

4465056_1
SEQUENCE LISTING

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<110> APOGENIX GMBH
<120> SINGLE-CHAIN TRAIL-RECEPTOR AGONIST PROTEINS
<130> 566215: BBI-999PC
<140> PCT/US2015/27270
<141> 2015-04-23
<150> 61/983,152
<151> 2014-04-23
<160> 31
<170> PatentIn version 3.5
<210> 1
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<212> PRT
<213> Homo sapiens
<220>
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20          25          30

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

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

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

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

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

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

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

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

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His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
165 170 175

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

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

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

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

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
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Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
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Ser Phe Phe Gly Ala Phe Leu Val Gly
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<210> 2
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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Gly Ser Gly Ser Gly Ser Gly Ser
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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
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1 5

<210> 9
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 Gly Gly Asn Gly Ser Gly
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Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 20 25 30

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

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

Glu Gln Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 65 70 75 80

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

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

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

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

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

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
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165

170

175

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 180 185 190

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

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

<210> 11

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

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His Thr Cys Pro Pro Cys
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<213> Artificial Sequence

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

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Ala Gly Asn Gly
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<210> 13

<211> 15

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<213> Artificial Sequence

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

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<210> 14
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
single-chain fusion polypeptide"

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20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg
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225		230		4465056_1 235		240									
Asn	Gly	Glu	Leu	Val ₂₄₅	Ile	His	Glu	Lys	Gly ₂₅₀	Phe	Tyr	Tyr	Ile	Tyr ₂₅₅	Ser
Gln	Thr	Tyr	Phe ₂₆₀	Arg	Phe	Gln	Glu	Glu ₂₆₅	Ile	Lys	Glu	Asn	Thr ₂₇₀	Lys	Asn
Asp	Lys	Gln ₂₇₅	Met	Val	Gln	Tyr	Ile ₂₈₀	Tyr	Lys	Tyr	Thr	Ser ₂₈₅	Tyr	Pro	Asp
Pro	Ile ₂₉₀	Leu	Leu	Met	Lys	Ser ₂₉₅	Ala	Arg	Asn	Ser	Cys ₃₀₀	Trp	Ser	Lys	Asp
Ala ₃₀₅	Glu	Tyr	Gly	Leu	Tyr ₃₁₀	Ser	Ile	Tyr	Gln	Gly ₃₁₅	Gly	Ile	Phe	Glu	Leu ₃₂₀
Lys	Glu	Asn	Asp	Arg ₃₂₅	Ile	Phe	Val	Ser	Val ₃₃₀	Thr	Asn	Glu	His	Leu ₃₃₅	Ile
Asp	Met	Asp	His ₃₄₀	Glu	Ala	Ser	Phe	Phe ₃₄₅	Gly	Ala	Phe	Leu	Val ₃₅₀	Gly	Gly
Ser	Gly	Ser ₃₅₅	Gly	Asn	Gly	Ser	Arg ₃₆₀	Val	Ala	Ala	His	Ile ₃₆₅	Thr	Gly	Thr
Arg	Gly ₃₇₀	Arg	Ser	Asn	Thr	Leu ₃₇₅	Ser	Ser	Pro	Asn	Ser ₃₈₀	Lys	Asn	Glu	Lys
Ala ₃₈₅	Leu	Gly	Arg	Lys	Ile ₃₉₀	Asn	Ser	Trp	Glu	Ser ₃₉₅	Ser	Arg	Ser	Gly	His ₄₀₀
Ser	Phe	Leu	Ser	Asn ₄₀₅	Leu	His	Leu	Arg	Asn ₄₁₀	Gly	Glu	Leu	Val	Ile ₄₁₅	His
Glu	Lys	Gly	Phe ₄₂₀	Tyr	Tyr	Ile	Tyr	Ser ₄₂₅	Gln	Thr	Tyr	Phe	Arg ₄₃₀	Phe	Gln
Glu	Glu	Ile ₄₃₅	Lys	Glu	Asn	Thr	Lys ₄₄₀	Asn	Asp	Lys	Gln	Met ₄₄₅	Val	Gln	Tyr
Ile	Tyr ₄₅₀	Lys	Tyr	Thr	Ser	Tyr ₄₅₅	Pro	Asp	Pro	Ile	Leu ₄₆₀	Leu	Met	Lys	Ser
Ala ₄₆₅	Arg	Asn	Ser	Cys	Trp ₄₇₀	Ser	Lys	Asp	Ala	Glu ₄₇₅	Tyr	Gly	Leu	Tyr	Ser ₄₈₀
Ile	Tyr	Gln	Gly	Gly ₄₈₅	Ile	Phe	Glu	Leu	Lys ₄₉₀	Glu	Asn	Asp	Arg	Ile ₄₉₅	Phe
Val	Ser	Val	Thr	Asn	Glu	His	Leu	Ile	Asp	Met	Asp	His	Glu	Ala	Ser

500

505

510

Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser
 515 520 525
 Ser Ser Gly Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 530 535 540
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 545 550 555 560
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 565 570 575
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 580 585 590
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 595 600 605
 Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 610 615 620
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 625 630 635 640
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 645 650 655
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 660 665 670
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 675 680 685
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 690 695 700
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 705 710 715 720
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 725 730 735
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<210> 15

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<211> 774

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

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20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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Asn Gly Glu Leu Val₂₄₅ Ile His Glu Lys Gly₂₅₀ Phe Tyr Tyr Ile Tyr₂₅₅ Ser
 Gln Thr Tyr Phe₂₆₀ Arg Phe Gln Glu Glu₂₆₅ Ile Lys Glu Asn Thr₂₇₀ Lys Asn
 Asp Lys Gln₂₇₅ Met Val Gln Tyr Ile₂₈₀ Tyr Lys Tyr Thr Ser₂₈₅ Tyr Pro Asp
 Pro Ile₂₉₀ Leu Leu Met Lys Ser₂₉₅ Ala Arg Asn Ser Cys₃₀₀ Trp Ser Lys Asp
 Ala Glu Tyr Gly Leu Tyr₃₁₀ Ser Ile Tyr Gln Gly₃₁₅ Gly Ile Phe Glu Leu₃₂₀
 Lys Glu Asn Asp Arg₃₂₅ Ile Phe Val Ser Val₃₃₀ Thr Asn Glu His Leu₃₃₅ Ile
 Asp Met Asp His₃₄₀ Glu Ala Ser Phe Phe₃₄₅ Gly Ala Phe Leu Val₃₅₀ Gly Gly
 Ser Gly Ser₃₅₅ Gly Asn Gly Ser Arg₃₆₀ Val Ala Ala His Ile₃₆₅ Thr Gly Thr
 Arg Gly₃₇₀ Arg Ser Asn Thr Leu₃₇₅ Ser Ser Pro Asn Ser₃₈₀ Lys Asn Glu Lys
 Ala Leu Gly Arg Lys Ile₃₉₀ Asn Ser Trp Glu Ser₃₉₅ Ser Arg Ser Gly His₄₀₀
 Ser Phe Leu Ser Asn₄₀₅ Leu His Leu Arg Asn₄₁₀ Gly Glu Leu Val Ile₄₁₅ His
 Glu Lys Gly Phe₄₂₀ Tyr Tyr Ile Tyr Ser₄₂₅ Gln Thr Tyr Phe Arg₄₃₀ Phe Gln
 Glu Glu Ile₄₃₅ Lys Glu Asn Thr Lys₄₄₀ Asn Asp Lys Gln Met₄₄₅ Val Gln Tyr
 Ile Tyr₄₅₀ Lys Tyr Thr Ser Tyr₄₅₅ Pro Asp Pro Ile Leu₄₆₀ Leu Met Lys Ser
 Ala Arg Asn Ser Cys Trp₄₇₀ Ser Lys Asp Ala Glu₄₇₅ Tyr Gly Leu Tyr Ser₄₈₀
 Ile Tyr Gln Gly Gly₄₈₅ Ile Phe Glu Leu Lys₄₉₀ Glu Asn Asp Arg Ile₄₉₅ Phe
 Val Ser Val Thr₅₀₀ Asn Glu His Leu Ile₅₀₅ Asp Met Asp His Glu₅₁₀ Ala Ser

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Phe Phe Gly Ala Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser
 515 520 525
 Ser Ser Gly Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 530 535 540
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 545 550 555 560
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 565 570 575
 Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 580 585 590
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 595 600 605
 Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 610 615 620
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
 625 630 635 640
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 645 650 655
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
 660 665 670
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 675 680 685
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 690 695 700
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 705 710 715 720
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 725 730 735
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 740 745 750
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 755 760 765
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<210> 16
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<220>
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 DNA polynucleotide sequence encoding a
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aacaccctgt ccagcccca ctccaagaac gagaaggccc tgggccggaa gatcaactcc      180
tgggagtcct ccagatccgg ccactccttt ctgtccaacc tgcacctgag aaacggcgag      240
ctggatcatcc acgagaaggg cttctactac atctactccc agacctactt caggtttcag      300
gaagagatca aagagaacac aaagaacgac aagcagatgg tgcagtatat ctacaagtac      360
acctcctacc ccgaccccat cctgctgatg aagtccgccc ggaactcctg ctgggtccaag      420
gatgctgagt acggcctgta cagcatctac cagggcgcca tcttcgagct gaaagagaac      480
gaccggatct tcgtgtccgt gaccaacgag cacctgatcg acatggacca cgaggccagc      540
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cacattaccg gaaccagagg ccggtccaac accctgagca gccctaacag caaaaatgag      660
aaagctctcg ggcgaagat caacagctgg gaatctagca gaagcggcca cagctttctg      720
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cagatgggcc agtacattta taagtatacc agctaccctg atcctatcct cctcatgaag      900
tctgccagaa actcttggtg gagcaaggac gccgagtatg gactgtactc tatctatcag      960
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ctcattgata tggatcatga agctagtttc ttcggggcat tcctcgtggg aggctccggc     1080
tctggcaacg gatctagagt cgccgcacac atcacagga ccagaggcag aagcaatacc     1140
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agcagcagat ccgggcacag ttttctgtct aatctccatc tgaggaatgg ggagctggtg     1260
attcacgaaa aaggatttta ctacatttac agtcagactt actttcgttt tcaggaagag     1320
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tatcctgacc caattctgct catgaagagt gcccgaaca gctgctggtc taaagacgcc     1440
gaatacgggc tgtattccat ttaccagggg ggaatttttg agctgaagga aaatgatcgg     1500
atttttgtct ctgtcacaaa cgaacacctc atcgatatgg atcacgaagc ctctttcttt     1560
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aagacccaca cctgtccccc ttgtcctgcc cctgaactgc tgggcggacc ttccgtgttc 1680
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gagtccaacg gccagcctga gaacaactac aagaccaccc cccctgtgct ggactccgac 2160
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<210> 17

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

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

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

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```

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

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

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

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

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

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

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

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

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

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
180 185 190

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

Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 18
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<212> PRT
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<220>
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20 25 30

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

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

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

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

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

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

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

130

135

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

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

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

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

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

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

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

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

Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp
275 280 285

Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp
290 295 300

Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu
305 310 315 320

Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile
325 330 335

Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly
340 345 350

Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr
355 360 365

Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys
370 375 380

Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His
385 390 395 400

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

675

680

685

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

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

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

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

Leu Ser Leu Ser Pro Gly Lys
 755

<210> 19

<211> 740

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 19

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

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

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

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

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

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

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

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

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

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His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175
 Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190
 Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205
 Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220
 Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly
 325 330 335
 Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
 340 345 350
 Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
 355 360 365
 Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
 370 375 380
 Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe
 385 390 395 400
 Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys
 405 410 415

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Glu Asn Thr Lys₄₂₀ Asn Asp Lys Gln Met₄₂₅ Val Gln Tyr Ile Tyr₄₃₀ Lys Tyr
 Thr Ser Tyr₄₃₅ Pro Asp Pro Ile Leu₄₄₀ Leu Met Lys Ser Ala₄₄₅ Arg Asn Ser
 Cys Trp₄₅₀ Ser Lys Asp Ala Glu₄₅₅ Tyr Gly Leu Tyr Ser₄₆₀ Ile Tyr Gln Gly
 Gly₄₆₅ Ile Phe Glu Leu Lys₄₇₀ Glu Asn Asp Arg Ile₄₇₅ Phe Val Ser Val Thr₄₈₀
 Asn Glu His Leu Ile₄₈₅ Asp Met Asp His Glu₄₉₀ Ala Ser Phe Phe Gly₄₉₅ Ala
 Phe Leu Val Gly₅₀₀ Gly Pro Gly Ser Ser₅₀₅ Ser Ser Ser Ser Ser₅₁₀ Gly Ser
 Cys Asp Lys₅₁₅ Thr His Thr Cys Pro₅₂₀ Pro Cys Pro Ala Pro₅₂₅ Glu Leu Leu
 Gly Gly₅₃₀ Pro Ser Val Phe Leu₅₃₅ Phe Pro Pro Lys Pro₅₄₀ Lys Asp Thr Leu
 Met₅₄₅ Ile Ser Arg Thr Pro₅₅₀ Glu Val Thr Cys Val₅₅₅ Val Val Asp Val Ser₅₆₀
 His Glu Asp Pro Glu₅₆₅ Val Lys Phe Asn Trp₅₇₀ Tyr Val Asp Gly Val₅₇₅ Glu
 Val His Asn Ala₅₈₀ Lys Thr Lys Pro Arg₅₈₅ Glu Glu Gln Tyr Ser₅₉₀ Ser Thr
 Tyr Arg Val₅₉₅ Val Ser Val Leu Thr₆₀₀ Val Leu His Gln Asp₆₀₅ Trp Leu Asn
 Gly Lys₆₁₀ Glu Tyr Lys Cys Lys₆₁₅ Val Ser Asn Lys Ala₆₂₀ Leu Pro Ala Pro
 Ile₆₂₅ Glu Lys Thr Ile Ser₆₃₀ Lys Ala Lys Gly Gln₆₃₅ Pro Arg Glu Pro Gln₆₄₀
 Val Tyr Thr Leu Pro₆₄₅ Pro Ser Arg Glu Glu₆₅₀ Met Thr Lys Asn Gln Val₆₅₅
 Ser Leu Thr Cys₆₆₀ Leu Val Lys Gly Phe₆₆₅ Tyr Pro Ser Asp Ile₆₇₀ Ala Val
 Glu Trp Glu₆₇₅ Ser Asn Gly Gln Pro₆₈₀ Glu Asn Asn Tyr Lys₆₈₅ Thr Thr Pro

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

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

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

Ser Pro Gly Lys
740

<210> 20

<211> 754

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 20

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
260 265 270

Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
275 280 285

Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
290 295 300

Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
305 310 315 320

Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Gly
325 330 335

Asn Gly Ser Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser
340 345 350

Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg
355 360 365

Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser
370 375 380

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

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

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

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Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser
 435 440 445
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 450 455 460
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 465 470 475 480
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser
 500 505 510
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 515 520 525
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 530 535 540
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 545 550 555 560
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 565 570 575
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ser Ser Thr
 580 585 590
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 595 600 605
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 610 615 620
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 625 630 635 640
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 645 650 655
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 660 665 670
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 675 680 685
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 690 695 700

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

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

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

Glu Lys

<210> 21
 <211> 739
 <212> PRT
 <213> Artificial Sequence

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

<400> 21
 Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 1 5 10 15

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

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

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

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

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

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

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

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

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

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

435 440 445
 Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly
 450 455 460
 Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr
 465 470 475 480
 Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser
 500 505 510
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
 515 520 525
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 530 535 540
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 545 550 555 560
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 565 570 575
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 580 585 590
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 595 600 605
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
 610 615 620
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 625 630 635 640
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 645 650 655
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 660 665 670
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 675 680 685
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 690 695 700
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

705 710 715 720

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser

725 730 735

Pro Gly Lys

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

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

<400> 23
Gly ser Gly ser
1
```

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

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

<400> 24
Gly Ser Gly
1
```

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

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

<400> 25
Gly Pro Gly Ser Ser Ser Ser Ser Ser Gly Ser Cys Asp Lys Thr His
```

1

5

10

15

Thr Cys Pro Pro Cys
20

<210> 26

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 26

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala
 485 490 495
 Phe Leu Val Gly Gly Pro Gly Ser Ser Ser Ser Ser Gly Ser Asp
 500 505 510
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
 515 520 525
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 530 535 540
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 545 550 555 560
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 565 570 575
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 580 585 590
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 595 600 605
 Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
 610 615 620
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 625 630 635 640
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 645 650 655
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 660 665 670
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 675 680 685
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 690 695 700
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 705 710 715 720
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 725 730 735
 Ser Ser Ser Ser Ser Ser Ala Trp Ser His Pro Gln Phe Glu Lys
 740 745 750

<210> 27
 <211> 750
 <212> PRT
 <213> Artificial Sequence

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

<400> 27
 Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr
 1 5 10 15
 Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile
 20 25 30
 Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu
 35 40 45
 His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr
 50 55 60
 Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn
 65 70 75 80
 Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser
 85 90 95
 Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp
 100 105 110
 Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile
 115 120 125
 Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu
 130 135 140
 His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu
 145 150 155 160
 Val Gly Gly Ser Gly Ser Gly Asn Gly Ser Arg Val Ala Ala His Ile
 165 170 175
 Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys
 180 185 190
 Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg
 195 200 205
 Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu
 210 215 220

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Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe
 225 230 235 240
 Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met
 245 250 255
 Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu
 260 265 270
 Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly
 275 280 285
 Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp
 290 295 300
 Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His
 305 310 315 320
 Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly Gly Ser Gly Ser Arg
 325 330 335
 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 340 345 350
 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 355 360 365
 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 370 375 380
 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 385 390 395 400
 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 405 410 415
 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 420 425 430
 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 435 440 445
 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 450 455 460
 Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
 465 470 475 480
 Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 485 490 495

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 28
<211> 750
<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 28

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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Gln Glu Glu Ile Lys₂₄₅ Glu Asn Thr Lys Asn₂₅₀ Asp Lys Gln Met Val₂₅₅ Gln
 Tyr Ile Tyr Lys₂₆₀ Tyr Thr Ser Tyr Pro₂₆₅ Asp Pro Ile Leu Leu₂₇₀ Met Lys
 Ser Ala Arg₂₇₅ Asn Ser Cys Trp Ser₂₈₀ Lys Asp Ala Glu Tyr₂₈₅ Gly Leu Tyr
 Ser Ile₂₉₀ Tyr Gln Gly Gly Ile₂₉₅ Phe Glu Leu Lys Glu₃₀₀ Asn Asp Arg Ile
 Phe Val Ser Val Thr Asn₃₁₀ Glu His Leu Ile Asp₃₁₅ Met Asp His Glu Ala₃₂₀
 Ser Phe Phe Gly Ala₃₂₅ Phe Leu Val Gly Gly₃₃₀ Ser Gly Ser Gly Ser Arg₃₃₅
 Val Ala Ala His₃₄₀ Ile Thr Gly Thr Arg₃₄₅ Gly Arg Ser Asn Thr₃₅₀ Leu Ser
 Ser Pro Asn₃₅₅ Ser Lys Asn Glu Lys₃₆₀ Ala Leu Gly Arg Lys₃₆₅ Ile Asn Ser
 Trp Glu₃₇₀ Ser Ser Arg Ser Gly₃₇₅ His Ser Phe Leu Ser₃₈₀ Asn Leu His Leu
 Arg Asn Gly Glu Leu Val₃₉₀ Ile His Glu Lys Gly₃₉₅ Phe Tyr Tyr Ile Tyr₄₀₀
 Ser Gln Thr Tyr Phe₄₀₅ Arg Phe Gln Glu Glu₄₁₀ Ile Lys Glu Asn Thr₄₁₅ Lys
 Asn Asp Lys Gln₄₂₀ Met Val Gln Tyr Ile₄₂₅ Tyr Lys Tyr Thr Ser Tyr Pro
 Asp Pro Ile₄₃₅ Leu Leu Met Lys Ser₄₄₀ Ala Arg Asn Ser Cys₄₄₅ Trp Ser Lys
 Asp Ala₄₅₀ Glu Tyr Gly Leu Tyr₄₅₅ Ser Ile Tyr Gln Gly₄₆₀ Gly Ile Phe Glu
 Leu Lys Glu Asn Asp Arg₄₇₀ Ile Phe Val Ser Val₄₇₅ Thr Asn Glu His Leu₄₈₀
 Ile Asp Met Asp His₄₈₅ Glu Ala Ser Phe Phe₄₉₀ Gly Ala Phe Leu Val₄₉₅ Gly
 Gly Pro Gly Ser₅₀₀ Ser Ser Ser Ser Ser₅₀₅ Ser Gly Ser Cys₅₁₀ Asp Lys Thr

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His Thr Cys₅₁₅ Pro Pro Cys Pro Ala₅₂₀ Pro Glu Leu Leu Gly₅₂₅ Gly Pro Ser

Val Phe₅₃₀ Leu Phe Pro Pro Lys₅₃₅ Pro Lys Asp Thr Leu₅₄₀ Met Ile Ser Arg

Thr₅₄₅ Pro Glu Val Thr Cys₅₅₀ Val Val Val Asp Val₅₅₅ Ser His Glu Asp Pro₅₆₀

Glu Val Lys Phe Asn₅₆₅ Trp Tyr Val Asp Gly₅₇₀ Val Glu Val His Asn₅₇₅ Ala

Lys Thr Lys Pro₅₈₀ Arg Glu Glu Gln Tyr₅₈₅ Ser Ser Thr Tyr Arg₅₉₀ Val Val

Ser Val Leu₅₉₅ Thr Val Leu His Gln₆₀₀ Asp Trp Leu Asn Gly₆₀₅ Lys Glu Tyr

Lys Cys₆₁₀ Lys Val Ser Asn Lys₆₁₅ Ala Leu Pro Ala Pro₆₂₀ Ile Glu Lys Thr

Ile₆₂₅ Ser Lys Ala Lys Gly₆₃₀ Gln Pro Arg Glu Pro₆₃₅ Gln Val Tyr Thr Leu₆₄₀

Pro Pro Ser Arg Glu₆₄₅ Glu Met Thr Lys Asn₆₅₀ Gln Val Ser Leu Thr₆₅₅ Cys

Leu Val Lys Gly₆₆₀ Phe Tyr Pro Ser Asp₆₆₅ Ile Ala Val Glu Trp₆₇₀ Glu Ser

Asn Gly Gln₆₇₅ Pro Glu Asn Asn Tyr₆₈₀ Lys Thr Thr Pro Pro₆₈₅ Val Leu Asp

Ser Asp₆₉₀ Gly Ser Phe Phe Leu₆₉₅ Tyr Ser Lys Leu Thr₇₀₀ Val Asp Lys Ser

Arg Trp Gln Gln Gly Asn₇₁₀ Val Phe Ser Cys Ser₇₁₅ Val Met His Glu Ala₇₂₀

Leu His Asn His Tyr₇₂₅ Thr Gln Lys Ser Leu₇₃₀ Ser Leu Ser Pro Gly₇₃₅ Ser

Ser Ser Ser Ser₇₄₀ Ser Ala Trp Ser His₇₄₅ Pro Gln Phe Glu Lys₇₅₀

<210> 29

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

polypeptide"

<400> 29

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu

260

265

270

Met Lys Ser₂₇₅ Ala Arg Asn Ser Cys₂₈₀ Trp Ser Lys Asp Ala₂₈₅ Glu Tyr Gly

Leu Tyr₂₉₀ Ser Ile Tyr Gln Gly₂₉₅ Gly Ile Phe Glu Leu₃₀₀ Lys Glu Asn Asp

Arg Ile Phe Val Ser Val₃₁₀ Thr Asn Glu His Leu₃₁₅ Ile Asp Met Asp His₃₂₀

Glu Ala Ser Phe Phe₃₂₅ Gly Ala Phe Leu Val₃₃₀ Gly Gly Ser Gly Ser₃₃₅ Arg

Val Ala Ala His₃₄₀ Ile Thr Gly Thr Arg₃₄₅ Gly Arg Ser Asn Thr₃₅₀ Leu Ser

Ser Pro Asn₃₅₅ Ser Lys Asn Glu Lys₃₆₀ Ala Leu Gly Arg Lys₃₆₅ Ile Asn Ser

Trp Glu₃₇₀ Ser Ser Arg Ser Gly₃₇₅ His Ser Phe Leu Ser₃₈₀ Asn Leu His Leu

Arg Asn Gly Glu Leu Val₃₉₀ Ile His Glu Lys Gly₃₉₅ Phe Tyr Tyr Ile Tyr₄₀₀

Ser Gln Thr Tyr Phe₄₀₅ Arg Phe Gln Glu Glu₄₁₀ Ile Lys Glu Asn Thr₄₁₅ Lys

Asn Asp Lys Gln₄₂₀ Met Val Gln Tyr Ile₄₂₅ Tyr Lys Tyr Thr Ser₄₃₀ Tyr Pro

Asp Pro Ile₄₃₅ Leu Leu Met Lys Ser₄₄₀ Ala Arg Asn Ser Cys₄₄₅ Trp Ser Lys

Asp Ala Glu Tyr Gly Leu Tyr₄₅₅ Ser Ile Tyr Gln Gly₄₆₀ Gly Ile Phe Glu

Leu Lys Glu Asn Asp Arg₄₇₀ Ile Phe Val Ser Val₄₇₅ Thr Asn Glu His Leu₄₈₀

Ile Asp Met Asp His₄₈₅ Glu Ala Ser Phe Phe₄₉₀ Gly Ala Phe Leu Val₄₉₅ Gly

Gly Pro Gly Ser₅₀₀ Ser Ser Ser Ser Ser₅₀₅ Ser Gly Ser Cys₅₁₀ Asp Lys Thr

His Thr Cys₅₁₅ Pro Pro Cys Pro Ala₅₂₀ Pro Glu Leu Leu Gly₅₂₅ Gly Pro Ser

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg

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540

530

535

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

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

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

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

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

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

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

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

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

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

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

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

<210> 30

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 30

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

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

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

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

4465056_1

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

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

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

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

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

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

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

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

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

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

<210> 31

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 31

Asp Glu Val Asp

1