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<110> R-Pharm Overseas, Inc.

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<170> PatentIn version 3.5

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Ser Ile Thr Ile Ser Cys
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Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Lys Tyr Ala Gln Arg Phe
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Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr Thr Ala Tyr
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Met Glu Leu Ser Ser Leu Ile Ser Asp Asp Thr Ala Leu Tyr Tyr Cys
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Gly Thr Leu Val Thr Val Ser Ser
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Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro Arg
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20                  25                  30

Ser Ala Ser Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35                  40                  45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asp Asp Tyr Ala
    50                  55                  60

Val Ser Val Lys Gly Arg Ile Ser Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95

Tyr Tyr Cys Ala Arg Ser Gln Gly Arg Tyr Phe Val Asn Tyr Gly Met
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Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30


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


Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Arg
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Gly Ile Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
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            20                  25                  30


Lys Ala Ala Trp Tyr Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35                  40                  45


Trp Leu Gly Arg Thr Tyr Phe Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50                  55                  60


Asp Ser Val Lys Ser Arg Leu Thr Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80


Gln Phe Ser Leu Gln Leu Lys Ser Val Ser Pro Glu Asp Thr Ala Val
                85                  90                  95


Tyr Tyr Cys Ala Arg Gly Gln Tyr Thr Ala Phe Asp Ile Trp Gly Gln
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Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asn Val Gly Gly Tyr
            20                  25                  30


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


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


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


Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Arg
                85                  90                  95


Arg Leu His Gly Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
            100                 105                 110


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


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


Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Lys Tyr Ala Gln Arg Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr Thr Ala Tyr
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65 70 75 80

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

Thr Thr Ser Arg Gly Phe Ser Tyr Gly Trp Phe Asp Tyr Trp Gly Gln
100 105 110

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

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asp Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Ser Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Ser Gln Gly Arg Tyr Phe Val Asn Tyr Gly Met
100 105 110

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

Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Arg
                85                  90                  95

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

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

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Arg
                85                  90                  95

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gcacagaggt tccagggcag ggtcacgatt accgcggacg aatcgacgac cacagcctac 240

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cagttctccc tgcagctgaa ctctgtgact cccgaggaca cggctgtgta ttactgtgca 300

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aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240

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gggaaagccc ctaagctcct ggtctatggt gcatccagtt tgcaaagtgg ggtcccatca 180

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20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

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His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                325                 330
```

<210> 69
<211> 996
<212> DNA
<213> IgG1

<400> 69

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gccagcacta aggggccctc tgtgtttcca ctcgcccctt ctagcaaaag cacttccgga       60

ggcactgcag cactcgggtg tctggtcaaa gattatttcc ctgagccagt caccgtgagc      120

tggaactctg gcgccctcac ctccggggtt cacacctttc cagccgtcct gcagtcctcc      180

ggcctgtact ccctgagcag cgtcgttacc gtgccatcct cttctctggg gacccagaca      240

tacatctgca atgtcaacca taagcctagc aacaccaagg tggacaaaaa ggtcgagcca      300

aagagctgcg ataagacaca cacctgccct ccatgccccg cacctgaact cctgggcggg      360

ccttccgttt tcctgtttcc tcccaagccc aaggatacac tgatgattag ccgcaccccc      420

gaagtcactt gcgtggtggt ggatgtgagc catgaagatc cagaagttaa gtttaactgg      480

tatgtggacg gggtcgaggt gcacaatgct aaaacaaagc ccagggagga gcaatataac      540

tccacataca gagtggtgtc cgttctgaca gtcctgcacc aggactggct gaacgggaag      600

gaatacaagt gcaaggtgtc taataaggca ctgccagccc ccatagagaa gacaatctct      660
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aaagctaaag gccaaccacg cgagcctcag gtctacacac tgccaccatc cagggacgaa 720

ctgaccaaga atcaggtgag cctgacttgt ctcgtcaaag gattctaccc aagcgacatc 780

gccgtggagt gggaatccaa cggccaacca gagaacaact acaagaccac cccaccagtc 840

ctggactctg atgggagctt tttcctgtat tccaagctga cagtggacaa gtctcggtgg 900

caacagggca acgtgttcag ctgctccgtg atgcatgaag ccctgcataa ccactatacc 960

cagaaaagcc tcagcctgtc ccccgggaaa taatga 996

<210> 70
<211> 107
<212> PRT
<213> Kappa

<400> 70

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 71
<211> 321
<212> DNA
<213> Kappa

<400> 71
cgtacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60

ggtaccgcta gcgttgtgtg cctgctgaat aacttttatc cacgggaggc taaggtgcag 120

tggaaagtgg acaatgccct ccagagcgga aatagccaag agtccgttac cgaacaggac 180

tctaaagact ctacatactc cctgtcctcc acactgaccc tctccaaggc cgactatgag 240

aaacacaagg tttacgcatg cgaggtcaca caccagggac tctcctctcc cgtgaccaag 300

agcttcaacc ggggagaatg c 321

<210> 72
<211> 106
<212> PRT
<213> lamda

<400> 72

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

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Val Ser Asp
20 25 30

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

Val Lys Val Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg Ser Tyr Ser Cys Arg Val Thr His Glu Gly Ser Thr Val
85 90 95

Glu Lys Thr Val Ala Pro Ala Glu Cys Ser
100 105

<210> 73
<211> 318
<212> DNA
<213> lamda

<400> 73
ggtcagccca aggctgcccc ctcggtcact ctgttcccac cctcctctga ggagcttcaa 60

gccaacaagg ccacactggt gtgtctcgta agtgacttct acccgggagc cgtgacagtg 120

gcctggaagg cagatggcag ccccgtcaag gtgggagtgg agaccaccaa accctccaaa 180

caaagcaaca acaagtatgc ggccagcagc tacctgagcc tgacgcccga gcagtggaag 240

tcccacagaa gctacagctg ccgggtcacg catgaaggga gcaccgtgga gaagacagtg 300

gcccctgcag aatgctct 318

<210> 74
<211> 37
<212> DNA
<213> Synthetic

<400> 74
gcgcaagctt gccaccatga tcttcctcct gctaatg 37

<210> 75
<211> 31
<212> DNA
<213> Synthetic

<400> 75
gccgaattcg atagcactgt tcacttccct c 31

<210> 76
<211> 37
<212> DNA
<213> Synthetic

<400> 76
gcgcaagctt gccaccatgc tgcgtcggcg gggcagc 37

<210> 77
<211> 34
<212> DNA
<213> Synthetic

<400> 77
gcgcgaattc ggctatttct tgtccatcat cttc 34

<210> 78
<211> 21
<212> DNA
<213> Synthetic

<400> 78
gtacgagcta aaagtacagt g 21

<210> 79
<211> 20
<212> DNA
<213> Synthetic

<400> 79
tagataccca tacgacgttc 20

<210> 80
<211> 24
<212> DNA
<213> Synthetic

<400> 80
tctggtggtg gtggttctgc tagc 24

<210> 81
<211> 59
<212> DNA
<213> Synthetic

<400> 81
gccagatctc gagctattac aagtcttctt cagaaataag cttttgttct agaattccg 59

<210> 82
<211> 20
<212> DNA
<213> Synthetic

<400> 82
taatacgact cactataggg 20

<210> 83
<211> 24
<212> DNA
<213> Synthetic

<400> 83
ggcagcccca taaacacaca gtat 24

<210> 84
<211> 60
<212> PRT
<213> Synthetic

<400> 84

Ala Thr Gly Gly Ala Gly Ala Cys Ala Gly Ala Cys Ala Cys Ala Cys
1 5 10 15

Thr Cys Cys Thr Gly Cys Thr Ala Thr Gly Gly Gly Thr Ala Cys Thr
20 25 30

Gly Cys Thr Gly Cys Thr Cys Thr Gly Gly Gly Thr Thr Cys Cys Ala
35 40 45

Gly Gly Thr Thr Cys Cys Ala Cys Cys Gly Gly Thr
50 55 60

<210> 85
<211> 450
<212> PRT
<213> Homo sapiens

<400> 85

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Lys Tyr Ala Gln Arg Phe
50 55 60

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Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80

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

Thr Thr Ser Arg Gly Phe Asn Tyr Gly Trp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                245                 250                 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg
    290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320
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Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                325                 330                 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            340                 345                 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
        355                 360                 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    370                 375                 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385                 390                 395                 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
                405                 410                 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            420                 425                 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly Lys
    450
```

<210> 86
<211> 1353
<212> DNA
<213> Homo sapiens

<400> 86
caggtccagc ttgtgcagtc tggagctgag gtgaagaagc ctgcgtcctc ggtcaaagtc 60

tcctgcacgg cttctggcgg ctccttcagc acctatgcta tcagttgggt gcgacaggct 120

cctggacaag ggcttgaatg gatgggcggg atcatcccca tctttggtac aactaagtac 180

gcacagaggt tccagggcag ggtcacgatt accgcggacg aatcgacgac cacagcctac 240

atggagctga gcagcctgat atctgacgac acggccctgt attattgtac gacgtctcgt 300

ggattcaact atggctggtt tgactactgg ggccagggta ccctggtcac cgtctcctca 360

gccagcacta aggggccctc tgtgtttcca ctcgcccctt ctagcaaaag cacttccgga 420

ggcactgcag cactcgggtg tctggtcaaa gattatttcc ctgagccagt caccgtgagc 480

tggaactctg gcgccctcac ctccggggtt cacacctttc cagccgtcct gcagtcctcc 540

ggcctgtact ccctgagcag cgtcgttacc gtgccatcct cttctctggg gacccagaca 600

tacatctgca atgtcaacca taagcctagc aacaccaagg tggacaaaaa ggtcgagcca 660

aagagctgcg ataagacaca cacctgccct ccatgccccg cacctgaact cctgggcggg 720

ccttccgttt tcctgtttcc tcccaagccc aaggatacac tgatgattag ccgcaccccc 780

gaagtcactt gcgtggtggt ggatgtgagc catgaagatc cagaagttaa gtttaactgg 840

tatgtggacg gggtcgaggt gcacaatgct aaaacaaagc ccagggagga gcaatatgcc 900

tccacataca gagtggtgtc cgttctgaca gtcctgcacc aggactggct gaacgggaag 960

gaatacaagt gcaaggtgtc taataaggca ctgccagccc ccatagagaa gacaatctct 1020

aaagctaaag gccaaccacg cgagcctcag gtctacacac tgccaccatc cagggaggaa 1080

atgaccaaga atcaggtgag cctgacttgt ctcgtcaaag gattctaccc aagcgacatc 1140

gccgtggagt gggaatccaa cggccaacca gagaacaact acaagaccac cccaccagtc 1200

ctggactctg atgggagctt tttcctgtat tccaagctga cagtggacaa gtctcggtgg 1260

caacagggca acgtgttcag ctgctccgtg atgcatgaag ccctgcataa ccactatacc 1320

cagaaaagcc tcagcctgtc ccccgggaaa taa 1353

<210> 87
<211> 214
<212> PRT
<213> Homo sapiens

<400> 87

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ile His
20 25 30

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

Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro Arg
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

```
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 88
<211> 642
<212> DNA
<213> Homo sapiens

<400> 88
gaaattgtaa tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgta gggccagtca gagtgttggc atacacttag cctggtatca acagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccagta gggccactgg catcccagac 180

aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240

gaagattttg cagtgtatta ctgtcagcag tatggttctt tacctcggac gttcggccaa 300

gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggtaccgct agcgttgtgt gcctgctgaa taacttttat 420

ccacgggagg ctaaggtgca gtggaaagtg gacaatgccc tccagagcgg aaatagccaa 480

gagtccgtta ccgaacagga ctctaaagac tctacatact ccctgtcctc cacactgacc 540

ctctccaagg ccgactatga gaaacacaag gtttacgcat gcgaggtcac acaccaggga 600

ctctcctctc ccgtgaccaa gagcttcaac cggggagaat gc 642