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<110> BAXALTA INCORPORATED
BAXALTA GMBH

<120> VIRAL VECTORS ENCODING RECOMBINANT FVIII VARIANTS WITH INCREASED
EXPRESSION FOR GENE THERAPY OF HEMOPHILIA A

<130> 008073-5107-WO

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<150> 62/255,317

<151> 2015-11-13

<160> 109

<170> PatentIn version 3.5

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
 35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
 50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
 65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
 85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser

115

120

125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
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Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
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Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
 195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
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Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
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Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
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Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
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Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
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Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
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Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
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Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
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His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
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Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
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Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
820 825 830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
835 840 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
850 855 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
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Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
885 890 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
900 905 910

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915 920 925

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930 935 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
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Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
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985

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<223> Description of Artificial Sequence: Synthetic
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<223> Description of Artificial Sequence: Synthetic polynucleotide

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atcactgcct ccagctactt caccaacatg tttgccacct ggagcccaag caaggccagg	3960
ctgcacctcc aggggaaggag caatgcctgg agggcccagg tcaacaaccc aaaggagtgg	4020
ctgcaggtgg acttccagaa gaccatgaag gtcactgggg tgaccacca gggggtcaag	4080
agcctgtca ccagcatgta tgtgaaggag ttcctgatca gctccagcca ggatggccac	4140
cagtggaccc tcttcttcca gaatggcaag gtcaaggtgt tccagggcaa ccaggacagc	4200
ttcaccctg tggatgaacag cctggacccc cccctcctga ccagatacct gaggattcac	4260

ccccagagct ggggccacca gattgccctg aggatggagg tcctgggatg tgaggcccag 4320
gacctgtact ga 4332

<210> 10
<211> 1443
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 10
Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser
755 760 765

Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys
770 775 780

Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
785 790 795 800

Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg
805 810 815

Leu Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg
820 825 830

Ala Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu
835 840 845

Phe Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn
850 855 860

Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp
865 870 875 880

Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe
885 890 895

Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
900 905 910

Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp
915 920 925

Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys
930 935 940

Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser
945 950 955 960

Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro
965 970 975

Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr
980 985 990

Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg
995 1000 1005

Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe
1010 1015 1020

Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp
1025 1030 1035

Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp
1040 1045 1050

Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His
1055 1060 1065

Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys
1070 1075 1080

Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu
1085 1090 1095

Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile
1100 1105 1110

Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr
1115 1120 1125

Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile
1130 1135 1140

Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala
1145 1150 1155

Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp
1160 1165 1170

Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala
1175 1180 1185

Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys
1190 1195 1200

Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu
1205 1210 1215

Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr
1220						1225					1230			
Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His
1235						1240					1245			
Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His
1250						1255					1260			
Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met
1265						1270					1275			
Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser
1280						1285					1290			
Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr
1295						1300					1305			
Asn	Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
1310						1315					1320			
Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys
1325						1330					1335			
Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly
1340						1345					1350			
Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val
1355						1360					1365			
Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr
1370						1375					1380			
Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln
1385						1390					1395			
Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp	Pro	Pro	Leu	Leu
1400						1405					1410			
Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp	Val	His	Gln	Ile
1415						1420					1425			

Ala	Leu	Arg	Met	Glu	Val	Leu	Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr
1430						1435					1440			

<210> 11
 <211> 4368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 11
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 accaggagat actacctggg ggctgtggag ctttcttggg actacatgca gtctgacctg 120
 ggggagctgc ctgtggatgc caggttccca cccagagtgc ccaaatcctt cccattcaac 180
 acctctgtgg tctacaagaa gaccctcttt gtggagttca ctgaccacct gttcaacatt 240
 gccaaacca ggccaccctg gatgggactc ctgggacca ccattcaggc tgagggtgat 300
 gacactgtgg tcatcacctt caagaacatg gcctcccacc ctgtgagcct gcatgctgtg 360
 ggggtcagct actggaaggc ctctgagggg gctgagtatg atgaccagac ctcccagagg 420
 gagaaggagg atgacaaagt gttccctggg ggcagccaca cctatgtgtg gcaggtcctc 480
 aaggagaatg gccccatggc ctctgacca ctctgcctga cctactccta cttttctcat 540
 gtggacctgg tcaaggacct caactctgga ctgattgggg ccctgctggt gtgcagggag 600
 ggctccctgg ccaaagagaa gaccagacc ctgcacaagt tcattctcct gtttgctgtc 660
 tttgatgagg gcaagagctg gcactctgaa accaagaact ccctgatgca ggacagggat 720
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 ctgcctggac tcattggctg ccacaggaaa tctgtctact ggcatgtgat tggcatgggg 840
 acaaccctg aggtgcactc cattttctctg gagggccaca ctttctggt caggaaccac 900
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 gacctggac agttcctgct gttctgccac atcagctccc accagcatga tggcatggag 1020
 gcctatgtca aggtggacag ctgccctgag gagccacagc tcaggatgaa gaacaatgag 1080
 gaggctgagg actatgatga tgacctgact gactctgaga tggatgtggt ccgctttgat 1140

gatgacaaca gcccatcctt cattcagatc aggtctgtgg ccaagaaaca cccaagacc	1200
tgggtgcact acattgctgc tgaggaggag gactgggact atgccccact ggtcctggcc	1260
cctgatgaca ggagctacaa gagccagtac ctcaacaatg gcccacagag gattggacgc	1320
aagtacaaga aagtcagggt catggcctac actgatgaaa ctttcaagac caggagggcc	1380
attcagcatg agtctggcat cctgggcca ctctgtatg gggagggtgg ggacaccctg	1440
ctcatcatct tcaagaacca ggcctccagg ccctacaaca tctaccaca tggcatcact	1500
gatgtcaggc ccctgtacag ccgcaggctg ccaaaggggg tgaaacacct caaggacttc	1560
cccattctgc ctggggagat cttcaagtac aagtggactg tctactgtga ggatggacca	1620
accaaattctg accccagggt cctcaccaga tactactcca gctttgtgaa catggagagg	1680
gacctggcct ctggcctgat tggcccactg ctcatctgct acaaggagtc tgtggaccag	1740
aggggaaacc agatcatgtc tgacaagagg aatgtgattc tgttctctgt ctttgatgag	1800
aacaggagct ggtacctgac tgagaacatt cagcgcttcc tgcccaacc tgctggggtg	1860
cagctggagg accctgagtt ccaggccagc aacatcatgc actccatcaa tggctatgtg	1920
tttgacagcc tccagctttc tgtctgcctg catgagggtg cctactggta cattctttct	1980
attggggccc agactgactt cttttctgtc ttcttctctg gctacacctt caaacacaag	2040
atggtgtatg aggacaccct gaccctcttc ccattctctg gggagactgt gttcatgagc	2100
atggagaacc ctggcctgtg gattctggga tgccacaact ctgacttccg caacaggggc	2160
atgactgccc tgctcaaagt ctctcctgtg gacaagaaca ctggggacta ctatgaggac	2220
agctatgagg acatctctgc ctacctgtc agcaagaaca atgccattga gcccaggagc	2280
ttcagccaga attccagaca cccagcacc agggagatca ccaggaccac cctccagtct	2340
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gacatctatg acgaggacga gaaccagagc ccaaggagct tccagaagaa gaccaggcac	2460
tacttcattg ctgctgtgga ggcctgtgg gactatggca tgagctccag ccccatgtc	2520
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ttcactgatg gcagcttcac ccagcccctg tacagagggg agctgaatga gcacctggga	2640
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caggcctcca ggccctacag cttctacagc tccctcatca gctatgagga ggaccagagg	2760

cagggggctg agccacgcaa gaactttgtg aaaccaatg aaaccaagac ctacttctgg	2820
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ttctctgatg tggacctgga gaaggatgtg cactctggcc tgattggccc actcctggtc	2940
tgccacacca acaccctgaa ccctgccccat ggaaggcaag tgactgtgca ggagtttgcc	3000
ctcttcttca ccatctttga tgaaaccaag agctgggtact tcactgagaa catggagcgc	3060
aactgcaggg ccccatgcaa cattcagatg gaggacccca cttcaaaga gaactaccgc	3120
ttccatgcca tcaatggcta catcatggac accctgcctg ggcttgtcat ggcccaggac	3180
cagaggatca ggtggtacct gctttctatg ggctccaatg agaacattca ctccatccac	3240
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gtggagtgcc tcattgggga gcacctgcat gctggcatga gcaccctgtt cctggtctac	3420
agcaacaagt gccagacccc cctgggaatg gcctctggcc acatcaggga cttccagatc	3480
actgcctctg gccagtatgg ccagtgggcc cccaagctgg ccaggctcca ctactctgga	3540
tccatcaatg cctggagcac caaggagcca ttcagctgga tcaaagtgga cctgctggcc	3600
cccatgatca tccatggcat caagaccag ggggccaggc agaagttctc cagcctgtac	3660
atcagccagt tcatcatcat gtacagcctg gatggcaaga aatggcagac ctacagaggc	3720
aactccactg gaacactcat ggtcttcttt ggcaatgtgg acagctctgg catcaagcac	3780
aacatcttca acccccaat catcgccaga tacatcaggc tgcacccac ccactacagc	3840
atccgcagca ccctcaggat ggagctgatg ggctgtgacc tgaactcctg cagcatgccc	3900
ctgggcatgg agagcaaggc ctttctgat gcccagatca ctgcctccag ctacttcacc	3960
aacatgtttg ccacctggag cccaagcaag gccaggctgc acctccaggg aaggagcaat	4020
gcctggaggc cccaggtcaa caacccaaag gagtggctgc aggtggactt ccagaagacc	4080
atgaaggatca ctgggggtgac caccagggg gtcaagagcc tgctcaccag catgtatgtg	4140
aaggagttcc tgatcagctc cagccaggat ggccaccagt ggaccctctt cttccagaat	4200
ggcaaggatca aggtgttcca gggcaaccag gacagcttca cccctgtggt gaacagcctg	4260
gacccccccc tcctgaccag atacctgagg attcaccccc agagctgggt ccaccagatt	4320
gccctgagga tggaggtcct gggatgtgag gcccaggacc tgtactga	4368

<210> 12

<211> 1455

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 12

Met	Gln	Ile	Glu	Leu	Ser	Thr	Cys	Phe	Phe	Leu	Cys	Leu	Leu	Arg	Phe
1				5					10					15	

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

Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg
		35					40					45			

Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val
	50					55					60				

Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile
65				70					75					80	

Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln
				85					90					95	

Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser
			100					105					110		

His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser
		115					120					125			

Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp
	130					135					140				

Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu
145					150					155					160

Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser
				165					170					175	

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr

385		390		395		400									
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro
				405					410					415	
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn
			420					425					430		
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met
		435					440					445			
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu
	450					455					460				
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu
465					470					475					480
Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro
				485					490					495	
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys
			500					505					510		
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe
		515					520					525			
Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp
	530					535					540				
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg
545					550					555					560
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu
				565					570					575	
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val
			580					585					590		
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu
		595					600					605			

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro
755 760 765

Ser Thr Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu
770 775 780

Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe
785 790 795 800

Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys
805 810 815

Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr

830

Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn
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Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
1040 1045 1050

Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu
1055 1060 1065

Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly
1070 1075 1080

His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu
1085 1090 1095

Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro
1100 1105 1110

Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His
1115 1120 1125

Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys
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Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe
1145 1150 1155

Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu
1160 1165 1170

Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys
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Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
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Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser
1205 1210 1215

Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys
1220 1225 1230

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

1235	1240	1245
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Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp 1280 1285 1290		
Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile 1295 1300 1305		
Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe 1310 1315 1320		
Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg 1325 1330 1335		
Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu 1340 1345 1350		
Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr 1355 1360 1365		
Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe 1370 1375 1380		
Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe 1385 1390 1395		
Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe 1400 1405 1410		
Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr 1415 1420 1425		
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Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
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<210> 13

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

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<211> 4374
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polynucleotide

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<210> 16

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 16

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<210> 17

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 17

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<210> 18

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 18

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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
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Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
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Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
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Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
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Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
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His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
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Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
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Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
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Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
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Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
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Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
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Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp

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Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
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Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
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Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
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Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
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Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
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Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
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Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
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Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
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Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu

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1155

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Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile
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Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly
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Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr
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Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu
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Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu
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Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His
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Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
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Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp
1895 1900 1905

Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn
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Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His
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Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met
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Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser

1955	1960	1965
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Val Arg 1985	Lys Lys Glu Glu Tyr 1990	Tyr Asn Leu Tyr 1995
Pro Gly 2000	Val Glu Met Leu Pro 2005	Ser Lys Ala Gly 2010
Ile Trp 2015	Arg Val Glu Cys Leu 2020	Ile Gly Glu His Leu 2025
Met Ser 2030	Thr Leu Phe Leu Val 2035	Tyr Ser Asn Lys Cys 2040
Leu Gly 2045	Met Ala Ser Gly His 2050	Ile Arg Asp Phe Gln 2055
Ser Gly 2060	Gln Tyr Gly Gln Trp 2065	Ala Pro Lys Leu Ala 2070
Tyr Ser 2075	Gly Ser Ile Asn Ala 2080	Trp Ser Thr Lys Glu 2085
Trp Ile 2090	Lys Val Asp Leu Leu 2095	Ala Pro Met Ile Ile 2100
Lys Thr 2105	Gln Gly Ala Arg Gln 2110	Lys Phe Ser Ser Leu 2115
Gln Phe 2120	Ile Ile Met Tyr Ser 2125	Leu Asp Gly Lys Lys 2130
Tyr Arg 2135	Gly Asn Ser Thr Gly 2140	Thr Leu Met Val Phe 2145
Val Asp 2150	Ser Ser Gly Ile Lys 2155	His Asn Ile Phe Asn 2160

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Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln
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Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser
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Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
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Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe
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Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
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Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser
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Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys
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Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
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Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
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tacgtgaagg agttcctgat cagcagcagc caggacggcc accagtggac cctgttcttc	4200
cagaacggca aagtgaaggt gttccagggc aaccaggaca gcttcacccc cgtggtgaac	4260
agcctggacc cccccctgct gaccaggtat ctgaggatcc acccccagag ctgggtgcac	4320
cagatcgccc tgagaatgga agtgctggga tgcgaggccc aggacctgta ctga	4374

<210> 21

<211> 1457

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 21

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
755 760 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
770 775 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
785 790 795 800

Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
805 810 815

Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
820 825 830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
835 840 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
850 855 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
865 870 875 880

Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
885 890 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
900 905 910

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
915 920 925

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
930 935 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
945 950 955 960

Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
965 970 975

Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
980 985 990

Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
995 1000 1005

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn
1010 1015 1020

Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys
1025 1030 1035

Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr
1040 1045 1050

Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr
1055 1060 1065

Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe
1070						1075					1080			
Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met
1085						1090					1095			
Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met
1100						1105					1110			
Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly
1115						1120					1125			
Glu	His	Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser
1130						1135					1140			
Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg
1145						1150					1155			
Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro
1160						1165					1170			
Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser
1175						1180					1185			
Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro
1190						1195					1200			
Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe
1205						1210					1215			
Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp
1220						1225					1230			
Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu
1235						1240					1245			
Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn
1250						1255					1260			

Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro
1265 1270 1275

Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly
1280 1285 1290

Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys
1295 1300 1305

Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn
1310 1315 1320

Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln
1325 1330 1335

Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
1340 1345 1350

Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val
1355 1360 1365

Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys
1370 1375 1380

Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu
1385 1390 1395

Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
1400 1405 1410

Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr
1415 1420 1425

Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala
1430 1435 1440

Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1445 1450 1455

<210> 22

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 22

gccaccagga gatactacct gggcgccgtg gagctgagct gggactacat gcagtctgac	60
ctgggcgagc tgcctgtgga cgccaggttc cccccagag tgcccaagag cttccccttc	120
aacacctcag tgggtgtacaa gaagaccctg ttcgtggagt tcaccgacca cctgttcaac	180
atgccaaagc ccaggccccc ctggatgggc ctgctgggcc ccaccatcca ggccgaggtg	240
tacgacaccg tggatgatcac cctgaagaac atggccagcc acccctgag cctgcacgcc	300
gtgggctga gctactggaa ggcctctgag ggcgccgagt atgacgacca gaccagccag	360
agggagaagg aggacgaaa ggtgttcccc ggcggcagcc acacctacgt gtggcaggtg	420
ctgaaggaga acggccccc atggcagcgac cccctgtgcc tgacctacag ctacctgagc	480
cacgtggacc tggatgaagga cctgaactct ggcctgatcg gcgccctgct ggtgtgcagg	540
gagggcagcc tggccaagga gaagaccag accctgcaca agttcatcct gctgttcgcc	600
gtgttcgatg agggcaagag ctggcacagc gagaccaaga acagcctgat gcaggacagg	660
gatgccgcct ctgccagggc ctggcccaag atgcacaccg tgaacggcta cgtgaacagg	720
agcctgcccg gcctgatcgg ctgccacagg aagtctgtgt actggcacgt gatcggcatg	780
ggcaccaccc ccgagggtga cagcatcttc ctggagggcc acaccttcct ggtgaggaac	840
cacaggcagg ccagcctgga gatcagcccc atcaccttc tgaccgcca gaccctgctg	900
atggacctgg gccagttcct gctgttctgc cacatcagca gccaccagca cgacggcatg	960
gaggcctacg tgaagggtga cagctgcccc gaggagcccc agctgaggat gaagaacaac	1020
gaggaggccg aggactatga tgatgacctg accgactctg agatggacgt ggtgaggttt	1080
gatgatgaca acagccccag cttcatccag atcaggtctg tggccaagaa gcacccaag	1140
acctgggtgc actacatcgc cgccgaggag gaggactggg actacgcccc cctggtgctg	1200
gccccgacg acaggagcta caagagccag tacctgaaca acggcccca gaggatcggc	1260
aggaagtaca agaaggctag attcatggcc tacaccgacg agaccttcaa gaccaggag	1320
gcatccagc acgagtctgg catcctgggc cccctgctgt acggcgaggt gggcgacacc	1380

ctgctgatca tcttcaagaa ccaggccagc aggccctaca acatctaccc ccacggcatc	1440
accgatgtga ggcccctgta cagcaggagg ctgcccgaagg gcgatgaagca cctgaaggac	1500
ttcccatcc tgcccggcga gatcttcaag tacaagtgga ccgtgaccgt ggaggatggc	1560
cccaccaagt ctgacccag gtgcctgacc aggtactaca gcagcttcgt gaacatggag	1620
agggacctgg cctctggcct gatcggcccc ctgctgatct gctacaagga gagcgtggac	1680
cagaggggca accagatcat gtctgacaag aggaacgtga tcctgtttctc tgtgttcgat	1740
gagaacagga gctggatatct gaccgagaac atccagaggt tcctgcccga ccccgccggc	1800
gtgcagctgg aggacccga gttccaggcc agcaacatca tgcacagcat caacggctac	1860
gtgttcgaca gcctgcagct gtctgtgtgc ctgcacgagg tggcctactg gtacatcctg	1920
agcatcggcg cccagaccga cttcctgtct gtgttcttct ctggctacac cttcaagcac	1980
aagatggtgt acgaggacac cctgaccctg ttccccttca gcggcgagac cgtgttcgatg	2040
agcatggaga accccggcct gtggatcctg ggctgccaca acagcgactt caggaacagg	2100
ggcatgaccg ccctgctgaa agtcagcagc tgcgacaaga acaccggcga ctactacgag	2160
gacagctacg aggacatcag cgcctacctg ctgagcaaga acaacgccat cgagcccagg	2220

<210> 23

<211> 2052

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 23

gagatcacca ggaccacct gcagagcgac caggaggaga tcgactatga tgacaccatc	60
agcgtggaga tgaagaagga ggacttcgac atctacgacg aggacgagaa ccagagcccc	120
aggagcttcc agaagaagac caggcactac ttcacgccc ccgtggagag gctgtgggac	180
tatggcatga gcagcagccc ccacgtgctg aggaacaggg cccagagcgg cagcgtgccc	240
cagttcaaga aggtggtgtt ccaggagttc accgacggca gcttcaccca gcccctgtac	300
agaggcgagc tgaacgagca cctgggcctg ctgggcccct acatcagggc cgaggtggag	360
gacaacatca tggtgacctt caggaaccag gccagcaggc cctacagctt ctacagcagc	420
ctgatcagct acgaggagga ccagaggcag ggcgccgagc ccaggaagaa cttcgtgaag	480

cccaacgaga ccaagaccta cttctggaag gtgcagcacc acatggcccc caccaaggac	540
gagttcgact gcaaggcctg ggcctacttc tctgatgtgg acctggagaa ggacgtgcac	600
agcggcctga tcggccccct gctgggtgtgc cacaccaaca ccctgaaccc cgcccacggc	660
aggcaggtga ccgtgcagga gttcgccctg ttcttcacca tcttcgacga gaccaagagc	720
tggtacttca ccgagaacat ggagaggaac tgcagggccc cctgcaacat ccagatggag	780
gaccccacct tcaaggagaa ctacaggttc cacgccatca acggctacat catggacacc	840
ctgcccggcc tggatgatggc ccaggaccag aggatcaggt ggtatctgct gagcatgggc	900
agcaacgaga acatccacag catccacttc agcggccacg tgttcaccgt gaggaagaag	960
gaggagtaca agatggccct gtacaacctg taccgccggc tgttcgagac cgtggagatg	1020
ctgcccagca aggccggcat ctggagggtg gagtgcctga tcggcgagca cctgcacgcc	1080
ggcatgagca ccctgttcct ggtgtacagc aacaagtgcc agacccccct gggcatggcc	1140
agcggccaca tcagggactt ccagatcacc gcctctggcc agtacggcca gtgggcccc	1200
aagctggcca ggctgcacta cagcggcagc atcaacgcct ggagcaccaa ggagcccttc	1260
agctggatca aggtggacct gctggcccc atgatcatcc acggcatcaa gaccagggc	1320
gccaggcaga agttcagcag cctgtacatc agccagttca tcatcatgta cagcctggac	1380
ggcaagaagt ggacagaccta caggggcaac agcaccggca ccctgatggt gttcttcggc	1440
aacgtggaca gcagcggcat caagcacaac atcttcaacc ccccatcat cgccaggtag	1500
atcaggctgc acccaccca ctacagcatc aggagcacc tcgcatgga actgatgggc	1560
tcgacactga acagctgcag catgcccctg ggcatggaga gcaaggccat ctctgacgcc	1620
cagatcaccg ccagcagcta cttaccaaac atgttcgcca cctggagccc cagcaaggcc	1680
aggctgcacc tgcagggcag gagcaacgcc tggaggcccc aggtgaacaa cccaaggag	1740
tggctgcagg tggacttcca gaagaccatg aaggtgaccg gcgtgaccac ccagggcgtg	1800
aagagcctgc tgaccagcat gtacgtgaag gagttcctga tcagcagcag ccaggacggc	1860
caccagtgga ccctgttctt ccagaacggc aaagtgaagg tgttcaggga caaccaggac	1920
agcttcaccc ccgtggtgaa cagcctggac cccccctgc tgaccaggta tctgaggatc	1980
cacccccaga gctgggtgca ccagatcgcc ctgagaatgg aagtgctggg atgcgaggcc	2040
caggacctgt ac	2052

<210> 24
<211> 2220
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 24
gccaccagga gatactacct gggggctgtg gaactttctt gggactacat gcagtctgac 60
ctgggagagc tgcctgtgga tgccaggttc ccaccagag tgcccaagtc cttcccattc 120
aacacctctg tggctctaca gaagacactc tttgtggaat tcactgacca cctgtttcaac 180
attgcaaaac ccagaccacc ctggatggga ctcctgggac ccaccattca ggctgagggtg 240
tatgacactg tggatcatcac cctcaagaac atggcatccc accctgtgtc tctgcatgct 300
gtgggagtct catactggaa agcctctgaa ggggctgagt atgatgacca gacatcccag 360
agagagaaaag aggatgacaa ggtgtttcct gggggatctc acacctatgt gtggcaagtc 420
ctcaaggaga atggacccat ggcatctgac ccactctgcc tgacatactc ctacctttct 480
catgtggacc tggtaagga cctcaactct ggactgattg gggcactgct ggtgtgcagg 540
gaaggatccc tggccaagga gaaaaccag acactgcaca agttcattct cctgtttgct 600
gtctttgatg agggcaagtc ttggcactct gaaacaaaga actccctgat gcaagacagg 660
gatgctgcct ctgccagggc atggcccaag atgcacactg tgaatggcta tgtgaacaga 720
tcactgcctg gactcattgg ctgccacagg aaatctgtct actggcatgt gattggcatg 780
gggacaaccc ctgaagtga ctccattttc ctggagggac acaccttcct ggtcaggaac 840
cacagacaag cctctctgga gatctctccc atcaccttcc tcactgcaca gacactgctg 900
atggaccttg gacagttcct gctgttctgc cacatctctt cccaccagca tgatggcatg 960
gaagcctatg tcaaggtgga ctcatgccct gaggaaccac agctcaggat gaagaacaat 1020
gaggaggctg aggactatga tgatgacctg actgactctg agatggatgt ggtcagatgt 1080
gatgatgaca actctccatc cttcattcag atcaggctctg tggcaaagaa acacccaag 1140
acatgggtgc actacattgc tgctgaggaa gaggactggg actatgcacc actggtcctg 1200
gcccctgatg acaggagcta caagtctcag tacctcaaca atggcccaca aagaattgga 1260

agaaagtaca agaaagtcag attcatggcc tacactgatg aaaccttcaa gacaagagaa	1320
gccattcagc atgagtctgg cattctggga ccactcctgt atggggaagt gggagacacc	1380
ctgctcatca tcttcaagaa ccaggcctcc aggccctaca acatctaccc acatggcatc	1440
actgatgtca ggcccctgta cagcaggaga ctgccaaaag ggggtgaaaca cctcaaggac	1500
ttccccattc tgcctggaga gatcttcaag tacaagtgga ctgtcactgt ggaggatgga	1560
ccaacaaagt ctgaccccag gtgcctcacc agatactact cctcttttgt gaacatggag	1620
agagacctgg catctggact gattggacca ctgctcatct gctacaagga gtctgtggac	1680
cagagaggca accagatcat gtctgacaag agaaatgtga ttctgttctc tgtctttgat	1740
gagaacagat catggtacct gactgagaac attcagagat tcctgcccaa ccctgctggg	1800
gtgcaactgg aagaccctga gttccaggca agcaacatca tgcactccat caatggctat	1860
gtgtttgact ctctccagct ttctgtctgc ctgcatgagg tggcctactg gtacattctt	1920
tctattgggg cacaaactga cttcctttct gtcttcttct ctggatacac cttcaagcac	1980
aagatggtgt atgaggacac cctgacactc ttcccattct ctggggaaac tgtgttcatg	2040
agcatggaga accctggact gtggattctg ggatgccaca actctgactt cagaaacagg	2100
ggaatgactg cactgctcaa agtctcctcc tgtgacaaga acactgggga ctactatgag	2160
gactcttatg aggacatctc tgcctacctg ctgagcaaga acaatgccat tgagcccaga	2220

<210> 25

<211> 2052

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 25

gagatcacca ggacaaccct ccagtctgac caggaagaga ttgactatga tgacaccatt	60
tctgtggaga tgaagaagga ggactttgac atctatgatg aggacgagaa ccagtctcca	120
agatcattcc agaagaagac aagacactac ttcatgtctg ctgtggaaag actgtgggac	180
tatggcatgt cttcctctcc ccatgtcctc aggaacaggg cacagtctgg ctctgtgcc	240
cagttcaaga aagtggctct ccaggagttc actgatggct cattcaccca gccctgtac	300
agaggggaac tgaatgagca cctgggactc ctgggacat acatcagggc tgaggtggaa	360

gacaacatca tgggtgacatt cagaaaccag gcctccaggc cctacagctt ctactctttcc	420
ctcatcagct atgaggaaga ccagagacaa ggggctgagc caagaaagaa ctttgtgaaa	480
cccaatgaaa ccaagaccta cttctggaaa gtccagcacc acatggcacc caccaaggat	540
gagtttgact gcaaggcctg ggcatacttc tctgatgtgg acctggagaa agatgtgcac	600
tctggcctga ttggcccact cctggtctgc cacaccaaca ccctgaacct tgcacatgga	660
aggcaagtga ctgtgcagga gtttgcctc ttcttcacca tctttgatga aaccaagtca	720
tgggtacttca ctgagaacat ggagagaaac tgcagagcac catgcaacat tcagatggaa	780
gacccccact tcaaggagaa ctacaggttc catgccatca atggctacat catggacacc	840
ctgcctgggc ttgtcatggc acaggaccag agaatcagat ggtacctgct ttctatggga	900
tccaatgaga acattcactc catccacttc tctgggcatg tcttcactgt gagaaagaag	960
gaggaataca agatggccct gtacaacctc taccctgggg tctttgagac tgttgagatg	1020
ctgccctcca aagctggcat ctggagggtg gaatgcctca ttggggagca cctgcatgct	1080
ggcatgtcaa ccctgttcct ggtctacagc aacaagtgcc agacaccct gggaatggcc	1140
tctggccaca tcagggactt ccagatcact gcctctggcc agtatggcca gtgggcaccc	1200
aaactggcca ggctccacta ctctggctcc atcaatgcat ggtcaaccaa ggagccattc	1260
tcttggatca aggtggacct gctggcacc atgatcattc atggcatcaa gacacagggg	1320
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<210> 26
 <211> 4332
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

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<210> 27
<211> 4368
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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<210> 28

<211> 4332

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 28

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<210> 29

<211> 4368

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 29

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gagaaggagg acgacaaggt gttccccggc ggagccaca cctacgtgtg gcaggtgctg	480
aaggagaacg gccccatggc cagcgacccc ctgtgcctga cctacagcta cctgagccac	540
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gacccccccc tgctgaccag gtatctgagg atccaccccc agagctgggt gcaccagatc	4320
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<210> 30

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 30

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

1

5

10

<210> 31
<211> 24
<212> PRT
<213> Sus sp.

<400> 31
Ser Phe Ala Gln Asn Ser Arg Pro Pro Ser Ala Ser Ala Pro Lys Pro
1 5 10 15

Pro Val Leu Arg Arg His Gln Arg
20

<210> 32
<211> 16
<212> PRT
<213> Sus sp.

<400> 32
Ser Phe Ser Gln Asn Ser Arg His Gln Ala Tyr Arg Tyr Arg Arg Gly
1 5 10 15

<210> 33
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 33
Thr Thr Tyr Val Asn Arg Ser Leu
1 5

<210> 34
<211> 7
<212> PRT
<213> Homo sapiens

<400> 34
Pro Gln Leu Arg Met Lys Asn
1 5

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 35

Val Asp Gln Arg Gly Asn Gln
1 5

<210> 36

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 36

agcttcagcc agaatgtgag caacaatgtg agcaacaatg ccaccaataa tgctaccaac 60

ccacctgtcc tgaaacgcca ccagagg 87

<210> 37

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 37

agcttcagcc agaatgtgag caacaatgcc accaacaatg tgagcaaccc acctgtcctg 60

aaacgccacc agagg 75

<210> 38

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 38

agcttcagcc agaatgtgag caataatgcc accaaccac ctgtcctgaa acgccaccag 60

agg 63

<210> 39

<211> 54
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 39
 agcttcagcc agaatgtgag caataatcca cctgtcctga aagccacca gagg 54

 <210> 40
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 40
 agcttcagcc agaataggag cctgccacct gtcctgaaac gccaccagag g 51

 <210> 41
 <211> 93
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 41
 agcttcagcc agaatgccac taatgtgtct aacaactctg ctacctctgc tgactctgct 60

 gtgagcccac ctgtcctgaa acgccaccag agg 93

 <210> 42
 <211> 69
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 42
 agcttcagcc agaatgccac caactatgtg aacaggagcc tgccacctgt cctgaaacgc 60

 caccagagg 69

<210> 43
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 43
agcttcagcc agaatgccac caactatgtg aacaggagcc tgtctgccac ctctgctgac 60
tctgctgtga gccagaatcc acctgtcctg aaacgccacc agagg 105

<210> 44
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 44
agcttcagcc agaatgtgag caacaatgtg agcaatgctg tgtctgctgt gtctgctcca 60
cctgtcctga aacgccacca gagg 84

<210> 45
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 45
agcttcagcc agaatatcac tgtggcctct gccacctcta acatcactgt ggcctctgct 60
gaccacctg tcctgaaacg ccaccagagg 90

<210> 46
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 46
agcttcagcc agaatatcac tgtgaccaac atcactgtga ctgccccacc tgtcctgaaa 60
cgccaccaga gg 72

<210> 47
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 47
agcttcagcc agaatcagac tgtgaccaac atcactgtga ctgccccacc tgtcctgaaa 60
cgccaccaga gg 72

<210> 48
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 48
agcttcagcc agaatgccac taatgtgtct aacaacagca acaccagcaa tgacagcaat 60
gtgtctccac ctgtcctgaa acgccaccag agg 93

<210> 49
<211> 4374
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 49
atgcagattg agctgtccac ctgcttcttt ctgtgcctgc tgagattctg cttctctgcc 60
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ggagagctgc ctgtggatgc caggttccca cccagagtgc ccaagtcctt cccattcaac 180
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gcaaaaccca gaccaccctg gatgggactc ctgggaccca ccattcaggc tgaggtgtat	300
gacactgtgg tcatcacct caagaacatg gcatcccacc ctgtgtctct gcatgctgtg	360
ggagtctcat actggaaagc ctctgaaggg gctgagtatg atgaccagac atcccagaga	420
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<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 51

Val	Ser	Asn	Asn	Val	Ser	Asn	Asn	Ala	Thr	Asn	Asn	Ala	Thr	Asn
1				5				10					15	

<210> 52

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>

<221> CDS

<222> (1)..(33)

<400> 52

gtg	agc	aac	aat	gcc	acc	aac	aat	gtg	agc	aac
Val	Ser	Asn	Asn	Ala	Thr	Asn	Asn	Val	Ser	Asn
1				5				10		

33

<210> 53

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 53

Val	Ser	Asn	Asn	Ala	Thr	Asn	Asn	Val	Ser	Asn
1				5				10		

<210> 54

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> CDS
<222> (1)..(21)

<400> 54
gtg agc aat aat gcc acc aac
Val Ser Asn Asn Ala Thr Asn
1 5

21

<210> 55
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 55
Val Ser Asn Asn Ala Thr Asn
1 5

<210> 56
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(12)

<400> 56
gtg agc aat aat
Val Ser Asn Asn
1

12

<210> 57
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 57
Val Ser Asn Asn
1

<210> 58
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(9)

<400> 58
agg agc ctg
Arg Ser Leu
1

9

<210> 59
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 59
Arg Ser Leu
1

<210> 60
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(51)

<400> 60
gcc act aat gtg tct aac aac tct gct acc tct gct gac tct gct gtg 48
Ala Thr Asn Val Ser Asn Asn Ser Ala Thr Ser Ala Asp Ser Ala Val
1 5 10 15

agc 51
Ser

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 61
Ala Thr Asn Val Ser Asn Asn Ser Ala Thr Ser Ala Asp Ser Ala Val
1 5 10 15

Ser

<210> 62
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(27)

<400> 62
gcc acc aac tat gtg aac agg agc ctg 27
Ala Thr Asn Tyr Val Asn Arg Ser Leu
1 5

<210> 63
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 63

Ala Thr Asn Tyr Val Asn Arg Ser Leu
1 5

<210> 64

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>

<221> CDS

<222> (1)..(63)

<400> 64

gcc acc aac tat gtg aac agg agc ctg tct gcc acc tct gct gac tct 48
Ala Thr Asn Tyr Val Asn Arg Ser Leu Ser Ala Thr Ser Ala Asp Ser
1 5 10 15

gct gtg agc cag aat 63
Ala Val Ser Gln Asn
20

<210> 65

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 65

Ala Thr Asn Tyr Val Asn Arg Ser Leu Ser Ala Thr Ser Ala Asp Ser
1 5 10 15

Ala Val Ser Gln Asn
20

<210> 66

<211> 42

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(42)

<400> 66
gtg agc aac aat gtg agc aat gct gtg tct gct gtg tct gct 42
Val Ser Asn Asn Val Ser Asn Ala Val Ser Ala Val Ser Ala
1 5 10

<210> 67
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 67
Val Ser Asn Asn Val Ser Asn Ala Val Ser Ala Val Ser Ala
1 5 10

<210> 68
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(48)

<400> 68
atc act gtg gcc tct gcc acc tct aac atc act gtg gcc tct gct gac 48
Ile Thr Val Ala Ser Ala Thr Ser Asn Ile Thr Val Ala Ser Ala Asp
1 5 10 15

<210> 69
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 69

Ile	Thr	Val	Ala	Ser	Ala	Thr	Ser	Asn	Ile	Thr	Val	Ala	Ser	Ala	Asp
1				5				10					15		

<210> 70

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>

<221> CDS

<222> (1)..(30)

<400> 70

atc	act	gtg	acc	aac	atc	act	gtg	act	gcc	30
Ile	Thr	Val	Thr	Asn	Ile	Thr	Val	Thr	Ala	
1				5				10		

<210> 71

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 71

Ile	Thr	Val	Thr	Asn	Ile	Thr	Val	Thr	Ala
1				5				10	

<210> 72

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> CDS
<222> (1)..(30)

<400> 72
cag act gtg acc aac atc act gtg act gcc 30
Gln Thr Val Thr Asn Ile Thr Val Thr Ala
1 5 10

<210> 73
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 73
Gln Thr Val Thr Asn Ile Thr Val Thr Ala
1 5 10

<210> 74
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> CDS
<222> (1)..(51)

<400> 74
gcc act aat gtg tct aac aac agc aac acc agc aat gac agc aat gtg 48
Ala Thr Asn Val Ser Asn Asn Ser Asn Thr Ser Asn Asp Ser Asn Val
1 5 10 15

tct 51
Ser

<210> 75
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 75

Ala Thr Asn Val Ser Asn Asn Ser Asn Thr Ser Asn Asp Ser Asn Val
1 5 10 15

Ser

<210> 76

<211> 405

<212> PRT

<213> Homo sapiens

<400> 76

Met Pro Leu Leu Leu Tyr Thr Cys Leu Leu Trp Leu Pro Thr Ser Gly
1 5 10 15

Leu Trp Thr Val Gln Ala Met Asp Pro Asn Ala Ala Tyr Val Asn Met
20 25 30

Ser Asn His His Arg Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe
35 40 45

Ser Leu Tyr Lys His Leu Val Ala Leu Ser Pro Lys Lys Asn Ile Phe
50 55 60

Ile Ser Pro Val Ser Ile Ser Met Ala Leu Ala Met Leu Ser Leu Gly
65 70 75 80

Thr Cys Gly His Thr Arg Ala Gln Leu Leu Gln Gly Leu Gly Phe Asn
85 90 95

Leu Thr Glu Arg Ser Glu Thr Glu Ile His Gln Gly Phe Gln His Leu
100 105 110

His Gln Leu Phe Ala Lys Ser Asp Thr Ser Leu Glu Met Thr Met Gly
115 120 125

Asn Ala Leu Phe Leu Asp Gly Ser Leu Glu Leu Leu Glu Ser Phe Ser
130 135 140

Ala Asp Ile Lys His Tyr Tyr Glu Ser Glu Val Leu Ala Met Asn Phe
145 150 155 160

Gln Asp Trp Ala Thr Ala Ser Arg Gln Ile Asn Ser Tyr Val Lys Asn
165 170 175

Lys Thr Gln Gly Lys Ile Val Asp Leu Phe Ser Gly Leu Asp Ser Pro
180 185 190

Ala Ile Leu Val Leu Val Asn Tyr Ile Phe Phe Lys Gly Thr Trp Thr
195 200 205

Gln Pro Phe Asp Leu Ala Ser Thr Arg Glu Glu Asn Phe Tyr Val Asp
210 215 220

Glu Thr Thr Val Val Lys Val Pro Met Met Leu Gln Ser Ser Thr Ile
225 230 235 240

Ser Tyr Leu His Asp Ser Glu Leu Pro Cys Gln Leu Val Gln Met Asn
245 250 255

Tyr Val Gly Asn Gly Thr Val Phe Phe Ile Leu Pro Asp Lys Gly Lys
260 265 270

Met Asn Thr Val Ile Ala Ala Leu Ser Arg Asp Thr Ile Asn Arg Trp
275 280 285

Ser Ala Gly Leu Thr Ser Ser Gln Val Asp Leu Tyr Ile Pro Lys Val
290 295 300

Thr Ile Ser Gly Val Tyr Asp Leu Gly Asp Val Leu Glu Glu Met Gly
305 310 315 320

Ile Ala Asp Leu Phe Thr Asn Gln Ala Asn Phe Ser Arg Ile Thr Gln
325 330 335

Asp Ala Gln Leu Lys Ser Ser Lys Val Val His Lys Ala Val Leu Gln
340 345 350

Leu Asn Glu Glu Gly Val Asp Thr Ala Gly Ser Thr Gly Val Thr Leu
355 360 365

Asn Leu Thr Ser Lys Pro Ile Ile Leu Arg Phe Asn Gln Pro Phe Ile
370 375 380

Ile Met Ile Phe Asp His Phe Thr Trp Ser Ser Leu Phe Leu Ala Arg
385 390 395 400

Val Met Asn Pro Val
405

<210> 77
<211> 4
<212> PRT
<213> Homo sapiens

<400> 77
Asn Met Ser Asn
1

<210> 78
<211> 4
<212> PRT
<213> Homo sapiens

<400> 78
Asn Leu Thr Glu
1

<210> 79
<211> 4
<212> PRT
<213> Homo sapiens

<400> 79
Asn Lys Thr Gln
1

<210> 80
<211> 4
<212> PRT
<213> Homo sapiens

<400> 80
Asn Gly Thr Val
1

<210> 81
<211> 4
<212> PRT
<213> Homo sapiens

<400> 81
Asn Phe Ser Arg
1

<210> 82
<211> 4
<212> PRT
<213> Homo sapiens

<400> 82
Asn Leu Thr Ser
1

<210> 83
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83
Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ala
1 5 10 15

Thr Asn Val Ser Asn Asn Ser Asn Thr Ser Asn Asp Ser Asn Val Ser
20 25 30

Pro Pro Val Leu Lys Arg His Gln Arg
35 40

<210> 84
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 84
Asn Ala Thr Asn
1

<210> 85
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 85
Asn Val Ser Asn
1

<210> 86
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 86
Asn Asn Ser Asn
1

<210> 87
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 87
Asn Thr Ser Asn
1

<210> 88
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 88

Asn Asp Ser Asn
1

<210> 89
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 89
Asn Val Ser Pro
1

<210> 90
<211> 4377
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 90
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accaggagat actacctggg ggctgtggaa ctttcttggg actacatgca gtctgacctg 120
ggagagctgc ctgtggatgc caggttccca cccagagtgc ccaagtcctt cccattcaac 180
acctctgtgg tctacaagaa gacactcttt gtggaattca ctgaccacct gttcaacatt 240
gcaaaaccca gaccacctg gatgggactc ctgggaccca ccattcaggc tgagggtgtat 300
gacactgtgg tcatcacctt caagaacatg gcatcccacc ctgtgtctct gcatgctgtg 360
ggagtctcat actggaaagc ctctgaaggg gctgagtatg atgaccagac atcccagaga 420
gagaaagagg atgacaaggt gttccctggg ggatctcaca cctatgtgtg gcaagtcctc 480
aaggagaatg gacccatggc atctgacca ctctgcctga catactccta cttttctcat 540
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ggatccctgg ccaaggagaa aaccagaca ctgcacaagt tcattctcct gtttgctgtc 660
tttgatgagg gcaagtcttg gcactctgaa acaaagaact ccctgatgca agacagggat 720
gctgcctctg ccagggcattg gcccaagatg cacactgtga atggctatgt gaacagatca 780

ctgcctggac tcattggctg ccacaggaaa tctgtctact ggcatgtgat tggcatgggg	840
acaaccctg aagtgcactc cttttcctg gagggacaca ctttcctggt caggaaccac	900
agacaagcct ctctggagat ctctcccatc accttcctca ctgcacagac actgctgatg	960
gaccttggac agttcctgct gtcctgccac atctcttccc accagcatga tggcatggaa	1020
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tgggtgcact acattgctgc tgaggaagag gactgggact atgcaccact ggtcctggcc	1260
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gatgtcaggc ccctgtacag caggagactg caaaaggggg tgaaacacct caaggacttc	1560
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acaaagtctg accccaggtg cctcaccaga tactactcct cttttgtgaa catggagaga	1680
gacctggcat ctggactgat tggaccactg ctcatctgct acaaggagtc tgtggaccag	1740
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aacagatcat ggtacctgac tgagaacatt cagagattcc tgcccaacc tgctggggtg	1860
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gaggactttg acatctatga tgaggacgag aaccagtctc caagatcatt ccagaagaag	2460
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ccccatgtcc tcaggaacag ggcacagtct ggctctgtgc cacagttcaa gaaagtggtc	2580
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atgtatgtga aggagttcct gatctcttcc tcacaggatg gccaccagtg gacactcttc	4200
ttccagaatg gcaaagtcaa ggtgttccag ggcaaccagg actctttcac acctgtggtg	4260
aactcactgg accccccct cctgacaaga tacctgagaa ttcaccccca gtcttggtgc	4320
caccagattg ccctgagaat ggaagtcctg ggatgtgagg cacaagacct gtactga	4377

<210> 91

<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 91

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accaggagat actacctggg ggctgtggaa ctttcttggg actacatgca gtctgacctg	120
ggagagctgc ctgtggatgc caggttccca cccagagtgc ccaagtcctt cccattcaac	180
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aaggagaatg gaccactgc atctgacca ccctgcctga catactccta cttttctcat	540
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gctgcctctg ccagggcctg gcccaagatg cacactgtga atggctatgt gaacagatca	780
ctgcctggac tcattggctg ccacaggaaa tctgtctact ggcatgtgat tggcatgggg	840
acaaccctg aagtgcactc cttttctctg gagggacaca ctttcttggt caggaaccac	900
agacaagcct ctctggagat ctctcccatc accttctca ctgcacagac actgctgatg	960

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tctctgtaca	tctcacagtt	catcatcatg	tactctctgg	atggcaagaa	gtggcagaca	3720
tacagaggca	actccactgg	caccctcatg	gtcttctttg	gcaatgtgga	cagctctggc	3780
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<210> 92

<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 92

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<210> 93

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 93

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<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 94

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<210> 95

<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

polynucleotide

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<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 97

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<210> 98

<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

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<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 100

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<210> 101

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 101

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<210> 102

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 102

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<210> 103

<211> 4377

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 103

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agcatgcccc tgggcatgga gagcaaggcc atctctgacg cccagatcac cgccagcagc	3960
tacttcacca acatgttcgc cacctggagc cccagcaagg ccaggctgca cctgcagggc	4020
aggagcaacg cctggaggcc ccaggtgaac aacccaagg agtggctgca ggtggacttc	4080
cagaagacca tgaaggtgac cggcgtgacc acccagggcg tgaagagcct gctgaccagc	4140
atgtacgtga aggagtctct gatcagcagc agccaggacg gccaccagtg gaccctgttc	4200
ttccagaacg gcaaagtga ggtgttcag ggcaaccagg acagcttcac cccgtggtg	4260
aacagcctgg accccccct gctgaccagg tatctgagga tccacccca gagctgggtg	4320
caccagatcg ccctgagaat ggaagtgctg ggatgagagg cccaggacct gtactga	4377

<210> 104

<211> 1458

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 104

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Val Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ser Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Lys Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Thr Thr Tyr Val Asn Arg Ser Leu Ser Gln Asn Pro Pro Val
755 760 765

Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp
770 775 780

Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys
785 790 795 800

Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser
805 810 815

Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu
820 825 830

Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala
835 840 845

Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe
850 855 860

Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu
865 870 875 880

His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn
885 890 895

Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr
900 905 910

Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro
915 920 925

Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys
930 935 940

Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala
945 950 955 960

Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly
965 970 975

Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala
980 985 990

His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile
995 1000 1005

Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg
1010 1015 1020

Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe
1025 1030 1035

Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp
1040 1045 1050

Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp
1055 1060 1065

Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His
1070 1075 1080

Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys
1085 1090 1095

Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu
1100 1105 1110

Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile
1115 1120 1125

Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr
1130 1135 1140

Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile
1145 1150 1155

Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala
1160 1165 1170

Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp
1175 1180 1185

Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala
1190 1195 1200

Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys
1205 1210 1215

Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu
1220 1225 1230

Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr
	1235					1240					1245			
Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His
	1250					1255					1260			
Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His
	1265					1270					1275			
Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met
	1280					1285					1290			
Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser
	1295					1300					1305			
Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr
	1310					1315					1320			
Asn	Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
	1325					1330					1335			
Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys
	1340					1345					1350			
Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly
	1355					1360					1365			
Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val
	1370					1375					1380			
Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr
	1385					1390					1395			
Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln
	1400					1405					1410			
Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp	Pro	Pro	Leu	Leu
	1415					1420					1425			
Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp	Val	His	Gln	Ile
	1430					1435					1440			

Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1445 1450 1455

<210> 105

<211> 1458

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 105

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Thr Thr Tyr Val Asn Arg Ser Leu Ser Gln Asn Pro Pro Val
755 760 765

Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp
770 775 780

Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys
785 790 795 800

Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser
805 810 815

Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu
820 825 830

Trp Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala
835 840 845

Gln Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe
850 855 860

Thr Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu
865 870 875 880

His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn
885 890 895

Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr
900 905 910

Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro
915 920 925

Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys
930 935 940

Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala
945 950 955 960

Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly
965 970 975

Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala
980 985 990

His Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile
995 1000 1005

Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg
1010 1015 1020

Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe
1025 1030 1035

Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp
1040 1045 1050

Thr Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp
1055 1060 1065

Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His
1070 1075 1080

Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys
1085 1090 1095

Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu
1100 1105 1110

Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile
1115 1120 1125

Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr
1130 1135 1140

Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile
1145 1150 1155

Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala
1160 1165 1170

Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp
1175 1180 1185

Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala
1190 1195 1200

Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys
1205 1210 1215

Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu
1220						1225					1230			
Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr
1235						1240					1245			
Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His
1250						1255					1260			
Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His
1265						1270					1275			
Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met
1280						1285					1290			
Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser
1295						1300					1305			
Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr
1310						1315					1320			
Asn	Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
1325						1330					1335			
Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys
1340						1345					1350			
Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly
1355						1360					1365			
Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val
1370						1375					1380			
Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr
1385						1390					1395			
Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln
1400						1405					1410			
Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp	Pro	Pro	Leu	Leu
1415						1420					1425			

Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile
1430 1435 1440

Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1445 1450 1455

<210> 106

<211> 1457

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 106

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Val Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ser Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Lys Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Ser Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
755 760 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
770 775 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
785 790 795 800

Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
805 810 815

Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
820 825 830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
835 840 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
850 855 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
865 870 875 880

Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
885 890 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
900 905 910

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
915 920 925

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
930 935 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
945 950 955 960

Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
965 970 975

Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
980 985 990

Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
995 1000 1005

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn
1010 1015 1020

Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys
1025 1030 1035

Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr
1040 1045 1050

Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr
1055 1060 1065

Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe
1070 1075 1080

Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met
1085 1090 1095

Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met
1100 1105 1110

Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly
1115 1120 1125

Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser
1130 1135 1140

Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg
1145 1150 1155

Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro
1160 1165 1170

Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser
1175 1180 1185

Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro
1190 1195 1200

Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe
1205 1210 1215

Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp
1220 1225 1230

Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu
1235 1240 1245

Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn
1250 1255 1260

Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro
1265 1270 1275

Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly
1280 1285 1290

Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys
1295 1300 1305

Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn
1310 1315 1320

Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln
1325 1330 1335

Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
1340 1345 1350

Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val
1355 1360 1365

Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys
1370 1375 1380

Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu
1385 1390 1395

Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
1400 1405 1410

Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr
1415 1420 1425

Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala
1430 1435 1440

Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1445 1450 1455

<210> 107

<211> 1457

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 107

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

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Val Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ser Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Lys Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Thr Ala Ser Asp Pro Pro Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Ser Cys His Ile Ser Ser His Gln His
325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
645 650 655

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

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
755 760 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
770 775 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
785 790 795 800

Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
805 810 815

Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
820 825 830

Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
835 840 845

Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
850 855 860

Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
865 870 875 880

Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
885 890 895

Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
900 905 910

Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
915 920 925

Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
930 935 940

Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
945 950 955 960

Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
965 970 975

Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
980 985 990

Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
995 1000 1005

Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn
1010 1015 1020

Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys
1025 1030 1035

Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr
1040 1045 1050

Leu Pro Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr
1055 1060 1065

Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe
1070 1075 1080

Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met
1085 1090 1095

Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met
1100 1105 1110

Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly
1115 1120 1125

Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser
1130 1135 1140

Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg
1145 1150 1155

Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro
1160 1165 1170

Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser
1175 1180 1185

Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro
1190 1195 1200

Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe
1205 1210 1215

Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp
1220 1225 1230

Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu
1235 1240 1245

Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn
1250 1255 1260

Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro
1265 1270 1275

Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly
1280 1285 1290

Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys
1295 1300 1305

Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn
1310 1315 1320

Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln
1325 1330 1335

Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
1340 1345 1350

Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val
1355 1360 1365

Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys
1370 1375 1380

Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu
1385 1390 1395

Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln	Asp
1400						1405					1410			

Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp	Pro	Pro	Leu	Leu	Thr
1415						1420					1425			

Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp	Val	His	Gln	Ile	Ala
1430						1435					1440			

Leu	Arg	Met	Glu	Val	Leu	Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr
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<210> 108

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 108

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acctctgtgg tctacaagaa gacactcttt gtggaattca ctgaccacct gttcaacatt	240
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gacactgtgg tcgtcaccct caagaacatg gcatcccacc ctgtgtctct gcatgctgtg	360
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<210> 109

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 109

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