 360

ccgtccttta tgcaagccct tcccatgggg gctctgcccc aagggccaat gcagaacgt 420
acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
cttaaagttt accctctctt gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600
gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacttccaa ggaaagcctg 660

gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg	720
atggacagca agaagatgac ccagaagaac cgcaagaccc ggaaggccgc cagagagaag	780
cacagaaaga ccgacaacct ggacctgcag caccagcgca gacgcaaaaa gaagaaggac	840
aaggtcgaga tccggaatcg gagccctaag gccaatagca ccgagtgtca gggcgagcac	900
agcagagagc agaacctgct gaacctggtg caattgaacc ctacagccc tcaccaccgg	960
aaggacgagg aagatcacca gaagagacac caccaccaca atcaaaagaa gatgtccgtc	1020
aacgagggca acaaccactg gcctagagt gaaatgccta ccggttggt gctcgtgggc	1080
tacaacacca gaaacacagc ccagaatcct cggtgcagc agcacctgaa aactggcag	1140
cagtgcacca gagccagatg gtgtcaagag cctgtcaga cctgacctt cttccacttc	1200
ttcttctttt tcaaacggg gtcctgtgc tgccccggct ggtctaaagg acaacctcct	1260
ccacctggcc tgaagcttc tagcctggct tctcaggtgg ccagaaccac aggcgtgtac	1320
cagcacgtgt ggctgatctg cttcgtgttt ttcgtgtgcg tggaaccgg cttctgtcac	1380
gtggcccaag tgggactcga gagactcgtt agcctgagcg gcatcaccga cgtgaaccat	1440
tgggcccagc ctaagccatc tcctagcaaa ggccaccggca tgaacagacc catcggcctg	1500
agagttggca aaggcgtgtg ggctagactg tggtgaaga actggaagcg gttcaagctc	1560
aaaaagaaat acacaggcat ggaaatcctg ctgtggattc tgctgaagat ggaaattcag	1620
atcttcaaga ttigcctggg cgagatgcag ctgtgcctca agaagaaagt caacgcctgc	1680
agcaacgcca agaaaatgcc cttccagtgc cggtgcagac gcgagtacag agtgaccatg	1740
attcagaaga agaaacagaa gtccccgtg ttcttccacg gcgacctgtg cagaccttct	1800
ccttgctgt ctiggagcag caggatcgtg gtcctggac acgccctgag ctgtcggact	1860
cgtagaagat ggtccagcaa gatggccaag aagtcccagc agcctctgtg tagaggcggc	1920
ccttctgcca gcgatagatg ctgtagctgt agccccagcg gctttagcgc tggaagaggc	1980
agatgtcctg tgcagggatg tctgaggcca cacagagttc agctgctgag aagatggggc	2040
cctggatctc ctgctggcca gagactgtct aagggttcc aactgctgcg ttggtgggga	2100
ccaggatctc cagctcctga gcctagaaag ggccatttc caccacctga tcctccatgg	2160
cctgtgaccg ctgtgacagt gatggctggc tctgtgccta gcgtcagtc tgtggatgct	2220
ctggaatccc ctggacctt ggctctcgaa ggccctagca gccctagaaa cctgctctgg	2280
cgggaaatga gcatcttct gcctggcatc ttcaacctgc acctgtgcta ctaccacagc	2340
cagagcaacc ggaacaagag ccggcagatg gaatccctgg gcatgaagct gcagatcaca	2400

cacccattcg ccagccagcc actgggcca aagatgcca acaacacca gatcagactg 2460

ctgaagcccc gccaggcctt tggcagcttt tccgccgatt tttcagcccc tcagcaggcc 2520

cctctgagac tgtggtcttg gtgcggcaca agccagacct acttcggctc tatcgaagcc 2580

ctgacagccc tgttcacctg tagaaccgcc agcatcagcg tgaacatcag caccctgatg 2640

agcatcctgg aagccatcct ggccatgaca ctgacctga atggcagccc tctgtgggac 2700

tgcagacaaa caacaggcac acaccacggc tgcctgtggg agatcccttc tgttaccttg 2760

ctggctaccg ccaaaaagag ccctaccagc tttctgtgtc agcggcctcc tctgcagcca 2820

gtggaagaga agaagaacgg ccggatcagc agcgtgccac cttctccacc tcttgccttg 2880

ggccctagaa tgcagctctg caccagctg gcccggttct tccctattac acctcctgtg 2940

tggcacatcc tgggacctca gagacacacc cctctgtga cccctgacac cagatggatc 3000

ttctccaacc agctgcagac cgtgcagatg ctgtgtctgc ctccactgaa gcagggcgag 3060

agaatcatct ggctctcgg cggtcttcag atcccaact tcttttgag cctcggcatc 3120

ggacacactg gcgctgtg gcatactgga agcggagaa gagaatggg cggcagcacc 3180

gtgtctagaa gccactgtg gatcagctcc atgatctacc tgagaggcat ggccttcgcc 3240

tccgacagca gcatcagaac caccagagt tctgtgtgtc ggagatgtgg cgccaaaagc 3300

gccgcagcca gcagcgacaa gaagaagaaa agcaccgaaa agaccaagaa caagatcatc 3360

tgaagggcc acagaatcac ccaggtgtg ctgagactgg gcaacctgcc tccattcttc 3420

agaggcagcg aggtgccctt tcttagacct tgcggacca agtgccagaa gaaggttcca 3480

agcgcctctc cttggggact gcaccaaga acagcctcca tcacactgcc taccaccagc 3540

ctgaaggcca gcagaacaag ctgtgtcccc agatctcacc ccagactgcc cagaacaaag 3600

tggcctctgc agtgctgtc gcacagcctg ggaacaactg gaacactcgt gtgggaaagg 3660

ggcgtgtgc agatgagaag tctggaagct cactgccttc tgcagacatt ccacctccac 3720

cactgcagaa ccagcctag ctctgtcct ccagcctgga ttctgtacca aggacagtgg 3780

agcggagccg tctgtggact tagacctgtg gctcaccatc tgccaagacc tatccagggg 3840

ctgactgtc ctgagctcc tcatcaacca gctctgtcct ggggaaagtg gccctggga 3900

atgacaggac ccgccagatg ttgccgttg cctagaagaa tgtgtagctc tctggcctg 3960

ccaaccggcc tgacatctct gatctgtcct agcagtgate tggccgtgtg gatctctagc 4020

tccaccagcc actttctgat gcggagccca gtgtgtccaa gcagcagact gacatgtgcc 4080

tctccacagc tgcctcgat gtggacatgg tctagctggc tgaaagagtg gggaggacag 4140

gcccacagac agcggaactg tagagtgaac gccgttgagg aactgcacag caggcggatg 4200
tctgtcggga tctgaagaa ttgggtgtcc tgcgtttacg tgcggctgag tgcagtggga 4260
ctgtctactt ggagcgccct ggattccctg atcctgtcct tccagagagt gaaaaccagc 4320
cggatactga acctccaggt gctgaagaag atcctgcgga gctttatgaa gctgtaccac 4380
tctctcgtga tgtgcctgcg gctgcggacc aagctggaaa aagctctgag cgctctgttt 4440
atctggcccc agcacagcta caaaggccag gcattcggaa gcctgtgcca gctgggtgtct 4500
gccgatttca gcgcccctca agtgaccaga ctgcggagcc tgaaccatct gctgattcgg 4560

tggatcttta gcaatcagct gacagtccaa atgctctgcc tgccgatcat caagaaaatg 4620
aagaaacgga tcatggtgca cgtcttgaag aagaatcgga agcagattat ctgtatcaag 4680
aatatgttcc tgcagcggaa gggattcctg aacctgagcc acgtggaaaa gttcagagag 4740
agcaccctgg gcaatttctg gatgaagctc ctgcagctgc caccagcttg cacctctaag 4800
gcctggacac ccagaaagct tgtggggaga gccgtgcgga gaaagggcgt cgtgatcaac 4860
ctgaagagac tgcagaaatt ccgggctagc gtgtccttct ggactctgct gcctacaaca 4920
ggcgtgcgga caagagctc tccactgaga ctgactctgt ggctccaag aagccagaaa 4980

agccagcacc actgcgcctt gagaaagatc gagtgggcca caaagctgtc cctcggcggc 5040
aaagcaggac cacaggctca agagaaggcc aacatcctga acagcctgcc ttctctatg 5100
gaaatcgccg tgcgtcaaga aatgctgaac cagaagtgtc tggccccctt cgagcttaag 5160
aagaacctcc tgcgtccaac ctacacacc cactctgtc ggacacacct taaaaagaag 5220
cccagagaca tctgcagaat cagcggtac ccctacgatg tccctgacta tgcgtcctaa 5280
aggcgcgcct agcgccgc 5299

<210> 1215

<211> 5299

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 1D

<400> 1215

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
ggtttctcca tctcgtgac actgttctg gcgggacagg caacaactgc gtatttcttg 240
tatcagcagc aaggaagact ggataagctt acagttacat ccagaatct ccaacttgaa 300

aacctcagaa tgaagcttcc gaagccccc aagcccgctc ccaaaatgag gatggcgaca 360

 ccgtctctta tgcaagccct tcccatgggg gctctgcccc aagggccaat gcagaacgct 420
 acaaagtatg gaaatatgac agaggatcat gtcattgcatt tgcttcaaaa cgctgatccc 480
 cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
 acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600
 gagatgtccc ggcatctctt ggagcaaaag ccgacggacg cacctcccaa ggaaagcctg 660
 gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720
 atggccgaca agaaaaacgt gcggagcgct agttctctg gacatcctt tggccccaga 780

 agaatgacca gacggacat gaccaccacc aaaatgatga tgatgcggcg gaccaagcgg 840
 cggagaagaa aaagacgccg gatgaccatg atgaccagaa gaacctgct gaccaagaaa 900
 acctgtctga cccctagaac cagcgccgcc aaaaagctc tgcccagaca gacaatcagc 960
 cagcggaggc ctatccagac acctcctgga acaagcctgg ccatctgggg cagaagaagc 1020
 aagatcgagg cctctctat cggcagcatc acccctctga gcatcagcag acctaccagc 1080
 agagccagac agagctgttg cctgcctgga ctgacacacc ctgctcatca gcctctgggc 1140
 tctatggttg gagctggaac aggcggagga cctgcttgtg tgcctgtggc cgaagcttct 1200

 acaggcgctt ggacagctga aggcgctgcc ggacacaagat gtagagccag cagagccct 1260
 tgcagacagc tgctgtctc tagccctacc aagtgcgaga tctgcgtgaa gagaagaagg 1320
 cggcgcaagc ggagcagcca gtctagatct cccgtgccta agaaacgcga gcggatgatg 1380
 ctccctgtgc gggccagaac agctagatct gctctgccac aaggcagggc tcctctggaa 1440
 ggaatgcttc tgcttagagc actgcccagc ctgctgagca gaatgcctgc cagaagagag 1500
 agcagattct ggctggccct gcagccctt ggactcagac ctctctatct gcctagctgt 1560
 caccctctgc ctcaactgct tggacctctt ccacctcacc aggcacctgg cgagaaaaac 1620

 gacctgcagc tgctcgtgat gacgacacc acctacaaga tctactggac cgtgatcctg 1680
 ctgaacctt gcggcaacct gcacctgaaa accaccagcc tgaacgcaa gaaaatggaa 1740
 gatatgatct gggagagcaa ccagcagctg aagtggaccc ctacatctt gaagtcggcc 1800
 tctatcgcca agaagcgat caagctgcgg cggaacagca ccagacggga aatgccttct 1860
 caggccacac ctctccacc tggaccttgg agagccgctc tgggcaaaga agtgaagcgg 1920
 agccagagca agctgagact gagaacaca agcccttctg aaaaaaggg ctttgtatc 1980
 ctgagcaaca tgggcgga cgggtctatc tgctgacca tcgtgttctt tctggccct 2040

tacttcccca tgcctagcag ctggcttagc agcggcagaa ccagactgcc tctgaggcca	2100
cagagaggcc ctagacctct gcatagatgg ctgcagcaga ccaccggctg ctctcagaga	2160
agaggcgact gcccaagaac catggccgga ccatctgctt ctctgcaccc tgcacttggc	2220
agagcctcca gaaagacctg gcagagaagg ctgagagcct gtagagcagg cggacctgct	2280
ggatgggcta gacaggccag aaaacgcaag agagagaagc ggtcccagaa gtccagacag	2340
aacctatgc agctgaaaag ctgcagacgg aagatcagca actggtctaa gctgcggagc	2400
ccctggatct tcgaggccaa aaagagcatg aagagatccc agcggcctcc tcggagcatc	2460
ctgagcctgt tcaagaagaa gaagcccctg acattcagcc ccagcgtgtc caagaagagg	2520
ctgcctaagc tgaagggcaa gaaacgccgg aaagaaatcc agcgggaaggt ggtcaagaac	2580
cccagccagc ctgtgccact gagaaatgac ggcatcacca acggcaacga cagcaccggg	2640
tcttgacga tcagcctgaa gaaaagcctg gaaaagatgc ccctgatgcg gagcctgctg	2700
tactccagaa tgtgcctggt gcagatcccc acacacacct gggagcccga ctactttgtg	2760
tccctgccta tgatgttcag ctgggccaca cagagctttc cagtgggcgc cgtgtttctg	2820
accagacctg ccattccttg ctgtagctgt accagccact ccaatccttg gagccagtcc	2880
acactggcca tccggtttat ctctgccct cagccaagca gcagcacctg tacagctgct	2940
cctagcggcc agtattttgc cctgcggagt atgccaaga gccggaacca ggtgctgttt	3000
cggagaaatc tgacccaag ccagctgcgg aactggccc ctccatatat gctgctgcct	3060
cagtctctgt ccagagcct gtctcggaag cagatcccat ctcagtcct gctcgtgcgg	3120
accagctga cactgacagg cactagaagc tccggcacca gagcctctcc atctgccgtg	3180
tgtctgtgct gctggacatg ccccagcaga agctttcctg ccgctctcc aagcggactg	3240
agagcacctg ttggagcaca ggctcctcca gaagtacac tgagagccag ctgtgccagc	3300
tccgccagca aagcttgtgc aggactttgg ccttggggag cccaagtgcg gatgaagaag	3360
aaggacagca ccatcttcat ctaccccagg ctgaaaacct tcggcgtgcc actgggcagc	3420
attctgtgtc tggttggaag cctgagcacg atgatgatca ttagcaccac cagacaagag	3480
tgcggcagac gggccagcgt gccctgtaga cctatgatcg gaagcgccag acctggacca	3540
tggcggacaa gtgctatgcc ttctgccatg ggagtcgcc tgcctaccag ctgtgaaagc	3600
ggaagatctc ctctgccac cggcggaaga atgccaggat ctcagtctat catgatgagc	3660
tggatgcctc cactggctcc ctgcgtgct tgccttggt ctctgtctcc tacactgtgc	3720
cctgtctacc ctgctagagc accaacagcc gtgcctgcct ttacaccct gtctgtctat	3780
cctgtgccag tctgtctggt atgtcacctg gctgtgcgga cctccatgct taccttgctg	3840
ccaatgatga ccctgaaggc cctggtcaag acatggaccc agttcagaaa ctacccaga	3900

cggcacccctc acagaagccc accaacaagc tgcctccac tgctcgaggc ctttccactg 3960
 ccaagagcca gcctgagagc taccgtgcct agacactcta gcgtgctggc cacaggactg 4020
 catctgcata ggcagattag cctgcctctg cggggcttcc tgctgcatca accactgcc 4080
 ggacaacacc tgggctgtc ccacagactg agactgcggc tgcctagaac aaccgagatc 4140

 cagctgacca tgaacgactc caagcacaag ctggaaagcc ccgctctgaa acaggtgtcc 4200
 ccagctagtc ctctacaca gcagcctcag acaccccagg attctagaca ggtgctggcc 4260
 gtgcctatga gcctggcctg tagcatcacc gtgtccttcg tgggccagat ctctaccctg 4320
 gtgctggacg tgcctccat cagccactgg aacggcatct gggaagtgat gccagaaca 4380
 ctggaaggct gcattccgt gaaggaccac cggacatccc agaaccacag caagtgcac 4440
 accgagtgtg tgcggacagc cctgaacacc aagtgtgaaa tttgtgtgaa gaacaccgcc 4500
 atcctggcta tcacctgat caccacacag gacctcacc tggacctgt gtgtcatccc 4560

 catagaaggc ccggttgaa gggacaccac agagtgggtg ttagccacca tccttccggc 4620
 agcaccaagt ctactggca gcagagagaa agaggcggag gccgcagaga aaagaagggc 4680
 tgtagagagg caagcagagc cggccagttt cctgtgtggc ggagaacatc tagaggcatg 4740
 tccttgcagt ggaagtccg caatgcctgc acacctctga gatgtcccag cagatctcca 4800
 gccaccttcc tgactgccct gaacggctgg catagatctg gactgagggc ccagaccgcc 4860
 ttctttctgc tggacatcat cctgcggaga gcccggccta caagctgcag cacatgtaga 4920
 atgtgtggc ggctgccctg caaagtgacc gaaagctccc tggccaagaa aacctgacc 4980

 aatcagccta gcttgcccgg accttgtgt agcctgtgt ctacactgag ccagccacca 5040
 cctcaggctc ctagccaagt ttggacagcc gctacactgc ggtgtcctgc tgtgcctgct 5100
 gctgcatgtc cacctctgaa gctggtcca ctgcaagtga ccacaacact gaagtgate 5160
 ctggtcatgc tggaaatcgt gaccgagaac aaagttcggc agaacttcaa gcggaactcc 5220
 agcttcttct acaccagcga cagaggctac ccctacgatg tccctgacta tgcgtcctaa 5280
 aggcgcgcct agcgccgc 5299

 <210> 1216
 <211> 5281
 <212> DNA
 <213> Artificial Sequence

 <220><223> Cloning cassette hINV 2D
 <400> 1216
 gaattcggat cccgcgactt cgccgcatg catcgacggc gtcacggag ttgccgggaa 60

gacccaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
 atgcttggta ggcgccctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
 ggttttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtattttcttg 240
 tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa 300
 aacctcagaa tgaagcttcc gaagcccca aagcccgtct ccaaatgag gatggcgaca 360

 ccgtcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt 420
 acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
 cttaaagttt accctctctt gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
 acgatggaaa cgattgactg gaaggtgttt gagagctgga tgcaccattg gctcctgttc 600
 gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctcccaa ggaaagcctg 660
 gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg acccgtgccg 720
 atgcggaaga tgcagagcct gaatcacccc agcagactga ccaacaatcc tcggagaaag 780

 acctggaaga tgcggaagaa gtacgccag aagcctagcc agaagaacca cctgtaccgg 840
 cagatcaacc ggcgcaagct gcagagaaaag aagtccagaa gccacctgga cttcagcccc 900
 tactggatga agaaagtga gcgggccaga aaccggaaca tgaagaaaac catgagccac 960
 ctgatcgccc atcaggccct gaagatgtct ggctgagac tgtttcacc cagactgctg 1020
 accagaaaga agcccgcaa gcagaaaaag ggccacatga tcttcagccg gcggaagtgg 1080
 cagatccggc acgtgctgaa gaatctgatc cccagcctga acgcccagtg gatgttcctg 1140
 agaatcgcta gccacagat catgcagaga accagcgccg accggttccg gatgaagcgg 1200

 agaatgcaga acctggacaa tctgggcgtg ccctggcctc tgttgccctgg attgctgctg 1260
 gcccataatg acggcttcag cacctacggc acccagaaag gcgagtgcgt gtgtctgcag 1320
 tgtctgagcg gcagcagcct gttcatcctg aagcagcccc tggacctgaa gatctccaag 1380
 accttcattg ccagccctca gattatgcag cggatgagcg ccgtgaactt cgagacaatc 1440
 ctgcaggccc atctcaggt gccagctctt gctcctcaag cttggtggcc cgctagaaga 1500
 ggccctctga catctgtcc aagcgcacag cagtccctga cacggacact ggaaagcgcc 1560
 ggactgtttc ctiggctgca caccagtg cgggccttca ttcacacacc tagaagccct 1620

 ggctgcagcg tgtacccaa catgtgctgg cgtacaaga aacggggagt gatcgccctg 1680
 cggatctacc ctctagcac atgcagcctg ccttgagag gccgatcct gattcagcac 1740
 ggcggcactt tcaccttccg gttctgggtc gagaagctga gctggaacat ctgcaagaac 1800
 ctgagcctgt acctggataa gttcgtgcag cggctgctgt acgtgtacat catcgagaca 1860
 aacgtgttcg tgctgaacct gttccactg ccagtgaacc agatcttcat gatggccttc 1920

tacctgaagt acaccgagaa ggcctgggtc atggaactgg aatggctgat ccagcagcag	1980
tgctaccagc ggaagagaat gaagaccggc gccatccaag agaagggcgc tattcaagag	2040
aaaggggcca tgaccaagcg gatctgcgtg gtcaatttcg aggcctgcag agagatggaa	2100
agcctgagcg cccctgagaa gatcacccctg ttgaagccc acatggcccgt gtgcaccagc	2160
atcaatgtgc tgtgtgtcag ggccagcctg atcgagaaac tgatgaaaga aaagcgcaag	2220
atgaagcgca accaggtggc atcccctcaa atcatgcaac ggctgttcat caagggtac	2280
cagaacaacc acttcacgtt ccacctcaa aacttcgcct tcttcagctc cttcggaac	2340
aacaagtata tcaacatcct gacctttctg cccagcagat tcccttgggg acctcctca	2400
ctgggagccc ttagagctac agctcctgct acagctgctc cccaggcaca gacacctcat	2460
tggagagccg ccaccacaag cagcatgagc agctctccaa gagccgagcc taccagctct	2520
agctcttggg ccacttgcgt gcctagatgc tgcagctcca gctgctattg gacgtgtct	2580
agctggcctc ctgctggcgc tgccgaagcc acaaatacca gaaccagaag cgcgagagc	2640
cagcggggaa gaatgtgac ttggagaagc tcctgtggc tgcagggcac cagatgtttt	2700
acaggcgtgc ggaccagctc caggtgcagc ctgatggaac agatccctca cctgaagtct	2760
aacagccgga agaaactgct cgaggacatg aagcagaacg gcttcaccag acggcggaac	2820
agcagaaagc agagccaagt gcagctggcc atccaggtgc tgcgtgtgga caagcacaag	2880
tactttctgt tcggcagagc cacatttctg ctggctctgt gggagtgtag cctgcctcag	2940
gctagactgt gcctgatcgt gtctagaacc ctgctgctcg tgcagtctag acaccaagc	3000
tggccttggg ccagatgcct gagaatgcgg cctccacgca gccactggaa ctctgcctac	3060
ctggggagaa cactgctcgt gacctgcac ctgtaccaca gatggatcgt gaccagcatg	3120
tgccagagcc agagatggct gacctccacc acctctagaa gctctgccct gatgtggacc	3180
tgggtgtgta caagaggtgg cggcaagcgg aagaaaaaga tgtgcaaggt gtccggcggc	3240
tgcaccgcct gtgttgaaag atgtccttgg aaggcatct gttggaagt gcctgtgaca	3300
gtggccgcca tgagcagaac acctccaaga cgcgtgtgcg gccacagaga gggcagcgag	3360
tctgataatc tgggcctgct gtactccttt ccacctgtgc tgttcaaggc cgaccagagc	3420
gaaagctctc tgagcagcgg caacagcgtg atcgtgcaca agatcgtgct ggtgttcctg	3480
aagtccttga gcagctacaa ctgcgagaga agaatcagcg gcatccagaa gagagccatc	3540
gagttcgccg tctgaagct gctgaacatg gacctcggca agggactgac acacccctg	3600
cctctgaaga ggacctgca gaacaagcgg aacaagaaca tcaagcgggt caaccagaag	3660

aagggaaca tcaagaggaa gtccatcctg ctgcatctga ttgtgctgaa cagccccgag 3720

agcaaccggg aaaagatcat caaccccacc atcagctgcc ctttcagag cccacaaaag 3780

agactgggaa gccctcctct gcacctgtgt cagcctctga ggcctatcc tatcagcgag 3840

ggcctgacca tgaccaccgg cagaaacatc aacagcaact cctgatgac caactgcctg 3900

ttcagcccca ttttctgtg ccaccacgcc atcatgcacc ggaagatgac aagccctcac 3960

ttcagactgt tctccagaa gateccacat ccacaggtcc caagtgtggt ggccctgtgc 4020

aagtttacac acccctgcac catgctgctg cccaaggcg ctttttgaa gcctcctagc 4080

cagggcctct ccagctgtct gatgacaggc tgttggcagt ggtccagcgt gacaagcctg 4140

gaatggacag cccaagagag aggcgtgtcc tctggctga tgaagcaaac atggatgaag 4200

tcttggctcc tgcgggaccc cagctacaga tccatcctgg aatacgtgtc cacacgggtg 4260

ctgtggatgc ccacctctac cgtgcctaag tttttctga ccttcagcca gatccgatg 4320

tgcgccctgt ctaccctag cttctacatc agctccaccg tgtgctttct gagcaagcac 4380

tgcattgacc cctgcacacc tggaccacgc ctgcagtgtt acctgaacct ggccaacggc 4440

ctgtggttca acctgatctt ccggaacaaa aagaccaagc tgtggttctc cctgattaac 4500

atccaccacc gcaagaaccc actgctgccc atgcggctgg aaaaaaggc cacttgatg 4560

cggcggaccg agctgtctct ggaaccttgg attccttacc tgcatcagca gaaaaccag 4620

tggctcccca tgagaagcct gggcgagcct tggcgagctg gatttcagtg gggagagtct 4680

ccctggcaag tgatggcctc tctgacaggc agacgcaaga aaagagagga tctctcgga 4740

ctgcaagaga aaaaaagccg gaagctgatg tccagctgcg ccgtcctcc acatagactg 4800

ctgggacctc gcagatgggg aagctgtggg agagcctgtt cttgtggcag aggcctgtga 4860

accctagag gcgactggaa gagacacca cctcggcgga ttctgtttca cgtgcggaac 4920

atcgtgtacg gaatccaagt gatgctgtgc tgtcaccccg cctggctgtc tccaatcagc 4980

gcttgtctc gcctgtgcc ttatccattc caggttctgg ccctggaagt gacattccct 5040

ccaggcactg ccatgcctca gatgcaattg caggcactgg caatgtggga gaaaggctgg 5100

gacaagcctc tgaaaaacac acagatcccc aggacaagcc cactgtggaa gatcacaatg 5160

gtgctgacat accccaactg cgtggtgcac gtctgatgt tcggcggcaa gaagcggagc 5220

aagttcggct acccctacga tgctcctgac tatgctcct aaaggcgcgc ctacggcgcc 5280

c 5281

<210> 1217

<211> 5296

<212> DNA

<213> Artificial Sequence

<220><223> Cloning cassette hINV 3D

<400> 1217

gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa	60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg	120
atgcttggtg ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact	180
ggtttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg	240
tatcagcagc aaggaagact ggataagctt acagttacat cccagaatct ccaacttgaa	300
aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca	360
ccgctcctta tgcaagccct tcccatgggg gctctgcccc aaggccaat gcagaacgt	420
acaaagtatg gaaatatgac agaggatcat gtcattgatt tgcttcaaaa cgctgatccc	480
cttaaagttt acctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac	540
acgatggaaa cgattgactg gaagtggtt gagagctgga tgcaccattg gtcctgttc	600
gagatgtccc ggcattctct ggagcaaaag ccgacggacg cacctccaa ggaaagcctg	660
gaattggagg acccgagtag tgggctgggc gtcacaaagc aagacctggg accctgccc	720
atgcagaaca ccagaagcac caacctggaa aagaaccca gcctgaagaa gcagagccag	780
cgagaggaa agctgagcag cagaaagaag ggccacacca agaaccggcg gaaggccaag	840
agaaagcccc agatcagcca gaagaaggac cctgccggca agctgaagaa acacctgaac	900
cggaagctgc acctgaccag atcctgcctg atcgacctga ccatgatgat gagccagaag	960
ctgtggaaga accagcgcaa gagaatccct ctgccttctc cacggcagca tctgtgcct	1020
cagtatccac tgcattctcc acctccatgc ctgctgtgc tccaccacag acacctctg	1080
gcctttctcg agatggcctg cagcagccag cacaccaca gcatcaagat ctggatcagc	1140
ttcagccagc aggacctgcc tagaatgtg ccatcagca gccctctgca cagaccccag	1200
atgcctttct ggacctgcac ctttctgcc accacatggg gcacatggga gacaccttct	1260
acatggggct ggcggacatt cggccctgtg tactacgtgt gcaaccggat gaacgtgtcc	1320
agcgtgctga agcctttcct gttcaccgtg cctatcgagg acatgagaga gtgcaccctg	1380
ggcagaaaca gaatgaatgt gtcctctgtg ctgaaacct gtctgatccc cgtgccaatc	1440
ctgaccacac tgagcttctg gctgatcgag gaaagccggc ggaacagacg gtacagaaag	1500
atctacgggg agctgaagat gtcctgcag gccctgcctc tgaccttag cacactgtg	1560

tgggacagca gacacaccac caccacaagc agccccagaa gatccccctgc tctgagagct	1620
agaggcggca ccacaatcgg cgaagtgaca agcagaggcg ccagcagctc taccagcaga	1680
gacagcagaa gctttttcac cagcgtcac cccagcagac cctgcagaat gagactgtac	1740
cagagcaacg gcatggaagc ctgcggcaca caccctacac ctagactgtc tagaggccct	1800
ccactgcaca ccagaacctat gagcctgagc aacatcctga tgaagtccg gctgatgctg	1860
cagaagcagt gctgctacaa cctcgtgac aagcacctc tgatcttcg gatcaacctg	1920
cggagacagg gcaagaccaa agacggcgtt gtgcagagcc tgggcttcct gaaccagcag	1980
atcatcctgc agaaagagtt cttcatctgc ctgctgatgt tcatcaagcg gtggaagcca	2040
gccgccacaa agacacctcc accactgatt ctgtggcctc aggccgctcc tgtgcacaag	2100
aagagaggcc tggtcagcct gttcttctcc cactgcctgt gccaccagat gaagtgcctg	2160
accgccgtgg attgtctgca ggccttctgg gacatgatga ttgcgaagat ccagaagcgg	2220
cggagaaccg ccaaccggct gaaaaagaaa tacctggtgc agtgtaccaa cctgagcgtg	2280
cccatgatgc tgaccatcct gatctggaag cgggtgttca tcctcctgct gagcgacaag	2340
aagtgtctga gactcagatg cggcggatgg ctgtgtggct ggacacctag aggcaagaac	2400
aagaagcggg gaaagctgcg gcccaagcac ctgaagaaaa ccagcgccaa ggtgtccgtg	2460
atcaccatga agctctggga gaagcacttc aagggcctga actggaacct ggtcgtgtgg	2520
attctgaacc tgaagatgat gtggctcaag aagtccacca agagcagaca gagcagccca	2580
ttcctggctc ggagctgaa taccatgcaa tggaacaaca agaaaatggc catgaccgtg	2640
atcgtggcg cccaccactg tcagtacaag ctgacctaca ccaaagtgtg gaagatgaat	2700
tggaagaaaa tgatgatcgg ctcccagcac ctctgttta gccactgga ttcaagccca	2760
ctgcagtgc tgctgcacc tcacggcaag agatgcaacc cttgtgcag actgacctgg	2820
atgagcagag agtgggaaaa gcggaagcag atcctcggcg gagcggcaa gtacaaagag	2880
tacttctga agcggattct catccggaag gctatgacag tgctggccgg cgataagaaa	2940
ggcctgggaa gattcatgag atgcgtgcag agcgagacaa aggccgtgtc tctgcagctg	3000
cctctcggcc gaagaaagtc cggcgtgatg aagtgttggg atctgtgcc cagactggac	3060
tttccccca gatctagctc tggcggcgag aagctgaagc actgtttcaa agcctggggc	3120
ctgtgtttt tctacctgt gtacttcgag aagaaacggc ccgagtggct gagcgttgac	3180
cctcctggat ctgtctggat tctgccctgc atggacctgg acggaatgct gacagtgatc	3240
ggccagggac tcgtgggcat gaccctaga gatctgggaa cagtggctgg cgccaccgca	3300

cagattcaga ggcctatcca ggtgcagaca ggcggcagac tgttcctgat tcacctgaga	3360
aaggtggaca cccaccatct gcaggtcgtg accaagaccg tgacagccac aacagctgac	3420
ggccagagga tgcggagact gaagtgaag gcctgtcggc tgagatgggc cagacctgaa	3480
cctgtctcac aggtctctcc aaagagccac ttccacctc atcctagcgg cccctccaga	3540
acctctagcc tgcagctcag acccattcct ccacacctga gacacccact gctgtgaag	3600
ggaaagaaca gcccctgtg ccaaaagaaa ctgcgggtgc agaaccaggg ccatctgtg	3660
atgatcctgc tgcataacgc cagacagccc agcaggccta ccggaagaac ccctaccaca	3720
agactgatgg cccctgtggg cagcgtgatg tctttagacc tgtgacca gccatctcct	3780
gccagcgcat gtacaatgcc accactcctg catccacagt gggccccaca tagtgtgga	3840
ctgtctccag gcgcttgag acctgcctgt acctgcatca gcatgaccac catctccaga	3900
gccacatggc ggctgagaat cccaagcctg aggaagtacc ggcagaacat cgagatcacc	3960
cctcagcgtt ctaaggccca ggtttccgtg tacagcggca atctgtgag ctctccaga	4020
cggggcatga agagtagcgt gcggctgaag aacagcatcc ctacgtgcc aaaagccacc	4080
gccgtcact ctgtgacagt gaagctgcag tacctgtttt tctgaccgt gtgcggcttc	4140
gaccgggtgt tcttggttaa gatctgcaag aagaagctgc tcctcaagct gctgagaggc	4200
cccagacgga aagtgtgat ggtgctttgg ctcccccca accagagtct gcagaaaagc	4260
caggtgttcc agtgggtgct gcggaccgaa acctacatgg aaatgacta cggccatcag	4320
gcccctcagg tggccatgct gcctaaactg ctgtgtagac agatgctccc cactctgtcc	4380
acactccagc agaggcatcc tcagggacct tgtctctctc ctgtgacacc tctgagagtg	4440
cagtctgtgc tgtcctggg agtgcctcag acagccgctt ttagcggccg gattctgcac	4500
cagccagaaa tggccgccat gagactgatg cccaagtcc tgaactccac caacagctgg	4560
tggacagtgg ccctagatg tcctagaagc gcctggaca ttagccccgg acctacatct	4620
cctagcctgg cctcttgtgc ctctgtggcc attggaagc tggcactgct gggcgcatct	4680
gccccttgtg gcgcagctgg tgcctagagag gctggaagat ttgccgtgct gggcaccatg	4740
gttatgaagg gtgtgcccgc agcctcctgt cagtctctc catctccaag agagacaacc	4800
cctagcagcg acgccaccag acggacaaga cctattgccg ctacagagca aaagaccatg	4860
actgccgccg gactgacccc tcggagaaac ctgcagagaa atctgaaggt cctgggcgcc	4920
aagaagatca ccttctgag aaacagcaga cgcgccacac ctacctctaa gggcagcctg	4980
agaagaaagt acctgagagt gaacatccgc aagctcatct ggaccaagca gcggagcttc	5040
ctgtctctgt tcccaagct gagagccacc gagcagatga ccaatgtggg atgcctgtc	5100
aagaaaagca gccaatcgcg gcggagctgg cgcaatgtgt cccggtacag caacatggaa	5160

cacaggctga ccatggacag cgccctgagc ctgacaaaga gagagggccc tgagacaagc 5220
gagaagaaga ggaagttgcc tggctacccc tacgatgtcc ctgactatgc gtccctaaagg 5280
cgcgccctagc ggccgc 5296
<210> 1218
<211> 5299
<212> DNA
<213> Artificial Sequence

<220><223> Cloning cassette hINV 4D
<400> 1218
gaattcggat cccgcgactt cgccgccatg catcgacggc gctcacggag ttgccgggaa 60
gacaaaaagc ctgtgatgga cgatcagcgg gaccttattt ctaacaatga acaacttccg 120
atgcttggta ggcggcctgg agcaccagag tccaagtgtt ctaggggcgc cctgtacact 180
ggttttctcca tctcgtgac actgttgctg gcgggacagg caacaactgc gtatttcttg 240
tatcagcagc aaggaagact ggataagctt acagttacat ccagaatct ccaacttgaa 300
aacctcagaa tgaagcttcc gaagcccca aagcccgctt ccaaatgag gatggcgaca 360

ccgtcctta tgcaagccct tcccatgggg gctctgcccc aagggccaat gcagaacgt 420
acaaagtatg gaaatatgac agaggatcat gtcatgcatt tgcttcaaaa cgctgatccc 480
cttaaagttt accctcctct gaaggggagc ttccagaaa atcttcgaca tctcaagaac 540
acgatggaaa cgattgactg gaagtggtt gagagctgga tgcaccattg gctcctgttc 600
gagatgtccc ggcattctct ggagcaaaaag ccgacggacg cacctccaa ggaaagcctg 660
gaattggagg acccgagtag tgggtgggc gtcacaaagc aagacctggg acccgtgccg 720
atgaacagaa agaccagaaa ggccgccaga gagaagcacc gcaagaccga cgacaagaag 780

aagaagtcca ccgaaaagac caagaacgcc aagaagatgc cttccagca gcggcctcct 840
ctgcagcctg ttaacctgga tctgcagcac cagcgcagac gcaaaaagaa gaaagacaag 900
gtcgaaatcc ggaatcgag ccctaaggcc aatagcaccg agtgtcagg cgagcacagc 960
agagagcaga acctgctgaa tctggtgcag ctgaacctc acagccctca ccacagaaag 1020
gacgaagagg accaccagaa gcggcaccac caccacaatc aaaagaaaat gagcgtgcgg 1080
gctagcgtgt ccttctggac acttttgcca acaaccggcg tgcggacaag aggctctcca 1140
ctgagactga cactgtggcc tccacgggtt ccaccttctc cacctcttgc tctgggcccc 1200

agaatgcagc tgtgtaccca gctcggccgg ttcttcctta tcacacctcc tgtgtggcac 1260
atcctgggac ctgagagaca cacacctcag gctcctctga ggctgtggtc ttggtgcggc 1320

acaagccaga cctacttcgg cagcagacca tctccttgcc tgagctggtc cagcagaatt	1380
gtggccctg gacacgcct gagctgtcgg actagaagaa gatggtctag caagcggtgg	1440
atcttctcca accagctgac cgtgcagatg ctgtgcctgc caatcacaca cccattcgcc	1500
tctcagcctc tgggacaaga gatgccaac aacaccaga tccggctgct gaagccctgc	1560
agagtgaacg ccgtggaaga actgcacagc aggcggatgt ctgtgcggat cgtgaagaac	1620
tgggtgtcct gctgttacgt gcggtgtct gctgtgggcc tgtctacttg gagtgcctg	1680
gacgaggaag agaagaacgg ccggatcagc agcctgaaa agaaagtga tgcctgcagc	1740
tccctgatcc tgagcttcca gcgctgaaa accggcatgg aaatcctgct gtggattctg	1800
ctgaagatgg aaattcagat cttcaagatt tgcctgggcg agatgcagct ctgcggccag	1860
gcctttggaa gccttagcgc cgatttcagc gccctcaga tcattaagaa gatgaagaaa	1920
cggatcatgg tgcacgagct gaagaagaat ctgctgtgc ctatgtgtc cagcctggct	1980
ctgccaacag gcctgacatc tctgatcctg cctagcagcg atctggcgt gctgatctct	2040
agctccacca gccactttct gatgcggagc cctgtgtgc caagcagcag actgacttgt	2100
gcctctccac agctgccccg gatgtggact tggcttagct ggctgaagaa cgagggaac	2160
aaccactggc ctagagtga aatgcctacc ggctggctgc tcgtcggcta caacaccaga	2220
aacacagccc agaatcctcg gctgcagcag cacctgaaac actggcagca gtgcaccaga	2280
gccagatggt gtcaagagcc ctgtcagacc ctgacctct tccatttctt cttctttttc	2340
aaaacggtgt cctgtgttg ccccggtgg tctaaaggac aacctctcc acctggcctg	2400
aagccttcta gcctggcttc tcaggtggcc agaaccacag gcgtgtacca gcacgtgtgg	2460
ctgatctgtt tcgtgttttt cgtgtgtgtg gaaaccggct tctgtcacgt ggcccaagtg	2520
ggactcgaga gactggtgtc tctgtccggc atcaccgacg tgaaccattg ggccagcct	2580
aagccatctc ctagcaaagg caccggcatg aacagacca tcggcctgag agttggcaaa	2640
ggcgtgtggg ccagactgat cctggccatg aactgacct tgaacggcat ggccaagaag	2700
tcccagcagc ctctgcaggt cgtgtctgaga ctgggaaacc tgcctccatt cttcagaggc	2760
agcgagggtc ctttctctag acctgtctgg accaagcctg cctgcacaag caaggcctgg	2820
actcccagaa aactcgtggg gagagccgtg cggagaaagg gatctccact ctgggattgc	2880
tccaccacaa caggcacaca ccacggatgc ctgtgggaga tcccatctgt gacctgctg	2940
gcccaccta gaaccgctc tatcacctg cctaccacaa gcctgaaggg ctccagaacc	3000
agctgtgcc ctagatctca cccagactg cctaggacca aatggccct gcagtgtctg	3060
ctgcacagcc tgggaacaac cggaacactc gtttgggaaa ggggcgtcct gcagatgaga	3120
tccctgaag cccattgtcc actgcagacc ttccatctgc accactgcag gaccagcct	3180

agctcttgtc ctcttcctg gattctgtac caaggacagt ggagcggagc cgtcgtggga 3240
cttagacctg tggctcacca tctgcctaga cctatccagg gcctgcactg tccacaggca 3300

ccctcatcaac ctgctctgag ctggggaaaa tggcccgtgg gaatgacagg ccctgccaga 3360
tgttgcatat ggcccagacg gtgccagaag aaggttccat cagcctctcc atggggcctc 3420
gtgctcaaaa agaaccggaa acagatgctg aaccagaagt gtctggcccc ttttagagag 3480
agcacctgg gcaatttctg gatgaagctg ctccagctgc ctgtcgtgat caacctgaag 3540
agactgcaga agttcaacct gcacctgtgc tactaccaca gccagagcaa cagaaacaag 3600
agccgccaga tggatccctt gggcatgaag ttgcagtcct agaaatccca gcaccactgt 3660
gccctgcgga agatcgagtg ggccacaaaag ttgtctctcg gcggaaaagc cggaccacag 3720

gtcgaagaga aggccacctc tcggattctg aacctgcaag tgctcaagaa gatcctgcgg 3780
agctttatga agctgtacca ctctctggtc atgtgcctgc ggctgaggac caagctggaa 3840
aaggctctga gcgcccgtt catctggccc cagcacagct acaagcccct gttctttcac 3900
ggcgacctgt gcgagtgggg aggccaggct catagacagc ggaactggct gaaaaactgg 3960
aagcggttca agcttaaaaa gaagtacatc cagaagaaga agcagaagtc taacaagatc 4020
atctgcaagg gccaccgat caccatcatc tgtatcaaga atatgttctt gcagcgcaag 4080
ggcttctga acctgagcca cgtggaaaag ttctgtagag gcggccctag cgccagcgat 4140

agatgctgtt ctgttagccc cagcggcttc agtgccggca gaggaagatg tcctgttcag 4200
ggctgtctga ggccccacag agttcaactg ctgagaagat ggggccctgg ctctcctgct 4260
ggacagaggc tgtctaaggg ctttcagctg ctccgttggg ggggaccagg atctcctgct 4320
cctgagccta gaaaggggcc atttcacca cctgacctc catggcctgt gaccgctgtg 4380
acagtgatgg ctggatctgt gcctagtgtc cagtctgtgg acgccctgga atctcctgga 4440
cctctggctc tcgaaggacc tagcagccct agaaacctgc tttggagaga gatgagcatc 4500
tttctgcccg gcattctcac cgccaagaaa agccccacca gcttttgctg caatatcctg 4560

aacagcctgc caagctctat ggaaatcgcc gtgctgcaag aggacagcaa aaagatgacc 4620
cagaagggcc aagccttcgg ctccctgtgt cagcttgtgt ccgctgactt ctctgccct 4680
caagtgacct ggctgcggag cctgaatcat ctgctgatca cctacacacc ccacatctgc 4740
agacacaccc tgttgacccc tgacaccaga tggatcttta gcaatcagct gcagacagtc 4800
cagatgctct gtctgcctcc actgaagcag ggcgagagaa tcatttggcc cctcggcggc 4860
tttcagatcc ccaacttctt ttggagcctc ggcatcggac acactggcgc ctggtggcat 4920

actggaaggc ggagaagaga atggggcggc agcaccgtgt ctagaagccc tctgtggatc 4980

agctccatga tctacctgag aggcatggcc ttcgccagcg acagcagcat cagaaccacc 5040

agagtgtcct ggtgcagaag atgcggcgcc aaaagcgctg ccgccagctc tattgaagct 5100

ctgaccgctc tgttacctg ccggaccgcc agcatcagcg tgaacatcag caccctgatg 5160

tccatcctgg aagcacttaa gaagaaaccc agagacatct gccgcatcag ctgccggtgt 5220

agacgcgagt acagagtac tatgggctac ccctacgatg tccctgacta tgcgtcctaa 5280

aggcgcgcct agcggccgc 5299

<210> 1219

<211> 37184

<212> DNA

<213> Great Ape Adenovirus

<400> 1219

catcatcaat aatatacctt attttggatt gaggccaata tgataatgag gtgggcgggg 60

cgaggcgggg cgggtgacgt aggacgcgcg agtagggttg ggaggtgtgg cggaagtgtg 120

gcatttgcga gtgggaggag ctgacatgca atcttccgtc gcggaaaatg tgacgttttt 180

gatgagcgcc gcctacctcc ggaagtgcc attttcgcgc gcttttcacc ggatatcgta 240

gtaatttttg gcgggaccat gtaagatttg gccattttcg cgcgaaaagt gaaacgggga 300

agtgaaaact gaataatagg gcgttagtca tagcgcgtaa tatttaccga gggccgaggg 360

actttgaccg attacgtgga ggactcgccc aggtgttttt tacgtgaatt tccgcgttcc 420

gggtcaaagt ctccgttttt attgtcgccg tcactctgacg cggagggtat ttaaaccgcg 480

tgcgtcctca aagaggccac tcttgagtgc cagcgagaag agttttctcc tccgtctcgt 540

ttcggcgatc gaaaaatgag acatttagcc tgcactccgg gtcttttctc cggccggcg 600

gcgtccgagc ttttggacgc tttgtcaat gaggttctga gcgatgattt tccgtctact 660

accacttta gccacctac tcttcacgaa ctgtacgacg tggatgtact ggtggatgtg 720

aacgatccca acgaggagcg ggtttctacg ttttttcccg agtctgcgt tttggtgcc 780

caggagggat ttgacctaca cactccgccg ctgcctatct tagagtctcc gctgccggag 840

cccagtggta taccttatat gcctgaactg ctcccgaag tggtagacct gacctgccac 900

gagccgggct ttccgcccag cgacgatgag ggtgagcctt ttgctttaga ctatgctgag 960

atacctgggc tcggttgacg gtctttgtca tatcatcaga gggttaccgg agaccccgag 1020

gttaagtgtt cgctgtgcta tatgaggtcg acctcttctt ttatctacag taagtttttt 1080

tgtgtagggt ggcttttttg gtaggtgggt tttgtggcag gacaggtgta aatgttgctt 1140

gtgttttttg tacctgcagg tccggtgtcc gagccagacc cggagcccga ccgcgatccc	1200
gagccggatc ccgagcctcc tcgcaggcca aggaaattac cttccatttt gtgcaagcct	1260
aagacacctg tgaggaccag cgaggcggac agcactgact ctggcacttc tacctctcct	1320
cctgaaattc acccagtggg tccctctggg atacatagac ctgttgctgt tagagtttgc	1380
gggcgcagcc ctgcagtaga gtgcattgag gacttgctta acgatcccga gggacctttg	1440
gacttgagca ttaaagcccc taggcaataa accccaccta agtaataaac cccacctaag	1500
taataaactt taccgccctt ggttattgag atgacgcca atgtttgctt ttgaatgact	1560
tcatgtgtat aataaaagtg agtgtggtca taggtctctt gtttgtctgg gcggggttta	1620
agggtatata agtttctcgg ggctaaactt ggttacactt gaccccaatg gaggcgtggg	1680
ggtgcttgga ggagtttgcg gacgtgcgcc gtttgcctga cgagagctct agcaatacct	1740
atagtatttg gaggtatctg tggggctcta ctcaggccaa gttggtcttc agaattaagc	1800
aggattacaa gtgcgatttt gaagagcttt ttagttcctg tggtagctt ttgcaatcct	1860
tgaatctggg ccaccagct atcttccagg aaaaggttct ctgactttg gatttttcca	1920
ctccggggcg caccgccgt tgtgtggctt ttgtgtcttt tgtgcaagat aaatggagcg	1980
gggagaccca ctgagtcac ggctacgtgc tggatttcat ggcatggct ctttgagggg	2040
cttacaacaa atggaagatt cagaaggaac tgtacggttc cgcctacgt cgtccacttc	2100
tgcagcggca ggggctgatg tttcccgacc atcgccagca tcagaatctg gaagacgagc	2160
gagcggagaa gatcagcttg agagccggcc tggaccctcc tcaggaggaa tgaatctccc	2220
gcaggtaggt gagctgttcc ccgaactgag acgggtcctg actatcaggg aggatggta	2280
gttttgaag aagctgaaga gggatcgggg tgaggagat gatgagcgg ctagcaattt	2340
agcttttagt ctgataactc gccaccgacc ggaatgtatt acctatcagc agattaagga	2400
gagttgtgcc aacgagctgg atcttttggg tcagaagtat agcatagaac agcttaccac	2460
ttactggctt cagccggggg atgattggga agaggcgatt aggggtgatg caaaggtggc	2520
cctgcggccc gattgcaagt ataagattac taagttgggt aatattagaa actgctgcta	2580
tatttctgga aacggggccg aagtggagat agatactgag gacagggtgg ctattaggtg	2640
ttgcatgata aacatgtggc ccgggatact ggggatggat ggggtgatat ttatgaatgt	2700
gaggttcacg ggccccaaact ttaatggtac ggtgttcacg ggcaacacca acttgctcct	2760
gcatggtgcg agtttctatg ggtttaacaa cacctgtata gaggcctgga ccgatgtaaa	2820
ggttcgaggt tgttctttt atagctgttg gaaggcgggt gtgtgtcgcc ctaaaagcag	2880

gggttctgtg aagaaatgct tgtttgaaag gtgcacccta ggtatccttt ctgagggcaa 2940

ctccagggtg cgccataatg tggcttcgaa ctgcggttgc ttcatgcaag tgaagggggt 3000

gagcggtatc aagcataact cggctctgtg aaactgcgag gatcgcgct ctcagatgct 3060

gacctgcttt gatggcaact gtcacctgtt gaagaccatt catataagca gtcacccag 3120

aaaggcctgg cccgtgtttg agcataacat tctgaccgcg tgttccttgc atctgggggt 3180

caggaggggt atgttctgc cttaccagtg taactttagc cactataaaa tcctgctgga 3240

acccgagtgc atgactaagg tcagcctgaa tgggtgtgtt gatgtgagtc tgaagatttg 3300

gaaggtgctg aggtatgatg agaccaggac caggtgccga ccctgcgagt gcggcggcaa 3360

gcacatgaga aatcagcctg tgatgttgga tgtgaccgag gagcttaggc ctgaccatct 3420

ggtgctggcc tgcaccaggc ccgagtttgg gtctagcgat gaggataccg attgaggtgg 3480

gtaaggtggg cgtggctagc aggggtggcg tgtataaatt gggggtctaa ggggtctctc 3540

tgtttgtctt gcaacagccg ccgcatgag cgacaccggc aacagctttg atggaagcat 3600

ctttagtccc tatctgacag tgcgcatgcc tctctgggcc ggagtgcgtc agaattgat 3660

gggttccaac gtggatggac gtcccgttct gccttcaaat tcttctaact tggcctacgc 3720

gaccgtggga ggaactccg tggacgccg gacctccgc gccgcctccg ccgccccgc 3780

gaccgcgcgc agcatggcta cggaccttta cagctctttg gtggcgagca gcgcggcctc 3840

tcgcgcgtct gctcgggatg agaaactgac tgcctctgtg cttaaactgg aagacttgac 3900

ccgggagctg ggtcaactga ccagcaggt ttccagcttg cgtgagagca gccttgccctc 3960

cccataatgg ccataatat aaataaaagc cagtctgttt ggattaagca agtgtatgtt 4020

ctttatttaa ctctccgcgc gcggtaaagc cgggaccagc ggtctcggtc gtttagggtg 4080

cgggtgattt ttccaacac gtggtacagg tgctctgga tgtttagata catgggcatg 4140

agtcacatcc tggggtggag gtagcaccac tgcagagctt cgtgctcggg ggtggtgttg 4200

tatatgatcc agtcgtagca ggagcgctgg gcgtggtgct gaaaaatgtc cttagcaag 4260

aggcttatag ctagggggag gcccttggtg taagtgttta caaatctgct tagctgggag 4320

gggtgcatcc ggggggatat gatgtgcatc ttggactgga ttttaggtt ggctatgttc 4380

ccgccagat cccttctggg attcatgttg tgcaggacca ccagcacggt atatccagtg 4440

cacttgggaa atttatctg gagcttagac gggaatgcat ggaagaactt ggagacgccc 4500

ttgtggcctc ccagattttc catacattcg tccatgatga tggcaatggg cccgtgggaa 4560

gtgcctgag caaaaacgtt tctggcatcg ctacatcgt agttatgttc cagggtgagg 4620

tcacataggg acatctttac gaatcggggg cgaagggtcc cggactgggg gatgatggta	4680
ccctcggggc ccggggcgta gtcccccctca cagatctgca tctcccaggc ttccatttca	4740
gagggaggga tcataccac ctgcggggcg atgaaaaaga cagtttctgg cgcaggggag	4800
attaactggg atgagagcag gtttctgagc agctgtgact ttccacagcc ggtgggcccc	4860
tatatcacgc ctatcaccgg ctgcagctgg tagttaagag agctgcagct gccgtcctcc	4920
cggagcaggg gggccacctc gttgagcata tccctgacgt ggatgttctc cctgaccagt	4980
tccgccagaa ggcgctcgcc gccagcgaa agcagctctt gcaaggaagc aaaatttttc	5040
agcggtttca ggccatcggc cgtgggcatg tttttcagcg tctgggtcag cagctccagc	5100
ctgtcccaga gctcgggat gtgctctacg gcacatcgat ccagcagatc tctcgtttc	5160
gcgggttggg gcggctttcg ctgtagggca ccagccgatg ggcgtccagc ggggccagag	5220
tcatgtcctt ccatgggcgc agggctcctc tcagggtggt ctgggtcacg gtgaagggt	5280
gcgtccggg ttgggactg gccaggggtgc gcttgaggct ggttctgctg gtgctgaatc	5340
gctgccgctc ttgccctgc gcgtcgcca ggtagcattt gaccatggtc tcgtagtcga	5400
gacctcggc ggcgtgcccc ttggcgcgga gctttccctt ggaggtggcg ccgcacgagg	5460
ggcactgcag gctcttcagg gcgtagagct tgggagcgag aaacacggac tctggggagt	5520
aggcgtccgc gccgcaggcc gagcagaccg tctcgattc caccagccaa gtgagttccg	5580
ggcggtcagg gtcaaaaac aggttgcccc catgcttttt gatgcgtttc ttaccttggc	5640
tctccatgag gcggtgtccc ttctcgggtga cgaagaggct gtccgtgtcc ccgtagaccg	5700
acttcagggg cctgtcttcc agcggagtgc ctctgtcctc ctctagaga aactctgacc	5760
actctgagac gaaggccgc gtccaggcca ggacgaagga ggccacgtgg gaggggtagc	5820
ggtcgtgtgc cactagcggg tccaccttct ccagggtgtg caggcacatg tccccctct	5880
ccgcgtccag aaaagtgatt ggctttagg ttaggacac gtgaccgggg gttcccaacg	5940
gggggggtata aaagggggtg ggtgcccttt catcttcact ctcttccga tcgtgtctg	6000
cgagagccag ctgctgggtt aagtattccc tctcgaaggc gggcatgacc tcagcgtca	6060
ggttgtcagt ttctaaaaat gaggaggatt tgatgttcac ctgtccggag gtgatacctt	6120
tgagggtacc tgggtccatc tggtcagaaa aactatttt tttgttatca agcttgggtg	6180
cgaatgacct gtagaggcg ttggagagca gcttggcgat ggagcgcagg gtctgtttt	6240
tgtcgcggtc ggctcgtcc ttggccgcga tgttagttg cacgtactc ggggccacgc	6300
acttcactc ggggaacacg gtggtgcgt cgtctgggat caggcgcacc ctccagccgc	6360
ggttgtgcag ggtgacctg tcgacgttg tggcgacctc accgcgcaga cgctcgttgg	6420
tccagcagag gcggccgccc ttgcgcgagc agaagggggg taggggttcc agctggtcct	6480

cgtttggggg gtccgcgtcg atggtaaaga ccccggggag caggcgcggg tcaaagtagt 6540

cgatcttgca agcttgcag tccagagccc gctgccattc gcggcgcgcg agcgcgcgct 6600

cgtaggggtt gagggcgggg cccaggggca tgggtgggt gagcgcgag gcgtacatgc 6660

cgcagatgtc atacacgtac aggggttccc tgaggatacc gaggtagggt gggtagcagc 6720

gcccccgcg gatgctggcg cgcacgtagt catagagctc gtgggagggg gccagcatgt 6780

tgggcccag gttggtgcgc tggggcgct cgcgcgga gacgatctgc ctgaagatgg 6840

cgtgggagtt ggaggagatg gtggccgct ggaagacgtt gaagcttgct tcttgcaagc 6900

ccaggagtc cctgacgaag gagcgtagg actcgcgag cttgtgcacc agctcgcgcg 6960

tgacctggac gtcgagcga cagtagtcga gggtctcgcg gatgatgtca tacctatcct 7020

cccccttctt ttccacagc tcgcggttga ggacgaactc ttcgcggtct ttccagtact 7080

cttgagggg aaacccgtcc gtgtccgaac ggtaagagcc tagcatgtag aactggttga 7140

cggcctggta ggggcagcag ccttctcca cgggcagcgc gtaggcctgc gccgccttgc 7200

ggaggagggt gtgggtgagg gcgaaagtgt ccctgacat gactttgagg tattgatgtc 7260

tgaagtctgt gtcacgcag ccgcccgtt cccacagggt gtagtcctg cgctttttgg 7320

agcgcggtt gggcaggag aaggtaggt cattgaagag gatcttccc gtcgaggca 7380

tgaagttct ggtgatgcga aaggccctg ggaccgagga gcggttgtg atgacctggg 7440

cggccaggac gatctgtca aagccgttta tgttgttcc cacgatgtag agctccagga 7500

agcggggctg gcccttgatg gaggggagct ttttaagttc ctctaggta agctcctcgg 7560

gcgattccag gccgtgtcc tccagggcc agtcttgcaa gtgagggtg gccgccagga 7620

aggatcgcca gaggtcgcg gccatagggt tctgcaggcg gtcgcggaag gttctgaact 7680

gccgccccac ggccatttt tcgggggtga tgcagtagaa ggtgagggg tctttctccc 7740

aggggtccca tctgagctct cgggcgaggt cgcgcgcggc agcgaccaga gcctcgtcgc 7800

ccccagttt catgaccagc atgaaggga cgagttgctt gccaaaggct cccatccaag 7860

tgtagtttc tacatcgtag gtgacaaaga ggcgtccgt gcgaggatga gagccgattg 7920

ggaagaactg gatctccgc caccagttgg aggattggct gttgatgtg tgaaagtaga 7980

agtcctgtct gcgggcccag cactcgtgct ggcttttgta aaagcgaccg cagtactggc 8040

agcgtgcac gggttgtata tcttgacga ggtgaacctg gcgacctctg acgaggaagc 8100

gcagcgggaa tciaagtc ccgctgggg tcccgtgtgg ctggtggtct tttactttgg 8160

ttgtctggc gccagcatct gtctcctgga ggcgatggt ggaacagacc accacgccgc 8220

gagagccga ggtccagatc tcggcgctcg gcggcgagg tttgatgacg acatcgcgca 8280

cattggagct gtccatggtc tccagctccc gcggcgag gtcagccggg agttcctgga 8340

ggttcacctc gcagagacgg gtcaaggcgc ggacagtgtt gagatggat ctgatttcaa 8400

 ggggcatgtt ggaggcggag tcgatggctt gcaggaggcc gcagccccgg gggggccacga 8460
 tggttccccg cggggcgcga ggggaggcgg aagctggggg tgtgttcaga agcggtgacg 8520
 cgggcgggccc cccggaggta ggggggggttc cgccccaca ggcatgggcg gcaggggcac 8580
 gtcttcgccg cgcgcgggca ggggctgggt ctggctccga agagcgcttg cgtgcgcgac 8640
 gacgcgacgg ttggtgtcct gtatctggcg cctctgagtg aagaccacgg gtcccgtgac 8700
 cttgaacctg aaagagagtt cgacagaatc aatctcggca tcgttgacag cggcctggcg 8760
 caggatctcc tgcacgtcgc ccgagttgtc ctggtaggcg atttctgcca tgaactgctc 8820

 gatctcttcc tcttgagat ctctctgtcc ggcgcgctcc acggtggcgc ccaggtcgtt 8880
 ggagatgcga cccatgagct gcgagaaggc gttgagtcgc ccctcgttcc agaccggct 8940
 gtagaccacg cccccctcgg cgtcgcgggc gcgcatgacc acctgggcca gtttagctc 9000
 cacgtgtcgc gtgaagacgg cgtagtgtcg caggcgctgg aaaaggtagt tcagggtggt 9060
 ggcggtgtgc tcggcgacga agaagtacat gaccacgcgc cgcaactgg attcattgat 9120
 gtcccccaag gcctccaggc gctccatggc ctctagaag tccacggcga agttgaaaaa 9180
 ctgggagttg cgagcggaca cggtaactc ctctccaga agacggatga gctcggcgac 9240

 agtgtcgcgc acctcgcgt cgaaggccac ggggggcgct tcttctctt ccacctctt 9300
 ttccatgatt gcttcttctt ctctctcagc cgggacggga gggggcggcg gcgggggagg 9360
 ggcgcgccgg cgcgccgggc gcaccgggag gcggtcgatg aagcgctcga tcctctccc 9420
 ccgcatgcgg cgcattgct cggtagcggc gcggccgttc tcccgggggc gcagctcgaa 9480
 gacgcgcct ctatttcgc cgcggggcgg gcggccgtga ggtagcgaga cggcgctgac 9540
 tatgcatctt aacaattgct gtgtaggtac gccccaagg gacctgattg agtccagatc 9600
 caccggtacc gaaaacctt ggaggaaagc gtctatccag tcgcagtcgc aaggtaggt 9660

 gagcaccgtg gcggggcggg gcgggtcggg agagttcctg gcggagatgc tgctgatgat 9720
 gtaattaaag taggcggtct tgagaaggcg gatggtggac aggagcacca tgtctttggg 9780
 tccggcctgt tggatgcgga ggcggtcggc catgccccag gcctcgttct gacaccggcg 9840
 caggctcttg tagtaatctt gcatgagtct ttccaccggc acttcttctc ctctcttctc 9900
 ttcatctcgc cgttggttct tcgcgccgcc catgcgcgtg accccaaagc ccctgagcgg 9960
 ctgcagcagg gccaggtcgg cgaccacgcg ctcgccaag atggcctgct gtacctgagt 10020
 gagggctctc tcgaagtcac ccatgtccac gaagcgggtg taggcaccgc tgttgatggt 10080

gtagggtgcag ttggccatga cggaccagtt gacggtctgg tgtcccggct gcgagagctc	10140
cgtgtaccgc aggcgcgaga aggcgcggga atcgaacacg tagtcgttgc aagtcgcac	10200
cagatactgg tagcccacca ggaagtgcgg cggaggttgg cgatagaggg gccagcgctg	10260
ggtggcgggg gcgcccggcg ccaggctctt cagcatgagg cggtggtatc cgtagatgta	10320
cctggacatc caggtgatgc ctgcggcggg ggtgggtggcg cgcgcgtagt cgcggacccg	10380
gttccagatg tttcgcaggg gcgagaagtg ttccatggtc ggacacgtct ggccggtgag	10440
gcgcgcgcag tcgttgacgc tctatacaca cacaaaaacg aaagcgttta cagggtcttc	10500
gttctgtagc ctggaggaaa gtaaatgggt tgggttgcgg tgtgccccgg ttcgagacca	10560
agctgagctc agccgggtga agccgcagct aacgtggtat tggcagtccc gtctcgaccc	10620
aggccctgta tcctccagga tacggtcgag agcccttttg ctttcttggc caagcggccg	10680
tggcgcgcatc tgggatagat ggtcgcgatg agaggacaaa agcggctcgc ttccgtagtc	10740
tggagaaaca atcgccaggg ttgcgttgcg gcgtaccccg gttcgagccc ctatggcggc	10800
ttggatcggc cggaaccgcg gctaacctgg gctgtggcag ccccgctctc aggacccgc	10860
cagccgactt ctccagttac gggagcgagc cccttttgtt tttttatttt ttagatgcat	10920
cccgtgctgc ggcagatgcg cccctcgccc cggcccgatc agcagcagca acagcaggca	10980
tgcagacccc cctctctct ccccgccccg gtcaccacgg ccgcggcggc cgtgtccggt	11040
gcggggggcg cgttgagtc agatgagcca ccgcggcggc gacctaggca gtatctggac	11100
ttggaagagg gcgagggact ggcgcggtg gggcgagct ctccagagcg ccaccgcgg	11160
gtgcagttag aaaggacgc gcgtgaggcg tacctgccgc ggcaaacct gtttcgcgac	11220
cgcgggggcg aggagcccga ggagatgcgg gactgcaggt tccaagcggg gcgcgagctg	11280
cgccgcggct tggacagaca gcgcctgctg cgcgaggagg actttgagcc cgacacgcag	11340
acgggcatca gccccgcg cgcgcacgtg gcgcggccg acctggtgac cgcctacgag	11400
cagacggtga accaggagcg caacttcaa aaaagcttca acaaccacgt gcgcacgctg	11460
gtggcgcg aggaggtgac cctgggtctc atgcatctgt gggacctggt ggaggcgatc	11520
gtgcagaacc ccagcagcaa gcccctgacc gcgcagctgt tcctggtggt gcagcacagc	11580
agggacaacg aggccttcag ggaggcgctg ctgaacatca ccgagccgga ggggcgctgg	11640
ctctggacc tgataaacat cctgcagagc atagtgtg gcaggcgcag cctgagcctg	11700
gccgagaagg tggcggccat taactattct atgctgagcc tgggcaagtt ctacgtcgc	11760
aagatctaca agacccccta cgtgcccata gacaaggagg tgaagataga cagcttctac	11820
atgcgcatgg cgtgaaggt gctaacctg agcgacgacc tgggagtgt cgcgaacgag	11880
cgcatccaca aggccgtgag cgccagccgg cggcgcgagc tgagcgaccg cgaactgatg	11940

cacagtcctgc agcgcgcgct gaccggcgcg ggcgagggcg acagggaggt cgagtcctac	12000
tttgacatgg gggccgacct gcactggcag ccgagccgcc gcgccctgga agcggcgggg	12060
gcgtacggcg gccccctggc ggccgatgac gaggaagagg aggactatga gctagaggag	12120
ggcgagtacc tggaggactg acctggctgg tgggtgtttg gtatagatgc aagatccgaa	12180
cgtggcggac ccggcgggtcc gggcggcgct gcagagccag ccgtccggca ttaactcctc	12240
tgacgactgg gcccgggcca tgggtcgcat catggccctg accgcgcgca accccgaggc	12300
cttcaggcag cagcctcagg ctaaccggct ggcgggccatc ttggaagcgg tagtgcccgc	12360
gcgtccaac cccaccacg agaaggtgct ggccatagtc aacgcgctgg cggagagcag	12420
ggccatccgg gcagacgagg ccggactggt gtacgatgcg ctgctgcagc ggggtggcgcg	12480
gtacaacagc ggcaacgtgc agaccaacct ggaccgcctg gtgacggacg tgcgcgaggc	12540
cgtggcgcgag cgcgagcgct tgcacagga cggcaacctg ggctcgctgg tggcgctaaa	12600
cgcccttcctt agcaccacg cgccaacgt accgcggggg caggaggact acaccaactt	12660
cttgagcgcg ctgcggctga tggtagccga ggtccctcag agcgaggtgt accagtcggg	12720
gcccactac ttcttcaga ccagcagaca gggcttgcaa accgtgaacc tgagccaggc	12780
tttcaagaac ctgcgggggc tgtggggagt gaaggcgccc accggcgacc gggctacggt	12840
gtccagcctg ctaaccccc aactcgcct gctgctgctg ctgatcgcg ccttcacgga	12900
cagcgggagc gtctcgggg agacctatct gggccacctg ctgacgctgt accgcgaggc	12960
catcgggcag gcgcaggtag acgagcacac ctccaggag atcaccagcg tgagccacgc	13020
gctggggcag gaggacacgg gcagcctgca ggcgacctg aactacctgc tgaccaacag	13080
gcggcagaag attcccacg tgcacagcct gaccaggag gaggagcgca tcttgcgcta	13140
cgtgcagcag agcgtgagcc tgaacctgat gcgcgacggc gtgacgcca gcgtggcgct	13200
ggacatgacc gcgcgaaca tggaaccggg catgtacgt tcccagcggc cgttcacaa	13260
ccgcctgatg gactacttg atcgggcggc ggccgtgaac cccgagtact tcaccaatgc	13320
cattctgaat cccactgga tgccccctcc gggtttctac aacggggact tcgaggtgcc	13380
tgaggtcaac gatgggttcc tctgggatga catggatgac agtgtgttct ccccaaccc	13440
gctgcgcgcc gcgtctctgc gattgaagga gggctctgac agggaaggac caaggagtct	13500
ggcctcctcc ctggctctgg gggcgggtggg cgccacgggc gcggcggcg gcgggcagcag	13560
ccccctcccc agcctggcgg actctctgaa tagcgggcgg gtgagcaggc cccgcttgct	13620
aggcgaggag gagtatctga acaactcct gctgcagccc gtgagggaca aaaacgtca	13680
gcggcagcag ttccccaa atgggataga gacctggtg gacaagatgt ccagatggaa	13740
gacgtatgcg caggagtaca aggagtggga ggaccgccag ccgcggcccc tgccgcccc	13800

tagacagcgc tggcagcggc gcgcgtccaa ccgccgtgg aggcaggggc ccgaggacga	13860
tgatgactct gcagatgaca gcagcgtgtt ggacctgggc gggagcggga accccttttc	13920
gcacctgcgc ccacgcctgg gcaagatgtt ttaaaagaga aaaataaaaa ctcaccaagg	13980
ccatggcgac gagcgttggc tttttgttcc ctcccttagt atgcggcgcg cggcgatgtt	14040
cgaggagggg cctccccct cttacgagag cgcgatggga atttctctg cggcgccct	14100
gcagcctccc tacgtgcctc ctccgtacct gcaacctaca ggggggagaa atagcatctg	14160
ttactctgag ctgcagcccc tgtacgatac caccagactg tacctggtgg acaacaagtc	14220
cgcggacgtg gcctccctga actaccagaa cgaccacagc gattttttga ccacggtgat	14280
ccaaaacaac gacttcacc caaccgaggc cagtaccag accataaacc tggacaacag	14340
gtcgaactgg ggcggcgacc tgaagactat cctgcacacc aatatgcca acgtgaacga	14400
gttcatgttc accaactctt ttaaggcgcg ggtgatggcg gcgcgcgagc agggggaggc	14460
gaagtacgag tgggtggact tcacgtgcc cgagggaac tactcagaga ccatgactct	14520
cgacctgatg aacaatcgca tcgtggaaca ctatctgaaa gtgggcagc agaacggggt	14580
gaaggagagc gatatcgggg tcaagtttga caccagaaac ttccgtctgg gctgggacct	14640
tgtgaccggg ctggtcatgc cgggggtcta caccaacgag gcctttcatc ccgatatagt	14700
gctcctgccc ggcgtgtggg tggacttcac ccagagccgg ctgagcaacc tgctgggcgt	14760
tcgaagcgg caacctttcc aggagggttt caagatcacc tatgaggatc tggagggggg	14820
caacattccc gcgtccttg atctggacgc ctacgaggag agcttgaaac ccgaggagag	14880
cgctggcgac agcggcgaga gtggcgagga gcaagccggc ggcgcgga cgcgctcggc	14940
agaaaacgaa agtactccc cagtggcggc ggacgctcg gaggtcgagc cggaggccat	15000
gcagcaggac gcagaggagg gcgcgcagga ggacatgaac aatggggaga tcagggcgca	15060
cactttcgcc acccggggcg aagaaaaaga ggcagaggcg gcggcgga cggcggaagc	15120
cgaaaccgag gcagaggcag agcccagac cgaagttagt gaagacatga atgatggaga	15180
acgtaggggt gacacgtttg ccaccgggg cgaagagaag gcggcgagg cagaagccgc	15240
ggctgaggag gcggctcgcg ctgcggccaa ggctgaggct gcggctgagg ctaaggtcga	15300
agccgatgtt gcggttagg ctacggctga ggaggaggcg gcggctgaag cagttaagga	15360
aaaggccag gcagagcagg aagagaaaa acctgtcatt caacctctaa aagaagatag	15420
caaaaagcgc agttacaacg tcattgaggg cagcaccttt acccaatacc gcagctggta	15480
cctggcttac aactacggcg acccgggtcaa gggggtgcgc tcgtggacct tgctctgcac	15540

gccggacgtc acctgcggt ccgagcagat gtactgggtc ctgccaaaca tgatgcaaga 15600
cccgtgacc ttccgttcca cgcggcaggt tagcaacttt ccggtgggtg gcgccgaact 15660
gtgtccagta cactccaaga gtttttaciaa cgagcaggcc gtctactccc agctgatccg 15720
ccaggccacc tcctgaccc acgtgttcaa tcgctttccc gagaaccaga ttttggcgcg 15780
cccgccggcc cccacatca ccaccgtcag tgaaaacgtt cctgcctca cagatcacgg 15840
gacgtaccg ctgcgaaca gcatctcagg agtcacgca gtgaccatta ctgacgccag 15900
acgccggacc tgccctiacg tttacaaggc ctggggcata gtctcgccgc gcgtcctctc 15960

cagtgcact ttttaaaaca catccacca cacgtccaa aatcatgtcc gtactcatct 16020
cgcccagcaa caacaccggc tgggggctgc gcgcaccag caagatgttt ggaggggcaa 16080
ggaagcgctc cgaccagcac ccggtgcgcg tgcgcggcca ctaccgcgcg ccctggggtg 16140
cgcacaagcg cgggcgcaca gggcgacca ctgtggatga tgtcattgac tccgtagtgg 16200
agcaggcgcg ccactacaca cccggcgcg cgaccgcctc cgccgtgtcc accgtggacc 16260
aggcgatcga aagcgtggta cagggggcg ggactatgc caaccttaa agtcgccgc 16320
gccgcgtggc gcgccccat cgccggagac cccgggctac tgccgcgcg cgccttacca 16380

aggctctgct caagcgccc aggcgaactg gccaccgggc cgccatgagg gccgcacggc 16440
gggctgccg tgccgcgagc gccgtggccc cgcgggcacg aaggcgcgcg gccgtgccg 16500
ccgccccgc catttcagc ttggcctcga cgcggcgcg taacatatac tgggtgcgcg 16560
actcggtag cggcacagct gtgcccgtgc gctttcgccc cccacggaat tagcacaaga 16620
caacatacac actgagtctc ctgctgttgt gtatccagc ggcgaccgtc agcagcgcg 16680
acatgtcaa gcgcaaaatt aaagaagaga tgtccaggt catcgcgccg gagatctatg 16740
ggccccgaa gaaggaggag gaggattaca agccccgaa gctaaagcgg gtcaaaaaga 16800

aaaagaaaga tgatgacgtt gacgaggcgg tggagtttgt ccgccgcagtg gcgccaggc 16860
gccctgtgca gtggaagggt cggcgctgc agcagtcct gcgccccgc accgcggtgg 16920
tctttacgc cgcgagcgt tccacgcga ctttcaagcg ggtgtacgat gaggtgtacg 16980
gcgacgagga tctgttgag caggccaacc atcgatttgg ggagtttgca tatgggaaac 17040
ggcctcgca gactctaaaa gaggacctgc tggcgctacc gctggacgag ggcaatcca 17100
ccccagttc gaagccggtg accctgcaac aggtgctgcc tttgagcgcg cccagcgagc 17160
agaagcgagg gttaaagcg gagggcgggg acctggcacc caccgtgcag ttgatggtgc 17220

ccaagcgga gaagctggag gacgtgctgg agaaaatgaa agtagagccc gggatccagc 17280
ccgagatcaa ggtccgcct atcaagcagg tggcgcccgg cgtgggagtc cagaccgtgg 17340
acgttaggat tcccaggag gagatggaaa cccaaaccgc cactccctct tcggcagcaa 17400

gcgccaccac cggcgccgct tcggtagagg tgcagacgga cccctggcta cccgccgcca	17460
ctatcgccgt cggcgccgcc ccccgttcgc gcggacgcaa gagaaattat ccagcggcca	17520
gcgcgcttat gccccagtat gcgctgcac catccatcgc gcccaccccc ggctaccgcg	17580
ggtactcgta ccgccccgcg agatcagccg gcactcgcg cggcgccgc cgtgcgacca	17640
caaccagccg ccgccgtcgc cggcgccgcc agccagtgt gacccccgtg tctgtaagga	17700
aggtggctcg ctcggggagc acgctgggtg tgcccagagc gcgctaccac ccagcatcg	17760
tttaaagccg gtctctgtat ggttcttgca gatatggccc tcaattgtcg ctttcgcttc	17820
ccggtgccgg gataccgagg aagaactcac cggcgagggg gcatggcggg cagcggcttc	17880
cgcggcgccc gtcgcatcg ccggcgcgca aagagcaggc gcatgcgcgg cgggtgtgtg	17940
cccctgctgg tcccgtact cggcgcgcg atcgcgccg tgcccgggat cgcctccgtg	18000
gccctgcagg cgtcccagaa acattgactc ttgcaacctt gcaagcttgc atttttggag	18060
gaaaaataa aaaagtctag actctcacgc tcgcttggtc ctgtgactat tttgtagaaa	18120
aaagatggaa gacatcaact ttgcgtcgt ggcccccggt cacggctcgc gcccgttcat	18180
gggagactgg acagatacgc gcaccagcaa tatgagcggg ggcgcccttca gctggggcag	18240
tctgtggagc ggccttaaaa attttgggtc caccattaag aactatggca acaaagcgtg	18300
gaacagcagc acgggtcaga tgctgagaga caagttgaaa gagcagaact tccaggagaa	18360
ggtggcgagc ggcctggcct ctggcatcag cggggtggtg gacatagcta accagccgt	18420
gcagaaaaag ataaacagtc atctggaccc ccgccctcag gtggaggaaa cgcctccagc	18480
catggagacg gtgtctcccg agggcaaagg cgaagcgc cgcggcccg acagggaaga	18540
gaccttggtg tcacacaccg aggagccgcc ctcttacgag gaggcagtca aggccgcct	18600
gcccaccact cggcccatg ctccatggc caccggtgtg gtgggtcaca ggcaacacac	18660
ccccgaaca ctagatcgc ccccgccgtc cgagccgact cgccagccaa aggcggtgac	18720
ggtgtccgt cctccactt ccgcccga cagagtcct ctgcgccgcg ctgcgagcgg	18780
ccccgggcc tcgcgagta gcggcaactg gcagagcaca ctgaacagca tcgtgggcct	18840
gggagtgagg agtgtgaagc gccgccgtt ctactgaatg agcaagctag ctaacgtgtt	18900
glatgtgtgt atgcgtccta tgtcgccgc agaggagctg ttgagccgc ggcgccgtct	18960
gcactccagc gaatttcaag atggcgaccc catcgatgat gcctcagtgg tcgtacatgc	19020
acatctcggg ccaggacgct tcggagtacc tgagccccgg gctggtgcag ttcgcccgcg	19080
ccacagacac ctacttcaac atgagtaaca agttcaggaa cccactgtg gcgcccaccc	19140
acgatgtgac cacggaccgg tcgcagcgcc tgacgtgcg gttcatcccc gtggatcggg	19200
aggacaccgc ttactcttac aaggcgcggt tcacgtggc cgtgggcgac aaccgcgtgc	19260

tggacatggc ctccacttac ttgacatcc ggggggtgct ggacaggggc cccactttta	19320
agccctactc gggcactgcc tacaaccccc tggcccccaa gggcgcccc aattcttgtg	19380
agtgggaaca agaggaaaat caggtggtcg ctgcagatga tgaacttgaa gatgaagaag	19440
cgcaagcaca agaggaagcc cctgtgaaaa aaattcatgt atatgctcag gcgcctcttt	19500
ctggcgaaaa gatttccaag gatgtatcc aaataggtac tgaagtcgta ggagatacat	19560
ctaaggacac ttttgcagat aaaacattcc aaccgaacc tcagataggc gagtctcagt	19620
ggaacgaggc tgatgccaca gcagcaggag gtagagtttt gaaaaagact acccctatga	19680
gaccttgcta tggatcctat gccaggccta ccaatgcca cgggggtcaa ggaattatgg	19740
ttgccaatga acaaggagtg ttggagtcta aagtagaaat gcaatttttc tctaacacca	19800
caacccttaa tgcgcgggat ggaaccggca atcccgaacc aaagtggtg ttgtacagcg	19860
aagatgtcca cttggaatct cccgatactc atctgtctta caagcccaa aaggatgatg	19920
ttaatgcaa aatcatgttg ggtcagcaag ccatgccaa cagaccaac ctcatggat	19980
ttagagataa tttcattggg cttatgtttt acaacagcac cggtaacatg ggagtgtctg	20040
cgggtcaggc ctctcagttg aatgtgttg tggacttgca ggatagaaac acagaactgt	20100
catatcagct tctgcttgat tcaattgggg atagaaccag atacttctcc atgtggaacc	20160
aggcagtgga tagctatgat ccagatgtca gaattattga aaaccatggg actgaggatg	20220
aactgcccaa ctactgttc ctttgggcg gcataggagt tactgatact tatcaaggga	20280
taaaaatac caatggcaat ggtcagtgga ccaaagatga tcagttcgcg gaccgcaacg	20340
aaataggggt gggaaacaac ttcgccatgg agatcaacat ccaggccaac ctttgagaa	20400
acttctctta tgcaaactg gggctctacc tgccagacaa gctcaagtac aacccacca	20460
acgtggacat ctctgacaac cccaacacct atgactacat gaacaagcgg gtggtggccc	20520
ctggcctggt ggactgttt gtcaatgtgg gagccagggt gtcctggac tacatggaca	20580
acgtcaacc cttcaaccac caccgcaatg cgggtctgcg ctaccgtcc atgatcctgg	20640
gcaacgggcg ctatgtgcc ttccacatcc aggtacccca gaagttcttt gccatcaaga	20700
acctctgct cctgcccggc tcttacacct acgagtggaa cttcaggaag gatgtgaaca	20760
tggctctaca gagctctctg ggcaatgacc ttaggggtgga tggggccagc atcaagtttg	20820
acagcatcac cctctatgct acatttttcc ccatggccca caacaccgcc tccacgttg	20880
aggccatgct gagaaacgac accaacgacc agtcctttaa tgactacctc tctggggcca	20940
acatgtctta cccaatccca gccaaaggcca ccaacgtgcc catctccatc ccctctcgca	21000

actgggccgc ctttagaggc tgggccttta cccgccttaa gaccaaggag accccctccc	21060
tgggctcggg ttttgatccc tactttgttt actcgggata catcccctac ctggatggca	21120
ccttctacct caaccacact ttcaagaaga tatccatcat gtatgactcc tccgtcagct	21180
ggccgggcaa cgaccgcttg ctacccccca atgagttcga ggtcaagcgc gccgtggacg	21240
gcgagggcta caacgtggcc cagtgcaca tgaccaagga ctggttcctg gtgcagatgc	21300
tggccaacta caacataggc taccagggtt ttacatccc agagagctac aaggacagga	21360
tgtactcctt cticagaaat ttccaacca tgagccgaca ggtggtggac gagaccaatt	21420
acaaggacta tcaagccatt ggcatcacc accagcaca caactcgggt ttcgtgggct	21480
acctggcgcc caccatgcgc gaggtcagg cctacccgc caactcccc tacccttga	21540
taggcaagac cgcggtcgac agcgtcacc agaaaaagt cctctcgac cgcacctct	21600
ggcgcatccc ctctctagc aacttcatt ccatgggtgc gctcacggac ctgggcaaaa	21660
acctgttta tgccaactct gcccatgcgc tggacatgac tttgagggtg gacccatgg	21720
acgagccac cttctctat attgtgttg aagtgttca cgtggtcaga gtgcaccagc	21780
cgcaccgagg tgtcatcgag accgtgtacc tgcgtacgc cttctcagcc ggcaacgcca	21840
ccacctaagg agacagcgc gccgcgcct gcatgacggg ttccaccgag caagagctca	21900
gggccattgc cagagacctg ggatgcggac cctattttt gggcacctat gacaaacgt	21960
tcccgggctt tatctccga gacaagctcg cctgcgcat tgtcaacac gccgcgcgcg	22020
agaccggggg cgtgcactgg ctggcctttg gctgggacc gcgtccaaa acttgctacc	22080
tctttgacc ctttggttc tccgatcag gcctcaggca gatttatgag tttgagtacg	22140
aggggctgct gcgccgcag gcgtcgcct cctgcgccga ccgtgcac acccttgaga	22200
agtccaccga aaccgtgcag gggcccccact cggccgcctg cggctctctc tgttgcatgt	22260
ttttgcacgc ctttgtcac tggcctcaga gtcccatgga ttgcaacccc accatgaact	22320
tgctaaagg agtgcccaac gccatgctcc agagcccca ggtccagccc accctgcgc	22380
gcaaccagga acagctttac cgcttcctgg agcgccact cccctactc cgcagccaca	22440
gcgcgcgcat cgggggggac acctctttt gccacttgca agaaaacatg caagacggaa	22500
aatgatgtac agcatgctt taataaatgt aaagactgtg cactttaatt atacacgggc	22560
tctttctggt tattttatca acaccgccgt cgccatttag aaatcgaaag ggttctgccg	22620
tgcgtcgccg tgcgccagg gcagagacac gttgcgata tggaagcggc tcgcccactt	22680
gaactcgggc accacatgc ggggcagtgg ttctcgggg aagtctcgc tccacagggt	22740
gcgggtcagc tgcagcgc tcaggaggtc gggagccgag atcttgaagt cgcagttggg	22800
gccggaaccc tgcgcgcgc agttgcggt cagggggtg cagcactgga acaccagcag	22860

ggccggatta ttacagctgg ccagcaggct ctcgctcgctg atcatgtcgc tgtccagatc	22920
ctccgcgttg ctcagggcga atggggatcat ctctgcagacc tgcctgcca ggaaggcg	22980
gagccaggc ttgccgttg agtcgcagcg caggggcatt agcagggtgcc cacggcccga	23040
ctgcgcctgc gggtaacaac gcgcgatgaa ggcttcgata tgcctaaaag ccacctgggt	23100
cttggctccc tccgaaaaga acatcccaca ggacttgctg gagaactggt tcgcgggaca	23160
gctggcatcg tgcaggcagc agcgcgcgtc agtggttgga atctgcacca cgttgcgacc	23220
ccaccggttt ttactatct tggccttgga agcctgctcc tttagcgcgc gctggccgtt	23280
ctcgctggtc acatccatct ctatcacctg ttccttggtg atcatgttg tcccgtgcag	23340
acacttagg tcgcccctcg tctgggtgca gcggtgctcc cacagcgcgc aaccggtggg	23400
ctcccaattc ttgtgggtca ccccccgta ggctgcagg taggcctgca ggaagcgccc	23460
catcatggtc ataaaggtct tctggctcgt aaaggtcagc tgcaggccgc gatgctcttc	23520
gttcagccag gtcttcgaga tggcgccag cgcctcggtc tgctcgggca gcatctaaa	23580
atttgtcttc aggtcgttat ccacgtggta ctgtccatc atggcacgcg ccgcctccat	23640
gcccctctcc caggcggaca ccatgggcag gcttaggggg tttatcactt ccagcggcga	23700
ggacaccgta ctttcgattt cttctctctc cccctcttcc cggcgcgcgc ccccgctgtt	23760
gcgcgctctt accgcctgca ccaaggggtc gtcttcaggc aagcgccga ccgagcgctt	23820
gccgcccctg acctgcttga tcagtaccgg cgggttgctg aagcccacca tggtcagcgc	23880
cgctgctct tcttcgtctt cgctgtctac cactatttct ggggaggggc ttctccgctc	23940
tgccgcaaag gcggcggatc gcttcttttt tttcttggga gccgccgca tggagtccgc	24000
cacggcgacc gaggtcgagg gcgtggggct gggggtgcgc ggtaccaggg cctcgtcgcc	24060
ctcggactct tctctgact ccaggcggcg gcggagtgc tcttttggg gcgcgcgcgt	24120
cagcggcggc ggagacgggg acggggacgg ggacgggacg ccctccacag ggggtggtct	24180
tcgcgcagac ccgcggccgc gctcgggggt cttctcgcgc tggctctggt cccgactggc	24240
cattgtatcc tctctctct aggcagagag acataaggag tctatcatgc aagtcagaaa	24300
ggaggagagc ttaaccaccc cctcagagac cgccgatgcg cccgccgtcg ccgtcgcccc	24360
cgctaccgcc gacgcgcccc ccacaccgag cgacaccccc acggaccccc ccgccgacgc	24420
acccctgttc gaggaagcgg ccgtggagca ggacccgggc tttgtctcgg cagaggagga	24480
tttgcaagag gaggagaata aggaggagaa gccctcagt ccaaaagatc ataaagagca	24540
agacgagcac gacgcagacg cacaccaggg tgaagtctgg cggggggacg gagggcatgg	24600
cggcgccgac tacctagacg aaggaaacga cgtgctcttg aagcacctgc atcgtcagt	24660
cgccatcgct tcgcagcctc tgcaggagcg cagcgagggt cccctcagcg tggcggagg	24720

cagccgcgcc tacgagctca gcctcttttc cccccgggtg cccccccgcc gccgcgaaaa	24780
cggcacatgc gagcccaacc cgcgcctcaa ctctacccc gcctttgttg tgcccagagt	24840
cctggccacc tatcacatct tctttcaaaa ttgcaagatc cccatctcgt gccgcgcaa	24900
ccgtagccgc gccgataaga tgctggccct gcgccagggc gaccacatac ctgatatcg	24960
cgctttggaa gatgtgccaa agatcttcga gggctctgggg cgcaacgaga agcgggcagc	25020
aaactctctg caacaggaaa acagcgaaaa tgagagtcac actggagcgc tggtaggagt	25080
ggagggcgac aacgcccgc tggcgggtgt caagcgagc atcgaggtca cccactttgc	25140
ctaccccgcg ctcaacctgc ccccaaaagt catgaacggt gtcattggacg ggctgatcat	25200
gcgccgcggc cggcccctcg ctccagatgc aaacttgcac gaggagaccg aggacggtca	25260
gcccgtggtc agcgacgagc agctgacggt ctggctggag agcgcgacc cggccgaact	25320
ggaggagcgg cgcaagatga tgatggccgc ggtgtgtgtc accgtagagc tggagtgtct	25380
gcagcgcttc ttcgggtgac ccgagatgca gagaaaggtc gaggagacc tacactacac	25440
cttcgccag ggctacgtgc gccaggcttg caagatctcc aacgtggagc tcagcaacct	25500
ggtgtcctac ctgggcatct tgcatgaaaa ccgccttggg cagagcgtgc tacactccac	25560
cctgcgcggg gaggcgccgc gcgactacgt gcgcgactgc gtttacctct tctctgcta	25620
caactggcag acggccatgg gggctctggca gcagtgcctg gaggagcgca acctcaagga	25680
gttgagaag ctctgcagc gcgcgtcaa agacctctgg acgggcttca acgagcgctc	25740
ggtggccgcc gcgtagccg acctcatctt ccccgagcgc ctgctcaaaa cctccagca	25800
ggggctgccc gacttacca gccaaagcat gttgcaaaat tttaggaaact ttatctgga	25860
gcgttctggc atctacccg ccacctgtgt cgcctgccc agcgactttg tccccctgt	25920
gtaccgcgag tgcccccg cgtgtgggg cactgtctac ctgttccaac tggccaacta	25980
cctgtcctac cagcgggacc tcatggagga ctccagcggc gaggggctca tggagtcca	26040
ctgccgtgc aacctctgca cgcaccaccg ctccctggtc tgcaacacc aactgtcag	26100
cgagagttag attatcggtc ctttcgagct acagggtccg tctcctcag acgagaagtc	26160
cgcggtccg gggctaaaaac tcatccggg gctgtggact tccgcctacc tgcgcaaatt	26220
tgtacctgaa gactaccag cccacgaaat caggttttac gaggaccaat cccgcccgc	26280
caaggcgag ctgaccgct gcgtcatcac ccaggcgag atcctaggcc aattgcaagc	26340
catcaaaaa gcccgcaag agttttgtct gaagaggggt cggggggtgt atctggacc	26400
ccagtgggt gaggagctca acccggttc cccgtgcca ccgcccggg accttcttc	26460

ccaggataag catcgccatg gctcccagaa agaagcagca gcggccgccg ctgccgccgc 26520

cccacatgct ggaggaagag gaggaatact gggacagtca ggagaggag gtctcgacg 26580

aggaggagcc ggagacggag atggaagagt gggaggagga cagcttagac gaggaggctt 26640

ccgaagccga agaggcaggc gcaacaccgt caccctcggc cgcagccccc tcgcaggcgc 26700

ccccgaagtc cgtccccagc atcagcagca acagcagcgc tataacctcc gctcctccac 26760

cgccgcgacc caccggccgac cgcagaccca accgtagatg ggacaccacc ggaaccgggg 26820

ccggttaagtc ctccgggaga ggcaagcaag cgcagcgcca aggctaccgc tcgtggcgcg 26880

ctcacaagaa cgccatagtc gcttgcttgc aagactgcgg ggggaacatc tccttcgccc 26940

gccgttccct gctcttcac caccgtgtgg ccttcccccg taacgtcctg cattactacc 27000

gtcatctcta cagcccctac tgcggcggca gtgagccaga ggcggccagc ggcggcggcg 27060

cccgtttcgg tgcctaggaa gaccagggc aagacttcag ccaagaaact cgcggcgacc 27120

gcggcgaacg cggtcgcggg ggccctgcgc ctgacggtga acgaacctt gtcgaccgc 27180

gaactgagga accgaatctt cccactctc tatgcatct tccagcagag cagagggcag 27240

gatcaggaac tgaaagtaaa aaacaggtct ctgcgtccc tcaccgcag ctgtctgtat 27300

cacaagagcg aagaccagct tcggcgcacg ctggaggacg ctgaggcact cttcagcaaa 27360

tactgcgcgc tcaactctaa ggactagctc cgcgcccttc tcgaatttag gcgggaacgc 27420

ctacgtcatc gcagcgccgc cgtcatgagc aaggacattc ccacgccata catgtggagc 27480

tatcagccgc agatgggact cgcggcgggc gcctccaag actactccac ccgatgaac 27540

tggctcagtg ccggcccaca catgatctca caggttaatg acatccgcac ccatcgaaac 27600

caaatattgg tgaagcaggc ggcaattacc accacgccc gcaataatcc caaccccagg 27660

gagtggcccc cgtccctggt gtatcaggaa attccccgcc ccaccaccgt actattccg 27720

cgtgattccc aggccgaagt ccaaatgact aactcagggg cacagctcgc gggcggtgt 27780

cgtcacaggg tgcggcctcc tcgccagggt ataactcacc tggagatccg aggcagaggt 27840

attcagctca acgacgagtc ggtgagctcc tcgtcggtc tcagacctga cgggaccttc 27900

cagatagccg gagccggccg atcttccttc acgccccgc aggcgtaact gactctgcag 27960

agctcgtcct cggcgccgcg ctcgggcggc atcgggactc tccagttcgt gcaggagttt 28020

gtgccctcgg tctacttcaa cccctctcgc ggctctcccg gtcgtaccc ggaccagttt 28080

atcccgaact ttgacgcgc gagggactcg gtggacggct acgactgaat gtcgggtgga 28140

cccgtgacg agcaacttcg cctgaagcac ctgaccact gccgccgcc tcagtgttt 28200

gcccgtgtc agaccggtga gttccagtac tttccctgc ccgactcgca cccggacggc 28260

ccggcgacg ggtgctgtt tttcatccc agtcaggctc gctctaccct aatcaggag 28320

ttcaccgccc gtccccctact ggcggagttg gaaaaggggc cttctatcct aaccattgcc	28380
tgcatttgct ctaaccctgg attacaccaa gatctttgct gtcatttggtg tgctgagtat	28440
aataaaggct gagatcagaa tctactcggg ctctgtgcgc catcctgtca acgccaccgt	28500
ccaagcccgg ccgatcagc ccgaggtgaa cctcacctgt ggtctgcacc ggcgccctgag	28560
gaaataccta gcttggctact acaacagcac tccctttgtg gttacaaca gctttgacca	28620
ggacggggtc tcaactgaggg ataacctctc gaacctgagc tactccatca ggaagaacaa	28680
caccctcgag ctacttctc cttacctgcc cgggacttac cagtgtgtca ccggcccctg	28740
caccacacc cacctgttga tcgtaaacga ctctcttcg agaacagacc tcaataactc	28800
ctctccgag tttcccagaa caggagggtga gctcaggaaa ccccggttaa agaagggtgg	28860
acaagagtta acacttgtgg ggtttctggt atatgtgacg ctgggtgggtg ctcttttgat	28920
taaggctttt ctttccatgt ctgaactatc cctcttcttt tatgaacaac tcgactagt	28980
ctaacgggac ctiaccaac gaatcgggat tgaatatcgg taaccaggtt gcagtttcac	29040
ttttgattac cttcatagtc ctcttctgc tagtgctgtc gcttctgtgc ctgcggatcg	29100
ggggctgctg catccacgtt tatacttggt gctggctgtt tagaaggttc ggagaccacc	29160
gcaggtagaa taatgctgct taccctcttt gtcttgccgc tggctgccag ctgccaagcc	29220
ttttccgagg ctgacttcat agagccccag tgcaatatca cttataaatc tgaactgcc	29280
atctgtacta ttctaataca atgtgttact caacacgata aggtgactgt taaatacaaa	29340
gatcaattaa aaaaagacgc actttacagc agctggcaac caggagatga tcaaaaatac	29400
aatgtaaccg tcttccaggg caaactctcc aaaacttaca attacaattt cccatttgag	29460
cagatgtgtg actttgtcat gtacatggaa aagcagtaca agctgtggcc tccaactccc	29520
cagggtgtg tgaaaaatcc aggtcttttc tgtatgatct ctctctgtgt aactgtgctg	29580
gcactaatac tcacgttct gtatctcaga tttaaatcaa ggcaaagctt cattgatgaa	29640
aagaaaatgc cataatcgct caacgttga ttgctaacac cgggttttta tccgcagaat	29700
gattggaatc accctactaa tcacctccct ccttgcgatt gccatgggt tggaacgaat	29760
cgaagtccct gtgggggcca atgttacct ggtggggcct gtcggcaatg ctacattaat	29820
gtgggaaaaa tatactaaaa atcaatgggt ttcttactgc actaacaaaa acagccacaa	29880
gcccagagcc atctgcgatg ggcaaaatct aaccttgatt gatgttcaat tgctggatgc	29940
gggctactat taigggcagc tgggtacaat gattaattac tggagacccc acagagatta	30000
catgcttcac gtagtaaagg gtccattag cagcccaacc accacctcta ccacaccac	30060
taccaccact actcccacca ccagcactgc cggccagcct cctcatagca gaacaaccac	30120
ttttatcaat tccaagtccc actccccca cattgcccgc ggccctccg cctcagactc	30180

cgagaccacc gagatctgct tctgcaaatg ctctgacgcc attgccagg atttgaaga 30240

tcacaggaa gatgagcatg actacgcaga tgcattgccag gcatcagagg cagaagcgct 30300

accggtggcc ctaaaacagt atgcagactc ccacaccacc cccaaccttc ctccaccttc 30360

ccagaagcca agtttcctgg gggaaaatga aactctgcct ctttcatac tagctctgac 30420

atctgttctg attttggccg ctctgctggt gcttctatgc tctatatgct acctgatctg 30480

ctgcagaaag aaaaaatctc acggccatgc tcaccagccc ctcattgact tcccttacc 30540

tccagagctg ggcgaccaca aactttaagt ctgcagtagc tatctgccca tcccttgtca 30600

gtcgacagcg atgagcccca ctaatctaac agcctctgga cttacaacat tgtctcttaa 30660

tgagaccacc gctcctcaag acctgtacga tgggtgtctcc gcgctgggta accagtggga 30720

tcacctgggc atattggtggc tctcatagg agcagtgacc ctgtgcctaa tcttggctctg 30780

gatcatctgc tgcataaaa gcagaagacc caggcgccgg cccatctaca ggcccttcgt 30840

catcacacct gaagataatg atgatgatga caccacctcc aggcctgcaga gcctaagca 30900

gctactcttc tcttttacag catggtaaat tgaatcatgc cccgcatctt catctacttg 30960

cttctccttc cactttttct gggctcctct acattggcca ctgtgtccca catcgaggta 31020

gactgcctca cgccttcac agtctacctg cttttcggt tttcatctg cacctttgtc 31080

tgacagctta tcaactgtagt gatctgcttc atacagtga tcgactacat ctgtgtgcgg 31140

gtggcctact ttagacacca cccccagtat cgcaacaggg acatagcggc tctcctaaga 31200

cttgtttaaa tcatggccaa attacctgtg attggtcttc tgattatctg ctgcgtccta 31260

gccgcgattg ggactcaacc taataccacc accagcgctc ccagaaagag acatgtatcc 31320

tgcagcttca agcgtccctg gaatatacc caatgcttta ctgatgaacc tgaaatctct 31380

ttggcttggt acttcagcg caccgccctt ctcatctct gcagtacgtt tattgtcttt 31440

gccatctacc ctcccttaa cctgggctgg aatgctgtca actctatgga atateccacc 31500

ttcccagaac cagacctgcc agacctggtt gttctaaacg cgtttctcc tctccagtt 31560

caaaatcagt ttgcctctc gtcctctacg cccactgagg tcagctactt taatctaaca 31620

ggcggagatg actgaaaacc tagacctaga aatggacggt ctctgcagcg agcaacgcac 31680

actagagagg cgcggcaaa aagcagagct cgagcgtctt aaacaagagc tccaagacgc 31740

cgtggccata caccagtga aaaaagggt cttctgtctg gtaaaacagg ccacgtcac 31800

ctatgaaaaa acaggtgaca cccaccgctt aggatacaag ctgccacac agcgccaaaa 31860

gtttgccctt atgataggtg aacaacccat caccgtcacc cagcactccg tggagacaga 31920

aggctgcatt catgctccct gcaggggcgc tgactgcctc tacaccttga tcaaaaccct	31980
ctgcggtctc agagacctta tccctttcaa ttgatcataa ctgtaatcaa taaaaaatca	32040
cttacttgaa atctgatagc aagactctgt ccaatttttt cagcaaacct tccttcccct	32100
cctcccaact ctggtactct aggcgcctcc tagctgcaaa cttcctccac agtctgaagg	32160
gaatgtcaga ttctctctcc tgctccctccg caccacgat cttcatgttg ttacagatga	32220
aacgcgcgag atcgtctgac gagaccttca acccctgtga cccctacgat accgagatcg	32280
ctccgacttc tgiccccttc cttacccttc cctttgtatc atccgcagga atgcaagaaa	32340
atccagctgg ggtgctgtcc ctgcacctgt cagagcccct taccaccac aatggggccc	32400
tgactctaaa aatggggggc ggcctgacctc tggacaagga agggaatctc acttcccaaa	32460
acatcaccag tgtcgtatccc cctctcaaaa aaagcaagaa caacatcagc cttcagaccg	32520
ccgcaccctc cgcctgacgc tccggggccc taaccttttt tgccactccc cccctagcgg	32580
tcagtggcga caaccttact gtgcagtctc aggccctctt tactttggaa gactcaaaac	32640
taactctggc caccaaagga cccctaactg tgtccgaagg caaacttgtc ctagaacag	32700
agcctccctc gcatgcaagt gacagcagta gcctgggcct tagcgtcacg gcccactta	32760
gcattaacaa tgacagccta ggactagaca tgcaagcgcc catcagctct cgagatggaa	32820
aactggctct aacagtggcg gccccctaa ctgtggccga gggtatcaat gctttggcag	32880
tagccacagg taatggtatt ggactaaatg aaaccaacac acacctgcag gcaaaactgg	32940
tcgcgcccct aggcctttgat accaacggca acattaagct aagcgtcgca ggaggcatga	33000
ggctaacaa taacacactg atactagatg taaactaccc atttgaggct caaggccaac	33060
tgagcctaag agtgggctcg ggcccactat atgtagattc tagtagtcat aacctaacca	33120
ttagatgcct taggggattg tatgtaacat cttctaacaa ccaaaacggt ctaggaggca	33180
acattaaact aacaaaaggc cttgtgtatg acggaaatgc catagcagtt aatgttgga	33240
aagggttgga atacagccct actggcacia cagaaaaacc tatacagact aaaataggtc	33300
taggcatgga gtatgacact gagggagcca tgatgacaaa actaggctct ggactaagct	33360
ttgacaattc aggagccatt gtggtgggaa acaaaaatga tgacaggctt actttgtgga	33420
ccacaccgga cccatcgccc aactgtcaga ttactctga aaaagatgct aaactaacct	33480
tggtactgac taaatgtggc agtcagggtg taggcacagt atctattgcc gctcttaaag	33540
gtagccttgt gccaatcact agtgcaatca gtgtggttca gatataccta aggtttgatg	33600
aaaatggggt gctgatgagt aactcttcac ttaatggcga atactggaat tttagaaacg	33660
gagactcaac taatggcaca ccatatacaa acgcagtggg ttttatgcct aatctactgg	33720
cctatcctaa aggtcaaac acaactgcaa aaagtaacat tgtcagccag gtctacatga	33780

acggggacga tactaaacct atgacattta caatcaactt caatggcctt agtgaacag	33840
gggatacccc tgtcagtaaa tattccatga cattctcatg gaggtggcca aatggaagct	33900
acatagggca caatittgta acaaacctct ttactttctc ctacatcgcc caagaataaa	33960
gaaagcacag agatgcttgt ttttgatttc aaaattgtgt gcttttattt attttcaagc	34020
ttacagtatt tccagtagtc attagaatag agcttaatta aactgcatga gaacctttcc	34080
acatagctta aattatcacc agtgcaaatg gaaaaaaatc aacatacctt tttatccaga	34140
tatcaaagaa ctctagtggc cagtittccc ccacctccc agctcacaga atacacagtc	34200
ctttccccc ggctggcttt aaacaacact atctcatgg taacagacat atttttaggt	34260
gtaataatcc acacggtctc ttggcgggcc aaacgctggc ctgtgatgtt aataaactcc	34320
ccaggcagct ctttcaagtt cagctcgctg tccaactgct gaagcgctcg cggctccgac	34380
tgcgcctcta gcggaggcaa cggcagcacc cgatccttga tctataaagg agtagagtca	34440
taatccccc taagaatagg gcggtgatgc agcaacaagg cgcgagcaa ctctgccgc	34500
cgctctccg tacgacagga atgcaacggg gtggtgtct cctccgcat aatccgcacc	34560
gctcgagca tcagcatcct cgctctccgg gcacagcagc gcatcctgat ctactgaga	34620
tcggcgagc aagtgagca caacaccaag atgttattta agatcccaca gtgcaaagca	34680
ctgtacccaa agctcatggc gggaaggaca gccccacgt gaccatcgta ccagatcctc	34740
aggtaaatca aatgacgacc tctcataaac acgctggaca tatacatcac ctcttgggc	34800
atgagctgat tcaccacctc tcgataccac aggcacgct gattaattaa agaccctcg	34860
agcaccatcc tgaaccagga agccagcacc tgacccccg ccaggcactg cagggacccc	34920
ggtgaatcg agtggcagtg aagactccag cgctcgtagc cgtgaacat agagctggtc	34980
attatatcca cattggcaca acacagacac actttcatac acttttcat gattagcagc	35040
tcctctctag tcaagacat atccaagga atcaccact cttgaatcaa ggtaaatccc	35100
acacagcagg gcaggcctct cacataactc acgttatgca tagtgagcgt gtcgcaatct	35160
ggaaataccg gatgatcttc catcaccgaa gcccggtct cgtctcaaa gggaggtaaa	35220
cggctcctcg tgtagggaca gtggcgggat aatcgagatc gtgttgaacg tagagtcag	35280
ccaaaggga cagcggacgt actcatattt cctccagcag aaccaagtgc gcgcgtggca	35340
gtatccctg cgtcttctgt ctgcgcgct gcccgctcg gtgtagtagt tgtaatacag	35400
ccactccctc agaccgtcaa ggcgtccct ggctccgga tctataaaa caccgtcctg	35460
cagcgccgc ctgatgacat ccaccaccgt agagtatgcc aagcccagcc acgaaatgca	35520
ctcactttga cagcgagaga taggaggagc gggaagagat ggaagaacca tgatagtaaa	35580
agaactttta ttccaatcga tcctctaaa tgtcaaagt tagatctatc agatggcact	35640

ggtctcctcc gctgagtcga tcaaaaataa cagctaaacc acaacaaca cgattggtca 35700

 aatgctgcac aagggtttgc agcataaaat cgctcgaaa gtccaccgca agcataacat 35760
 caaagccacc gccctatca tgatctatga taaaaacccc acagctatcc accagaccca 35820
 tatagttttc atctctccat cgtgaaaaaa tatttacaag ctccctcttt aaatcacctc 35880
 caaccaattc aaaaagtga gccagaccgc cctccacctt cattttcagc atgcgcatca 35940
 tgattgcaa aattcaggct cctcagacac ctgtataaga ttgagaagcg gaacgttaac 36000
 atcaatgttt cgctcgcaa gatcgcgct cagtgcagc atgatataat cccacaggtc 36060
 ggagcggatc agcgaggaca tctccccgcc aggaaccaac tcaacggagc ctatgctgat 36120

 tataatacgc atattcgggg ctatgctaac cagcacggcc cccaaatagg cgtactgcat 36180
 aggcggcgac aaaaagtga cagtttgggt taaaaaatca ggcaaacact cgcgcaaaaa 36240
 agcaagaaca tcataacct gctcatgcaa atagatgcaa gtaagctcag gaacgaccac 36300
 agaaaaatgc acaatttttc tctcaaacat gactgcgagc cctgcaaaaa ataaaaaga 36360
 aacattacac aagagtagcc tgtcttacia tgggtagac tactctaacc aacataagac 36420
 ggccacgac atcgcccgcg tggccataaa aaaaattatc cgtgtgatta aaaagaagca 36480
 cagatagctg gccagtcata tccggagtca tcacgtgca acccgtgtag acccccgggt 36540

 tggacacatc ggccaaacaa agaaagcggc caatgtatcc cggaggaatg ataactaa 36600
 gacgaagata caacagaata accccatggg gggaataac aaagttagta ggtgaataaa 36660
 aacgataaac acccgaaact cctcctcgcg taggcaaaat agcgccctcc ccttcaaaa 36720
 caacatacag cgttccaca gcagccatga caaaagactc aaaacactca aaagactcag 36780
 tcttaccagg aaaataaaag cactctcaca gcaccagcac taatcagagt gtgaagaggg 36840
 ccaagtgccg aacgagtata tataggaatt aaaaatgacg taaatgtgta aaggtcaaaa 36900
 aacgcccaga aaaatacaca gaccaacgcc cgaaacgaaa acccgcgaaa aaatacccag 36960

 aagttcctca acaaccgcca ctccgcttt cccacgatac gtcacttcct caaaaatagc 37020
 aaactacatt tcccatatgt acaaaaccaa aaccctccc cttgtaccg cccacaactt 37080
 acataatcac aaacgtcaaa gcctacgtca cccgccccgc ctgccccgc ccacctcatt 37140
 atcatattgg cctcaatcca aaataaggta tattattgat gatg 37184

【심사관 직권보정사항】

【직권보정 1】

【보정항목】 청구범위

【보정세부항목】 청구항 6

【변경전】

제4항에 있어서, 하기 특징 중 적어도 하나를 갖는, 방법:

- (i) 각각의 암 샘플에 대한 CAFSPL이, CVP의 이미 일부분인 FSP의 아미노산 길이 및 상응하는 FSM이 상기 암 샘플 속에 존재하는 CFSP로부터의 새로운 FSP의 아미노산 길이를 함함으로써 결정됨;
- (ii) 역치 값이 특정 암 유형에 속하는 CS로부터의 샘플의 각각의 서브세트에 대해 별도로 정의됨;
- (iii) 점수는, 임의로 CF가 5% 미만인 암 유형으로부터의 CS 내 FSM을 계수함이 없이, FSP의 아미노산 길이와, FSP를 생성하는 FSM이 CS 내에서 관찰되는 전체적인 빈도 사이의 곱(product)으로서 정의됨;
- (iv) 암 샘플의 서브세트는 종양 유형으로부터의 모든 암 샘플을 포함하고 여기서 FSM은 5% 이상의 CF로 존재함;
- (v) 5% 미만의 전체적인 빈도로 FSM에 의해 생성된 FSP는 선택으로부터 배제됨;
- (vi) CVP로의 혼입이 CAFSPL이 여전히 TV 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지 또는 CVP 내에 존재하는 모든 FSP의 누적 길이가 V개 아미노산의 최대 값에 도달할 때까지 새로운 FSP 또는 변형된 FSP의 첨가가 진행됨; 및
- (vii) 동일한 FSM으로부터 유래된 FSP는 개개의 FSP의 점수의 합으로서 계산된 합해진(combined) 점수를 지닌 하나의 FSP로서 취급됨.

【변경후】

제4항에 있어서, 하기 특징 중 적어도 하나를 갖는, 방법:

- (i) 각각의 암 샘플에 대한 CAFSPL이, CVP의 이미 일부분인 FSP의 아미노산 길이 및 상응하는 FSM이 상기 암 샘플 속에 존재하는 CFSP로부터의 새로운 FSP의 아미노산 길이를 함함으로써 결정됨;
- (ii) 역치 값(threshold value; TV)이 특정 암 유형에 속하는 CS로부터의 샘플의 각각의 서브세트에 대해 별도로 정의됨;
- (iii) 점수는, 임의로 CF가 5% 미만인 암 유형으로부터의 CS 내 FSM을 계수함이 없이, FSP의 아미노산 길이와, FSP를 생성하는 FSM이 CS 내에서 관찰되는 전체적인 빈도 사이의 곱(product)으로서 정의됨;
- (iv) 암 샘플의 서브세트는 종양 유형으로부터의 모든 암 샘플을 포함하고 여기서 FSM은 5% 이상의 CF로 존재함;
- (v) 5% 미만의 전체적인 빈도로 FSM에 의해 생성된 FSP는 선택으로부터 배제됨;
- (vi) CVP로의 혼입이 CAFSPL이 여전히 TV 미만인 임의의 암 샘플의 CAFSPL을 증가시키는 추가의 FSP가 이용가능하지 않을 때까지 또는 CVP 내에 존재하는 모든 FSP의 누적 길이가 V개 아미노산의 최대 값에 도달할 때까지 새로운 FSP 또는 변형된 FSP의 첨가가 진행됨; 및
- (vii) 동일한 FSM으로부터 유래된 FSP는 개개의 FSP의 점수의 합으로서 계산된 합해진(combined) 점수를 지닌 하나의 FSP로서 취급됨.