SEQUENCE LISTING

<110> DAIICHI SANYKO CO., LTD.

<120> Anti-FGFR2 Antibodies

<130> FP1320WO

<160> 113

<170> PatentIn version 3.5

<210> 1
<211> 12
<212> PRT
<213> Rattus norvegicus

<400> 1

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
1 5 10

<210> 2
<211> 13
<212> PRT
<213> Rattus norvegicus

<400> 2

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

<210> 3
<211> 5

<212> PRT
<213> Rattus norvegicus

<400> 3

Gln Val Lys Leu Leu
1 5

<210> 4
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 4

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

Glu

<210> 5
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 5

Gln Val Lys Leu Leu
1 5

<210> 6

<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 6

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

Glu

<210> 7
<211> 28
<212> PRT
<213> Artifitial Sequence

<400> 7

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

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

<210> 8
<211> 20
<212> DNA
<213> Artifitial Sequence

<400> 8
ggttctccca ctcagtaatc 20

<210> 9
<211> 20
<212> DNA
<213> Artifitial Sequence

<400> 9
catatgatca gtgtcctctc 20

<210> 10
<211> 20
<212> DNA
<213> Artifitial Sequence

<400> 10
atatgatcag tgtcctctcc 20

<210> 11
<211> 366
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(366)

<400> 11
gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtg cag cct gga agg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

tct ctg aaa cta tcc tgt gta gcc tct gga ttc aga ttc aat gac ttt 96

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe Asn Asp Phe
20 25 30

tgg atg acc tgg atc cgc cag gct cca ggg aag ggg ctg gag tgg gtt 144
Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gca tcc att act tat act ggt gat aac act tac tat gca ggc tct gtg 192
Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala Gly Ser Val
50 55 60

aag ggc cga atc act atc tcc aga gat aat gcg aag agc acc cta tac 240
Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr
65 70 75 80

ctg caa atg aac agt ctg agg tct gag gac acg gcc act tat tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

aca aga gat gac tac gga gga tat agc ccc tac tat atg gat gcc tgg 336
Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met Asp Ala Trp
100 105 110

ggt caa gga act tca gtc act gtc tcc tca 366
Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 12
<211> 122
<212> PRT
<213> Rattus norvegicus

<400> 12

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe Asn Asp Phe
20 25 30

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

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

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

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met Asp Ala Trp
100 105 110

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

<210> 13
<211> 354
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(354)

<400> 13

```
cag gtt aag ctg ctg cag tct ggg gct gag ctg gta aaa cct ggt gct        48
Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                  10                  15

tca gtg aag ttg tcc tgc aag act tct ggt ttt acc ttc agc act agc        96
Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
            20                  25                  30

tat atg agt tgg ttg aag cag gtg cct gga ccg agt att gag tgg att       144
Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile Glu Trp Ile
        35                  40                  45

gga tgg att tat gct gga gat ggt ggt act aag tat aat cag aag ttc       192
Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
    50                  55                  60

aag ggc aag gcc aca ctg aca gta gac aaa tct tct agc aca gca tac       240
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

atg gat ctc agc agc ctg aca tct gag gac gct gca gtc tat ttt tgt       288
Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Phe Cys
                85                  90                  95

gca acg gat ggt tat ggg gat tgg ttt gct tac tgg ggc caa ggc act       336
Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtc act gtc tct tca                                               354
Leu Val Thr Val Ser Ser
```

115

<210> 14
<211> 118
<212> PRT
<213> Rattus norvegicus

<400> 14

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

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
20 25 30

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

Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 15
<211> 354
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(354)

<400> 15
cag gtt aag ctg ctg cag tct ggg gct gag ctg gta aaa cct ggt gct 48
Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

tca gtg aag ttg tcc tgc aag act tct ggt ttt aca ttc agc act agt 96
Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
20 25 30

tat atg agt tgg ttg aag cag gtg cct gga ccg agt act gag tgg att 144
Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr Glu Trp Ile
35 40 45

gga tgg att tat gct gga gat ggt ggt act aag tat aat cag aag ttc 192
Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
50 55 60

aag ggc aag gcc aca ctg aca gta gac aaa ttt tct agc aca gca tac 240
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Phe Ser Ser Thr Ala Tyr
65 70 75 80

atg gat ctc agc agc ctg aca tct gag gac gct gca gtc tat ttc tgt 288
Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Phe Cys
85 90 95

gca acg gat ggt tat ggg gat tgg ttt act tac tgg ggc caa ggc act 336
Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly Gln Gly Thr
100 105 110

ctg gtc act gtc tct tca 354
Leu Val Thr Val Ser Ser
115

<210> 16
<211> 118
<212> PRT
<213> Rattus norvegicus

<400> 16

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

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe Ser Thr Ser
20 25 30

Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr Glu Trp Ile
35 40 45

Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 17
<211> 29
<212> DNA
<213> Artifitial Sequence

<400> 17
ttcatgaggc acacgactga ggcacctcc 29

<210> 18
<211> 20
<212> DNA
<213> Artifitial Sequence

<400> 18
tccagttgct aactgttccg 20

<210> 19

<211> 19
<212> DNA
<213> Artifitial Sequence

<400> 19
cagtggtatc aacgcagag 19

<210> 20
<211> 327
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(327)

<400> 20
gac atc cag atg acc cag tct cca tct tcc ctg tct gca ttt ctg gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Leu Gly
1 5 10 15

gac aga gtc act att act tgc cgg gca agt caa gac att gga aat tat 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Tyr
20 25 30

tta aga tgg ttc cag cag aaa ccg ggg aaa tct cct agg ctt atg att 144
Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

tat ggt gca acc aac ttg gca aat ggg gtc cca tca agg ttc agt ggc 192
Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt agg tct ggg tca gat tat tct ctg acc atc aac aac ttg gag tct 240

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn Asn Leu Glu Ser
65 70 75 80

gaa gac atg gct att tat tac tgt ctg aag cat aat gag tat cca ttc 288
Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn Glu Tyr Pro Phe
85 90 95

acg ttc ggc tca ggg acg aag ttg gaa ata aaa cgg gct 327
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
100 105

<210> 21
<211> 109
<212> PRT
<213> Rattus norvegicus

<400> 21

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

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

Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Arg Leu Met Ile
35 40 45

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn Asn Leu Glu Ser

65 70 75 80

Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn Glu Tyr Pro Phe
85 90 95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala
100 105

<210> 22
<211> 28
<212> DNA
<213> Artifitial Sequence

<400> 22
tacgtgctgt ctttgctgtc ctgatcag 28

<210> 23
<211> 330
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDA
<222> (1).. (330)

<220>
<221> CDS
<222> (1).. (330)

<400> 23
gac atc cag atg aca cag tct cca gct tcc ctg tct gca tct ctg gga 48

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

gaa act gtc acc atc gaa tgt cga gca agt gag gac att tac agt aat        96
Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn
            20                  25                  30

tta gcg tgg tat cag cag aaa cca ggg aac tct cct cag ctc ctg atc       144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro Gln Leu Leu Ile
        35                  40                  45

tat gat gca aat atc ttg gca gat ggg gtc cca tca cgg ttc agt ggc       192
Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggc aca cag tat tct cta aag ata aac agc ctg caa tct       240
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

gaa gat gtc gca agt tat ttc tgt caa cag tat aac aat tat cct ccg       288
Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Pro
                85                  90                  95

ttc acg ttt gga gtt ggg acc aag ctg gaa ctg aaa cgg gct               330
Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys Arg Ala
            100                 105                 110
```

<210> 24
<211> 110
<212> PRT
<213> Rattus norvegicus

<400> 24

```
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
```

1 5 10 15

Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn
20 25 30

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

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

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

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

Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys Arg Ala
100 105 110

<210> 25
<211> 330
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(330)

<400> 25

gac atc cag atg aca cag tct cca gct tcc ctg tct gca tct ctg gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa act gtc acc atc gaa tgt cga gca agt gag gac ata tac agt aat 96
Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn
20 25 30

tta gcg tgg tat cag cag aaa cca ggg aac tct cct cag ctc ctg atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro Gln Leu Leu Ile
35 40 45

tat gat gca aat atc ctg gca gat ggg gtc cca tca cgg ttc agt ggc 192
Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt ggg tct ggc aca cag tat tct cta aag ata aac agc ctg caa tct 240
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

gaa gat gtc gca agt tat ttc tgt caa cag tat aac aat tat cct ccg 288
Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Pro
85 90 95

ttc acg ttt gga gct ggg acc aag ctg gaa ctg aaa cgg gct 330
Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
100 105 110

<210> 26
<211> 110
<212> PRT
<213> Rattus norvegicus

<400> 26

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

Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp Ile Tyr Ser Asn
20 25 30

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

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

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65 70 75 80

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

Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala
100 105 110

<210> 27
<211> 449
<212> DNA
<213> Homo sapiens

<400> 27

gcctccggac tctagagcca ccatggtgct gcagacccag gtgttcatct ccctgctgct 60

gtggatctcc ggcgcgtacg gcgatatcgt gatgattaaa cgtacggtgg ccgccccctc 120

cgtgttcatc ttcccccccct ccgacgagca gctgaagtcc ggcaccgcct ccgtggtgtg 180

cctgctgaat aacttctacc ccagagaggc caaggtgcag tggaaggtgg acaacgccct 240

gcagtccggg aactcccagg agagcgtgac cgagcaggac agcaaggaca gcacctacag 300

cctgagcagc accctgaccc tgagcaaagc cgactacgag aagcacaagg tgtacgcctg 360

cgaggtgacc caccagggcc tgagctcccc cgtcaccaag agcttcaaca gggggggagtg 420

ttaggggccc gtttaaacgg gggaggcta 449

<210> 28
<211> 30
<212> DNA
<213> Artifitial Sequence

<400> 28
tataccgtcg acctctagct agagcttggc 30

<210> 29
<211> 30
<212> DNA
<213> Artifitial Sequence

<400> 29
gctatggcag ggcctgccgc cccgacgttg 30

<210> 30

<211> 1132

<212> DNA

<213> Homo sapiens

<400> 30

gcctccggac tctagagcca ccatgaaaca cctgtggttc ttcctcctgc tggtggcagc 60

tcccagatgg gtgctgagcc aggtgcaatt gtgcaggcgg ttagctcagc ctccaccaag 120

ggcccaagcg tcttcccccc ggcaccctcc tccaagagca cctctggcgg cacagccgcc 180

ctgggctgcc tggtcaagga ctacttcccc gaacccgtga ccgtgagctg gaactcaggc 240

gccctgacca gcggcgtgca caccttcccc gctgtcctgc agtcctcagg actctactcc 300

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 360

gtgaatcaca agcccagcaa caccaaggtg gacaagagag ttgagcccaa atcttgtgac 420

aaaactcaca catgcccacc ctgcccagca cctgaactcc tgggggggacc ctcagtcttc 480

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 540

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 600

gtggaggtgc ataatgccaa gacaaagccc cgggaggagc agtacaacag cacgtaccgg 660

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc 720

aaggtctcca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggc 780

cagccccggg aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 840

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 900

gagagcaatg gccagcccga gaacaactac aagaccaccc ctcccgtgct ggactccgac 960

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcagggcaac 1020

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacaccca gaagagcctc 1080

tccctgtctc ccggcaaatg agatatcggg cccgtttaaa cgggggaggc ta 1132

<210> 31
<211> 702
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(702)

<400> 31

atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gcg tac ggc gac atc cag atg acc cag tct cca tct tcc ctg tct 96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

gca ttt ctg gga gac aga gtc act att act tgc cgg gca agt caa gac 144
Ala Phe Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

att gga aat tat tta aga tgg ttc cag cag aaa ccg ggg aaa tct cct 192
Ile Gly Asn Tyr Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
50 55 60

agg ctt atg att tat ggt gca acc aac ttg gca aat ggg gtc cca tca 240

```
Arg Leu Met Ile Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser
65                  70                  75                  80

agg ttc agt ggc agt agg tct ggg tca gat tat tct ctg acc atc aac      288
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn
                85                  90                  95

aac ttg gag tct gaa gac atg gct att tat tac tgt ctg aag cat aat      336
Asn Leu Glu Ser Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn
            100                 105                 110

gag tat cca ttc acg ttc ggc tca ggg acg aag ttg gaa ata aaa cgg      384
Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125

gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag cag      432
Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc tac      480
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145                 150                 155                 160

ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag tcc      528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc acc      576
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
            180                 185                 190

tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag aag      624
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205

cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc ccc      672
```

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

gtc acc aag agc ttc aac agg ggg gag tgt 702
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 32
<211> 234
<212> PRT
<213> Artifitial Sequence

<400> 32

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Phe Leu Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
35 40 45

Ile Gly Asn Tyr Leu Arg Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro
50 55 60

Arg Leu Met Ile Tyr Gly Ala Thr Asn Leu Ala Asn Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Asn

85 90 95

Asn Leu Glu Ser Glu Asp Met Ala Ile Tyr Tyr Cys Leu Lys His Asn
100 105 110

Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225 230

<210> 33
<211> 48
<212> DNA
<213> Artifitial Sequence

<400> 33
atctccggcg cgtacggcga catccagatg acccagtctc catcttcc 48

<210> 34
<211> 44
<212> DNA
<213> Artifitial Sequence

<400> 34
ggaggggcg gccacagccc gttttatttc caacttcgtc cctg 44

<210> 35
<211> 1413
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1).. (1413)

<400> 35
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtg cag 96
Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

cct gga agg tct ctg aaa cta tcc tgt gta gcc tct gga ttc aga ttc 144
Pro Gly Arg Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe
35 40 45

aat gac ttt tgg atg acc tgg atc cgc cag gct cca ggg aag ggg ctg 192
Asn Asp Phe Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

gag tgg gtt gca tcc att act tat act ggt gat aac act tac tat gca 240
Glu Trp Val Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala
65 70 75 80

ggc tct gtg aag ggc cga atc act atc tcc aga gat aat gcg aag agc 288
Gly Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

acc cta tac ctg caa atg aac agt ctg agg tct gag gac acg gcc act 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr
100 105 110

tat tac tgt aca aga gat gac tac gga gga tat agc ccc tac tat atg 384
Tyr Tyr Cys Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met
115 120 125

gat gcc tgg ggt caa gga act tca gtc act gtc agc tca gcc tcc acc 432
Asp Ala Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
130 135 140

aag ggc cca agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct 480
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

```
ggc ggc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa      528
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                165                 170                 175

ccc gtg acc gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac      576
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            180                 185                 190

acc ttc ccc gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc      624
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        195                 200                 205

gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc      672
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    210                 215                 220

aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag      720
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225                 230                 235                 240

ccc aaa tct tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct      768
Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

gaa ctc ctg ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag      816
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
            260                 265                 270

gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg      864
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
        275                 280                 285

gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac      912
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
```

ggc gtg gag gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac 960
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

aac agc acg tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac 1008
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc 1056
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg 1104
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

gaa cca cag gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag 1152
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac 1200
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

atc gcc gtg gag tgg gag agc aat ggc cag ccc gag aac aac tac aag 1248
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

acc acc cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc 1296
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

aag ctc acc gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca 1344
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

tgc tcc gtg atg cat gag gct ctg cac aac cac tac acc cag aag agc 1392
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

ctc tcc ctg tct ccc ggc aaa 1413
Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 36
<211> 471
<212> PRT
<213> Artifitial Sequence

<400> 36

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
20 25 30

Pro Gly Arg Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Arg Phe
35 40 45

Asn Asp Phe Trp Met Thr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ala Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala
65 70 75 80

Gly Ser Val Lys Gly Arg Ile Thr Ile Ser Arg Asp Asn Ala Lys Ser
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr
100 105 110

Tyr Tyr Cys Thr Arg Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met
115 120 125

Asp Ala Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr
130 135 140

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
145 150 155 160

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

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
195 200 205

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
210 215 220

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
225 230 235 240

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
245 250 255

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
275 280 285

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
290 295 300

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
305 310 315 320

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
325 330 335

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
340 345 350

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
355 360 365

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys
370 375 380

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
385 390 395 400

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
405 410 415

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
420 425 430

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
435 440 445

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
450 455 460

Leu Ser Leu Ser Pro Gly Lys
465 470

<210> 37
<211> 47
<212> DNA
<213> Artifitial Sequence

<400> 37
ccagatgggt gctgagcgag gtgcagctgg tggagtctgg gggaggc 47

<210> 38
<211> 48
<212> DNA
<213> Artifitial Sequence

<400> 38
cttggtggag gctgagctga cagtgactga agttccttga ccccaggc 48

<210> 39
<211> 705
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(705)

<400> 39
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gcg tac ggc gac atc cag atg aca cag tct cca gct tcc ctg tct 96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

gca tct ctg gga gaa act gtc acc atc gaa tgt cga gca agt gag gac 144
Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
35 40 45

att tac agt aat tta gcg tgg tat cag cag aaa cca ggg aac tct cct 192
Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
50 55 60

cag ctc ctg atc tat gat gca aat atc ttg gca gat ggg gtc cca tca 240
Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65 70 75 80

cgg ttc agt ggc agt ggg tct ggc aca cag tat tct cta aag ata aac 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
85 90 95

agc ctg caa tct gaa gat gtc gca agt tat ttc tgt caa cag tat aac 336
Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
100 105 110

aat tat cct ccg ttc acg ttt gga gtt ggg acc aag ctg gaa ctg aaa 384
Asn Tyr Pro Pro Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys
115 120 125

cgg gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag 432
Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145 150 155 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag 528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc 576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt 705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 40
<211> 235
<212> PRT
<213> Artifitial Sequence

<400> 40

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

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

Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
50 55 60

Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
85 90 95

Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
100 105 110

Asn Tyr Pro Pro Phe Thr Phe Gly Val Gly Thr Lys Leu Glu Leu Lys
115 120 125

Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 41
<211> 48
<212> DNA
<213> Artifitial Sequence

<400> 41
atctccggcg cgtacggcga catccagatg acacagtctc cagcttcc 48

<210> 42
<211> 45
<212> DNA
<213> Artifitial Sequence

<400> 42
ggaggggcg gccacagccc gtttcagttc cagcttggtc ccaac 45

<210> 43
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1).. (1401)

<400> 43
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

```
1               5                  10                  15

gtg ctg agc cag gtt aag ctg ctg cag tct ggg gct gag ctg gta aaa        96
Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggt gct tca gtg aag ttg tcc tgc aag act tct ggt ttt acc ttc       144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe
        35                  40                  45

agc act agc tat atg agt tgg ttg aag cag gtg cct gga ccg agt att       192
Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile
    50                  55                  60

gag tgg att gga tgg att tat gct gga gat ggt ggt act aag tat aat       240
Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aag ttc aag ggc aag gcc aca ctg aca gta gac aaa tct tct agc       288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95

aca gca tac atg gat ctc agc agc ctg aca tct gag gac gct gca gtc       336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val
            100                 105                 110

tat ttt tgt gca acg gat ggt tat ggg gat tgg ttt gct tac tgg ggc       384
Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
        115                 120                 125

caa ggc act ctg gtc act gtc agc tca gcc tcc acc aag ggc cca agc       432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc       480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
```

```
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
```

```
  290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
```

435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 44
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 44

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Ile
50 55 60

Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

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

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

Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 45
<211> 47
<212> DNA
<213> Artifitial Sequence

<400> 45

ccagatgggt gctgagccag gttaagctgc tgcagtctgg ggctgag 47

<210> 46
<211> 46
<212> DNA
<213> Artifitial Sequence

<400> 46
cttggtggag gctgagctga cagtgaccag agtgccttgg ccccag 46

<210> 47
<211> 705
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(705)

<400> 47
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gcg tac ggc gac atc cag atg aca cag tct cca gct tcc ctg tct 96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

gca tct ctg gga gaa act gtc acc atc gaa tgt cga gca agt gag gac 144
Ala Ser Leu Gly Glu Thr Val Thr Ile Glu Cys Arg Ala Ser Glu Asp
35 40 45

ata tac agt aat tta gcg tgg tat cag cag aaa cca ggg aac tct cct 192

```
Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
    50                  55                  60

cag ctc ctg atc tat gat gca aat atc ctg gca gat ggg gtc cca tca      240
Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

cgg ttc agt ggc agt ggg tct ggc aca cag tat tct cta aag ata aac      288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
                85                  90                  95

agc ctg caa tct gaa gat gtc gca agt tat ttc tgt caa cag tat aac      336
Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
            100                 105                 110

aat tat cct ccg ttc acg ttt gga gct ggg acc aag ctg gaa ctg aaa      384
Asn Tyr Pro Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
        115                 120                 125

cgg gct gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag      432
Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc      480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag      528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc      576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag      624
```

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt 705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 48
<211> 235
<212> PRT
<213> Artifitial Sequence

<400> 48

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30

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

Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ser Pro
50 55 60

Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser

65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn
85 90 95

Ser Leu Gln Ser Glu Asp Val Ala Ser Tyr Phe Cys Gln Gln Tyr Asn
100 105 110

Asn Tyr Pro Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125

Arg Ala Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

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

210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 49
<211> 45
<212> DNA
<213> Artifitial Sequence

<400> 49
ggaggggcg gccacagccc gtttcagttc cagcttggtc ccagc 45

<210> 50
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 50
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtt aag ctg ctg cag tct ggg gct gag ctg gta aaa 96
Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

cct ggt gct tca gtg aag ttg tcc tgc aag act tct ggt ttt aca ttc 144

```
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Phe Thr Phe
        35                  40                  45

agc act agt tat atg agt tgg ttg aag cag gtg cct gga ccg agt act        192
Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr
    50                  55                  60

gag tgg att gga tgg att tat gct gga gat ggt ggt act aag tat aat        240
Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aag ttc aag ggc aag gcc aca ctg aca gta gac aaa ttt tct agc        288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Phe Ser Ser
                85                  90                  95

aca gca tac atg gat ctc agc agc ctg aca tct gag gac gct gca gtc        336
Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val
            100                 105                 110

tat ttc tgt gca acg gat ggt tat ggg gat tgg ttt act tac tgg ggc        384
Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

caa ggc act ctg gtc act gtc agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
```

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1008
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
```

Pro Gly Lys
465

<210> 51
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 51

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Lys Leu Leu Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Leu Lys Gln Val Pro Gly Pro Ser Thr
50 55 60

Glu Trp Ile Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

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

Thr Ala Tyr Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Ala Ala Val

100 105 110

Tyr Phe Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 52
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 52

Asp Phe Trp Met Thr
1 5

<210> 53
<211> 17

<212> PRT
<213> Rattus norvegicus

<400> 53

Ser Ile Thr Tyr Thr Gly Asp Asn Thr Tyr Tyr Ala Gly Ser Val Lys
1 5 10 15

Gly

<210> 54
<211> 13
<212> PRT
<213> Rattus norvegicus

<400> 54

Asp Asp Tyr Gly Gly Tyr Ser Pro Tyr Tyr Met Asp Ala
1 5 10

<210> 55
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 55

Thr Ser Tyr Met Ser
1 5

<210> 56

<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 56

Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 57
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 57

Asp Gly Tyr Gly Asp Trp Phe Ala Tyr
1 5

<210> 58
<211> 5
<212> PRT
<213> Rattus norvegicus

<400> 58

Thr Ser Tyr Met Ser
1 5

<210> 59
<211> 17
<212> PRT
<213> Rattus norvegicus

<400> 59

Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn Gln Lys Phe Lys
1 5 10 15

Gly

<210> 60
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 60

Asp Gly Tyr Gly Asp Trp Phe Thr Tyr
1 5

<210> 61
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 61

Arg Ala Ser Gln Asp Ile Gly Asn Tyr Leu Arg
1 5 10

<210> 62
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 62

Gly Ala Thr Asn Leu Ala Asn
1 5

<210> 63
<211> 9
<212> PRT
<213> Rattus norvegicus

<400> 63

Leu Lys His Asn Glu Tyr Pro Phe Thr
1 5

<210> 64
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 64

Arg Ala Ser Glu Asp Ile Tyr Ser Asn Leu Ala
1 5 10

<210> 65
<211> 7

<212> PRT
<213> Rattus norvegicus

<400> 65

Asp Ala Asn Ile Leu Ala Asp
1 5

<210> 66
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 66

Gln Gln Tyr Asn Asn Tyr Pro Pro Phe Thr
1 5 10

<210> 67
<211> 11
<212> PRT
<213> Rattus norvegicus

<400> 67

Arg Ala Ser Glu Asp Ile Tyr Ser Asn Leu Ala
1 5 10

<210> 68
<211> 7
<212> PRT
<213> Rattus norvegicus

<400> 68

Asp Ala Asn Ile Leu Ala Asp
1 5

<210> 69
<211> 10
<212> PRT
<213> Rattus norvegicus

<400> 69

Gln Gln Tyr Asn Asn Tyr Pro Pro Phe Thr
1 5 10

<210> 70
<211> 822
<212> PRT
<213> Homo sapiens

<400> 70

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu
50 55 60

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys
195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys His Ser Gly Ile Asn Ser Ser
305 310 315 320

Asn Ala Glu Val Leu Ala Leu Phe Asn Val Thr Glu Ala Asp Ala Gly
325 330 335

Glu Tyr Ile Cys Lys Val Ser Asn Tyr Ile Gly Gln Ala Asn Gln Ser
340 345 350

Ala Trp Leu Thr Val Leu Pro Lys Gln Gln Ala Pro Gly Arg Glu Lys
355 360 365

Glu Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile
370 375 380

Gly Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg
385 390 395 400

Met Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val
405 410 415

His Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser
420 425 430

Ala Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile
435 440 445

Thr Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val
450 455 460

Ser Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp
465 470 475 480

Lys Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val
485 490 495

Val Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala
500 505 510

Val Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp
515 520 525

Leu Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys
530 535 540

His Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro
545 550 555 560

Leu Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr
565 570 575

Leu Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn
580 585 590

Arg Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr
595 600 605

Tyr Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile
610 615 620

His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val
625 630 635 640

Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp
645 650 655

Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala
660 665 670

Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp
675 680 685

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

Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly
705 710 715 720

His Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met
725 730 735

Met Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys
740 745 750

Gln Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu
755 760 765

Glu Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr
770 775 780

Pro Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser
785 790 795 800

Pro Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile
805 810 815

Asn Gly Ser Val Lys Thr
820

<210> 71
<211> 821
<212> PRT
<213> Homo sapiens

<400> 71

Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val Thr Met Ala
1 5 10 15

Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu Asp Thr Thr
20 25 30

Leu Glu Pro Glu Glu Pro Pro Thr Lys Tyr Gln Ile Ser Gln Pro Glu
35 40 45

Val Tyr Val Ala Ala Pro Gly Glu Ser Leu Glu Val Arg Cys Leu Leu

50 55 60

Lys Asp Ala Ala Val Ile Ser Trp Thr Lys Asp Gly Val His Leu Gly
65 70 75 80

Pro Asn Asn Arg Thr Val Leu Ile Gly Glu Tyr Leu Gln Ile Lys Gly
85 90 95

Ala Thr Pro Arg Asp Ser Gly Leu Tyr Ala Cys Thr Ala Ser Arg Thr
100 105 110

Val Asp Ser Glu Thr Trp Tyr Phe Met Val Asn Val Thr Asp Ala Ile
115 120 125

Ser Ser Gly Asp Asp Glu Asp Asp Thr Asp Gly Ala Glu Asp Phe Val
130 135 140

Ser Glu Asn Ser Asn Asn Lys Arg Ala Pro Tyr Trp Thr Asn Thr Glu
145 150 155 160

Lys Met Glu Lys Arg Leu His Ala Val Pro Ala Ala Asn Thr Val Lys
165 170 175

Phe Arg Cys Pro Ala Gly Gly Asn Pro Met Pro Thr Met Arg Trp Leu
180 185 190

Lys Asn Gly Lys Glu Phe Lys Gln Glu His Arg Ile Gly Gly Tyr Lys

195 200 205

Val Arg Asn Gln His Trp Ser Leu Ile Met Glu Ser Val Val Pro Ser
210 215 220

Asp Lys Gly Asn Tyr Thr Cys Val Val Glu Asn Glu Tyr Gly Ser Ile
225 230 235 240

Asn His Thr Tyr His Leu Asp Val Val Glu Arg Ser Pro His Arg Pro
245 250 255

Ile Leu Gln Ala Gly Leu Pro Ala Asn Ala Ser Thr Val Val Gly Gly
260 265 270

Asp Val Glu Phe Val Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile
275 280 285

Gln Trp Ile Lys His Val Glu Lys Asn Gly Ser Lys Tyr Gly Pro Asp
290 295 300

Gly Leu Pro Tyr Leu Lys Val Leu Lys Ala Ala Gly Val Asn Thr Thr
305 310 315 320

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

Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Ile Ser Phe

340 345 350

His Ser Ala Trp Leu Thr Val Leu Pro Ala Pro Gly Arg Glu Lys Glu
355 360 365

Ile Thr Ala Ser Pro Asp Tyr Leu Glu Ile Ala Ile Tyr Cys Ile Gly
370 375 380

Val Phe Leu Ile Ala Cys Met Val Val Thr Val Ile Leu Cys Arg Met
385 390 395 400

Lys Asn Thr Thr Lys Lys Pro Asp Phe Ser Ser Gln Pro Ala Val His
405 410 415

Lys Leu Thr Lys Arg Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala
420 425 430

Glu Ser Ser Ser Ser Met Asn Ser Asn Thr Pro Leu Val Arg Ile Thr
435 440 445

Thr Arg Leu Ser Ser Thr Ala Asp Thr Pro Met Leu Ala Gly Val Ser
450 455 460

Glu Tyr Glu Leu Pro Glu Asp Pro Lys Trp Glu Phe Pro Arg Asp Lys
465 470 475 480

Leu Thr Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val

485 490 495

Met Ala Glu Ala Val Gly Ile Asp Lys Asp Lys Pro Lys Glu Ala Val
500 505 510

Thr Val Ala Val Lys Met Leu Lys Asp Asp Ala Thr Glu Lys Asp Leu
515 520 525

Ser Asp Leu Val Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His
530 535 540

Lys Asn Ile Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu
545 550 555 560

Tyr Val Ile Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu
565 570 575

Arg Ala Arg Arg Pro Pro Gly Met Glu Tyr Ser Tyr Asp Ile Asn Arg
580 585 590

Val Pro Glu Glu Gln Met Thr Phe Lys Asp Leu Val Ser Cys Thr Tyr
595 600 605

Gln Leu Ala Arg Gly Met Glu Tyr Leu Ala Ser Gln Lys Cys Ile His
610 615 620

Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asn Asn Val Met

625 630 635 640

Lys Ile Ala Asp Phe Gly Leu Ala Arg Asp Ile Asn Asn Ile Asp Tyr
645 650 655

Tyr Lys Lys Thr Thr Asn Gly Arg Leu Pro Val Lys Trp Met Ala Pro
660 665 670

Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val Trp Ser
675 680 685

Phe Gly Val Leu Met Trp Glu Ile Phe Thr Leu Gly Gly Ser Pro Tyr
690 695 700

Pro Gly Ile Pro Val Glu Glu Leu Phe Lys Leu Leu Lys Glu Gly His
705 710 715 720

Arg Met Asp Lys Pro Ala Asn Cys Thr Asn Glu Leu Tyr Met Met Met
725 730 735

Arg Asp Cys Trp His Ala Val Pro Ser Gln Arg Pro Thr Phe Lys Gln
740 745 750

Leu Val Glu Asp Leu Asp Arg Ile Leu Thr Leu Thr Thr Asn Glu Glu
755 760 765

Tyr Leu Asp Leu Ser Gln Pro Leu Glu Gln Tyr Ser Pro Ser Tyr Pro

770 775 780

Asp Thr Arg Ser Ser Cys Ser Ser Gly Asp Asp Ser Val Phe Ser Pro
785 790 795 800

Asp Pro Met Pro Tyr Glu Pro Cys Leu Pro Gln Tyr Pro His Ile Asn
805 810 815

Gly Ser Val Lys Thr
820

<210> 72
<211> 705
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(705)

<400> 72
atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggc gcg tac ggc gac atc cag atg acc cag agc ccc agc agc ctg agc 96
Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

gcc agc gtg ggc gac aga gtg acc atc acc tgt cgg gcc agc gag gac 144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp

```
        35                  40                  45

atc tac agc aac ctg gcc tgg tat cag cag aag ccc ggc aag agc ccc        192
Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro
    50                  55                  60

cag ctg ctg atc tac gac gcc aac atc ctg gcc gac ggc gtg ccc agc        240
Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65                  70                  75                  80

aga ttc agc ggc agc ggc tcc ggc acc gac tac acc ctg acc atc tcc        288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
                85                  90                  95

agc ctg cag ccc gag gac ttc gcc acc tac tac tgc cag cag tac aac        336
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
            100                 105                 110

aac tac ccc cca ttc acc ttc ggc cag ggc acc aag gtg gaa atc aag        384
Asn Tyr Pro Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        115                 120                 125

cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc ccc tcc gac gag        432
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140

cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg ctg aat aac ttc        480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160

tac ccc aga gag gcc aag gtg cag tgg aag gtg gac aac gcc ctg cag        528
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175

tcc ggg aac tcc cag gag agc gtg acc gag cag gac agc aag gac agc        576
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
```

180 185 190

acc tac agc ctg agc agc acc ctg acc ctg agc aaa gcc gac tac gag 624
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

aag cac aag gtg tac gcc tgc gag gtg acc cac cag ggc ctg agc tcc 672
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

ccc gtc acc aag agc ttc aac agg ggg gag tgt 705
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 73
<211> 235
<212> PRT
<213> Artifitial Sequence

<400> 73

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

Gly Ala Tyr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asp
35 40 45

Ile Tyr Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ser Pro
50 55 60

Gln Leu Leu Ile Tyr Asp Ala Asn Ile Leu Ala Asp Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
100 105 110

Asn Tyr Pro Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
130 135 140

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

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 74
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 74
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc cag gga ctg 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

```
gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac      240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205
```

```
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350
```

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 75
<211> 467

<212> PRT
<213> Artifitial Sequence

<400> 75

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 76
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 76
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

```
cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc      144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc cag gga ctg      192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac      240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gcc gac aag agc acc agc      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175
```

```
agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320
```

```
cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460
```

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 77
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 77

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Ala Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 78
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 78
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa      96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc     144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc     192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac     240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc     288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg     336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc aca tac tgg ggc     384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc     432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc     480
```

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
```

```
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
```

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 79
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 79

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn

65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 80
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 80
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc atc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Ile
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgc gcc acc gac ggc tac ggc gac tgg ttc gcc tac tgg ggc 384
Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly

```
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

```
                260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg     1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc     1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag     1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc     1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
```

405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 81
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 81

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Ile
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Gly Tyr Gly Asp Trp Phe Ala Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 82
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 82

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95
```

```
acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gag ggc tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Glu Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240
```

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

```
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                         1401
Pro Gly Lys
465
```

<210> 83
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 83

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                   10                  15
```

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Glu Gly Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 84
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 84
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgc gcc acc gac gcc tac ggc gac tgg ttc aca tac tgg ggc 384
Tyr Tyr Cys Ala Thr Asp Ala Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

```
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350
```

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 85
<211> 467
<212> PRT

<213> Artifitial Sequence

<400> 85

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Ala Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 86
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 86
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144

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

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc        192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac        240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc        288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg        336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac gag tac ggc gac tgg ttc aca tac tgg ggc        384
Tyr Tyr Cys Ala Thr Asp Glu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
```

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1008
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
```

Pro Gly Lys
465

<210> 87
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 87

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val

100 105 110

Tyr Tyr Cys Ala Thr Asp Glu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly

245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu

385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 88
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 88
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

```
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa      96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc     144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc     192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac     240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc     288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg     336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac ttc tac ggc gac tgg ttc aca tac tgg ggc     384
Tyr Tyr Cys Ala Thr Asp Phe Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc     432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc     480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
```

```
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
```

```
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg     1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc     1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag     1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc     1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg     1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg     1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
```

435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 89
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 89

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Phe Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 90
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 90

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg       336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac cac tac ggc gac tgg ttc aca tac tgg ggc       384
Tyr Tyr Cys Ala Thr Asp His Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125
```

```
cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270
```

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 91
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 91

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp His Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 92
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 92

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95
```

```
acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg        336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac atc tac ggc gac tgg ttc aca tac tgg ggc        384
Tyr Tyr Cys Ala Thr Asp Ile Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240
```

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 93
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 93

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Ile Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 94
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 94
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240

```
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc      288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg      336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac aag tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Lys Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
```

```
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc     1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg     1104
```

```
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 95
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 95

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Lys Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 96
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 96
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe

35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgc gcc acc gac ctg tac ggc gac tgg ttc aca tac tgg ggc 384
Tyr Tyr Cys Ala Thr Asp Leu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala

```
          180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
       195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
   210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
               245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
          260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
       275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
   290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc     1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
```

```
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                         1401
Pro Gly Lys
```

465

<210> 97
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 97

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Leu Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 98
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 98
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

```
gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg       336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac atg tac ggc gac tgg ttc aca tac tgg ggc       384
Tyr Tyr Cys Ala Thr Asp Met Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc       432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc       480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160
```

```
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300
```

```
cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445
```

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 99
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 99

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Met Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 100
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>

<221> CDS
<222> (1)..(1401)

<400> 100

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg       336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac cag tac ggc gac tgg ttc aca tac tgg ggc       384
Tyr Tyr Cys Ala Thr Asp Gln Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125
```

```
cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc        432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc        480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg        528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct        576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg        624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac        672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270
```

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg 1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag 1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 101
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 101

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Gln Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 102
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 102

```
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg        48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1               5                  10                  15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg       336
```

```
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac cgg tac ggc gac tgg ttc aca tac tgg ggc      384
Tyr Tyr Cys Ala Thr Asp Arg Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc      432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc      480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
```

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac      960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc      1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
```

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc 1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg 1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 103
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 103

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Arg Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val

165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

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

450 455 460

Pro Gly Lys
465

<210> 104
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 104
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn

65 70 75 80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgc gcc acc gac gtg tac ggc gac tgg ttc aca tac tgg ggc 384
Tyr Tyr Cys Ala Thr Asp Val Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

```
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt        720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg        768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg        816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac        864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg        912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
```

```
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                          1401
Pro Gly Lys
465
```

<210> 105
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 105

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Val Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 106
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 106
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
35 40 45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc 192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac 240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc 288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgc gcc acc gac tgg tac ggc gac tgg ttc aca tac tgg ggc 384
Tyr Tyr Cys Ala Thr Asp Trp Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc 432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
130 135 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc 480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg 528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct 576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg 624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac 672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt 720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg 768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac 960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

```
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc      1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg      1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc      1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag      1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc      1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg      1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg      1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct      1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
    450                 455                 460

ccc ggc aaa                                                         1401
Pro Gly Lys
465
```

<210> 107
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 107

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Trp Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 108
<211> 1401
<212> DNA
<213> Artifitial Sequence

<220>
<221> CDS
<222> (1)..(1401)

<400> 108
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

```
gtg ctg agc cag gtg cag ctg gtg cag tct ggc gcc gaa gtg aag aaa        96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

cct ggg gct agc gtg aag gtg tcc tgc aag gcc agc ggc ttc acc ttc       144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Thr Phe
        35                  40                  45

agc acc agc tat atg agc tgg gtc cgc cag gct cca ggc ccc agc acc       192
Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
    50                  55                  60

gaa tgg atg ggc tgg atc tat gcc ggc gac ggc ggc acc aag tac aac       240
Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65                  70                  75                  80

cag aaa ttc aag ggc aga gtg acc ctg acc gtg gac aag agc acc agc       288
Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
                85                  90                  95

acc gcc tac atg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg       336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

tac tac tgc gcc acc gac tac tac ggc gac tgg ttc aca tac tgg ggc       384
Tyr Tyr Cys Ala Thr Asp Tyr Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
        115                 120                 125

cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca agc       432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    130                 135                 140

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca gcc       480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145                 150                 155                 160
```

```
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc gct      576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            180                 185                 190

gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg      624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        195                 200                 205

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    210                 215                 220

aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg ggg      768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
                245                 250                 255

gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg      816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            260                 265                 270

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac      864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
        275                 280                 285

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg      912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
    290                 295                 300
```

```
cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg tac        960
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305                 310                 315                 320

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc       1008
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                325                 330                 335

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc       1056
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
            340                 345                 350

gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag gtg       1104
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
        355                 360                 365

tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc       1152
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
    370                 375                 380

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag       1200
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385                 390                 395                 400

tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct ccc       1248
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
                405                 410                 415

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg       1296
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
            420                 425                 430

gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg atg       1344
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
        435                 440                 445
```

cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg tct 1392
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

ccc ggc aaa 1401
Pro Gly Lys
465

<210> 109
<211> 467
<212> PRT
<213> Artifitial Sequence

<400> 109

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

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

Ser Thr Ser Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Pro Ser Thr
50 55 60

Glu Trp Met Gly Trp Ile Tyr Ala Gly Asp Gly Gly Thr Lys Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Lys Ser Thr Ser
85 90 95

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

Tyr Tyr Cys Ala Thr Asp Tyr Tyr Gly Asp Trp Phe Thr Tyr Trp Gly
115 120 125

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
145 150 155 160

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

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Pro Gly Lys
465

<210> 110
<211> 39
<212> DNA
<213> Artifitial Sequence

<400> 110
ggcagagtga ccctgaccgc cgacaagagc accagcacc 39

<210> 111
<211> 39
<212> DNA
<213> Artifitial Sequence

<400> 111
ggtgctggtg ctcttgtcgg cggtcagggt cactctgcc 39

<210> 112
<211> 39
<212> DNA
<213> Artifitial Sequence

<400> 112
ggtgctggtg ctcttgtcgg cggtcagggt cactctgcc 39

<210> 113
<211> 42
<212> DNA
<213> Artifitial Sequence

<400> 113
cgcaagcttg tcgactcaaa caacatccag atgataggta tg 42