

Page 1
SEQUENCE LISTING

<110> APOGENIX GMBH

<120> SINGLE-CHAIN TRAIL-RECEPTOR AGONIST PROTEINS

<130> 566215: BBI-999PC

<140> PCT/US2015/27270

<141> 2015-04-23

<150> 61/983,152

<151> 2014-04-23

<160> 31

<170> PatentIn version 3.5

<210> 1

<211> 281

<212> PRT

<213> Homo sapiens

<220>

<221> source

<223> /note="human TRAIL"

<400> 1

Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
1 5 10 15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
20 25 30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
35 40 45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
50 55 60

Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65 70 75 80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
85 90 95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
100 105 110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
115 120 125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
130 135 140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145 150 155 160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile

165

175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
180 185 190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
195 200 205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
210 215 220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225 230 235 240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
245 250 255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly
275 280

<210> 2

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic linker peptide"

<400> 2

Gly Ser Gly Ser Gly Asn Gly Ser
1 5

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic linker peptide"

<400> 3

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

<210> 4

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic linker peptide"

linker peptide"

<400> 4

Gly Gly Ser Gly Ser Gly Ser Gly
1 5

<210> 5

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
linker peptide"

<400> 5

Gly Gly Ser Gly Ser Gly
1 5

<210> 6

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
linker peptide"

<400> 6

Gly Gly Ser Gly
1

<210> 7

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
linker peptide"

<400> 7

Gly Gly Ser Gly Asn Gly Ser Gly
1 5

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
linker peptide"

<400> 8

Gly Gly Asn Gly Ser Gly Ser Gly
1 5

<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic linker peptide"

<400> 9

Gly Gly Asn Gly Ser Gly
1 5

<210> 10

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic Fc fragment polypeptide"

<400> 10

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
1 5 10 15Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
20 25 30Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
35 40 45Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
50 55 60Glu Gln Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
65 70 75 80His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
85 90 95Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
100 105 110Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
115 120 125Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
130 135 140Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
145 150 155 160Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
165 170 175

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

180

185

190

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 195 200 205

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215

<210> 11

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic hinge-linker peptide"

<400> 11

Gly Pro Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr
 1 5 10 15

His Thr Cys Pro Pro Cys
 20

<210> 12

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic signal peptide"

<400> 12

Met Glu Thr Asp Thr Leu Leu Val Phe Val Leu Leu Val Trp Val Pro
 1 5 10 15

Ala Gly Asn Gly
 20

<210> 13

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic strep-tag + serine linker peptide"

<400> 13

Ser Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 1 5 10 15

<210> 14

<211> 760

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic single-chain fusion polypeptide"

<400> 14

Met Glu Thr Asp Thr Leu Leu Val Phe Val Leu Leu Val Trp Val Pro
 1 5 10 15

Ala Gly Asn Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
 20 25 30

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
 35 40 45

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
 50 55 60

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
 65 70 75 80

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
 85 90 95

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
 100 105 110

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
 115 120 125

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
 130 135 140

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
 145 150 155 160

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
 165 170 175

Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val
 180 185 190

Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
 195 200 205

Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
 210 215 220

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
 225 230 235 240

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
 245 250 255

Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
 260 265 270
 Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
 275 280 285
 Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
 290 295 300
 Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
 305 310 315 320
 Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
 325 330 335
 Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly
 340 345 350
 Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr
 355 360 365
 Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
 370 375 380
 Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
 385 390 395 400
 Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
 405 410 415
 Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
 420 425 430
 Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
 435 440 445
 Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
 450 455 460
 Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
 465 470 475 480
 Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
 485 490 495
 Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
 500 505 510
 Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser
 515 520 525

Ser Ser Gly Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 530 535 540
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 545 550 555 560
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 565 570 575
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 580 585 590
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 595 600 605
 Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 610 615 620
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 625 630 635 640
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 645 650 655
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 660 665 670
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 675 680 685
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 690 695 700
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 705 710 715 720
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 725 730 735
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 740 745 750
 Ser Leu Ser Leu Ser Pro Gly Lys
 755 760

<210> 15

<211> 774

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial sequence: Synthetic single-chain fusion polypeptide"

<400> 15

Met Glu Thr Asp Thr Leu Leu Val Phe Val Leu Leu Val Trp Val Pro
1 5 10 15

Ala Gly Asn Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
20 25 30

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
35 40 45

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
50 55 60

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
65 70 75 80

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
85 90 95

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
100 105 110

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
115 120 125

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
130 135 140

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
145 150 155 160

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
165 170 175

Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val
180 185 190

Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
195 200 205

Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
210 215 220

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
225 230 235 240

Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
245 250 255

Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
260 265 270

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
 275 280 285
 Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
 290 295 300
 Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
 305 310 315 320
 Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
 325 330 335
 Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly
 340 345 350
 Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr
 355 360 365
 Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
 370 375 380
 Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
 385 390 395 400
 Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
 405 410 415
 Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
 420 425 430
 Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
 435 440 445
 Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
 450 455 460
 Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
 465 470 475 480
 Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
 485 490 495
 Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
 500 505 510
 Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser
 515 520 525
 Ser Ser Gly Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 530 535 540

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
545 550 555 560

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
565 570 575

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
580 585 590

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
595 600 605

Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
610 615 620

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
625 630 635 640

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
645 650 655

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
660 665 670

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
675 680 685

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
690 695 700

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
705 710 715 720

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
725 730 735

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
740 745 750

Ser Leu Ser Leu Ser Pro Gly Ser Ser Ser Ser Ser Ser Ala Trp Ser
755 760 765

His Pro Gln Phe Glu Lys
770

<210> 16

<211> 2316

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial sequence: Synthetic
DNA polynucleotide sequence encoding a

<400> 16

gatatcggtta ccgccaccat ggaaccgac accctgctgg tgttcgtgct gctcgtgtgg

gtgccagccg gcaatggaca gagagtggcc gtcataata cgcgcacccg gggcagatct

aaacaccctgt ccagccccc aa ctccaagaa gagaaagccc tgggcccggaa gatcaactcc

tggagttcct ccagatccgg ccactccttt ctgtccaacc tgcaacctgag aaacggcggag

ctgtcatccc acgagaaggg ctctactaac atctactccc agaacctactt caggtttcag

gaaagatca aagagaacac aagaacgac aagcagatgg tgcagtatat ctacaagtac

acctctacc ccgaacccat cctgctgatg aagtcggccc ggaactcctg ctgtccaag

gatgctgagt acgacctgta cagcatctac caggcgggca tcttcgagct gaaagagaac

gaccggtact tctgttccgt gaccaacgag cactgatcg acatggacca cgaagccagc

tttttcggcg ccttctcgt gggcggatcc ggaagcggaa acgycagtag agtggctgcc

cacattaccg gaaccagagg ccgtccaac acctggagca gccctaacag caaaaatgag

aaagctctcg ggcgcagagt caacagctgg gaatctagca gaagcggcca cagctttctg

720
660
600
540
480
420
360
300
240
180
120
60

cagccccggg aaccccaggt gtacacactg ccccctagcc gggaagagat gaccaagaac 2040
 caggtgtccc tgacctgcct ggtcaagggc ttttaccctt cgcacattgc cgtggaatgg 2100
 gagtccaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggactccgac 2160
 ggctcattct tcctgtactc caagctgaca gtggacaagt cccggtggca gcagggcaac 2220
 gtgtttctct gctccgtgat gcacgaggcc ctgcacaacc actacacca gaagtccttg 2280
 tccctgagcc ccggcaaatg atagaagctt gatatc 2316

<210> 17

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic human Fc mutein polypeptide"

<400> 17

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1 5 10 15

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

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 100 105 110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 115 120 125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 130 135 140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 145 150 155 160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 165 170 175

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

180

185

190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 195 200 205

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 210 215

<210> 18

<211> 759

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 18

Met Glu Thr Asp Thr Leu Leu Val Phe Val Leu Leu Val Trp Val Pro
 1 5 10 15

Ala Gly Asn Gly Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
 20 25 30

Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
 35 40 45

Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
 50 55 60

Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
 65 70 75 80

Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
 85 90 95

Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
 100 105 110

Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
 115 120 125

Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
 130 135 140

Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
 145 150 155 160

Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
 165 170 175

Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val
 180 185 190

Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser
 195 200 205
 Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp
 210 215 220
 Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
 225 230 235 240
 Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser
 245 250 255
 Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn
 260 265 270
 Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
 275 280 285
 Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
 290 295 300
 Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
 305 310 315 320
 Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
 325 330 335
 Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly
 340 345 350
 Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr
 355 360 365
 Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
 370 375 380
 Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
 385 390 395 400
 Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His
 405 410 415
 Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln
 420 425 430
 Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr
 435 440 445
 Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser
 450 455 460

Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser
 465 470 475 480
 Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe
 485 490
 Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser
 500 505 510
 Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser
 515 520 525
 Ser Ser Gly Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 530 535 540
 Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 545 550 555 560
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 565 570 575
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 580 585 590
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 595 600 605
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 610 615 620
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 625 630 635 640
 Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 645 650 655
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
 660 665 670
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 675 680 685
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 690 695 700
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 705 710 715 720
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 725 730 735
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser

740

745

750

Leu Ser Leu Ser Pro Gly Lys
755

<210> 19

<211> 740

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 19

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
100 105 110

ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
115 120 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
130 135 140

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
145 150 155 160

val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
165 170 175

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
180 185 190

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
195 200 205

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220
 Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly
 325 330 335
 Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 340 345 350
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 355 360 365
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 370 375 380
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 385 390 395 400
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 405 410 415
 Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
 420 425 430
 Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 435 440 445
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 450 455 460
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 465 470 475 480

Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser
 500 505 510
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 515 520 525
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 530 535 540
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 545 550 555 560
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 565 570 575
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr
 580 585 590
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 595 600 605
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 610 615 620
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 625 630 635 640
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 645 650 655
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 660 665 670
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 675 680 685
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 690 695 700
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 705 710 715 720
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 725 730 735
 Ser Pro Gly Lys
 740
 <210> 20
 <211> 754

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
 20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
 35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
 50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 100 105 110

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 115 120 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160

Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly
 325 330 335
 Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 340 345 350
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 355 360 365
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 370 375 380
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 385 390 395 400
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 405 410 415
 Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
 420 425 430
 Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 435 440 445
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 450 455 460
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 465 470 475 480
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser
 500 505 510
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

515

520

525

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 530 535 540

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 545 550 555 560

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 565 570 575

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr
 580 585 590

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 595 600 605

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 610 615 620

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 625 630 635 640

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 645 650 655

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 660 665 670

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 675 680 685

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 690 695 700

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 705 710 715 720

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 725 730 735

Ser Pro Gly Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe
 740 745 750

Glu Lys

<210> 21

<211> 739

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 21

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
 20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
 35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
 50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 100 105 110

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 115 120 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160

Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175

Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190

Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205

Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220

Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240

Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly
 325 330 335
 Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 340 345 350
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 355 360 365
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 370 375 380
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 385 390 395 400
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 405 410 415
 Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
 420 425 430
 Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 435 440 445
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 450 455 460
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 465 470 475 480
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser
 500 505 510
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
 515 520 525
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

530

535

540

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 545 550 555 560

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 565 570 575

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 580 585 590

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 595 600 605

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
 610 615 620

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 625 630 635 640

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 645 650 655

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 675 680 685

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 690 695 700

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 705 710 715 720

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 725 730 735

Pro Gly Lys

<210> 22

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 22

Gly Ser Gly Ser Gly Ser
 1 5

<210> 23
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 23
 Gly Ser Gly Ser
 1

<210> 24
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 24
 Gly Ser Gly
 1

<210> 25
 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 25
 Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr His
 1 5 10 15

Thr Cys Pro Pro Cys
 20

<210> 26
 <211> 751
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 26
 Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 1 5 10 15

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
 20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
 35 40 45
 His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
 50 55 60
 Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 65 70 75 80
 Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 85 90 95
 Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 100 105 110
 Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 115 120 125
 Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140
 His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175
 Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190
 Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205
 Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220
 Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His

305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly
 325 330 335
 Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 340 345 350
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 355 360 365
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 370 375 380
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 385 390 395 400
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 405 410 415
 Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr
 420 425 430
 Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 435 440 445
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 450 455 460
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 465 470 475 480
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Gly Ser Asp
 500 505 510
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 515 520 525
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 530 535 540
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 545 550 555 560
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 565 570 575
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 580 585 590

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
595 600 605

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
610 615 620

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
625 630 635 640

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
645 650 655

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
660 665 670

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
675 680 685

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
690 695 700

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
705 710 715 720

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
725 730 735

Ser Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys
740 745 750

<210> 27

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 27

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 65 70 75 80
 Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 85 90 95
 Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 100 105 110
 Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 115 120 125
 Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140
 His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175
 Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190
 Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205
 Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220
 Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Arg
 325 330 335
 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser

340

345

350

Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 355 360 365
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 370 375 380
 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 385 390 395 400
 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 405 410 415
 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 420 425 430
 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 435 440 445
 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 450 455 460
 Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
 465 470 475 480
 Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 485 490 495
 Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr
 500 505
 His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 515 520 525
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 530 535 540
 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 545 550 555 560
 Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 565 570 575
 Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr Tyr Arg Val Val
 580 585 590
 Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 595 600 605
 Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser
725 730 735

Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys
740 745 750

<210> 28

<211> 750

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial sequence: Synthetic polypeptide"

<400> 28

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 100 105 110
 Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 115 120 125
 Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140
 His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gly Ser Gly Ser Gly Ser Arg Val Ala Ala His Ile Thr Gly
 165 170 175
 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
 180 185 190
 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
 195 200 205
 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
 210 215 220
 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
 225 230 235 240
 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
 245 250 255
 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
 260 265 270
 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
 275 280 285
 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
 290 295 300
 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
 305 310 315 320
 Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Ser Arg
 325 330 335
 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 340 345 350
 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 355 360 365
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu

370

375

Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
385 390 395 400

Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
405 410 415

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
420 425 430

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
435 440 445

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
450 455 460

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
465 470 475 480

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
485 490 495

Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr
500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
565 570 575

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr Tyr Arg Val Val
580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser
725 730 735

Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys
740 745 750

<210> 29

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 29

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
100 105 110

ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
115 120 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140
 His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175
 Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190
 Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205
 Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220
 Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Arg
 325 330 335
 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 340 345 350
 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 355 360 365
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 370 375 380
 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 385 390 395 400
 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Gly Ile Lys Glu Asn Thr Lys

405

415

Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
420 425 430

Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
435 440 445

Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
450 455 460

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
465 470 475 480

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
485 490 495

Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr
500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
565 570 575

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr Tyr Arg Val Val
580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 30

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 30

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

Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
20 25 30

Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
35 40 45

His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
50 55 60

Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
65 70 75 80

Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
85 90 95

Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
100 105 110

Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
115 120 125

Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
130 135 140

His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
145 150 155 160

Val Gly Gly Ser Gly Ser Gly Ser Arg Val Ala Ala His Ile Thr Gly
165 170 175

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Ser Pro Asn Ser Lys Asn Glu
 180 185 190
 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
 195 200 205
 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
 210 215 220
 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
 225 230 235 240
 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
 245 250 255
 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
 260 265 270
 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
 275 280 285
 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
 290 295 300
 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
 305 310 315 320
 Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly Ser Arg
 325 330 335
 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 340 345 350
 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 355 360 365
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 370 375 380
 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 385 390 395 400
 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 405 410 415
 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 420 425 430
 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 435 440 445
 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu

450

455

460

Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
465 470 475 480

Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
485 490 495

Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr
500 505 510

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
515 520 525

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
530 535 540

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
545 550 555 560

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
565 570 575

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr Tyr Arg Val Val
580 585 590

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
595 600 605

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
610 615 620

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
625 630 635 640

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
645 650 655

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
660 665 670

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
675 680 685

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
690 695 700

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
705 710 715 720

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
725 730 735

<210> 31
<211> 4
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

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Asp Glu Val Asp
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