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<110> Affinity Biosciences Pty Ltd
Matthew, Beasley

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<130> 512188

<160> 125

<170> PatentIn version 3.5

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Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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35 40 45

Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
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 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
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Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
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Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
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Thr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
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Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
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Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
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Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
 Page 9

65

70

75

80

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Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
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 <223> HVK2 F

<400> 33
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 cagaagccag gccagtcccc tgtgctggtc atctatcaag atagcaagcg gccctcaggg 180
 atccctgagc gattctctgg ctccaactct gggaacacag ccactctgac catcagcggg 240
 acccaggcta tggatgaggc tgactattac tgtcaggcgt gggacnntnn tnntggaggt 300
 nntnntnnta ctgtggtgtt cggcacgggc accaagctca tcatttcgtc tcagaccggt 360
 ggttctggtg gtggtggttc tggcggcggc ggctccggtg gtggtggatc cgaagtccaa 420

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 gcatccggtt ttactttcag cagctacgcg atgtcgtggg tgcgccaggc accgggcaag 540
 ggctctggagt gggtcagcgc catcagcggg agcggcggtt ctacgtatta tgcggacagc 600
 gtcaagggcc gtttcacat cagccgtgac aattccaaaa acaccctgta cttgcagatg 660
 aacagcttgc gtgcggaaga tacggctgtt tactactgtg cgaaanntnn tnntggannt 720
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 20 25 30

Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
 35 40 45

Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
 50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
 65 70 75 80

Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Xaa
 85 90 95

Xaa Xaa Gly Gly Xaa Xaa Xaa Thr Val Val Phe Gly Thr Gly Thr Lys
 100 105 110

pctau2012000970-seq1.txt

Val Thr Val Ser Ser Gln Thr Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser
130 135 140

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
145 150 155 160

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
165 170 175

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
180 185 190

Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
195 200 205

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Xaa Xaa Xaa Gly Xaa
225 230 235 240

Xaa Xaa Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
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 cagaagccag gccagtcccc tgtgctggtc atctatcaag atagcaagcg gccctcaggg 180
 atcccctgagc gattctctgg ctccaactct gggaacacag ccactctgac catcagcggg 240
 acccaggcta tggatgaggc tgactattac tgtcaggcgt gggactgaga cctagacggt 300
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 tttactttca gcagctacgc gatgtcgtgg gtgcgccagg caccgggcaa gggcctggag 240
 tgggtcagcg ccatcagcgg tagcggcggt tctacgtatt atgcggacag cgtcaagggc 300
 cgtttcacca tcagccgtga caattccaaa aacaccctgt acttgcagat gaacagcttg 360
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gtatcttc 68

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Pro Pro His Gly Ala Pro Ala
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Phe Asn Phe Gly Asn Ala Tyr
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Ile Asn Ser Gly Gly Ala Ser Phe
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Thr Ala Ala Gly Val Pro Phe
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Phe Ser Thr Gly Gly Cys Ala Phe
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Ala Ile Cys Gly Ala Thr Ala
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Pro Tyr Arg Gly Ser Phe Phe
 1 5

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Ile Ile Pro Gly Gly Leu Tyr Ala
 1 5

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Pro Val Ile Gly Ser Asn Thr
 1 5

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 20 25 30

Asn Pro Tyr Glu Gly Thr Gln Ile Leu Asp Leu Asn Val Thr Glu Gly
 35 40 45

Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Val Phe Gln Tyr
 50 55 60

Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Gln Asp Tyr Phe
 65 70 75 80

Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Met Thr Tyr
 85 90 95

Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile Ser Met Arg Gly
 100 105 110

Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Thr Asn Phe Pro Pro
 115 120 125

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

Glu Lys Met Tyr Val Glu Asp Gly Val Leu Lys Gly Asp Val Asn Met
 145 150 155 160

Arg Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Lys Thr
 165 170 175

Thr Tyr Lys Ala Lys Lys Glu Val Arg Leu Pro Asp Ala His Lys Ile
 180 185 190

Asp His Arg Ile Glu Ile Leu Lys His Asp Lys Asp Tyr Asn Lys Val
 195 200 205

Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met Leu Pro Ser Gln
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Ala Lys Ser Gly Gly Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu
 225 230 235 240

Trp His Glu Asp Thr Gly Gly Ser His His His His His
 245 250

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 20 25 30

Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
 35 40 45

Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
 50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
 65 70 75 80

Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Phe
 85 90 95

Asn Leu Gly Gly Cys Gly Asp Thr Val Val Phe Gly Thr Gly Thr Lys
 100 105 110

Val Thr Val Ser Ser Gln Thr Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser
 130 135 140

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 145 150 155 160

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
 165 170 175

Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
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185

190

Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 195 200 205

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 210 215 220

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Ile Asp Gly Pro
 225 230 235 240

Val Ala Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
 245 250 255

Ser Ser Ser Gln Thr Ser Ile Leu Val Ala
 260 265

<210> 112
 <211> 1176
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 112
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 gacacctcca gccgtaagct ggttgctggtg gatggcacca cgcacgggtgc tgccgttggc 180
 attcttgctg ttgctgctga ccagaccagc accacgctga cgttctacaa gtccggcacg 240
 ttccgttatg aggatgtgct ctggccggag gctgccagcg acgagacgaa aaaacggacc 300
 gcgtttgccg gaacggcaat cagcatcggt ggaggtagcg gcggatcgga tgacgacgat 360
 aagtctagaa atggcggaga cggtcagtct gtgctgactc agccaccctc agtgtccgtg 420
 tccccaggac agacagccag catcacctgc tctggagata aattggggga taaatatgct 480
 tgctggtatc agcagaagcc aggccagtcc cctgtgctgg tcatctatca agatagcaag 540
 cggccctcag ggatccctga gcgattctct ggctccaact ctgggaacac agccactctg 600
 accatcagcg ggaccaggc tatggatgag gctgactatt actgtcaggc gtgggacttt 660
 aatcttggcg gatgtggtga tactgtggtg ttcggcaccg gtacgaaagt gactgtctca 720
 tctcagaccg gtggttctgg tggcgggtgg tctggcggcg gcggctccgg tgggtggtga 780
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 gcaccgggca agggcctgga gtgggtcagc gccatcagcg gtagcggcgg ttctacgtat 960
 tatgcggaca gcgtcaaggg ccgtttcacc atcagccgtg acaattccaa aaacaccctg 1020
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aactcgagcg attacaagga cgatgatgac aaataa 1176

<210> 113
 <211> 391
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion protein

<400> 113

Met Thr Ser Lys Glu Thr Phe Thr His Tyr Gln Pro Gln Gly Asn Ser
 1 5 10 15

Asp Pro Ala His Thr Ala Thr Ala Pro Gly Gly Leu Ser Ala Lys Ala
 20 25 30

Pro Ala Met Thr Pro Leu Met Leu Asp Thr Ser Ser Arg Lys Leu Val
 35 40 45

Ala Trp Asp Gly Thr Thr Asp Gly Ala Ala Val Gly Ile Leu Ala Val
 50 55 60

Ala Ala Asp Gln Thr Ser Thr Thr Leu Thr Phe Tyr Lys Ser Gly Thr
 65 70 75 80

Phe Arg Tyr Glu Asp Val Leu Trp Pro Glu Ala Ala Ser Asp Glu Thr
 85 90 95

Lys Lys Arg Thr Ala Phe Ala Gly Thr Ala Ile Ser Ile Val Gly Gly
 100 105 110

Ser Gly Gly Ser Asp Asp Asp Asp Lys Ser Arg Asn Gly Gly Asp Gly
 115 120 125

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 130 135 140

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

Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
 165 170 175

Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 180 185 190

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
 195 200 205

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Phe Asn Leu Gly Gly

210

215

220

Cys Gly Asp Thr Val Val Phe Gly Thr Gly Thr Lys Val Thr Val Ser
 225 230 235 240

Ser Gln Thr Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 260 265 270

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 275 280 285

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 290 295 300

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
 305 310 315 320

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 325 330 335

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 340 345 350

Ala Val Tyr Tyr Cys Ala Lys His Ile Asp Gly Pro Val Ala Ala Phe
 355 360 365

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Asn Ser Ser Asp
 370 375 380

Tyr Lys Asp Asp Asp Asp Lys
 385 390

<210> 114
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 114

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
 20 25 30

Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
 35 40 45

Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
85

<210> 115
<211> 93
<212> PRT
<213> Homo sapiens
<400> 115

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val
1 5 10 15

Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly
20 25 30

Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
35 40 45

Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
65 70 75 80

Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
85 90

<210> 116
<211> 93
<212> PRT
<213> Homo sapiens
<400> 116

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val
1 5 10 15

Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly
20 25 30

Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
35 40 45

Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
65 70 75 80

Thr Gln Ala Met Asp Glu Ala His Tyr Tyr Cys Gln Thr
 85 90

<210> 117
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 117

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val
 1 5 10 15

Ser Pro Gly Gln Thr Ala Thr Ile Thr Cys Ser Gly Asp Lys Leu Gly
 20 25 30

Asp Lys Phe Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
 35 40 45

Leu Val Ile Tyr Gln Asp Tyr Gln Arg Pro Ser Gly Ile Pro Glu Arg
 50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
 65 70 75 80

Thr Gln Val Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala
 85 90

<210> 118
 <211> 87
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (41)..(41)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (61)..(61)
 <223> Xaa can be any naturally occurring amino acid

<400> 118

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

Ala Pro Glu Lys Thr Ala Thr Ile Ala Cys Gly Gly Asn Arg Ile Gly
 20 25 30

Ser Lys Ser Val His Trp Tyr Gln Xaa Lys Pro Gly Gln Ala Pro Val
 35 40 45

Leu Val Ile Tyr Asn Asp Asn Asp Arg Pro Ser Gly Xaa Pro Glu Arg
 50 55 60

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Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg
65 70 75 80

Val Glu Val Gly Asp Glu Ala
85

<210> 119
<211> 87
<212> PRT
<213> Homo sapiens
<400> 119

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val
1 5 10 15

Ala Pro Gly Lys Thr Ala Thr Ile Ala Cys Gly Gly Asn Arg Ile Gly
20 25 30

Ser Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val
35 40 45

Leu Val Ile Tyr Asn Asp Asn Asp Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg
65 70 75 80

Val Glu Val Gly Asp Glu Ala
85

<210> 120
<211> 83
<212> PRT
<213> Homo sapiens
<400> 120

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Tyr Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala

<210> 121
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 121

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val
 1 5 10 15

Ala Pro Gly Lys Thr Ala Thr Ile Thr Cys Gly Gly Asn Asn Ile Glu
 20 25 30

Asp Lys Ser Val His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val
 35 40 45

Leu Val Ile Tyr Tyr Asp Thr Asp Arg Pro Ser Gly Ile Pro Glu Arg
 50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Arg
 65 70 75 80

Val Glu Ala Gly Asp Glu Ala
 85

<210> 122
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 122

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 1 5 10 15

Thr Val Thr Ile Ser Cys Thr Gly Ser Ser Gly Ser Ile Ala Ser Asn
 20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
 35 40 45

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

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
 65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp
 85 90 95

<210> 123
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 123

Met Gly Asp Gly Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu
 1 5 10 15

Ser Pro Gly Lys Thr Val Thr Ile Pro Cys Thr Gly Ser Ser Gly Ser
 20 25 30

Ile Ala Ser Asn Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala
 35 40 45

Pro Thr Thr Val Ile Tyr Glu Asp Lys Gln Lys Pro Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu
 65 70 75 80

Thr Ile Ser Gly Leu Lys Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
 85 90 95

Ser Tyr Asp

<210> 124

<211> 99

<212> PRT

<213> Homo sapiens

<400> 124

Met Gly Asp Gly Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu
 1 5 10 15

Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Thr Gly Ser Ser Gly Ser
 20 25 30

Ile Ala Ser Asn Ser Val Gln Arg Tyr Gln Gln Arg Pro Gly Ser Ala
 35 40 45

Pro Thr Thr Val Ile Tyr Glu Asp Asn Arg Arg Pro Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu
 65 70 75 80

Ile Ile Ser Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
 85 90 95

Ser Tyr Asp

<210> 125

<211> 99

<212> PRT

<213> Homo sapiens

<400> 125

Met Gly Asp Gly Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu
1 5 10 15

Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Thr Gly Arg Ser Gly Ser
20 25 30

Ile Ala Asp Asn Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Val
35 40 45

Pro Thr Ser Val Ile Phe Glu Asp Asn Gln Arg Pro Ser Gly Val Pro
50 55 60

Glu Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu
65 70 75 80

Thr Ile Ser Gly Leu Met Thr Glu Asp Glu Ala Asp Tyr His Cys Gln
85 90 95

Ser Tyr Asp