SEQUENCE LISTING

<110> AMGEN INC.

<120> VARIANT FC-POLYPEPTIDES WITH ENHANCED BINDING TO THE NEONATAL FC RECEPTOR

<130> A-1688-WO-PCT

<140> TO BE ASSIGNED
<141> 2012-12-17

<150> 61/729,050
<151> 2012-11-21

<150> 61/585,993
<151> 2012-01-12

<150> 61/578,780
<151> 2011-12-21

<160> 575

<170> PatentIn version 3.5

<210> 1
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<213> Homo sapiens

<400> 1

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Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
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145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
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Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
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Ser Leu Ser Leu Ser Pro Gly Lys
225 230

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<213> Homo sapiens

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acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 360

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gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480

gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540

cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc 600

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20 25 30

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        35                  40                  45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
    50                  55                  60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65                  70                  75                  80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
                85                  90                  95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
            100                 105                 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
    130                 135                 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
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Ser Pro Gly Lys
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acgtgcgtgg tggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg      180

gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg      240

ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac      300
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aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 480

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 540

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600

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agcctctccc tgtctccggg taaatga 687

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		20					25					30			
Glu	Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg	Cys	Pro	Glu
	35					40					45				
Pro	Lys	Ser	Cys	Asp	Thr	Pro	Pro	Pro	Cys	Pro	Arg	Cys	Pro	Ala	Pro
50					55					60					
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
65				70					75					80	
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
			85					90					95		
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Lys	Trp	Tyr	Val	Asp
		100					105					110			
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr
	115					120					125				
Asn	Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
130					135					140					
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu
145				150					155					160	
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg
			165					170					175		
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys
		180					185					190			

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Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
        195                 200                 205

Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn
    210                 215                 220

Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
225                 230                 235                 240

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser
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Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser
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Leu Ser Leu Ser Pro Gly Lys
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cccccatgcc cacggtgccc agagcccaaa tcttgtgaca cacctccccc gtgcccaagg      180

tgcccagcac ctgaactcct gggaggaccg tcagtcttcc tcttcccccc aaaacccaag      240

gataccctta tgatttcccg gacccctgag gtcacgtgcg tggtggtgga cgtgagccac      300

gaagaccccg aggtccagtt caagtggtac gtggacggcg tggaggtgca taatgccaag      360

acaaagccgc gggaggagca gtacaacagc acgttccgtg tggtcagcgt cctcaccgtc      420

ctgcaccagg actggctgaa cggcaaggag tacaagtgca aggtctccaa caaagccctc      480

ccagccccca tcgagaaaac catctccaaa accaaaggac agccccgaga accacaggtg      540

tacaccctgc ccccatcccg ggaggagatg accaagaacc aggtcagcct gacctgcctg      600

gtcaaaggct tctaccccag cgacatcgcc gtggagtggg agagcagcgg gcagccggag      660

aacaactaca acaccacgcc tcccatgctg gactccgacg gctccttctt cctctacagc      720

aagctcaccg tggacaagag caggtggcag caggggaaca tcttctcatg ctccgtgatg      780

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Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20                  25                  30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35                  40                  45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50                  55                  60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65                  70                  75                  80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
                85                  90                  95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100                 105                 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
        115                 120                 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130                 135                 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145                 150                 155                 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
                165                 170                 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180                 185                 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
        195                 200                 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
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Leu Ser Leu Gly Lys
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gtcacgtgcg tggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 180

gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 240

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa cggcaaggag 300

tacaagtgca aggtctccaa caaaggcctc ccgtcctcca tcgagaaaac catctccaaa 360

gccaaagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg 420

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc 480

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 540

gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag caggtggcag 600

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            20                  25                  30

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

Gly Ala Trp Val Trp Glu Asn Gln Val Ser Trp Tyr Trp Glu Lys Glu
    50                  55                  60

Thr Thr Asp Leu Arg Ile Lys Glu Lys Leu Phe Leu Glu Ala Phe Lys
65                  70                  75                  80

Ala Leu Gly Gly Lys Gly Pro Tyr Thr Leu Gln Gly Leu Leu Gly Cys
                85                  90                  95

Glu Leu Gly Pro Asp Asn Thr Ser Val Pro Thr Ala Lys Phe Ala Leu
            100                 105                 110

Asn Gly Glu Glu Phe Met Asn Phe Asp Leu Lys Gln Gly Thr Trp Gly
        115                 120                 125

Gly Asp Trp Pro Glu Ala Leu Ala Ile Ser Gln Arg Trp Gln Gln Gln
    130                 135                 140

Asp Lys Ala Ala Asn Lys Glu Leu Thr Phe Leu Leu Phe Ser Cys Pro
145                 150                 155                 160

His Arg Leu Arg Glu His Leu Glu Arg Gly Arg Gly Asn Leu Glu Trp
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165 170 175

Lys Glu Pro Pro Ser Met Arg Leu Lys Ala Arg Pro Ser Ser Pro Gly
180 185 190

Phe Ser Val Leu Thr Cys Ser Ala Phe Ser Phe Tyr Pro Pro Glu Leu
195 200 205

Gln Leu Arg Phe Leu Arg Asn Gly Leu Ala Ala Gly Thr Gly Gln Gly
210 215 220

Asp Phe Gly Pro Asn Ser Asp Gly Ser Phe His Ala Ser Ser Ser Leu
225 230 235 240

Thr Val Lys Ser Gly Asp Glu His His Tyr Cys Cys Ile Val Gln His
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Ala Gly Leu Ala Gln Pro Leu Arg Val Glu Leu
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<212> PRT
<213> Homo sapiens

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1 5 10 15

Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro
20 25 30

Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys
35 40 45

Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp Ser Phe Tyr Leu
50 55 60

Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys
65 70 75 80

Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp
85 90 95

Arg Asp Met

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<211> 235
<212> PRT
<213> Homo sapiens

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Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235

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

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Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val
            20                  25                  30

Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val Cys
        35                  40                  45

Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser
    50                  55                  60

Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile Gln
65                  70                  75                  80

Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu
                85                  90                  95

Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile
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Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
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<210> 13
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<213> Artificial Sequence

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      or "Tyr" or "Trp"

<220>
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<223> /note="Residues given in the sequence have no preference
      with respect to those in the annotations for said positions"

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<210> 14
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or "Tyr" or "Trp"

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or "Tyr" or "Trp"

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or "Tyr" or "Trp"

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<212> PRT
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or "Tyr" or "Trp"

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"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

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<210> 19
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<210> 22
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<213> Artificial Sequence

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<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 22
Gly Gly Gly Cys Lys Lys Lys Lys Lys Lys Cys Gly Gly Gly
1 5 10

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT
<222> (5)..(11)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (5)..(11)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 23
Gly Gly Gly Cys Lys Lys Lys Lys Lys Lys Lys Cys Gly Gly Gly
1 5 10 15

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (5)..(12)
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or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (5)..(12)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 24
Gly Gly Gly Cys Lys Lys Lys Lys Lys Lys Lys Lys Cys Gly Gly Gly
1 5 10 15

<210> 25
<211> 705
<212> DNA
<213> Artificial Sequence

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

<220>
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<222> (109)..(111)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>

<221> Variation
<222> (112)..(114)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (115)..(117)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (118)..(120)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (121)..(123)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (124)..(126)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (109)..(126)
<223> /note="nucleotides given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 25
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcaa aaaaaaaaaa 120

aaaaaaaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 180

aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 240

gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 300

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 360

aaaaccatct ccaaagccaa agggcagccc cgagagccac aggtgtacac cctgccccca 420

tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 480

cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 540

acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 600

aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 660

aaccactaca cgcagaagag cctctccctg tctccgggta aatga 705

<210> 26
<211> 234
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT
<222> (37)..(42)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (37)..(42)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 26
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Lys Lys Lys Lys Lys Lys Thr Pro Glu Val Thr Cys
35 40 45

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
50 55 60

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
65 70 75 80

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
85 90 95

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
100 105 110

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
115 120 125

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
130 135 140

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
145 150 155 160

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
165 170 175

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
180 185 190

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
195 200 205

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 27
<211> 711
<212> DNA
<213> Artificial Sequence

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

<220>
<221> Variation
<222> (277)..(279)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (280)..(282)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (283)..(285)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (286)..(288)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (289)..(291)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>

<221> Variation
<222> (292)..(294)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (277)..(294)
<223> /note="nucleotides given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 27
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccaaaa aaaaaaaaaa aaaacaccag 300

gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 360

atcgagaaaa ccatctccaa agccaaaggg cagccccgag agccacaggt gtacaccctg 420

cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 480

ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 540

aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 600

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 660

ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaatg a 711

<210> 28
<211> 236
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT
<222> (93)..(98)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (93)..(98)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 28

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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                  10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Lys Lys Lys Lys
                85                  90                  95

Lys Lys His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
            100                 105                 110

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
        115                 120                 125

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
    130                 135                 140

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
145                 150                 155                 160

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                165                 170                 175

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
            180                 185                 190

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
        195                 200                 205

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
    210                 215                 220

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225                 230                 235
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<210> 29
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<221> source

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

<220>
<221> Variation
<222> (286)..(288)
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<220>
<221> Variation
<222> (289)..(291)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (292)..(294)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (295)..(297)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (298)..(300)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (301)..(303)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (286)..(303)
<223> /note="nucleotides given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 29
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccggtg gttgtaaaaa aaaaaaaaaa 300

aaatgtggtg gtcaccagga ctggctgaat ggcaaggagt acaagtgcaa ggtctccaac 360

aaagccctcc cagccccat cgagaaaacc atctccaaag ccaaagggca gccccgagag 420

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 480

acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 540

cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc 600

ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 660

tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 720

ggtaaatga 729

<210> 30
<211> 242
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT
<222> (96)..(101)
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<220>
<221> misc_feature
<222> (96)..(101)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 30
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Gly Gly Cys Lys
85 90 95

Lys Lys Lys Lys Lys Cys Gly Gly His Gln Asp Trp Leu Asn Gly Lys

```
            100                 105                 110

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
        115                 120                 125

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
    130                 135                 140

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
145                 150                 155                 160

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
                165                 170                 175

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
            180                 185                 190

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
        195                 200                 205

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
    210                 215                 220

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
225                 230                 235                 240

Gly Lys
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<210> 31
<211> 705
<212> DNA
<213> Artificial Sequence

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

<220>
<221> Variation
<222> (646)..(648)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (649)..(651)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (652)..(654)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"

or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (655)..(657)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (658)..(660)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (646)..(660)
<223> /note="nucleotides given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> Variation
<222> (664)..(666)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (664)..(666)
<223> /note="nucleotides given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 31
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

cacacccctg aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag 180

ttcaactggt acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag 240

cagtacaaca gcacgtaccg tgtggtcagc gtcctcaccg tcctgcacca ggactggctg 300

aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa 360

accatctcca aagccaaagg gcagccccga gagccacagg tgtacaccct gccccatcc 420

cgggatgagc tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc 480

agcgacatcg ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg 540

cctcccgtgc tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag 600

agcaggtggc agcaggggaa cgtcttctca tgctccgtga tgcataaaaa aaaaaaaaaa 660

cacaaataca cgcagaagag cctctccctg tctccgggta aatga 705

<210> 32

<211> 234
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT
<222> (215)..(219)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (215)..(219)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> VARIANT
<222> (221)..(221)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (221)..(221)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 32
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Lys Lys Lys Lys Lys His Lys His Tyr Thr
210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 33
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
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<220>
<221> Variation
<222> (226)..(228)
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<220>
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<222> (229)..(231)
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<220>
<221> Variation
<222> (232)..(234)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or

"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (235)..(237)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (238)..(240)
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<220>
<221> misc_feature
<222> (223)..(240)
<223> /note="nucleotides given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 33
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatggtggtt gtaaaaaaaa aaaaaaaaaa 240

tgtggtggtg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 300

agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 360

tccaacaaag ccctcccagc ccccatcgag aaaaccatct ccaaagccaa agggcagccc 420

cgagagccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 480

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 540

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 600

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 660

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 720

tctccgggta aatga 735

<210> 34
<211> 244
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT

<222> (75)..(80)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (75)..(80)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 34

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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Gly Gly Cys Lys Lys Lys Lys Lys Lys
65                  70                  75                  80

Cys Gly Gly Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
                85                  90                  95

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
            100                 105                 110

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
        115                 120                 125

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
    130                 135                 140

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
145                 150                 155                 160

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            180                 185                 190

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        195                 200                 205

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    210                 215                 220
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Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
225 230 235 240

Ser Pro Gly Lys

<210> 35
<211> 735
<212> DNA
<213> Artificial Sequence

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

<220>
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<222> (517)..(519)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (520)..(522)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
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<222> (523)..(525)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
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<222> (526)..(528)
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<220>
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<222> (529)..(531)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (532)..(534)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT" or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or "GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (517)..(534)
<223> /note="nucleotides given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of substitutions and preferred embodiments"

<400> 35
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 360

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccgg 420

gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480

gacatcgccg tggagtggga gagcaatggt ggttgtaaaa aaaaaaaaaa aaaatgtggt 540

ggtgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 600

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 660

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 720

tctccgggta aatga 735

<210> 36
<211> 244
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (173)..(178)
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<220>
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<222> (173)..(178)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 36
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

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

35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gly Cys Lys Lys Lys Lys
165 170 175

Lys Lys Cys Gly Gly Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
180 185 190

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
195 200 205

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
210 215 220

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
225 230 235 240

Ser Pro Gly Lys

<210> 37
<211> 735
<212> DNA
<213> Artificial Sequence

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

<220>
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<222> (439)..(441)
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or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
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<222> (442)..(444)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (445)..(447)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (448)..(450)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (451)..(453)
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or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> Variation
<222> (454)..(456)
<223> /replace="AAC" or "ACT" or "ATC" or "ATG" or "CAG" or "CAT"
or "CCG" or "CGT" or "CTG" or "GAA" or "GAC" or "GCT" or
"GGT" or "GTT" or "TAC" or "TCT" or "TGG" or "TTC"

<220>
<221> misc_feature
<222> (439)..(456)
<223> /note="nucleotides given in the sequence have no preference
with respect to those in the annotations for said positions"

<220>
<221> source
<223> /note="see specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 37
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 360

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccgg 420

gatgagctgg gtggttgtaa aaaaaaaaaa aaaaaatgtg gtggtaccaa gaaccaggtc 480

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 540

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 600

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 660

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 720

tctccgggta aatga 735

<210> 38
<211> 244
<212> PRT
<213> Artificial Sequence

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

<220>
<221> VARIANT
<222> (147)..(152)
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<220>
<221> misc_feature
<222> (147)..(152)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 38

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Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125
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Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Gly
    130                 135                 140

Gly Cys Lys Lys Lys Lys Lys Lys Cys Gly Gly Thr Lys Asn Gln Val
145                 150                 155                 160

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            180                 185                 190

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
        195                 200                 205

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
    210                 215                 220

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
225                 230                 235                 240

Ser Pro Gly Lys
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<210> 39
<211> 735
<212> DNA
<213> Artificial Sequence

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

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<222> (439)..(440)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (442)..(443)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (445)..(446)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (448)..(449)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (451)..(452)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (454)..(455)
<223> a, c, t, g, unknown or other

<400> 39
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg 60

gggggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 120

acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180

aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240

tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300

ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 360

atctccaaag ccaaagggca gccccgagag ccacaggtgt acaccctgcc cccatcccgg 420

gatgagctgg gtggttgtnn knnknnknnk nnknnktgtg gtggtaccaa gaaccaggtc 480

agcctgacct gcctggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 540

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 600

ttcttcctct acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 660

tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 720

tctccgggta aatga 735

<210> 40
<211> 244
<212> PRT
<213> Artificial Sequence

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

<220>
<221> MOD_RES
<222> (147)..(152)
<223> Any amino acid

<400> 40
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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

65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Gly
130 135 140

Gly Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly Gly Thr Lys Asn Gln Val
145 150 155 160

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

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
180 185 190

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
195 200 205

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
210 215 220

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
225 230 235 240

Ser Pro Gly Lys

<210> 41
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 41
Gly Gly Cys His Leu Pro Phe Ala Val Cys Gly Gly
1 5 10

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

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

<400> 42
Gly Gly Cys Trp Pro Leu Gln Asp Tyr Cys Gly Gly
1 5 10

<210> 43
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 43
Gly Gly Cys Gly His Glu Tyr Met Trp Cys Gly Gly
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 44
Gly Gly Cys Val Phe Asn Met Phe Asn Cys Gly Gly
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 45
Gly Gly Cys Ala Leu Tyr Pro Thr Asn Cys Gly Gly
1 5 10

<210> 46
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 46
Gly Gly Cys Met Gln Val Trp Gly Ser Cys Gly Gly
1 5 10

<210> 47
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 47
Gly Gly Cys Gln Lys Gly Trp Val Phe Cys Gly Gly
1 5 10

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 48
Gly Gly Cys Met Val Pro Phe Ser Met Cys Gly Gly
1 5 10

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 49
Gly Gly Cys Val Asn Thr Trp Trp Ser Cys Gly Gly
1 5 10

<210> 50
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 50
Gly Gly Cys Ile Gly Pro Phe Trp Trp Cys Gly Gly
1 5 10

<210> 51
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source

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

<400> 51
Gly Gly Cys Asp Arg Pro Val Trp Phe Cys Gly Gly
1 5 10

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 52
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1 5 10

<210> 53
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 53
Gly Gly Cys Tyr Ile Thr Gln Lys Leu Cys Gly Gly
1 5 10

<210> 54
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 54
His Leu Pro Phe Ala Val
1 5

<210> 55
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<220>
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<400> 55
Trp Pro Leu Gln Asp Tyr
1 5

<210> 56
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<220>
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<400> 56
Gly His Glu Tyr Met Trp
1 5

<210> 57
<211> 6
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<213> Artificial Sequence

<220>
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<400> 57
Val Phe Asn Met Phe Asn
1 5

<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 58
Ala Leu Tyr Pro Thr Asn
1 5

<210> 59
<211> 6
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<220>
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<400> 59
Met Gln Val Trp Gly Ser
1 5

<210> 60
<211> 6
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<220>
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<400> 60
Gln Lys Gly Trp Val Phe
1 5

<210> 61
<211> 6
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 61
Met Val Pro Phe Ser Met
1 5

<210> 62
<211> 6
<212> PRT
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<220>
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<400> 62
Val Asn Thr Trp Trp Ser
1 5

<210> 63
<211> 6
<212> PRT
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<220>
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<400> 63
Ile Gly Pro Phe Trp Trp
1 5

<210> 64
<211> 6
<212> PRT
<213> Artificial Sequence

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

<400> 64
Asp Arg Pro Val Trp Phe
1 5

<210> 65

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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peptide"

<400> 65
Asn Met Leu Trp Gly Ser
1 5

<210> 66
<211> 6
<212> PRT
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<220>
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peptide"

<400> 66
Tyr Ile Thr Gln Lys Leu
1 5

<210> 67
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 67
Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly Gly
1 5 10

<210> 68
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
primer"

<400> 68
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cagccg 66

<210> 69
<211> 66
<212> DNA
<213> Artificial Sequence

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

primer"

<400> 69
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cacagc 66

<210> 70
<211> 66
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 70
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ccggag 66

<210> 71
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 71
ctccggctgc ccattaccac cacagaattc gatcggcata ccacaaccac cgctctccca 60

ctccac 66

<210> 72
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 72
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aacaac 66

<210> 73
<211> 66
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 73
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ctccca 66

<210> 74
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 74
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aactac 66

<210> 75
<211> 66
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<220>
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gctctc 66

<210> 76
<211> 66
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 76
agcaatgggc agccgggtgg ttgtggtatg ccgatcgaat tctgtggtgg tgagaacaac 60

tacaag 66

<210> 77
<211> 66
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 77
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attgct 66

<210> 78
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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aagacc 66

<210> 79
<211> 66
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

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cccatt 66

<210> 80
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<212> DNA
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<220>
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accacg 66

<210> 81
<211> 66
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 81
cgtggtcttg tagttaccac cacagaattc gatcggcata ccacaaccac cgttctccgg 60

ctgccc 66

<210> 82
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 82
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acgcct 66

<210> 83
<211> 66
<212> DNA
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

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cggctg 66

<210> 84
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 84
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aactac 66

<210> 85
<211> 66
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<220>
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<400> 85
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ctccac 66

<210> 86
<211> 72
<212> DNA
<213> Artificial Sequence

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

primer"

<400> 86
gtggagtggg agagcggtgg tggttgtggt atgccgatcg aattctgtgg tggtggtccg 60

gagaacaact ac 72

<210> 87
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic primer"

<400> 87
gtagttgttc tccggaccac caccacagaa ttcgatcggc ataccacaac caccaccgct 60

ctcccactcc ac 72

<210> 88
<211> 14
<212> PRT
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<220>
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<220>
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<222> (4)..(11)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (4)..(11)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 88
Gly Gly Cys Lys Lys Lys Lys Lys Lys Lys Lys Cys Gly Gly
1 5 10

<210> 89
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (4)..(13)

<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (4)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 89
Gly Gly Cys Lys Lys Lys Lys Lys Lys Lys Lys Lys Cys Gly Gly
1 5 10 15

<210> 90
<211> 12
<212> PRT
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<220>
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peptide"

<400> 90
Gly Gly Cys His Phe Asp Ile Met Asn Cys Gly Gly
1 5 10

<210> 91
<211> 12
<212> PRT
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<220>
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peptide"

<400> 91
Gly Gly Cys Val Ile Asp Phe Phe Gly Cys Gly Gly
1 5 10

<210> 92
<211> 12
<212> PRT
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<220>
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peptide"

<400> 92
Gly Gly Cys Asp Ile Met Ile Phe Glu Cys Gly Gly
1 5 10

<210> 93
<211> 12
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 93
Gly Gly Cys Met Thr Glu Phe Ala Ile Cys Gly Gly
1 5 10

<210> 94
<211> 12
<212> PRT
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<220>
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<400> 94
Gly Gly Cys Ile Gln Tyr Trp Gln Phe Cys Gly Gly
1 5 10

<210> 95
<211> 12
<212> PRT
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<220>
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<400> 95
Gly Gly Cys Pro Phe Ser Trp Ala Phe Cys Gly Gly
1 5 10

<210> 96
<211> 12
<212> PRT
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<220>
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<400> 96
Gly Gly Cys Gly Phe Ala Phe Met Tyr Cys Gly Gly
1 5 10

<210> 97
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 97
Gly Gly Cys Pro Val Leu Leu Phe Asn Cys Gly Gly
1 5 10

<210> 98
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 98
Gly Gly Cys Pro Phe Thr Trp Thr Lys Cys Gly Gly
1   5   10

<210> 99
<211> 12
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<220>
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<400> 99
Gly Gly Cys Tyr Leu Tyr Trp Gln Phe Cys Gly Gly
1   5   10

<210> 100
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 100
Gly Gly Cys Val Ile Asn Met Phe Pro Cys Gly Gly
1   5   10

<210> 101
<211> 12
<212> PRT
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<220>
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<400> 101
Gly Gly Cys Pro Phe Thr Trp Asn Thr Cys Gly Gly
1   5   10

<210> 102
<211> 12
<212> PRT
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<220>
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peptide"

<400> 102
Gly Gly Cys Pro Phe Gln Ile Gly Glu Cys Gly Gly
1 5 10

<210> 103
<211> 12
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<220>
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<400> 103
Gly Gly Cys Leu Asp Ile Ile Trp Met Cys Gly Gly
1 5 10

<210> 104
<211> 12
<212> PRT
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<220>
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<400> 104
Gly Gly Cys Met Phe Val Phe Pro Ala Cys Gly Gly
1 5 10

<210> 105
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<220>
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<400> 105
Gly Gly Cys Val Met Glu Gln Leu Trp Cys Gly Gly
1 5 10

<210> 106
<211> 12
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<400> 106
Gly Gly Cys Phe Lys Glu Tyr Thr Trp Cys Gly Gly
1 5 10

<210> 107

<211> 12
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<220>
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<400> 107
Gly Gly Cys Pro Lys Asp Tyr His Ile Cys Gly Gly
1 5 10

<210> 108
<211> 12
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<400> 108
Gly Gly Cys Glu Val Met Val Phe Pro Cys Gly Gly
1 5 10

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Gly Gly Cys Val Phe Asn Thr Val Phe Cys Gly Gly
1 5 10

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<211> 12
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<220>
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Gly Gly Cys Asn Leu Pro Gln Glu Trp Cys Gly Gly
1 5 10

<210> 111
<211> 12
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Gly Gly Cys Met Ile Ala Pro Met Tyr Cys Gly Gly
1 5 10

<210> 112
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<220>
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<400> 112
Gly Gly Cys Met Met Leu Tyr Pro Met Cys Gly Gly
1 5 10

<210> 113
<211> 12
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<220>
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<400> 113
Gly Gly Cys Ile Ile Gly Pro Phe Leu Cys Gly Gly
1 5 10

<210> 114
<211> 12
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<220>
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<400> 114
Gly Gly Cys Thr Gly Met Val Phe Phe Cys Gly Gly
1 5 10

<210> 115
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<220>
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<400> 115
Gly Gly Cys Leu Met Tyr Lys Asn Val Cys Gly Gly
1 5 10

<210> 116
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<212> PRT
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<220>
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<400> 116
Gly Gly Cys Ala Phe Gly Ile Met Trp Cys Gly Gly
1 5 10

<210> 117
<211> 12
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<400> 117
Gly Gly Cys Arg His Arg Lys Lys Trp Cys Gly Gly
1 5 10

<210> 118
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<400> 118
Gly Gly Cys Phe Met Gly Ile Trp Gln Cys Gly Gly
1 5 10

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<400> 119
Gly Gly Cys Pro Ser Leu Pro Gln Phe Cys Gly Gly
1 5 10

<210> 120
<211> 12
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<400> 120
Gly Gly Cys Pro Ser Val Phe Thr Trp Cys Gly Gly
1 5 10

<210> 121
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<212> PRT
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<220>
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<400> 121
Gly Gly Cys Gln Glu Tyr Trp Glu Phe Cys Gly Gly
1 5 10

<210> 122
<211> 12
<212> PRT
<213> Artificial Sequence

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<400> 122
Gly Gly Cys Gln Trp Pro Thr Glu Phe Cys Gly Gly
1 5 10

<210> 123
<211> 12
<212> PRT
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<400> 123
Gly Gly Cys Ile Lys Phe Phe Asp Trp Cys Gly Gly
1 5 10

<210> 124
<211> 12
<212> PRT
<213> Artificial Sequence

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

<400> 124
Gly Gly Cys Glu Met Ser Phe Phe Leu Cys Gly Gly
1 5 10

<210> 125
<211> 12
<212> PRT

<213> Artificial Sequence

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

<400> 125
Gly Gly Cys His Ser Glu Val Glu Tyr Cys Gly Gly
1 5 10

<210> 126
<211> 12
<212> PRT
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<400> 126
Gly Gly Cys Trp Glu His Pro His Tyr Cys Gly Gly
1 5 10

<210> 127
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 127
Gly Gly Cys Glu Thr Tyr Trp Leu Phe Cys Gly Gly
1 5 10

<210> 128
<211> 12
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<400> 128
Gly Gly Cys Arg Val Pro Tyr Pro Ser Cys Gly Gly
1 5 10

<210> 129
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<400> 129

Gly Gly Cys Gly Trp Pro Phe Val Met Cys Gly Gly
1   5   10

<210> 130
<211> 12
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<400> 130
Gly Gly Cys Met Leu Phe Leu Glu Ser Cys Gly Gly
1   5   10

<210> 131
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<400> 131
Gly Gly Cys Phe His Val Lys Arg Trp Cys Gly Gly
1   5   10

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<400> 132
Gly Gly Cys Val Trp Glu Gln Glu His Cys Gly Gly
1   5   10

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      peptide"

<400> 133
Gly Gly Cys Ile Leu His Phe Lys Asp Cys Gly
1   5   10

<210> 134
<211> 12
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<400> 134
Gly Gly Cys His Phe Glu Val Phe Gln Cys Gly Gly
1 5 10

<210> 135
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<400> 135
Gly Gly Cys Val Phe Glu Val Met Gln Cys Gly Gly
1 5 10

<210> 136
<211> 12
<212> PRT
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<400> 136
Gly Gly Cys Met Thr Glu Phe Ser Trp Cys Gly Gly
1 5 10

<210> 137
<211> 12
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<400> 137
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1 5 10

<210> 138
<211> 12
<212> PRT
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<400> 138
Gly Gly Cys Lys Gly His Met Trp Tyr Cys Gly Gly

1 5 10

<210> 139
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 139
Gly Gly Cys Glu Ala Tyr Trp Gln Phe Cys Gly Gly
1 5 10

<210> 140
<211> 12
<212> PRT
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Gly Gly Cys Val Phe Ser Arg Phe Trp Cys Gly Gly
1 5 10

<210> 141
<211> 12
<212> PRT
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<400> 141
Gly Gly Cys Met Met Pro Phe Trp Pro Cys Gly Gly
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<400> 522
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<210> 523
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<220>
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<210> 524
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<210> 525

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<210> 527
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substitutions and preferred embodiments"

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substitutions and preferred embodiments"

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substitutions and preferred embodiments"

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gtggtcagcg tcctcaccgg tggttgtaaa aaaaaaaaaa aaaaatgtgg tggtcaccag 60

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substitutions and preferred embodiments"

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substitutions and preferred embodiments"

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gtggagtggg agagcaatgg tggttgtaaa aaaaaaaaaa aaaaatgtgg tggtgggcag 60

ccggagaaca ac 72

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<211> 18
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<213> Artificial Sequence

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gttcctttct attctcac 18

<210> 535

<211> 18
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substitutions and preferred embodiments"

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ggtaccaacc aggtcagcct gacc 84

<210> 537
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aac 63

<210> 544
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<210> 545
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primer"

<400> 545
gagtgggaga gcaatggtgg ttgtgttttc aacatgttca actgtggtgg tgggcagccg 60

gagaac 66

<210> 546
<211> 66
<212> DNA
<213> Artificial Sequence

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

<400> 546
gttctccggc tgcccaccac cacagttgaa catgttgaaa acacaaccac cattgctctc 60

ccactc 66

<210> 547
<211> 66
<212> DNA
<213> Artificial Sequence

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

<400> 547
gagtgggaga gcaatggtgg ttgtgctctg tacccgacta actgtggtgg tgggcagccg 60

gagaac 66

<210> 548
<211> 66
<212> DNA
<213> Artificial Sequence

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

<400> 548
gttctccggc tgcccaccac cacagttagt cgggtacaga gcacaaccac cattgctctc 60

ccactc 66

<210> 549
<211> 6
<212> PRT
<213> Homo sapiens

<400> 549
Leu Met Ile Ser Arg Thr
1 5

<210> 550
<211> 8

<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (2)..(7)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (2)..(7)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 550
Leu Lys Lys Lys Lys Lys Lys Thr
1 5

<210> 551
<211> 8
<212> PRT
<213> Homo sapiens

<400> 551
Thr Val Leu His Gln Asp Trp Leu
1 5

<210> 552
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<220>
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<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (2)..(7)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 552
Thr Lys Lys Lys Lys Lys Lys His Gln Asp Trp Leu
1 5 10

<210> 553
<211> 18
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (5)..(10)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (5)..(10)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 553
Thr Gly Gly Cys Lys Lys Lys Lys Lys Lys Cys Gly Gly His Gln Asp
1 5 10 15

Trp Leu

<210> 554
<211> 9
<212> PRT
<213> Homo sapiens

<400> 554
Met His Glu Ala Leu His Asn His Tyr
1 5

<210> 555
<211> 11
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (3)..(7)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (3)..(7)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<220>
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<222> (9)..(9)
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or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (9)..(9)
<223> /note="Residue given in the sequence has no preference
with respect to the annotations for said position"

<400> 555
Met His Lys Lys Lys Lys Lys His Lys His Tyr
1 5 10

<210> 556
<211> 5
<212> PRT
<213> Homo sapiens

<400> 556
Glu Val His Asn Ala
1 5

<210> 557
<211> 17
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (8)..(13)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr"
or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or
"Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu"
or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (8)..(13)
<223> /note="Residues given in the sequence have no preference
with respect to those in the annotations for said positions"

<400> 557
Glu Val His Asn Gly Gly Cys Lys Lys Lys Lys Lys Lys Cys Gly Gly
1 5 10 15

Ala

<210> 558
<211> 6
<212> PRT
<213> Homo sapiens

<400> 558
Asn Gly Gln Pro Glu Asn
1 5

<210> 559
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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<220>
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<222> (5)..(10)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (5)..(10)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 559
Asn Gly Gly Cys Lys Lys Lys Lys Lys Lys Cys Gly Gly Gly Gln Pro
1 5 10 15

Glu Asn

<210> 560
<211> 7
<212> PRT
<213> Homo sapiens

<400> 560
Asp Glu Leu Thr Lys Asn Gln
1 5

<210> 561
<211> 21
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (7)..(14)
<223> Any amino acid

<400> 561
Asp Glu Leu Gly Gly Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly

1 5 10 15

Gly Thr Lys Asn Gln
20

<210> 562
<211> 21
<212> PRT
<213> Artificial Sequence

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

<220>
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<222> (7)..(14)
<223> /replace="Phe" or "Asn" or "Arg" or "Ser" or "Thr" or "Met" or "Ile" or "Glu" or "Asp" or "Gly" or "Ala" or "Val" or "Gln" or "His" or "Pro" or "Leu" or "Tyr" or "Trp"

<220>
<221> misc_feature
<222> (7)..(14)
<223> /note="Residues given in the sequence have no preference with respect to those in the annotations for said positions"

<400> 562
Asp Glu Leu Gly Gly Cys Lys Lys Lys Lys Lys Lys Lys Lys Cys Gly
1 5 10 15

Gly Thr Lys Asn Gln
20

<210> 563
<211> 13
<212> PRT
<213> Homo sapiens

<400> 563
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
1 5 10

<210> 564
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 564
Trp Glu Ser Asn Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly Gly
1 5 10 15

Gly Gln Pro Glu Asn Asn Tyr Lys Thr
20 25

<210> 565
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 565
Trp Glu Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly Gly Ser Asn
1 5 10 15

Gly Gln Pro Glu Asn Asn Tyr Lys Thr
20 25

<210> 566
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 566
Trp Glu Ser Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly Gly Asn
1 5 10 15

Gly Gln Pro Glu Asn Asn Tyr Lys Thr
20 25

<210> 567
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 567
Trp Glu Ser Asn Gly Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly
1 5 10 15

Gly Gln Pro Glu Asn Asn Tyr Lys Thr
20 25

<210> 568
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 568
Trp Glu Ser Asn Gly Gln Gly Gly Cys Gly Met Pro Ile Glu Phe Cys
1 5 10 15

Gly Gly Pro Glu Asn Asn Tyr Lys Thr
20 25

<210> 569
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 569
Trp Glu Ser Asn Gly Gln Pro Gly Gly Cys Gly Met Pro Ile Glu Phe
1 5 10 15

Cys Gly Gly Glu Asn Asn Tyr Lys Thr
20 25

<210> 570
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 570
Trp Glu Ser Asn Gly Gln Pro Glu Gly Gly Cys Gly Met Pro Ile Glu
1 5 10 15

Phe Cys Gly Gly Asn Asn Tyr Lys Thr
20 25

<210> 571
<211> 25
<212> PRT
<213> Artificial Sequence

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

<400> 571
Trp Glu Ser Asn Gly Gln Pro Glu Asn Gly Gly Cys Gly Met Pro Ile
1 5 10 15

Glu Phe Cys Gly Gly Asn Tyr Lys Thr
20 25

<210> 572

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

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

<400> 572
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Gly Gly Cys Gly Met Pro
1   5   10   15

Ile Glu Phe Cys Gly Gly Tyr Lys Thr
            20   25

<210> 573
<211> 22
<212> PRT
<213> Artificial Sequence

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

<400> 573
Trp Glu Ser Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly Gly Pro
1   5   10   15

Glu Asn Asn Tyr Lys Thr
            20

<210> 574
<211> 24
<212> PRT
<213> Artificial Sequence

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

<400> 574
Trp Glu Ser Gly Gly Gly Cys Gly Met Pro Ile Glu Phe Cys Gly Gly
1   5   10   15

Gly Pro Glu Asn Asn Tyr Lys Thr
            20

<210> 575
<211> 9
<212> PRT
<213> Artificial Sequence

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

<400> 575
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1 5