SEQUENCE LISTING

<110> FORERUNNER PHARMA RESEARCH CO., LTD.
THE UNIVERSITY OF TOKYO

<120> DIAGNOSIS AND TREATMENT OF CANCER USING ANTI-EREG ANTIBODY

<130> C1-A0617P

<140> PCT/JP2007/069988
<141> 2007-10-12

<150> JP 2006-278819
<151> 2006-10-12

<160> 152

<170> PatentIn version 3.4

<210> 1
<211> 15
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<400> 1
gacacctata tacag 15

<210> 2
<211> 5
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 2

Asp Thr Tyr Ile Gln
1 5

<210> 3
<211> 51
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<400> 3
aggattgatc ctctgaatgg taatactaaa tatgtcccga agttccaggg c 51

<210> 4
<211> 17
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 4

Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val Pro Lys Phe Gln
1 5 10 15

Gly

<210> 5
<211> 21
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<400> 5
tctgggaccc tctttgactt c 21

<210> 6
<211> 7
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 6

Ser Gly Thr Leu Phe Asp Phe
1 5

<210> 7
<211> 1413
<212> DNA
<213> Mus musculus

<220>

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

<220>
<221> sig_peptide
<222> (1)..(57)

<220>
<221> mat_peptide
<222> (58)..(1413)

<220>
<221> V_region
<222> (58)..(405)

<220>
<221> C_region
<222> (406)..(1413)

<400> 7

```
atg aaa tgc agc tgg gtt atc ttc ttc ctg atg gca gtg gct aca ggg      48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Ala Thr Gly
                -15                 -10                 -5

gtc aat tca gag gat cag ctg cag cag tct ggg gca gag ctt gtg aag      96
Val Asn Ser Glu Asp Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
        -1  1               5                  10

cca ggg gcc tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att     144
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
    15                  20                  25

aaa gac acc tat ata cag tgg gtg aag ctg agg cct gaa cag ggc ctg     192
Lys Asp Thr Tyr Ile Gln Trp Val Lys Leu Arg Pro Glu Gln Gly Leu
30                  35                  40                  45
```

```
gag tgg att gga agg att gat cct ctg aat ggt aat act aaa tat gtc      240
Glu Trp Ile Gly Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val
                50                  55                  60

ccg aag ttc cag ggc aag gcc act ata aca gca gac aca tcc tcc aat      288
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
            65                  70                  75

aca gcc tac ctg caa ctc agc agc ctg aca tct gag gac act gcc gtc      336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
        80                  85                  90

tat tac tgt gtt agg tct ggg acc ctc ttt gac ttc tgg ggc caa ggc      384
Tyr Tyr Cys Val Arg Ser Gly Thr Leu Phe Asp Phe Trp Gly Gln Gly
    95                  100                 105

acc act ctc aca gtc tcc tca gcc aaa aca aca ccc cca tca gtc tat      432
Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
110                 115                 120                 125

cca ctg gcc cct ggg tgt gga gat aca act ggt tcc tct gtg act ctg      480
Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
                130                 135                 140

gga tgc ctg gtc aag ggc tac ttc cct gag tca gtg act gtg act tgg      528
Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Ser Val Thr Val Thr Trp
            145                 150                 155

aac tct gga tcc ctg tcc agc agt gtg cac acc ttc cca gct ctc ctg      576
Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu
        160                 165                 170

cag tct gga ctc tac act atg agc agc tca gtg act gtc ccc tcc agc      624
Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser
    175                 180                 185
```

act tgg cca agt cag acc gtc acc tgc agc gtt gct cac cca gcc agc 672
Thr Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala Ser
190 195 200 205

agc acc acg gtg gac aaa aaa ctt gag ccc agc ggg ccc att tca aca 720
Ser Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser Thr
210 215 220

atc aac ccc tgt cct cca tgc aag gag tgt cac aaa tgc cca gct cct 768
Ile Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala Pro
225 230 235

aac ctc gag ggt gga cca tcc gtc ttc atc ttc cct cca aat atc aag 816
Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile Lys
240 245 250

gat gta ctc atg atc tcc ctg aca ccc aag gtc acg tgt gtg gtg gtg 864
Asp Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val
255 260 265

gat gtg agc gag gat gac cca gac gtc cgg atc agc tgg ttt gtg aac 912
Asp Val Ser Glu Asp Asp Pro Asp Val Arg Ile Ser Trp Phe Val Asn
270 275 280 285

aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat tac 960
Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
290 295 300

aac agt act atc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac 1008
Asn Ser Thr Ile Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
305 310 315

tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc 1056
Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
320 325 330

cca tca ccc atc gag aga acc atc tca aaa att aaa ggg cta gtc aga 1104
Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu Val Arg
335 340 345

gct cca caa gta tac atc ttg ccg cca cca gca gag cag ttg tcc agg 1152
Ala Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu Ser Arg
350 355 360 365

aaa gat gtc agt ctc act tgc ctg gtc gtg ggc ttc aac cct gga gac 1200
Lys Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro Gly Asp
370 375 380

atc agt gtg gag tgg acc agc aat ggg cat aca gag gag aac tac aag 1248
Ile Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn Tyr Lys
385 390 395

gac acc gca cca gtc cta gac tct gac ggt tct tac ttc ata tac agc 1296
Asp Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile Tyr Ser
400 405 410

aag ctc gat ata aaa aca agc aag tgg gag aaa aca gat tcc ttc tca 1344
Lys Leu Asp Ile Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser Phe Ser
415 420 425

tgc aac gtg aga cac gag ggt ctg aaa aat tac tac ctg aag aag acc 1392
Cys Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys Lys Thr
430 435 440 445

atc tcc cgg tct ccg ggt aaa 1413
Ile Ser Arg Ser Pro Gly Lys
450

<210> 8
<211> 471
<212> PRT

<213> Mus musculus

<400> 8

```
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Ala Thr Gly
                -15                 -10                 -5

Val Asn Ser Glu Asp Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
        -1  1                   5                   10

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
    15                  20                  25

Lys Asp Thr Tyr Ile Gln Trp Val Lys Leu Arg Pro Glu Gln Gly Leu
30                  35                  40                  45

Glu Trp Ile Gly Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val
                50                  55                  60

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
            65                  70                  75

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
        80                  85                  90

Tyr Tyr Cys Val Arg Ser Gly Thr Leu Phe Asp Phe Trp Gly Gln Gly
    95                  100                 105
```

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr
110 115 120 125

Pro Leu Ala Pro Gly Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
130 135 140

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

Asn Ser Gly Ser Leu Ser Ser Ser Val His Thr Phe Pro Ala Leu Leu
160 165 170

Gln Ser Gly Leu Tyr Thr Met Ser Ser Ser Val Thr Val Pro Ser Ser
175 180 185

Thr Trp Pro Ser Gln Thr Val Thr Cys Ser Val Ala His Pro Ala Ser
190 195 200 205

Ser Thr Thr Val Asp Lys Lys Leu Glu Pro Ser Gly Pro Ile Ser Thr
210 215 220

Ile Asn Pro Cys Pro Pro Cys Lys Glu Cys His Lys Cys Pro Ala Pro
225 230 235

Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Asn Ile Lys
240 245 250

Asp Val Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val Val Val
255 260 265

Asp Val Ser Glu Asp Asp Pro Asp Val Arg Ile Ser Trp Phe Val Asn
270 275 280 285

Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
290 295 300

Asn Ser Thr Ile Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
305 310 315

Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
320 325 330

Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ile Lys Gly Leu Val Arg
335 340 345

Ala Pro Gln Val Tyr Ile Leu Pro Pro Pro Ala Glu Gln Leu Ser Arg
350 355 360 365

Lys Asp Val Ser Leu Thr Cys Leu Val Val Gly Phe Asn Pro Gly Asp
370 375 380

Ile Ser Val Glu Trp Thr Ser Asn Gly His Thr Glu Glu Asn Tyr Lys
385 390 395

Asp Thr Ala Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Ile Tyr Ser
400 405 410

Lys Leu Asp Ile Lys Thr Ser Lys Trp Glu Lys Thr Asp Ser Phe Ser
415 420 425

Cys Asn Val Arg His Glu Gly Leu Lys Asn Tyr Tyr Leu Lys Lys Thr
430 435 440 445

Ile Ser Arg Ser Pro Gly Lys
450

<210> 9
<211> 1398
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1395)

<220>
<221> sig_peptide
<222> (1)..(57)

<220>
<221> mat_peptide
<222> (58)..(1398)

<220>
<221> V_region

<222> (58)..(405)

<220>
<221> C_region
<222> (406)..(1398)

<400> 9

```
atg aaa tgc agc tgg gtt atc ttc ttc ctg atg gca gtg gct aca ggg      48
Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Ala Thr Gly
                -15                 -10                 -5

gtc aat tca gag gat cag ctg cag cag tct ggg gca gag ctt gtg aag      96
Val Asn Ser Glu Asp Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
        -1  1               5                  10

cca ggg gcc tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att     144
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
    15                  20                  25

aaa gac acc tat ata cag tgg gtg aag ctg agg cct gaa cag ggc ctg     192
Lys Asp Thr Tyr Ile Gln Trp Val Lys Leu Arg Pro Glu Gln Gly Leu
30                  35                  40                  45

gag tgg att gga agg att gat cct ctg aat ggt aat act aaa tat gtc     240
Glu Trp Ile Gly Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val
                50                  55                  60

ccg aag ttc cag ggc aag gcc act ata aca gca gac aca tcc tcc aat     288
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
            65                  70                  75

aca gcc tac ctg caa ctc agc agc ctg aca tct gag gac act gcc gtc     336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
        80                  85                  90

tat tac tgt gtt agg tct ggg acc ctc ttt gac ttc tgg ggc caa ggc     384
```

```
Tyr Tyr Cys Val Arg Ser Gly Thr Leu Phe Asp Phe Trp Gly Gln Gly
    95                  100                 105

acc act ctc aca gtc tcc tca gct agc acc aag ggc cca tcg gtc ttc      432
Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110                 115                 120                 125

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg      480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
                130                 135                 140

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg      528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
            145                 150                 155

aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta      576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
        160                 165                 170

cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc      624
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
    175                 180                 185

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc      672
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190                 195                 200                 205

agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa      720
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
                210                 215                 220

act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg      768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
            225                 230                 235

tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc      816
```

```
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
        240                 245                 250

cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac      864
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
    255                 260                 265

cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat      912
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270                 275                 280                 285

gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg      960
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
                290                 295                 300

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag     1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
            305                 310                 315

tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa     1056
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
        320                 325                 330

acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc     1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
    335                 340                 345

ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc     1152
Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350                 355                 360                 365

tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag     1200
Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
                370                 375                 380

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg     1248
```

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

gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag 1296
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
400 405 410

agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag 1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
415 420 425

gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt 1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430 435 440 445

aaa tga 1398
Lys

<210> 10
<211> 465
<212> PRT
<213> Homo sapiens

<400> 10

Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Ala Thr Gly
-15 -10 -5

Val Asn Ser Glu Asp Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
-1 1 5 10

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile

15 20 25

Lys Asp Thr Tyr Ile Gln Trp Val Lys Leu Arg Pro Glu Gln Gly Leu
30 35 40 45

Glu Trp Ile Gly Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val
50 55 60

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
65 70 75

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
80 85 90

Tyr Tyr Cys Val Arg Ser Gly Thr Leu Phe Asp Phe Trp Gly Gln Gly
95 100 105

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
110 115 120 125

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

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

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

160 165 170

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
175 180 185

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
190 195 200 205

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

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

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
240 245 250

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
255 260 265

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
270 275 280 285

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

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

305 310 315

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
320 325 330

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
335 340 345

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
350 355 360 365

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

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
400 405 410

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
415 420 425

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
430 435 440 445

Lys

<210> 11
<211> 33
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<400> 11
aaggcaagcc aagacattca caagtatata gct 33

<210> 12
<211> 11
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 12

Lys Ala Ser Gln Asp Ile His Lys Tyr Ile Ala
1 5 10

<210> 13
<211> 21
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<400> 13
tacacatcta cattacagcc a 21

<210> 14
<211> 7
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 14

Tyr Thr Ser Thr Leu Gln Pro
1 5

<210> 15
<211> 24
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<400> 15
ctacagtatg ataatcttcg gacg 24

<210> 16
<211> 8
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 16

Leu Gln Tyr Asp Asn Leu Arg Thr
1 5

<210> 17
<211> 702
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(699)

<220>
<221> sig_peptide
<222> (1)..(60)

<220>
<221> mat_peptide
<222> (61)..(702)

<220>
<221> V_region
<222> (61)..(378)

<220>
<221> C_region
<222> (379)..(702)

<400> 17

```
atg aga ccg tct att cag ttc ctg ggg ctc ttg ttg ttc tgg ctt cat      48
Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
-20                 -15                 -10                 -5

ggt gct cag tgt gac atc cag atg aca cag tct cca tcc tca ctg tct      96
Gly Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
           -1  1               5                  10

gca tct ctg gga ggc aaa gtc acc atc act tgc aag gca agc caa gac     144
Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
        15                  20                  25

att cac aag tat ata gct tgg tac caa cac aag cct gga aaa ggt cct     192
Ile His Lys Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
    30                  35                  40

agg ctg ctc ata cag tac aca tct aca tta cag cca ggc atc cca tca     240
Arg Leu Leu Ile Gln Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
45                  50                  55                  60

agg ttc agt gga agt ggg tct ggg aga gat tat tcc ttc agc atc agc     288
Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
                65                  70                  75

aac ctg gag cct gaa gat att gca act tat tat tgt cta cag tat gat     336
Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
            80                  85                  90

aat ctt cgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgg gct     384
Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
        95                  100                 105

gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag cag tta     432
Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu
    110                 115                 120
```

aca tct gga ggt gcc tca gtc gtg tgc ttc ttg aac aac ttc tac ccc 480
Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro
125 130 135 140

aaa gac atc aat gtc aag tgg aag att gat ggc agt gaa cga caa aat 528
Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn
145 150 155

ggc gtc ctg aac agt tgg act gat cag gac agc aaa gac agc acc tac 576
Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr
160 165 170

agc atg agc agc acc ctc acg ttg acc aag gac gag tat gaa cga cat 624
Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His
175 180 185

aac agc tat acc tgt gag gcc act cac aag aca tca act tca ccc att 672
Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile
190 195 200

gtc aag agc ttc aac agg aat gag tgt tag 702
Val Lys Ser Phe Asn Arg Asn Glu Cys
205 210

<210> 18
<211> 233
<212> PRT
<213> Mus musculus

<400> 18

Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
-20 -15 -10 -5

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

Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
15 20 25

Ile His Lys Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
30 35 40

Arg Leu Leu Ile Gln Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
65 70 75

Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
80 85 90

Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
95 100 105

Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu
110 115 120

Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro
125 130 135 140

Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn
145 150 155

Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr
160 165 170

Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His
175 180 185

Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile
190 195 200

Val Lys Ser Phe Asn Arg Asn Glu Cys
205 210

<210> 19
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(699)

<220>
<221> sig_peptide
<222> (1)..(60)

<220>
<221> mat_peptide

<222> (61)..(702)

<220>
<221> V_region
<222> (61)..(378)

<220>
<221> C_region
<222> (379)..(702)

<400> 19

```
atg aga ccg tct att cag ttc ctg ggg ctc ttg ttg ttc tgg ctt cat      48
Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
-20                 -15                 -10                 -5

ggt gct cag tgt gac atc cag atg aca cag tct cca tcc tca ctg tct      96
Gly Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
           -1  1                5                  10

gca tct ctg gga ggc aaa gtc acc atc act tgc aag gca agc caa gac     144
Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
        15                  20                  25

att cac aag tat ata gct tgg tac caa cac aag cct gga aaa ggt cct     192
Ile His Lys Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
    30                  35                  40

agg ctg ctc ata cag tac aca tct aca tta cag cca ggc atc cca tca     240
Arg Leu Leu Ile Gln Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
45                  50                  55                  60

agg ttc agt gga agt ggg tct ggg aga gat tat tcc ttc agc atc agc     288
Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
                65                  70                  75

aac ctg gag cct gaa gat att gca act tat tat tgt cta cag tat gat     336
```

```
Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
            80                  85                  90

aat ctt cgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgt acg      384
Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr
        95                  100                 105

gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg      432
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
    110                 115                 120

aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc      480
Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
125                 130                 135                 140

aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt      528
Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
                145                 150                 155

aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac      576
Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
            160                 165                 170

agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac      624
Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
        175                 180                 185

aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc      672
Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
    190                 195                 200

aca aag agc ttc aac agg gga gag tgt tga                              702
Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210
```

<210> 20
<211> 233
<212> PRT
<213> Homo sapiens

<400> 20

Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
-20 -15 -10 -5

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

Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
15 20 25

Ile His Lys Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro
30 35 40

Arg Leu Leu Ile Gln Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
45 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
65 70 75

Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
80 85 90

Asn Leu Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr

95 100 105

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
110 115 120

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
125 130 135 140

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

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
160 165 170

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
175 180 185

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
190 195 200

Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210

<210> 21
<211> 510
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(507)

<400> 21

```
atg acc gcg ggg agg agg atg gag atg ctc tgt gcc ggc agg gtc cct      48
Met Thr Ala Gly Arg Arg Met Glu Met Leu Cys Ala Gly Arg Val Pro
1               5                  10                  15

gcg ctg ctg ctc tgc ctg ggt ttc cat ctt cta cag gca gtc ctc agt      96
Ala Leu Leu Leu Cys Leu Gly Phe His Leu Leu Gln Ala Val Leu Ser
            20                  25                  30

aca act gtg att cca tca tgt atc cca gga gag tcc agt gat aac tgc     144
Thr Thr Val Ile Pro Ser Cys Ile Pro Gly Glu Ser Ser Asp Asn Cys
        35                  40                  45

aca gct tta gtt cag aca gaa gac aat cca cgt gtg gct caa gtg tca     192
Thr Ala Leu Val Gln Thr Glu Asp Asn Pro Arg Val Ala Gln Val Ser
    50                  55                  60

ata aca aag tgt agc tct gac atg aat ggc tat tgt ttg cat gga cag     240
Ile Thr Lys Cys Ser Ser Asp Met Asn Gly Tyr Cys Leu His Gly Gln
65                  70                  75                  80

tgc atc tat ctg gtg gac atg agt caa aac tac tgc agg tgt gaa gtg     288
Cys Ile Tyr Leu Val Asp Met Ser Gln Asn Tyr Cys Arg Cys Glu Val
                85                  90                  95

ggt tat act ggt gtc cga tgt gaa cac ttc ttt tta acc gtc cac caa     336
Gly Tyr Thr Gly Val Arg Cys Glu His Phe Phe Leu Thr Val His Gln
            100                 105                 110

cct tta agc aaa gag tat gtg gct ttg acc gtg att ctt att att ttg     384
Pro Leu Ser Lys Glu Tyr Val Ala Leu Thr Val Ile Leu Ile Ile Leu
```

115 120 125

ttt ctt atc aca gtc gtc ggt tcc aca tat tat ttc tgc aga tgg tac 432
Phe Leu Ile Thr Val Val Gly Ser Thr Tyr Tyr Phe Cys Arg Trp Tyr
130 135 140

aga aat cga aaa agt aaa gaa cca aag aag gaa tat gag aga gtt acc 480
Arg Asn Arg Lys Ser Lys Glu Pro Lys Lys Glu Tyr Glu Arg Val Thr
145 150 155 160

tca ggg gat cca gag ttg ccg caa gtc tga 510
Ser Gly Asp Pro Glu Leu Pro Gln Val
165

<210> 22
<211> 169
<212> PRT
<213> Homo sapiens

<400> 22

Met Thr Ala Gly Arg Arg Met Glu Met Leu Cys Ala Gly Arg Val Pro
1 5 10 15

Ala Leu Leu Leu Cys Leu Gly Phe His Leu Leu Gln Ala Val Leu Ser
20 25 30

Thr Thr Val Ile Pro Ser Cys Ile Pro Gly Glu Ser Ser Asp Asn Cys
35 40 45

Thr Ala Leu Val Gln Thr Glu Asp Asn Pro Arg Val Ala Gln Val Ser
50 55 60

Ile Thr Lys Cys Ser Ser Asp Met Asn Gly Tyr Cys Leu His Gly Gln
65 70 75 80

Cys Ile Tyr Leu Val Asp Met Ser Gln Asn Tyr Cys Arg Cys Glu Val
85 90 95

Gly Tyr Thr Gly Val Arg Cys Glu His Phe Phe Leu Thr Val His Gln
100 105 110

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

Phe Leu Ile Thr Val Val Gly Ser Thr Tyr Tyr Phe Cys Arg Trp Tyr
130 135 140

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

Ser Gly Asp Pro Glu Leu Pro Gln Val
165

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

<220>

<223> An artificially synthesized peptide sequence

<400> 23

Gly Gly Gly Ser
1

<210> 24
<211> 4
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 24

Ser Gly Gly Gly
1

<210> 25
<211> 5
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 25

Gly Gly Gly Gly Ser
1 5

<210> 26
<211> 5
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 26

Ser Gly Gly Gly Gly
1 5

<210> 27
<211> 6
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 27

Gly Gly Gly Gly Gly Ser
1 5

<210> 28
<211> 6
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 28

Ser Gly Gly Gly Gly Gly
1 5

<210> 29
<211> 7
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 29

Gly Gly Gly Gly Gly Gly Ser
1 5

<210> 30
<211> 7
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 30

Ser Gly Gly Gly Gly Gly Gly
1 5

<210> 31
<211> 5

<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 31

Gly Gly Gly Gly Ser
1 5

<210> 32
<211> 5
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 32

Ser Gly Gly Gly Gly
1 5

<210> 33
<211> 1038
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>

<221> CDS
<222> (1)..(1035)

<400> 33

atg gag atg ctc tgt gcc ggc agg gtc cct gcg ctg ctg ctc tgc ctg 48
Met Glu Met Leu Cys Ala Gly Arg Val Pro Ala Leu Leu Leu Cys Leu
1 5 10 15

ggt ttc cat ctt cta cag gca gtc ctc agt aca act gtg att cca tca 96
Gly Phe His Leu Leu Gln Ala Val Leu Ser Thr Thr Val Ile Pro Ser
20 25 30

tgt atc cca gga gag tcc agt gat aac tgc aca gct tta gtt cag aca 144
Cys Ile Pro Gly Glu Ser Ser Asp Asn Cys Thr Ala Leu Val Gln Thr
35 40 45

gaa gac aat cca cgt gtg gct caa gtg tca ata aca aag tgt agc tct 192
Glu Asp Asn Pro Arg Val Ala Gln Val Ser Ile Thr Lys Cys Ser Ser
50 55 60

gac atg aat ggc tat tgt ttg cat gga cag tgc atc tat ctg gtg gac 240
Asp Met Asn Gly Tyr Cys Leu His Gly Gln Cys Ile Tyr Leu Val Asp
65 70 75 80

atg agt caa aac tac tgc agg tgt gaa gtg ggt tat act ggt gtc cga 288
Met Ser Gln Asn Tyr Cys Arg Cys Glu Val Gly Tyr Thr Gly Val Arg
85 90 95

tgt gaa cac ttc ttt tta acc gtc cac caa cct tta agc aaa gag tat 336
Cys Glu His Phe Phe Leu Thr Val His Gln Pro Leu Ser Lys Glu Tyr
100 105 110

gtg gct cgc gga ccg aca atc aag ccc tgt cct cca tgc aaa tgc cca 384
Val Ala Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
115 120 125

gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag 432
Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
130 135 140

atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg 480
Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
145 150 155 160

gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt 528
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe
165 170 175

gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag 576
Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
180 185 190

gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac 624
Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
195 200 205

cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa 672
Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
210 215 220

gac ctc cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca 720
Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
225 230 235 240

gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag atg 768
Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
245 250 255

act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg cct 816
Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
260 265 270

gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta aac 864
Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
275 280 285

tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc atg 912
Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
290 295 300

tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat agc 960
Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser
305 310 315 320

tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg act 1008
Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
325 330 335

aag agc ttc tcc cgg act ccg ggt aaa tga 1038
Lys Ser Phe Ser Arg Thr Pro Gly Lys
340 345

<210> 34
<211> 345
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 34

Met Glu Met Leu Cys Ala Gly Arg Val Pro Ala Leu Leu Leu Cys Leu
1 5 10 15

Gly Phe His Leu Leu Gln Ala Val Leu Ser Thr Thr Val Ile Pro Ser

20 25 30

Cys Ile Pro Gly Glu Ser Ser Asp Asn Cys Thr Ala Leu Val Gln Thr
35 40 45

Glu Asp Asn Pro Arg Val Ala Gln Val Ser Ile Thr Lys Cys Ser Ser
50 55 60

Asp Met Asn Gly Tyr Cys Leu His Gly Gln Cys Ile Tyr Leu Val Asp
65 70 75 80

Met Ser Gln Asn Tyr Cys Arg Cys Glu Val Gly Tyr Thr Gly Val Arg
85 90 95

Cys Glu His Phe Phe Leu Thr Val His Gln Pro Leu Ser Lys Glu Tyr
100 105 110

Val Ala Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro
115 120 125

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
130 135 140

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
145 150 155 160

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe

165 170 175

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu
180 185 190

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His
195 200 205

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

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser
225 230 235 240

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met
245 250 255

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro
260 265 270

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn
275 280 285

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met
290 295 300

Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser

305 310 315 320

Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr
325 330 335

Lys Ser Phe Ser Arg Thr Pro Gly Lys
340 345

<210> 35
<211> 3633
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(3630)

<400> 35
atg cga ccc tcc ggg acg gcc ggg gca gcg ctc ctg gcg ctg ctg gct 48
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

gcg ctc tgc ccg gcg agt cgg gct ctg gag gaa aag aaa gtt tgc caa 96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt 144
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat 192
Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn

50 55 60

ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc tta aag 240
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg 288
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac 336
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat 384
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg 432
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac gtg gag 480
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc aac atg 528
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca 576
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac tgc cag 624
Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln

195 200 205

aaa ctg acc aaa atc atc tgt gcc cag cag tgc tcc ggg cgc tgc cgt 672
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc 720
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc cga gac 768
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac aac ccc 816
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc ttt ggt 864
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac 912
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa 960
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg 1008
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat 1056
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn

340 345 350

gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat 1104
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act 1152
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa 1200
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac 1248
Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa 1296
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg 1344
His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca 1392
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg 1440
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa 1488
Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu

485 490 495

aac agc tgc aag gcc aca ggc cag gtc tgc cat gcc ttg tgc tcc ccc 1536
Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc tct tgc cgg aat 1584
Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac ctt ctg gag ggt 1632
Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

gag cca agg gag ttt gtg gag aac tct gag tgc ata cag tgc cac cca 1680
Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

gag tgc ctg cct cag gcc atg aac atc acc tgc aca gga cgg gga cca 1728
Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac tgc gtc 1776
Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg gtc tgg 1824
Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca aac tgc 1872
Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

acc tac gga tgc act ggg cca ggt ctt gaa ggc tgt cca acg aat ggg 1920
Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly

625 630 635 640

cct aag atc ccg tcc atc gcc act ggg atg gtg ggg gcc ctc ctc ttg 1968
Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

ctg ctg gtg gtg gcc ctg ggg atc ggc ctc ttc atg cga agg cgc cac 2016
Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

atc gtt cgg aag cgc acg ctg cgg agg ctg ctg cag gag agg gag ctt 2064
Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

gtg gag cct ctt aca ccc agt gga gaa gct ccc aac caa gct ctc ttg 2112
Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

agg atc ttg aag gaa act gaa ttc aaa aag atc aaa gtg ctg ggc tcc 2160
Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

ggt gcg ttc ggc acg gtg tat aag gga ctc tgg atc cca gaa ggt gag 2208
Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

aaa gtt aaa att ccc gtc gct atc aag gaa tta aga gaa gca aca tct 2256
Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

ccg aaa gcc aac aag gaa atc ctc gat gaa gcc tac gtg atg gcc agc 2304
Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

gtg gac aac ccc cac gtg tgc cgc ctg ctg ggc atc tgc ctc acc tcc 2352
Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser

770 775 780

acc gtg cag ctc atc acg cag ctc atg ccc ttc ggc tgc ctc ctg gac 2400
Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

tat gtc cgg gaa cac aaa gac aat att ggc tcc cag tac ctg ctc aac 2448
Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

tgg tgt gtg cag atc gca aag ggc atg aac tac ttg gag gac cgt cgc 2496
Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

ttg gtg cac cgc gac ctg gca gcc agg aac gta ctg gtg aaa aca ccg 2544
Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

cag cat gtc aag atc aca gat ttt ggg ctg gcc aaa ctg ctg ggt gcg 2592
Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

gaa gag aaa gaa tac cat gca gaa gga ggc aaa gtg cct atc aag tgg 2640
Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

atg gca ttg gaa tca att tta cac aga atc tat acc cac cag agt gat 2688
Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

gtc tgg agc tac ggg gtg acc gtt tgg gag ttg atg acc ttt gga tcc 2736
Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

aag cca tat gac gga atc cct gcc agc gag atc tcc tcc atc ctg gag 2784
Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu

915 920 925

aaa gga gaa cgc ctc cct cag cca ccc ata tgt acc atc gat gtc tac 2832
Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

atg atc atg gtc aag tgc tgg atg ata gac gca gat agt cgc cca aag 2880
Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

ttc cgt gag ttg atc atc gaa ttc tcc aaa atg gcc cga gac ccc cag 2928
Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

cgc tac ctt gtc att cag ggg gat gaa aga atg cat ttg cca agt cct 2976
Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980 985 990

aca gac tcc aac ttc tac cgt gcc ctg atg gat gaa gaa gac atg gac 3024
Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995 1000 1005

gac gtg gtg gat gcc gac gag tac ctc atc cca cag cag ggc ttc 3069
Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010 1015 1020

ttc agc agc ccc tcc acg tca cgg act ccc ctc ctg agc tct ctg 3114
Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
1025 1030 1035

agt gca acc agc aac aat tcc acc gtg gct tgc att gat aga aat 3159
Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
1040 1045 1050

ggg ctg caa agc tgt ccc atc aag gaa gac agc ttc ttg cag cga 3204
Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg

```
1055                1060                1065

tac agc  tca gac ccc aca ggc  gcc ttg act gag gac  agc ata gac      3249
Tyr Ser  Ser Asp Pro Thr Gly  Ala Leu Thr Glu Asp  Ser Ile Asp
    1070                1075                1080

gac acc  ttc ctc cca gtg cct  gaa tac ata aac cag  tcc gtt ccc      3294
Asp Thr  Phe Leu Pro Val Pro  Glu Tyr Ile Asn Gln  Ser Val Pro
    1085                1090                1095

aaa agg  ccc gct ggc tct gtg  cag aat cct gtc tat  cac aat cag      3339
Lys Arg  Pro Ala Gly Ser Val  Gln Asn Pro Val Tyr  His Asn Gln
    1100                1105                1110

cct ctg  aac ccc gcg ccc agc  aga gac cca cac tac  cag gac ccc      3384
Pro Leu  Asn Pro Ala Pro Ser  Arg Asp Pro His Tyr  Gln Asp Pro
    1115                1120                1125

cac agc  act gca gtg ggc aac  ccc gag tat ctc aac  act gtc cag      3429
His Ser  Thr Ala Val Gly Asn  Pro Glu Tyr Leu Asn  Thr Val Gln
    1130                1135                1140

ccc acc  tgt gtc aac agc aca  ttc gac agc cct gcc  cac tgg gcc      3474
Pro Thr  Cys Val Asn Ser Thr  Phe Asp Ser Pro Ala  His Trp Ala
    1145                1150                1155

cag aaa  ggc agc cac caa att  agc ctg gac aac cct  gac tac cag      3519
Gln Lys  Gly Ser His Gln Ile  Ser Leu Asp Asn Pro  Asp Tyr Gln
    1160                1165                1170

cag gac  ttc ttt ccc aag gaa  gcc aag cca aat ggc  atc ttt aag      3564
Gln Asp  Phe Phe Pro Lys Glu  Ala Lys Pro Asn Gly  Ile Phe Lys
    1175                1180                1185

ggc tcc  aca gct gaa aat gca  gaa tac cta agg gtc  gcg cca caa      3609
Gly Ser  Thr Ala Glu Asn Ala  Glu Tyr Leu Arg Val  Ala Pro Gln
```

1190 1195 1200

agc agt gaa ttt att gga gca tga 3633
Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 36
<211> 1210
<212> PRT
<213> Homo sapiens

<400> 36

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
645 650 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
660 665 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
675 680 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
690 695 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705 710 715 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
725 730 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
740 745 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
755 760 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
770 775 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785 790 795 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
805 810 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
820 825 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
835 840 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
850 855 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865 870 875 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
885 890 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
900 905 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
915 920 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
930 935 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945 950 955 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
965 970 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
980 985 990

Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp Met Asp
995 1000 1005

Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln Gly Phe
1010 1015 1020

Phe Ser Ser Pro Ser Thr Ser Arg Thr Pro Leu Leu Ser Ser Leu
1025 1030 1035

Ser Ala Thr Ser Asn Asn Ser Thr Val Ala Cys Ile Asp Arg Asn
1040 1045 1050

Gly Leu Gln Ser Cys Pro Ile Lys Glu Asp Ser Phe Leu Gln Arg
1055 1060 1065

Tyr Ser Ser Asp Pro Thr Gly Ala Leu Thr Glu Asp Ser Ile Asp
1070 1075 1080

Asp Thr Phe Leu Pro Val Pro Glu Tyr Ile Asn Gln Ser Val Pro
1085 1090 1095

Lys Arg Pro Ala Gly Ser Val Gln Asn Pro Val Tyr His Asn Gln
1100 1105 1110

Pro Leu Asn Pro Ala Pro Ser Arg Asp Pro His Tyr Gln Asp Pro
1115 1120 1125

His Ser Thr Ala Val Gly Asn Pro Glu Tyr Leu Asn Thr Val Gln
1130 1135 1140

Pro Thr Cys Val Asn Ser Thr Phe Asp Ser Pro Ala His Trp Ala
1145 1150 1155

Gln Lys Gly Ser His Gln Ile Ser Leu Asp Asn Pro Asp Tyr Gln
1160 1165 1170

Gln Asp Phe Phe Pro Lys Glu Ala Lys Pro Asn Gly Ile Phe Lys
1175 1180 1185

Gly Ser Thr Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro Gln
1190 1195 1200

Ser Ser Glu Phe Ile Gly Ala
1205 1210

<210> 37
<211> 2514

<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(2511)

<400> 37

```
atg gta ggg ctg gga gcc tgc acc ctg act gga gtt acc ctg atc ttc      48
Met Val Gly Leu Gly Ala Cys Thr Leu Thr Gly Val Thr Leu Ile Phe
1               5                  10                  15

ttg cta ctc ccc aga agt ctg gag agc tgt gga cac atc gag att tca      96
Leu Leu Leu Pro Arg Ser Leu Glu Ser Cys Gly His Ile Glu Ile Ser
            20                  25                  30

ccc cct gtt gtc cgc ctg ggg gac cct gtc ctg gcc tct tgc acc atc     144
Pro Pro Val Val Arg Leu Gly Asp Pro Val Leu Ala Ser Cys Thr Ile
        35                  40                  45

agc cca aac tgc agc aaa ctg gac caa cag gca aag atc tta tgg aga     192
Ser Pro Asn Cys Ser Lys Leu Asp Gln Gln Ala Lys Ile Leu Trp Arg
    50                  55                  60

ctg caa gat gag ccc atc caa cct ggg gac aga cag cat cat ctg cct     240
Leu Gln Asp Glu Pro Ile Gln Pro Gly Asp Arg Gln His His Leu Pro
65                  70                  75                  80

gat ggg acc caa gag tcc ctc atc act ctg cct cac ttg aac tac acc     288
Asp Gly Thr Gln Glu Ser Leu Ile Thr Leu Pro His Leu Asn Tyr Thr
                85                  90                  95

cag gcc ttc ctc ttc tgc tta gtg cca tgg gaa gac agc gtc caa ctc     336
Gln Ala Phe Leu Phe Cys Leu Val Pro Trp Glu Asp Ser Val Gln Leu
            100                 105                 110
```

ctg gat caa gct gag ctt cac gca ggc tat ccc cct gcc agc ccc tca 384
Leu Asp Gln Ala Glu Leu His Ala Gly Tyr Pro Pro Ala Ser Pro Ser
115 120 125

aac cta tcc tgc ctc atg cac ctc acc acc aac agc ctg gtc tgc cag 432
Asn Leu Ser Cys Leu Met His Leu Thr Thr Asn Ser Leu Val Cys Gln
130 135 140

tgg gag cca ggt cct gag acc cac ctg ccc acc agc ttc atc cta aag 480
Trp Glu Pro Gly Pro Glu Thr His Leu Pro Thr Ser Phe Ile Leu Lys
145 150 155 160

agc ttc agg agc cgc gcc gac tgt cag tac caa ggg gac acc atc ccg 528
Ser Phe Arg Ser Arg Ala Asp Cys Gln Tyr Gln Gly Asp Thr Ile Pro
165 170 175

gat tgt gtg gca aag aag agg cag aac aac tgc tcc atc ccc cga aaa 576
Asp Cys Val Ala Lys Lys Arg Gln Asn Asn Cys Ser Ile Pro Arg Lys
180 185 190

aac ttg ctc ctg tac cag tat atg gcc atc tgg gtg caa gca gag aat 624
Asn Leu Leu Leu Tyr Gln Tyr Met Ala Ile Trp Val Gln Ala Glu Asn
195 200 205

atg cta ggg tcc agc gag tcc cca aag ctg tgc ctc gac ccc atg gat 672
Met Leu Gly Ser Ser Glu Ser Pro Lys Leu Cys Leu Asp Pro Met Asp
210 215 220

gtt gtg aaa ttg gag cct ccc atg ctg cag gcc ctg gac att ggc cct 720
Val Val Lys Leu Glu Pro Pro Met Leu Gln Ala Leu Asp Ile Gly Pro
225 230 235 240

gat gta gtc tct cac cag cct ggc tgc ctg tgg ctg agc tgg aag cca 768
Asp Val Val Ser His Gln Pro Gly Cys Leu Trp Leu Ser Trp Lys Pro
245 250 255

tgg aag ccc agt gag tac atg gaa cag gag tgt gaa ctt cgc tac cag 816
Trp Lys Pro Ser Glu Tyr Met Glu Gln Glu Cys Glu Leu Arg Tyr Gln
260 265 270

cca cag ctc aaa gga gcc aac tgg act ctg gtg ttc cac ctg cct tcc 864
Pro Gln Leu Lys Gly Ala Asn Trp Thr Leu Val Phe His Leu Pro Ser
275 280 285

agc aag gac cag ttt gag ctc tgc ggg ctc cat cag gcc cca gtc tac 912
Ser Lys Asp Gln Phe Glu Leu Cys Gly Leu His Gln Ala Pro Val Tyr
290 295 300

acc cta cag atg cga tgc att cgc tca tct ctg cct gga ttc tgg agc 960
Thr Leu Gln Met Arg Cys Ile Arg Ser Ser Leu Pro Gly Phe Trp Ser
305 310 315 320

ccc tgg agc ccc ggc ctg cag ctg agg cct acc atg aag gcc ccc acc 1008
Pro Trp Ser Pro Gly Leu Gln Leu Arg Pro Thr Met Lys Ala Pro Thr
325 330 335

atc aga ctg gac acg tgg tgt cag aag aag caa cta gat cca ggg aca 1056
Ile Arg Leu Asp Thr Trp Cys Gln Lys Lys Gln Leu Asp Pro Gly Thr
340 345 350

gtg agt gtg cag ctg ttc tgg aag cca acg ccc ctg cag gaa gac agt 1104
Val Ser Val Gln Leu Phe Trp Lys Pro Thr Pro Leu Gln Glu Asp Ser
355 360 365

gga cag atc cag ggc tac ctg ctg tcc tgg aat tcc cca gat cat caa 1152
Gly Gln Ile Gln Gly Tyr Leu Leu Ser Trp Asn Ser Pro Asp His Gln
370 375 380

ggg cag gac ata cac ctt tgc aac acc acg cag ctc agc tgt atc ttc 1200
Gly Gln Asp Ile His Leu Cys Asn Thr Thr Gln Leu Ser Cys Ile Phe
385 390 395 400

ctc ctg ccc tca gag gcc cag aac gtg acc ctt gtg gcc tac aac aaa 1248
Leu Leu Pro Ser Glu Ala Gln Asn Val Thr Leu Val Ala Tyr Asn Lys
405 410 415

gca ggg acc tct tca cct act aca gtg gtt ttc ctg gag aac gaa ggt 1296
Ala Gly Thr Ser Ser Pro Thr Thr Val Val Phe Leu Glu Asn Glu Gly
420 425 430

cca gct gtg acc gga ctc cat gcc atg gcc caa gac ctt aac acc atc 1344
Pro Ala Val Thr Gly Leu His Ala Met Ala Gln Asp Leu Asn Thr Ile
435 440 445

tgg gta gac tgg gaa gcc ccc agc ctt ctg cct cag ggc tat ctc att 1392
Trp Val Asp Trp Glu Ala Pro Ser Leu Leu Pro Gln Gly Tyr Leu Ile
450 455 460

gag tgg gaa atg agt tct ccc agc tac aat aac agc tat aag tcc tgg 1440
Glu Trp Glu Met Ser Ser Pro Ser Tyr Asn Asn Ser Tyr Lys Ser Trp
465 470 475 480

atg ata gaa cct aac ggg aac atc act gga att ctg tta aag gac aac 1488
Met Ile Glu Pro Asn Gly Asn Ile Thr Gly Ile Leu Leu Lys Asp Asn
485 490 495

ata aat ccc ttt cag ctc tac aga att aca gtg gct ccc ctg tac cca 1536
Ile Asn Pro Phe Gln Leu Tyr Arg Ile Thr Val Ala Pro Leu Tyr Pro
500 505 510

ggc atc gtg gga ccc cct gta aat gtc tac acc ttc gct gga gag aga 1584
Gly Ile Val Gly Pro Pro Val Asn Val Tyr Thr Phe Ala Gly Glu Arg
515 520 525

gct cct cct cat gct cca gcg ctg cat cta aag cat gtt ggc aca acc 1632
Ala Pro Pro His Ala Pro Ala Leu His Leu Lys His Val Gly Thr Thr
530 535 540

tgg gca cag ctg gag tgg gta cct gag gcc cct agg ctg ggg atg ata 1680
Trp Ala Gln Leu Glu Trp Val Pro Glu Ala Pro Arg Leu Gly Met Ile
545 550 555 560

ccc ctc acc cac tac acc atc ttc tgg gcc gat gct ggg gac cac tcc 1728
Pro Leu Thr His Tyr Thr Ile Phe Trp Ala Asp Ala Gly Asp His Ser
565 570 575

ttc tcc gtc acc cta aac atc tcc ctc cat gac ttt gtc ctg aag cac 1776
Phe Ser Val Thr Leu Asn Ile Ser Leu His Asp Phe Val Leu Lys His
580 585 590

ctg gag ccc gcc agt ttg tat cat gtc tac ctc atg gcc acc agt cga 1824
Leu Glu Pro Ala Ser Leu Tyr His Val Tyr Leu Met Ala Thr Ser Arg
595 600 605

gca ggg tcc acc aat agt aca ggc ctt acc ctg agg acc cta gat cca 1872
Ala Gly Ser Thr Asn Ser Thr Gly Leu Thr Leu Arg Thr Leu Asp Pro
610 615 620

tct gac tta aac att ttc ctg ggc ata ctt tgc tta gta ctc ttg tcc 1920
Ser Asp Leu Asn Ile Phe Leu Gly Ile Leu Cys Leu Val Leu Leu Ser
625 630 635 640

act acc tgt gta gtg acc tgg ctc tgc tgc aaa cgc aga gga aag act 1968
Thr Thr Cys Val Val Thr Trp Leu Cys Cys Lys Arg Arg Gly Lys Thr
645 650 655

tcc ttc tgg tca gat gtg cca gac cca gcc cac agt agc ctg agc tcc 2016
Ser Phe Trp Ser Asp Val Pro Asp Pro Ala His Ser Ser Leu Ser Ser
660 665 670

tgg ttg ccc acc atc atg aca gag gaa acc ttc cag tta ccc agc ttc 2064
Trp Leu Pro Thr Ile Met Thr Glu Glu Thr Phe Gln Leu Pro Ser Phe
675 680 685

```
tgg gac tcc agc gtg cca tca atc acc aag atc act gaa ctg gag gaa     2112
Trp Asp Ser Ser Val Pro Ser Ile Thr Lys Ile Thr Glu Leu Glu Glu
    690                 695                 700

gac aag aaa ccg acc cac tgg gat tcc gaa agc tct ggg aat ggt agc     2160
Asp Lys Lys Pro Thr His Trp Asp Ser Glu Ser Ser Gly Asn Gly Ser
705                 710                 715                 720

ctt cca gcc ctg gtt cag gcc tat gtg ctc caa gga gat cca aga gaa     2208
Leu Pro Ala Leu Val Gln Ala Tyr Val Leu Gln Gly Asp Pro Arg Glu
                725                 730                 735

att tcc aac cag tcc cag cct ccc tct cgc act ggt gac cag gtc ctc     2256
Ile Ser Asn Gln Ser Gln Pro Pro Ser Arg Thr Gly Asp Gln Val Leu
            740                 745                 750

tat ggt cag gtg ctt gag agc ccc acc agc cca gga gta atg cag tac     2304
Tyr Gly Gln Val Leu Glu Ser Pro Thr Ser Pro Gly Val Met Gln Tyr
        755                 760                 765

att cgc tct gac tcc act cag ccc ctc ttg ggg ggc ccc acc cct agc     2352
Ile Arg Ser Asp Ser Thr Gln Pro Leu Leu Gly Gly Pro Thr Pro Ser
    770                 775                 780

cct aaa tct tat gaa aac atc tgg ttc cat tca aga ccc cag gag acc     2400
Pro Lys Ser Tyr Glu Asn Ile Trp Phe His Ser Arg Pro Gln Glu Thr
785                 790                 795                 800

ttt gtg ccc caa cct cca aac cag gaa gat gac tgt gtc ttt ggg cct     2448
Phe Val Pro Gln Pro Pro Asn Gln Glu Asp Asp Cys Val Phe Gly Pro
                805                 810                 815

cca ttt gat ttt ccc ctc ttt cag ggg ctc cag gtc cat gga gtt gaa     2496
Pro Phe Asp Phe Pro Leu Phe Gln Gly Leu Gln Val His Gly Val Glu
            820                 825                 830
```

gaa caa ggg ggt ttc tag 2514
Glu Gln Gly Gly Phe
835

<210> 38
<211> 837
<212> PRT
<213> Mus musculus

<400> 38

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

Leu Leu Leu Pro Arg Ser Leu Glu Ser Cys Gly His Ile Glu Ile Ser
20 25 30

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

Ser Pro Asn Cys Ser Lys Leu Asp Gln Gln Ala Lys Ile Leu Trp Arg
50 55 60

Leu Gln Asp Glu Pro Ile Gln Pro Gly Asp Arg Gln His His Leu Pro
65 70 75 80

Asp Gly Thr Gln Glu Ser Leu Ile Thr Leu Pro His Leu Asn Tyr Thr
85 90 95

Gln Ala Phe Leu Phe Cys Leu Val Pro Trp Glu Asp Ser Val Gln Leu
100 105 110

Leu Asp Gln Ala Glu Leu His Ala Gly Tyr Pro Pro Ala Ser Pro Ser
115 120 125

Asn Leu Ser Cys Leu Met His Leu Thr Thr Asn Ser Leu Val Cys Gln
130 135 140

Trp Glu Pro Gly Pro Glu Thr His Leu Pro Thr Ser Phe Ile Leu Lys
145 150 155 160

Ser Phe Arg Ser Arg Ala Asp Cys Gln Tyr Gln Gly Asp Thr Ile Pro
165 170 175

Asp Cys Val Ala Lys Lys Arg Gln Asn Asn Cys Ser Ile Pro Arg Lys
180 185 190

Asn Leu Leu Leu Tyr Gln Tyr Met Ala Ile Trp Val Gln Ala Glu Asn
195 200 205

Met Leu Gly Ser Ser Glu Ser Pro Lys Leu Cys Leu Asp Pro Met Asp
210 215 220

Val Val Lys Leu Glu Pro Pro Met Leu Gln Ala Leu Asp Ile Gly Pro
225 230 235 240

Asp Val Val Ser His Gln Pro Gly Cys Leu Trp Leu Ser Trp Lys Pro
245 250 255

Trp Lys Pro Ser Glu Tyr Met Glu Gln Glu Cys Glu Leu Arg Tyr Gln
260 265 270

Pro Gln Leu Lys Gly Ala Asn Trp Thr Leu Val Phe His Leu Pro Ser
275 280 285

Ser Lys Asp Gln Phe Glu Leu Cys Gly Leu His Gln Ala Pro Val Tyr
290 295 300

Thr Leu Gln Met Arg Cys Ile Arg Ser Ser Leu Pro Gly Phe Trp Ser
305 310 315 320

Pro Trp Ser Pro Gly Leu Gln Leu Arg Pro Thr Met Lys Ala Pro Thr
325 330 335

Ile Arg Leu Asp Thr Trp Cys Gln Lys Lys Gln Leu Asp Pro Gly Thr
340 345 350

Val Ser Val Gln Leu Phe Trp Lys Pro Thr Pro Leu Gln Glu Asp Ser
355 360 365

Gly Gln Ile Gln Gly Tyr Leu Leu Ser Trp Asn Ser Pro Asp His Gln
370 375 380

Gly Gln Asp Ile His Leu Cys Asn Thr Thr Gln Leu Ser Cys Ile Phe
385 390 395 400

Leu Leu Pro Ser Glu Ala Gln Asn Val Thr Leu Val Ala Tyr Asn Lys
405 410 415

Ala Gly Thr Ser Ser Pro Thr Thr Val Val Phe Leu Glu Asn Glu Gly
420 425 430

Pro Ala Val Thr Gly Leu His Ala Met Ala Gln Asp Leu Asn Thr Ile
435 440 445

Trp Val Asp Trp Glu Ala Pro Ser Leu Leu Pro Gln Gly Tyr Leu Ile
450 455 460

Glu Trp Glu Met Ser Ser Pro Ser Tyr Asn Asn Ser Tyr Lys Ser Trp
465 470 475 480

Met Ile Glu Pro Asn Gly Asn Ile Thr Gly Ile Leu Leu Lys Asp Asn
485 490 495

Ile Asn Pro Phe Gln Leu Tyr Arg Ile Thr Val Ala Pro Leu Tyr Pro
500 505 510

Gly Ile Val Gly Pro Pro Val Asn Val Tyr Thr Phe Ala Gly Glu Arg
515 520 525

Ala Pro Pro His Ala Pro Ala Leu His Leu Lys His Val Gly Thr Thr
530 535 540

Trp Ala Gln Leu Glu Trp Val Pro Glu Ala Pro Arg Leu Gly Met Ile
545 550 555 560

Pro Leu Thr His Tyr Thr Ile Phe Trp Ala Asp Ala Gly Asp His Ser
565 570 575

Phe Ser Val Thr Leu Asn Ile Ser Leu His Asp Phe Val Leu Lys His
580 585 590

Leu Glu Pro Ala Ser Leu Tyr His Val Tyr Leu Met Ala Thr Ser Arg
595 600 605

Ala Gly Ser Thr Asn Ser Thr Gly Leu Thr Leu Arg Thr Leu Asp Pro
610 615 620

Ser Asp Leu Asn Ile Phe Leu Gly Ile Leu Cys Leu Val Leu Leu Ser
625 630 635 640

Thr Thr Cys Val Val Thr Trp Leu Cys Cys Lys Arg Arg Gly Lys Thr
645 650 655

Ser Phe Trp Ser Asp Val Pro Asp Pro Ala His Ser Ser Leu Ser Ser
660 665 670

Trp Leu Pro Thr Ile Met Thr Glu Glu Thr Phe Gln Leu Pro Ser Phe
675 680 685

Trp Asp Ser Ser Val Pro Ser Ile Thr Lys Ile Thr Glu Leu Glu Glu
690 695 700

Asp Lys Lys Pro Thr His Trp Asp Ser Glu Ser Ser Gly Asn Gly Ser
705 710 715 720

Leu Pro Ala Leu Val Gln Ala Tyr Val Leu Gln Gly Asp Pro Arg Glu
725 730 735

Ile Ser Asn Gln Ser Gln Pro Pro Ser Arg Thr Gly Asp Gln Val Leu
740 745 750

Tyr Gly Gln Val Leu Glu Ser Pro Thr Ser Pro Gly Val Met Gln Tyr
755 760 765

Ile Arg Ser Asp Ser Thr Gln Pro Leu Leu Gly Gly Pro Thr Pro Ser
770 775 780

Pro Lys Ser Tyr Glu Asn Ile Trp Phe His Ser Arg Pro Gln Glu Thr
785 790 795 800

Phe Val Pro Gln Pro Pro Asn Gln Glu Asp Asp Cys Val Phe Gly Pro
805 810 815

Pro Phe Asp Phe Pro Leu Phe Gln Gly Leu Gln Val His Gly Val Glu
820 825 830

Glu Gln Gly Gly Phe
835

<210> 39
<211> 2583
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(2580)

<400> 39
atg cga cct tcc ggg acg gcc ggg gca gcg ctc ctg gcg ctg ctg gct 48
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

gcg ctc tgc ccg gcg agt cgg gct ctg gag gaa aag aaa gtt tgc caa 96
Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat cat ttt 144
Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt ggg aat 192

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc tta aag 240
Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65 70 75 80

acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac aca gtg 288
Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat atg tac 336
Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat gca aat 384
Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa atc ctg 432
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aat gtg gag 480
His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc aac atg 528
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt gat cca 576
Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac tgc cag 624

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

aaa ctg acc aaa atc atc tgt gcc cag cag tgc tcc ggg cgc tgc cgt 672
Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca ggc tgc 720
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc cga gac 768
Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac aac ccc 816
Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc ttt ggt 864
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca gat cac 912
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg gag gaa 960
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc aaa gtg 1008
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

tgt aac gga ata ggt att ggt gaa ttt aaa gac tca ctc tcc ata aat 1056

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

gct acg aat att aaa cac ttc aaa aac tgc acc tcc atc agt ggc gat 1104
Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

ctc cac atc ctg ccg gtg gca ttt agg ggt gac tcc ttc aca cat act 1152
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

cct cct ctg gat cca cag gaa ctg gat att ctg aaa acc gta aag gaa 1200
Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

atc aca ggg ttt ttg ctg att cag gct tgg cct gaa aac agg acg gac 1248
Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

ctc cat gcc ttt gag aac cta gaa atc ata cgc ggc agg acc aag caa 1296
Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

cat ggt cag ttt tct ctt gca gtc gtc agc ctg aac ata aca tcc ttg 1344
His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

gga tta cgc tcc ctc aag gag ata agt gat gga gat gtg ata att tca 1392
Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

gga aac aaa aat ttg tgc tat gca aat aca ata aac tgg aaa aaa ctg 1440
Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

ttt ggg acc tcc ggt cag aaa acc aaa att ata agc aac aga ggt gaa 1488

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

aac agc tgc aag gcc aca ggc cag gtc tgc cat gcc ttg tgc tcc ccc 1536
Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

gag ggc tgc tgg ggc ccg gag ccc agg gac tgc gtc tct tgc cgg aat 1584
Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

gtc agc cga ggc agg gaa tgc gtg gac aag tgc aac ctt ctg gag ggt 1632
Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

gag cca agg gag ttt gtg gag aac tct gag tgc ata cag tgc cac cca 1680
Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

gag tgc ctg cct cag gcc atg aac atc acc tgc aca gga cgg gga cca 1728
Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac tgc gtc 1776
Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg gtc tgg 1824
Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca aac tgc 1872
Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

acc tac gga tgc act ggg cca ggt ctt gaa ggc tgt cca acg aat ggg 1920

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

cct aag atc ccg tcc gat cca tct gac tta aac att ttc ctg gag atc 1968
Pro Lys Ile Pro Ser Asp Pro Ser Asp Leu Asn Ile Phe Leu Glu Ile
645 650 655

ctt tgc tta gta ctc ttg tcc act acc tgt gta gtg acc tgg ctc tgc 2016
Leu Cys Leu Val Leu Leu Ser Thr Thr Cys Val Val Thr Trp Leu Cys
660 665 670

tgc aaa cgc aga gga aag act tcc ttc tgg tca gat gtg cca gac cca 2064
Cys Lys Arg Arg Gly Lys Thr Ser Phe Trp Ser Asp Val Pro Asp Pro
675 680 685

gcc cac agt agc ctg agc tcc tgg ttg ccc acc atc atg aca gag gaa 2112
Ala His Ser Ser Leu Ser Ser Trp Leu Pro Thr Ile Met Thr Glu Glu
690 695 700

acc ttc cag tta ccc agc ttc tgg gac tcc agc gtg cca tca atc acc 2160
Thr Phe Gln Leu Pro Ser Phe Trp Asp Ser Ser Val Pro Ser Ile Thr
705 710 715 720

aag atc act gaa ctg gag gaa gac aag aaa ccg acc cac tgg gat tcc 2208
Lys Ile Thr Glu Leu Glu Glu Asp Lys Lys Pro Thr His Trp Asp Ser
725 730 735

gaa agc tct ggg aat ggt agc ctt cca gcc ctg gtt cag gcc tat gtg 2256
Glu Ser Ser Gly Asn Gly Ser Leu Pro Ala Leu Val Gln Ala Tyr Val
740 745 750

ctc caa gga gat cca aga gaa att tcc aac cag tcc cag cct ccc tct 2304
Leu Gln Gly Asp Pro Arg Glu Ile Ser Asn Gln Ser Gln Pro Pro Ser
755 760 765

cgc act ggt gac cag gtc ctc tat ggt cag gtg ctt gag agc ccc acc 2352

Arg Thr Gly Asp Gln Val Leu Tyr Gly Gln Val Leu Glu Ser Pro Thr
770 775 780

agc cca gga gta atg cag tac att cgc tct gac tcc act cag ccc ctc 2400
Ser Pro Gly Val Met Gln Tyr Ile Arg Ser Asp Ser Thr Gln Pro Leu
785 790 795 800

ttg ggg ggc ccc acc cct agc cct aaa tct tat gaa aac atc tgg ttc 2448
Leu Gly Gly Pro Thr Pro Ser Pro Lys Ser Tyr Glu Asn Ile Trp Phe
805 810 815

cat tca aga ccc cag gag acc ttt gtg ccc caa cct cca aac cag gaa 2496
His Ser Arg Pro Gln Glu Thr Phe Val Pro Gln Pro Pro Asn Gln Glu
820 825 830

gat gac tgt gtc ttt ggg cct cca ttt gat ttt ccc ctc ttt cag ggg 2544
Asp Asp Cys Val Phe Gly Pro Pro Phe Asp Phe Pro Leu Phe Gln Gly
835 840 845

ctc cag gtc cat gga gtt gaa gaa caa ggg ggt ttc tag 2583
Leu Gln Val His Gly Val Glu Glu Gln Gly Gly Phe
850 855 860

<210> 40
<211> 860
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 40

Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn
50 55 60

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

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
85 90 95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
100 105 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
115 120 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
130 135 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145 150 155 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
165 170 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
180 185 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
195 200 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
210 215 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225 230 235 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
245 250 255

Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
260 265 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
275 280 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
290 295 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 310 315 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
325 330 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
340 345 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 360 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
370 375 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385 390 395 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
405 410 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
420 425 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
435 440 445

Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
450 455 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465 470 475 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
485 490 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
500 505 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
515 520 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
530 535 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545 550 555 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
565 570 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
580 585 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
595 600 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
610 615 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625 630 635 640

Pro Lys Ile Pro Ser Asp Pro Ser Asp Leu Asn Ile Phe Leu Glu Ile
645 650 655

Leu Cys Leu Val Leu Leu Ser Thr Thr Cys Val Val Thr Trp Leu Cys
660 665 670

Cys Lys Arg Arg Gly Lys Thr Ser Phe Trp Ser Asp Val Pro Asp Pro
675 680 685

Ala His Ser Ser Leu Ser Ser Trp Leu Pro Thr Ile Met Thr Glu Glu
690 695 700

Thr Phe Gln Leu Pro Ser Phe Trp Asp Ser Ser Val Pro Ser Ile Thr
705 710 715 720

Lys Ile Thr Glu Leu Glu Glu Asp Lys Lys Pro Thr His Trp Asp Ser
725 730 735

Glu Ser Ser Gly Asn Gly Ser Leu Pro Ala Leu Val Gln Ala Tyr Val
740 745 750

Leu Gln Gly Asp Pro Arg Glu Ile Ser Asn Gln Ser Gln Pro Pro Ser
755 760 765

Arg Thr Gly Asp Gln Val Leu Tyr Gly Gln Val Leu Glu Ser Pro Thr
770 775 780

Ser Pro Gly Val Met Gln Tyr Ile Arg Ser Asp Ser Thr Gln Pro Leu
785 790 795 800

Leu Gly Gly Pro Thr Pro Ser Pro Lys Ser Tyr Glu Asn Ile Trp Phe
805 810 815

His Ser Arg Pro Gln Glu Thr Phe Val Pro Gln Pro Pro Asn Gln Glu
820 825 830

Asp Asp Cys Val Phe Gly Pro Pro Phe Asp Phe Pro Leu Phe Gln Gly
835 840 845

Leu Gln Val His Gly Val Glu Glu Gln Gly Gly Phe
850 855 860

<210> 41
<211> 24

<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized oligonucleotide sequence

<400> 41
caggggccag tggatagacc gatg 24

<210> 42
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized oligonucleotide sequence

<400> 42
gctcactgga tggtgggaag atg 23

<210> 43
<211> 348
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(348)

<220>
<221> V_region
<222> (1)..(348)

<400> 43

gag gat cag ctg cag cag tct ggg gca gag ctt gtg aag cca ggg gcc 48
Glu Asp Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc 96
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

tat ata cag tgg gtg aag ctg agg cct gaa cag ggc ctg gag tgg att 144
Tyr Ile Gln Trp Val Lys Leu Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

gga agg att gat cct ctg aat ggt aat act aaa tat gtc ccg aag ttc 192
Gly Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val Pro Lys Phe
50 55 60

cag ggc aag gcc act ata aca gca gac aca tcc tcc aat aca gcc tac 240
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

ctg caa ctc agc agc ctg aca tct gag gac act gcc gtc tat tac tgt 288
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gtt agg tct ggg acc ctc ttt gac ttc tgg ggc caa ggc acc act ctc 336
Val Arg Ser Gly Thr Leu Phe Asp Phe Trp Gly Gln Gly Thr Thr Leu
100 105 110

aca gtc tcc tca 348
Thr Val Ser Ser
115

<210> 44
<211> 116

<212> PRT

<213> Mus musculus

<400> 44

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

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

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

Gly Arg Ile Asp Pro Leu Asn Gly Asn Thr Lys Tyr Val Pro Lys Phe
50 55 60

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

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

Val Arg Ser Gly Thr Leu Phe Asp Phe Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
115

<210> 45
<211> 318
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(318)

<220>
<221> V_region
<222> (1)..(318)

<400> 45

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

ggc aaa gtc acc atc act tgc aag gca agc caa gac att cac aag tat       96
Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile His Lys Tyr
            20                  25                  30

ata gct tgg tac caa cac aag cct gga aaa ggt cct agg ctg ctc ata      144
Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
        35                  40                  45

cag tac aca tct aca tta cag cca ggc atc cca tca agg ttc agt gga      192
Gln Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aga gat tat tcc ttc agc atc agc aac ctg gag cct      240
Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65                  70                  75                  80
```

gaa gat att gca act tat tat tgt cta cag tat gat aat ctt cgg acg 288
Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Arg Thr
85 90 95

ttc ggt gga ggc acc aag ctg gaa atc aaa 318
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 46
<211> 106
<212> PRT
<213> Mus musculus

<400> 46

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

Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile His Lys Tyr
20 25 30

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

Gln Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 47
ccatggagtt agtttgggca gcagatcc 28

<210> 48
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 48
aac tac tgg atg aac 15
Asn Tyr Trp Met Asn
1 5

<210> 49
<211> 5
<212> PRT
<213> Mus musculus

<400> 49

Asn Tyr Trp Met Asn
1 5

<210> 50
<211> 51
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(51)

<400> 50
agg att cat cct tct gat agt gaa act cac tac aat caa aag ttc aag 48
Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

aac 51
Asn

<210> 51
<211> 17
<212> PRT
<213> Mus musculus

<400> 51

Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe Lys
1 5 10 15

Asn

<210> 52
<211> 24
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(24)

<400> 52
tta tat tac tat act atg gac tac 24
Leu Tyr Tyr Tyr Thr Met Asp Tyr
1 5

<210> 53
<211> 8
<212> PRT
<213> Mus musculus

<400> 53

Leu Tyr Tyr Tyr Thr Met Asp Tyr
1 5

<210> 54
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(33)

<400> 54
aag gca agc caa gac att aac aag aat ata gct 33
Lys Ala Ser Gln Asp Ile Asn Lys Asn Ile Ala
1 5 10

<210> 55
<211> 11
<212> PRT
<213> Mus musculus

<400> 55

Lys Ala Ser Gln Asp Ile Asn Lys Asn Ile Ala
1 5 10

<210> 56
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> CDS

<222> (1)..(21)

<400> 56
tac aca tct aca tta cag cca 21
Tyr Thr Ser Thr Leu Gln Pro
1 5

<210> 57
<211> 7
<212> PRT
<213> Mus musculus

<400> 57

Tyr Thr Ser Thr Leu Gln Pro
1 5

<210> 58
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 58
cta cag tat gat aat ctt ccg tat acg 27
Leu Gln Tyr Asp Asn Leu Pro Tyr Thr
1 5

<210> 59

<211> 9
<212> PRT
<213> Mus musculus

<400> 59

Leu Gln Tyr Asp Asn Leu Pro Tyr Thr
1 5

<210> 60
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 60
agc tac tgg atg cac 15
Ser Tyr Trp Met His
1 5

<210> 61
<211> 5
<212> PRT
<213> Mus musculus

<400> 61

Ser Tyr Trp Met His
1 5

<210> 62
<211> 51
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(51)

<400> 62
gag att aat cct tac aat ggt ggt act aac tac aat gag aag ttc aag 48
Glu Ile Asn Pro Tyr Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

agc 51
Ser

<210> 63
<211> 17
<212> PRT
<213> Mus musculus

<400> 63

Glu Ile Asn Pro Tyr Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 64
<211> 18
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(18)

<400> 64
tgg aag ttg ggg act tac 18
Trp Lys Leu Gly Thr Tyr
1 5

<210> 65
<211> 6
<212> PRT
<213> Mus musculus

<400> 65

Trp Lys Leu Gly Thr Tyr
1 5

<210> 66
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(33)

<400> 66
cgg gca agt cag gaa att agt ggt tac tta agc 33
Arg Ala Ser Gln Glu Ile Ser Gly Tyr Leu Ser
1 5 10

<210> 67
<211> 11
<212> PRT
<213> Mus musculus

<400> 67

Arg Ala Ser Gln Glu Ile Ser Gly Tyr Leu Ser
1 5 10

<210> 68
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(21)

<400> 68
gcc gca tcc act tta gat tct 21
Ala Ala Ser Thr Leu Asp Ser
1 5

<210> 69
<211> 7

<212> PRT
<213> Mus musculus

<400> 69

Ala Ala Ser Thr Leu Asp Ser
1 5

<210> 70
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 70
cta caa tat gct agt tat cct cgg acg 27
Leu Gln Tyr Ala Ser Tyr Pro Arg Thr
1 5

<210> 71
<211> 9
<212> PRT
<213> Mus musculus

<400> 71

Leu Gln Tyr Ala Ser Tyr Pro Arg Thr
1 5

<210> 72
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 72
gtt tat tct ttg cac 15
Val Tyr Ser Leu His
1 5

<210> 73
<211> 5
<212> PRT
<213> Mus musculus

<400> 73

Val Tyr Ser Leu His
1 5

<210> 74
<211> 51
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(51)

<400> 74

gtt att agt act tac tat ggt gat gct atc tac aac cag aag ttc aag 48
Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ile Tyr Asn Gln Lys Phe Lys
1 5 10 15

ggc 51
Gly

<210> 75
<211> 17
<212> PRT
<213> Mus musculus

<400> 75

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

Gly

<210> 76
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 76
gag ggg aat ggt aac ccc ctt gac tac 27
Glu Gly Asn Gly Asn Pro Leu Asp Tyr
1 5

<210> 77
<211> 9
<212> PRT
<213> Mus musculus

<400> 77

Glu Gly Asn Gly Asn Pro Leu Asp Tyr
1 5

<210> 78
<211> 36
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(36)

<400> 78
act gcc agc tca agt gta agt tcc agt tac ttg cac 36
Thr Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
1 5 10

<210> 79
<211> 12
<212> PRT

<213> Mus musculus

<400> 79

Thr Ala Ser Ser Ser Val Ser Ser Ser Tyr Leu His
1 5 10

<210> 80
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(21)

<400> 80
agc aca tcc aac ctg gct tct 21
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 81
<211> 7
<212> PRT
<213> Mus musculus

<400> 81

Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 82

<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 82
cac cag tat cat cgt tcc ccg ctc acg 27
His Gln Tyr His Arg Ser Pro Leu Thr
1 5

<210> 83
<211> 9
<212> PRT
<213> Mus musculus

<400> 83

His Gln Tyr His Arg Ser Pro Leu Thr
1 5

<210> 84
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 84
agt tat ggt gta cac 15
Ser Tyr Gly Val His
1 5

<210> 85
<211> 5
<212> PRT
<213> Mus musculus

<400> 85

Ser Tyr Gly Val His
1 5

<210> 86
<211> 48
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(48)

<400> 86
gtg ata tgg agg gat gga agc aca acc tat aat tca gct ctc aaa tcc 48
Val Ile Trp Arg Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys Ser
1 5 10 15

<210> 87
<211> 16
<212> PRT

<213> Mus musculus

<400> 87

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

<210> 88
<211> 24
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(24)

<400> 88
aat tgg aat ggt ctt atg gac tac 24
Asn Trp Asn Gly Leu Met Asp Tyr
1 5

<210> 89
<211> 8
<212> PRT
<213> Mus musculus

<400> 89

Asn Trp Asn Gly Leu Met Asp Tyr
1 5

<210> 90

<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(33)

<400> 90
agg gca agt cag gac att agc tat tat tta aac 33
Arg Ala Ser Gln Asp Ile Ser Tyr Tyr Leu Asn
1 5 10

<210> 91
<211> 11
<212> PRT
<213> Mus musculus

<400> 91

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

<210> 92
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(21)

<400> 92
tac aca tca aga tta cac tca 21
Tyr Thr Ser Arg Leu His Ser
1 5

<210> 93
<211> 7
<212> PRT
<213> Mus musculus

<400> 93

Tyr Thr Ser Arg Leu His Ser
1 5

<210> 94
<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 94
caa cag ggt cat acg gtt ccg tgg acg 27
Gln Gln Gly His Thr Val Pro Trp Thr
1 5

<210> 95
<211> 9
<212> PRT

<213> Mus musculus

<400> 95

Gln Gln Gly His Thr Val Pro Trp Thr
1 5

<210> 96
<211> 15
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(15)

<400> 96
agc tac tgg atg cac 15
Ser Tyr Trp Met His
1 5

<210> 97
<211> 5
<212> PRT
<213> Mus musculus

<400> 97

Ser Tyr Trp Met His
1 5

<210> 98

<211> 48
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(48)

<400> 98
gct att tat cct gga aac agt gat agc tac aac cag aag ttc aag ggc 48
Ala Ile Tyr Pro Gly Asn Ser Asp Ser Tyr Asn Gln Lys Phe Lys Gly
1 5 10 15

<210> 99
<211> 16
<212> PRT
<213> Mus musculus

<400> 99

Ala Ile Tyr Pro Gly Asn Ser Asp Ser Tyr Asn Gln Lys Phe Lys Gly
1 5 10 15

<210> 100
<211> 12
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(12)

<400> 100
gtt atg gcc tac 12
Val Met Ala Tyr
1

<210> 101
<211> 4
<212> PRT
<213> Mus musculus

<400> 101

Val Met Ala Tyr
1

<210> 102
<211> 33
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(33)

<400> 102
cgg gca agt cag gac att ggt aat agc tta aac 33
Arg Ala Ser Gln Asp Ile Gly Asn Ser Leu Asn
1 5 10

<210> 103
<211> 11
<212> PRT

<213> Mus musculus

<400> 103

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

<210> 104
<211> 21
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(21)

<400> 104
gcc aca tcc aat tta gat tct 21
Ala Thr Ser Asn Leu Asp Ser
1 5

<210> 105
<211> 7
<212> PRT
<213> Mus musculus

<400> 105

Ala Thr Ser Asn Leu Asp Ser
1 5

<210> 106

<211> 27
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(27)

<400> 106
cta caa tat gct agt tct ccg tgg acg 27
Leu Gln Tyr Ala Ser Ser Pro Trp Thr
1 5

<210> 107
<211> 9
<212> PRT
<213> Mus musculus

<400> 107

Leu Gln Tyr Ala Ser Ser Pro Trp Thr
1 5

<210> 108
<211> 351
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(351)

<400> 108

```
cag gtc caa ctg cag cag cct ggg gct gaa ctg gtg aag cct ggg gct        48
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

tca gtg aag ctg tcc tgc aag gct tct ggc tac act ttc acc aac tac        96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30

tgg atg aac tgg gtg aag cag agg cct gga cga ggc ctc gag tgg att       144
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
        35                  40                  45

gga agg att cat cct tct gat agt gaa act cac tac aat caa aag ttc       192
Gly Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
    50                  55                  60

aag aac aag gcc aca ctg act gta gac aaa tcc tcc agc aca gcc tac       240
Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

atc caa ctc agc agc ctg aca tct gag gac tct gcg gtc tat tat tgt       288
Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

gca aat tta tat tac tat act atg gac tac tgg ggt caa gga acc tca       336
Ala Asn Leu Tyr Tyr Tyr Thr Met Asp Tyr Trp Gly Gln Gly Thr Ser
            100                 105                 110

gtc acc gtc tcc tca                                                   351
Val Thr Val Ser Ser
        115
```

<210> 109

<211> 117

<212> PRT
<213> Mus musculus

<400> 109

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

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

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

Gly Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn Gln Lys Phe
50 55 60

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

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

Ala Asn Leu Tyr Tyr Tyr Thr Met Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> 110
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(321)

<400> 110

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

ggc aaa gtc acc atc act tgc aag gca agc caa gac att aac aag aat      96
Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Lys Asn
            20                  25                  30

ata gct tgg cac caa cac aag cct gga aaa ggt cct agg ctg ctc ata     144
Ile Ala Trp His Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
        35                  40                  45

tgg tac aca tct aca tta cag cca ggc atc cca tca agg ttc agt gga     192
Trp Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aga gat tat tcc ttc agc atc agc aac ctg gag cct     240
Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65                  70                  75                  80

gaa gat att gca act tat tac tgt cta cag tat gat aat ctt ccg tat     288
Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Pro Tyr
                85                  90                  95
```

acg ttc gga tcg ggg acc aag ctg gaa ata aaa 321
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 111
<211> 107
<212> PRT
<213> Mus musculus

<400> 111

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

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

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

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

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

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Pro Tyr
85 90 95

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

<210> 112
<211> 345
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(345)

<400> 112
cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag cct ggg gct 48
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

tca gtg aag ttg tcc tgc aag gct tct ggc tac acc ttc acc agc tac 96
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt gag tgg att 144
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

gga gag att aat cct tac aat ggt ggt act aac tac aat gag aag ttc 192
Gly Glu Ile Asn Pro Tyr Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

aag agc aag gcc aca ctg act gta gac aaa tcc tcc agc aca gcc tac 240
Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

atg caa ctc agc agc ctg aca tct gag gac tct gcg gtc tat tac tgt 288

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

aca ata tgg aag ttg ggg act tac tgg ggc caa ggg act ctg gtc act 336
Thr Ile Trp Lys Leu Gly Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

gtc tct gca 345
Val Ser Ala
115

<210> 113
<211> 115
<212> PRT
<213> Mus musculus

<400> 113

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

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

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

Gly Glu Ile Asn Pro Tyr Asn Gly Gly Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

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

Thr Ile Trp Lys Leu Gly Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 114
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(321)

<400> 114
gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile

35 40 45

tac gcc gca tcc act tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

gaa gat ttt gca gac tat tac tgt cta caa tat gct agt tat cct cgg 288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Tyr Pro Arg
85 90 95

acg ttc ggt gga ggc acc aag ctg gaa atc aaa 321
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 115
<211> 107
<212> PRT
<213> Mus musculus

<400> 115

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

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

Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 116
<211> 354
<212> DNA
<213> Mus musculus

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

<400> 116
cag gtc cag ctg cag cag tct ggg gct gag ctg gtg agg cct ggg gtc 48
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Val
1 5 10 15

tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gtt tat 96
Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Val Tyr
20 25 30

tct ttg cac tgg gtg aag cag agt cat gca agg agt cta gag tgg att 144
Ser Leu His Trp Val Lys Gln Ser His Ala Arg Ser Leu Glu Trp Ile
35 40 45

gga gtt att agt act tac tat ggt gat gct atc tac aac cag aag ttc 192
Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ile Tyr Asn Gln Lys Phe
50 55 60

aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat 240
Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt 288
Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95

gca aga gag ggg aat ggt aac ccc ctt gac tac tgg ggc caa ggc acc 336
Ala Arg Glu Gly Asn Gly Asn Pro Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

act ctc aca gtc tcc tca 354
Thr Leu Thr Val Ser Ser
115

<210> 117
<211> 118
<212> PRT
<213> Mus musculus

<400> 117

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

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

Ser Leu His Trp Val Lys Gln Ser His Ala Arg Ser Leu Glu Trp Ile
35 40 45

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

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

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

Ala Arg Glu Gly Asn Gly Asn Pro Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 118
<211> 324
<212> DNA
<213> Mus musculus

<220>

<221> CDS
<222> (1)..(324)

<400> 118

caa att gtt ctc acc cag tct cca gca atc atg tct gca tct cta ggg 48
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly
1 5 10 15

gaa cgg gtc acc atg acc tgc act gcc agc tca agt gta agt tcc agt 96
Glu Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

tac ttg cac tgg tac cag cag aag cca gga tcc tcc ccc aaa ctc tgg 144
Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp
35 40 45

att tat agc aca tcc aac ctg gct tct gga gtc cca gct cgc ttc agt 192
Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

ggc agt ggg tct ggg acc tct tac tct ctc aca atc acc aac atg gag 240
Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Thr Asn Met Glu
65 70 75 80

gct gaa gat tct gcc act tat tac tgc cac cag tat cat cgt tcc ccg 288
Ala Glu Asp Ser Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
85 90 95

ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa 324
Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 119
<211> 108
<212> PRT

<213> Mus musculus

<400> 119

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

Glu Arg Val Thr Met Thr Cys Thr Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Leu Trp
35 40 45

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

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

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

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

<210> 120
<211> 348
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(348)

<400> 120

```
cag gtg cag ctg aag gag tca gga cct ggc ctg gtg gcg ccc tca cag      48
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1               5                  10                  15

agc ctg tcc atc aca tgc acc gtc tca gga ttc tca tta agt agt tat      96
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ser Tyr
            20                  25                  30

ggt gta cac tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg     144
Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

gga gtg ata tgg agg gat gga agc aca acc tat aat tca gct ctc aaa     192
Gly Val Ile Trp Arg Asp Gly Ser Thr Thr Tyr Asn Ser Ala Leu Lys
    50                  55                  60

tcc aga ctg agc atc agc aag gac ggc tcc aag agc caa gtt ttc tta     240
Ser Arg Leu Ser Ile Ser Lys Asp Gly Ser Lys Ser Gln Val Phe Leu
65                  70                  75                  80

aaa atg aac agt ctc caa act gat gac aca gcc atg tac tac tgt gcc     288
Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95

aga aat tgg aat ggt ctt atg gac tac tgg ggt caa gga acc tca gtc     336
Arg Asn Trp Asn Gly Leu Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
            100                 105                 110

acc gtc tcc tca                                                    348
```

Thr Val Ser Ser
115

<210> 121
<211> 116
<212> PRT
<213> Mus musculus

<400> 121

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

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

Ser Arg Leu Ser Ile Ser Lys Asp Gly Ser Lys Ser Gln Val Phe Leu
65 70 75 80

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

Arg Asn Trp Asn Gly Leu Met Asp Tyr Trp Gly Gln Gly Thr Ser Val

100 105 110

Thr Val Ser Ser
115

<210> 122
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(321)

<400> 122
gat atc cag atg aca cag act aca tcc tcc ctg tct gcc tct ctg gga 48
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gac aga gtc acc atc agt tgc agg gca agt cag gac att agc tat tat 96
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Tyr Tyr
20 25 30

tta aac tgg tat cag cag aga cca gat gga act gtt aaa ctc ctg atc 144
Leu Asn Trp Tyr Gln Gln Arg Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

tac tac aca tca aga tta cac tca gga gtc cca tca agg ttc agt ggc 192
Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt ggg tct gga aca gaa tct tct ctc acc att agc aat ctg gaa caa 240
Ser Gly Ser Gly Thr Glu Ser Ser Leu Thr Ile Ser Asn Leu Glu Gln

65 70 75 80

gaa gat att gcc act tac ttt tgc caa cag ggt cat acg gtt ccg tgg 288
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly His Thr Val Pro Trp
85 90 95

acg ttc ggt gga ggc acc aag ctg gaa atc aaa 321
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 123
<211> 107
<212> PRT
<213> Mus musculus

<400> 123

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

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

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

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

Ser Gly Ser Gly Thr Glu Ser Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly His Thr Val Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 124
<211> 336
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(336)

<400> 124
gag gtt cag ctc cag cag tct ggg act gtg ctg gca agg cct ggg gct 48
Glu Val Gln Leu Gln Gln Ser Gly Thr Val Leu Ala Arg Pro Gly Ala
1 5 10 15

tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt acc agc tac 96
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

tgg atg cac tgg gtg aaa cag agg cct gga cag ggt ctg gaa tgg att 144
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

ggc gct att tat cct gga aac agt gat agc tac aac cag aag ttc aag 192
Gly Ala Ile Tyr Pro Gly Asn Ser Asp Ser Tyr Asn Gln Lys Phe Lys
50 55 60

ggc aag gcc aaa ctg act gca gtc aca tcc acc agc act gcc tac atg 240
Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Thr Ser Thr Ala Tyr Met
65 70 75 80

gag ctc agc agc ctg aca aat gag gac tct gcg gtc tat tac tgt aca 288
Glu Leu Ser Ser Leu Thr Asn Glu Asp Ser Ala Val Tyr Tyr Cys Thr
85 90 95

agt gtt atg gcc tac tgg ggt caa gga acc tca gtc acc gtc tcc tca 336
Ser Val Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
100 105 110

<210> 125
<211> 112
<212> PRT
<213> Mus musculus

<400> 125

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

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

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

Gly Ala Ile Tyr Pro Gly Asn Ser Asp Ser Tyr Asn Gln Lys Phe Lys
50 55 60

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

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

Ser Val Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
100 105 110

<210> 126
<211> 321
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(321)

<400> 126
gac atc cag atg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gac att ggt aat agc 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Ser
20 25 30

tta aac tgg ctt cag cag gaa cca gat gga act att aaa cgc ctg atc 144
Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

tac gcc aca tcc aat tta gat tct ggt gtc tcc aaa agg ttc agt ggc 192
Tyr Ala Thr Ser Asn Leu Asp Ser Gly Val Ser Lys Arg Phe Ser Gly
50 55 60

agt agg tct ggg tca gat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

gaa gat ttt gta gac tat tac tgt cta caa tat gct agt tct ccg tgg 288
Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Trp
85 90 95

acg ttc ggt gga ggc acc aag ctg gaa atc aag 321
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 127
<211> 107
<212> PRT
<213> Mus musculus

<400> 127

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

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

Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

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

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

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 128
<211> 1401
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

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

<400> 128
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca gca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

gtc cac tcc cag gtc caa ctg cag cag cct ggg gct gaa ctg gtg aag 96
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys

20 25 30

cct ggg gct tca gtg aag ctg tcc tgc aag gct tct ggc tac act ttc 144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

acc aac tac tgg atg aac tgg gtg aag cag agg cct gga cga ggc ctc 192
Thr Asn Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu
50 55 60

gag tgg att gga agg att cat cct tct gat agt gaa act cac tac aat 240
Glu Trp Ile Gly Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn
65 70 75 80

caa aag ttc aag aac aag gcc aca ctg act gta gac aaa tcc tcc agc 288
Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

aca gcc tac atc caa ctc agc agc ctg aca tct gag gac tct gcg gtc 336
Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

tat tat tgt gca aat tta tat tac tat act atg gac tac tgg ggt caa 384
Tyr Tyr Cys Ala Asn Leu Tyr Tyr Tyr Thr Met Asp Tyr Trp Gly Gln
115 120 125

gga acc tca gtc acc gtc tcc tca gct agc acc aag ggc cca tcg gtc 432
Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
130 135 140

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

ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg 528
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser

165 170 175

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

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

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

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

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

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

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

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

aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt 960
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg

305 310 315 320

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

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

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac 1104
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

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

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

gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg 1248
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
405 410 415

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

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

gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg 1392
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro

450 455 460

ggt aaa tga 1401
Gly Lys
465

<210> 129
<211> 466
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 129

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

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

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

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

Glu Trp Ile Gly Arg Ile His Pro Ser Asp Ser Glu Thr His Tyr Asn
65 70 75 80

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

Thr Ala Tyr Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Asn Leu Tyr Tyr Tyr Thr Met Asp Tyr Trp Gly Gln
115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
465

<210> 130
<211> 705
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

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

<400> 130

atg aga ccc tcc att cag ttc ctg ggg ctc ttg ttg ttc tgg ctt cat 48
Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
1 5 10 15

ggt gct cag tgt gac atc cag atg aca cag tct cca tcc tca ctg tct 96
Gly Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

gca tct ctg gga ggc aaa gtc acc atc act tgc aag gca agc caa gac 144
Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
35 40 45

att aac aag aat ata gct tgg cac caa cac aag cct gga aaa ggt cct 192
Ile Asn Lys Asn Ile Ala Trp His Gln His Lys Pro Gly Lys Gly Pro
50 55 60

agg ctg ctc ata tgg tac aca tct aca tta cag cca ggc atc cca tca 240
Arg Leu Leu Ile Trp Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
65 70 75 80

agg ttc agt gga agt ggg tct ggg aga gat tat tcc ttc agc atc agc 288
Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser
85 90 95

aac ctg gag cct gaa gat att gca act tat tac tgt cta cag tat gat 336
Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp
100 105 110

aat ctt ccg tat acg ttc gga tcg ggg acc aag ctg gaa ata aaa cgt 384

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

acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag      432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
    130                 135                 140

ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat      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 aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg      528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
                165                 170                 175

ggt aac tcc cag gag agt gtc aca 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 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa      624
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
        195                 200                 205

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc      672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
    210                 215                 220

gtc aca aag agc ttc aac agg gga gag tgt tga                         705
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230
```

<210> 131
<211> 234
<212> PRT
<213> Artificial

<220>

<223> Synthetic Construct

<400> 131

Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His
1 5 10 15

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

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

Ile Asn Lys Asn Ile Ala Trp His Gln His Lys Pro Gly Lys Gly Pro
50 55 60

Arg Leu Leu Ile Trp Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser
65 70 75 80

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

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

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

Thr 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> 132
<211> 1395
<212> DNA
<213> Artificial

<220>

<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(1395)

<400> 132

```
atg gga tgg agc tat atc atc ctc ttt ttg gta gca aca gtt aca gat       48
Met Gly Trp Ser Tyr Ile Ile Leu Phe Leu Val Ala Thr Val Thr Asp
1               5                  10                  15

gtc cac tcc cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag       96
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30

cct ggg gct tca gtg aag ttg tcc tgc aag gct tct ggc tac acc ttc      144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tac tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt      192
Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gag tgg att gga gag att aat cct tac aat ggt ggt act aac tac aat      240
Glu Trp Ile Gly Glu Ile Asn Pro Tyr Asn Gly Gly Thr Asn Tyr Asn
65                  70                  75                  80

gag aag ttc aag agc aag gcc aca ctg act gta gac aaa tcc tcc agc      288
Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
                85                  90                  95

aca gcc tac atg caa ctc agc agc ctg aca tct gag gac tct gcg gtc      336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
```

tat tac tgt aca ata tgg aag ttg ggg act tac tgg ggc caa ggg act 384
Tyr Tyr Cys Thr Ile Trp Lys Leu Gly Thr Tyr Trp Gly Gln Gly Thr
115 120 125

ctg gtc act gtc tct gca gct agc acc aag ggc cca tcg gtc ttc ccc 432
Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
130 135 140

ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc 480
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
145 150 155 160

tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac 528
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
165 170 175

tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag 576
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
180 185 190

tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc 624
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
195 200 205

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

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

cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca 768
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
245 250 255

gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg 816
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
260 265 270

acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct 864
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
275 280 285

gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc 912
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
290 295 300

aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc 960
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
305 310 315 320

agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac 1008
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
325 330 335

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

atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg 1104
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
355 360 365

ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc 1152
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

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

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac 1248
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

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

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1344
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
435 440 445

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa 1392
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

tga 1395

<210> 133
<211> 464
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 133

Met Gly Trp Ser Tyr Ile Ile Leu Phe Leu Val Ala Thr Val Thr Asp
1 5 10 15

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

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

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

Glu Trp Ile Gly Glu Ile Asn Pro Tyr Asn Gly Gly Thr Asn Tyr Asn
65 70 75 80

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

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

Tyr Tyr Cys Thr Ile Trp Lys Leu Gly Thr Tyr Trp Gly Gln Gly Thr
115 120 125

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

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

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
165 170 175

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

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

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

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
245 250 255

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

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

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

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
325 330 335

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

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
370 375 380

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
405 410 415

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
435 440 445

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 134
<211> 711
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(711)

<400> 134

```
atg gac atg agg gtt cct gct cac gtt ttt ggc ttc ttg ttg ctc tgg      48
Met Asp Met Arg Val Pro Ala His Val Phe Gly Phe Leu Leu Leu Trp
1               5                  10                  15

ttt cca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc      96
Phe Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30

tta tct gcc tct ctg gga gaa aga gtc agt ctc act tgt cgg gca agt     144
Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser
        35                  40                  45

cag gaa att agt ggt tac tta agc tgg ctt cag cag aaa cca gat gga     192
Gln Glu Ile Ser Gly Tyr Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly
    50                  55                  60

act att aaa cgc ctg atc tac gcc gca tcc act tta gat tct ggt gtc     240
Thr Ile Lys Arg Leu Ile Tyr Ala Ala Ser Thr Leu Asp Ser Gly Val
65                  70                  75                  80

cca aaa agg ttc agt ggc agt agg tct ggg tca gat tat tct ctc acc     288
```

```
Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr
                85                  90                  95

atc agc agc ctt gag tct gaa gat ttt gca gac tat tac tgt cta caa   336
Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln
            100                 105                 110

tat gct agt tat cct cgg acg ttc ggt gga ggc acc aag ctg gaa atc   384
Tyr Ala Ser Tyr Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        115                 120                 125

aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat   432
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac   480
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc   528
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac   576
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac   624
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc   672
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga               711
```

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

<210> 135
<211> 236
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 135

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

Phe Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

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

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

Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr
85 90 95

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

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

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

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

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

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

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

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

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

<210> 136
<211> 1404
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(1404)

<400> 136

```
atg ggt tgg agc tgt atc atc ttc ttt ctg gta gca aca gct aca ggt      48
Met Gly Trp Ser Cys Ile Ile Phe Phe Leu Val Ala Thr Ala Thr Gly
1               5                  10                  15

gtg cac tcc cag gtc cag ctg cag cag tct ggg gct gag ctg gtg agg      96
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            20                  25                  30

cct ggg gtc tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc     144
Pro Gly Val Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
        35                  40                  45

act gtt tat tct ttg cac tgg gtg aag cag agt cat gca agg agt cta     192
Thr Val Tyr Ser Leu His Trp Val Lys Gln Ser His Ala Arg Ser Leu
    50                  55                  60

gag tgg att gga gtt att agt act tac tat ggt gat gct atc tac aac     240
Glu Trp Ile Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ile Tyr Asn
65                  70                  75                  80
```

```
cag aag ttc aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc      288
Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser
                85                  90                  95

aca gcc tat atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc      336
Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile
            100                 105                 110

tat tac tgt gca aga gag ggg aat ggt aac ccc ctt gac tac tgg ggc      384
Tyr Tyr Cys Ala Arg Glu Gly Asn Gly Asn Pro Leu Asp Tyr Trp Gly
        115                 120                 125

caa ggc acc act ctc aca gtc tcc tca gct agc acc aag ggc cca tcg      432
Gln Gly Thr Thr Leu 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 ggg ggc aca gcg      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 ccg gtg acg gtg      528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                165                 170                 175

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

gtc cta 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 aaa gtt gag ccc aaa tct tgt      720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
225                 230                 235                 240

gac aaa act cac aca tgc cca ccg 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 ccg 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 ccg 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

cgt 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 ggg cag ccc cga 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 gat gag ctg acc aag aac cag gtc agc 1152
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu 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 ggg cag ccg gag aac aac tac aag acc acg 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 ggg 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 acg 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

ccg ggt aaa tga 1404
Pro Gly Lys
465

<210> 137
<211> 467
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 137

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

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

Pro Gly Val Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe
35 40 45

Thr Val Tyr Ser Leu His Trp Val Lys Gln Ser His Ala Arg Ser Leu
50 55 60

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

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

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

Tyr Tyr Cys Ala Arg Glu Gly Asn Gly Asn Pro Leu Asp Tyr Trp Gly
115 120 125

Gln Gly Thr Thr Leu 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 Lys 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 Asp Glu Leu 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> 138
<211> 714
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(714)

<400> 138
atg gat ttt cag gtg cag att ttc agc ttc ctg cta atc agt gcc tca 48
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

gtc ata atg tcc aga gga caa att gtt ctc acc cag tct cca gca atc 96
Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
20 25 30

atg tct gca tct cta ggg gaa cgg gtc acc atg acc tgc act gcc agc 144
Met Ser Ala Ser Leu Gly Glu Arg Val Thr Met Thr Cys Thr Ala Ser
35 40 45

tca agt gta agt tcc agt tac ttg cac tgg tac cag cag aag cca gga 192
Ser Ser Val Ser Ser Ser Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly
50 55 60

tcc tcc ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga 240
Ser Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly
65 70 75 80

gtc cca gct cgc ttc agt ggc agt ggg tct ggg acc tct tac tct ctc 288
Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95

aca atc acc aac atg gag gct gaa gat tct gcc act tat tac tgc cac 336
Thr Ile Thr Asn Met Glu Ala Glu Asp Ser Ala Thr Tyr Tyr Cys His
100 105 110

cag tat cat cgt tcc ccg ctc acg ttc ggt gct ggg acc aag ctg gag 384
Gln Tyr His Arg Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

ctg aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct 432
Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat 480
Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
145 150 155 160

aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc 528
Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
165 170 175

ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag 576
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
180 185 190

gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac 624
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
195 200 205

tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg 672
Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
210 215 220

agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga 714
Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 139
<211> 237
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 139

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
20 25 30

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

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

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

Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
85 90 95

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

Gln Tyr His Arg Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
130 135 140

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

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

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

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

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

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

<210> 140
<211> 1398
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(1398)

<400> 140
atg gct gtc ctg ggg ctg ctt ctc tgc ctg gtg act ttc cca agc tgt 48
Met Ala Val Leu Gly Leu Leu Leu Cys Leu Val Thr Phe Pro Ser Cys
1 5 10 15

gcc ctg tcc cag gtg cag ctg aag gag tca gga cct ggc ctg gtg gcg 96
Ala Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala

20 25 30

ccc tca cag agc ctg tcc atc aca tgc acc gtc tca gga ttc tca tta 144
Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45

agt agt tat ggt gta cac tgg gtt cgc cag cct cca gga aag ggt ctg 192
Ser Ser Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

gag tgg ctg gga gtg ata tgg agg gat gga agc aca acc tat aat tca 240
Glu Trp Leu Gly Val Ile Trp Arg Asp Gly Ser Thr Thr Tyr Asn Ser
65 70 75 80

gct ctc aaa tcc aga ctg agc atc agc aag gac ggc tcc aag agc caa 288
Ala Leu Lys Ser Arg Leu Ser Ile Ser Lys Asp Gly Ser Lys Ser Gln
85 90 95

gtt ttc tta aaa atg aac agt ctc caa act gat gac aca gcc atg tac 336
Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr
100 105 110

tac tgt gcc aga aat tgg aat ggt ctt atg gac tac tgg ggt caa gga 384
Tyr Cys Ala Arg Asn Trp Asn Gly Leu Met Asp Tyr Trp Gly Gln Gly
115 120 125

acc tca gtc acc gtc tcc tca gct agc acc aag ggc cca tcg gtc ttc 432
Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
130 135 140

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
145 150 155 160

ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg 528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp

165 170 175

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

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

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

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

act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg 768
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
245 250 255

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

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

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

gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg 960
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

305 310 315 320

gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag 1008
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
325 330 335

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

acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc 1104
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
355 360 365

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

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

agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg 1248
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
405 410 415

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

agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag 1344
Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt 1392
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

450 455 460

aaa tga 1398
Lys
465

<210> 141
<211> 465
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 141

Met Ala Val Leu Gly Leu Leu Leu Cys Leu Val Thr Phe Pro Ser Cys
1 5 10 15

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

Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45

Ser Ser Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

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

Ala Leu Lys Ser Arg Leu Ser Ile Ser Lys Asp Gly Ser Lys Ser Gln
85 90 95

Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr
100 105 110

Tyr Cys Ala Arg Asn Trp Asn Gly Leu Met Asp Tyr Trp Gly Gln Gly
115 120 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
435 440 445

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

Lys
465

<210> 142
<211> 705
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

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

<400> 142

atg atg tcc tct gct cag ttc ctt ggt ctc ctg ttg ctc tgt ttt caa 48
Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Cys Phe Gln
1 5 10 15

ggt acc aga tgt gat atc cag atg aca cag act aca tcc tcc ctg tct 96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
20 25 30

gcc tct ctg gga gac aga gtc acc atc agt tgc agg gca agt cag gac 144
Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
35 40 45

att agc tat tat tta aac tgg tat cag cag aga cca gat gga act gtt 192
Ile Ser Tyr Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Asp Gly Thr Val
50 55 60

aaa ctc ctg atc tac tac aca tca aga tta cac tca gga gtc cca tca 240
Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

agg ttc agt ggc agt ggg tct gga aca gaa tct tct ctc acc att agc 288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Ser Ser Leu Thr Ile Ser
85 90 95

aat ctg gaa caa gaa gat att gcc act tac ttt tgc caa cag ggt cat 336
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly His
100 105 110

acg gtt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc aaa cgt 384

Thr Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag 432
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 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 aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 528
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

ggt aac tcc cag gag agt gtc aca 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 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 624
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 672
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

gtc aca aag agc ttc aac agg gga gag tgt tga 705
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 143
<211> 234
<212> PRT
<213> Artificial

<220>

<223> Synthetic Construct

<400> 143

Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
1 5 10 15

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
20 25 30

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

Ile Ser Tyr Tyr Leu Asn Trp Tyr Gln Gln Arg Pro Asp Gly Thr Val
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Ser Ser Leu Thr Ile Ser
85 90 95

Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly His
100 105 110

Thr Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125

Thr 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> 144
<211> 1386
<212> DNA
<213> Artificial

<220>

<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(1386)

<400> 144

```
atg gaa tgt aac tgg ata ctt cct ttt att ctg tcg gta act tca ggg      48
Met Glu Cys Asn Trp Ile Leu Pro Phe Ile Leu Ser Val Thr Ser Gly
1               5                  10                  15

gtc tac tca gag gtt cag ctc cag cag tct ggg act gtg ctg gca agg      96
Val Tyr Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Val Leu Ala Arg
            20                  25                  30

cct ggg gct tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt     144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45

acc agc tac tgg atg cac tgg gtg aaa cag agg cct gga cag ggt ctg     192
Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
    50                  55                  60

gaa tgg att ggc gct att tat cct gga aac agt gat agc tac aac cag     240
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Ser Asp Ser Tyr Asn Gln
65                  70                  75                  80

aag ttc aag ggc aag gcc aaa ctg act gca gtc aca tcc acc agc act     288
Lys Phe Lys Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Thr Ser Thr
                85                  90                  95

gcc tac atg gag ctc agc agc ctg aca aat gag gac tct gcg gtc tat     336
Ala Tyr Met Glu Leu Ser Ser Leu Thr Asn Glu Asp Ser Ala Val Tyr
            100                 105                 110
```

```
tac tgt aca agt gtt atg gcc tac tgg ggt caa gga acc tca gtc acc      384
Tyr Cys Thr Ser Val Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
        115                 120                 125

gtc tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc      432
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
    130                 135                 140

tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc      480
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145                 150                 155                 160

aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc      528
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
                165                 170                 175

ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga      576
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
            180                 185                 190

ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc      624
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
        195                 200                 205

acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag      672
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
    210                 215                 220

gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc      720
Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
225                 230                 235                 240

cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc      768
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
                245                 250                 255
```

```
ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag      816
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
            260                 265                 270

gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag      864
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
        275                 280                 285

ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag      912
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
    290                 295                 300

ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc      960
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
305                 310                 315                 320

acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag     1008
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
                325                 330                 335

gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa     1056
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
            340                 345                 350

gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc     1104
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
        355                 360                 365

cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa     1152
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
    370                 375                 380

ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag     1200
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
385                 390                 395                 400
```

ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc 1248
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
405 410 415

tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag 1296
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
420 425 430

cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac 1344
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1386
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 145
<211> 461
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 145

Met Glu Cys Asn Trp Ile Leu Pro Phe Ile Leu Ser Val Thr Ser Gly
1 5 10 15

Val Tyr Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Val Leu Ala Arg
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35 40 45

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

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Ser Asp Ser Tyr Asn Gln
65 70 75 80

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

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

Tyr Cys Thr Ser Val Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
115 120 125

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

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

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
165 170 175

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly

180 185 190

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

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

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

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
245 250 255

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
260 265 270

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
275 280 285

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
290 295 300

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
305 310 315 320

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys

325 330 335

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

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
370 375 380

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
385 390 395 400

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
405 410 415

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
420 425 430

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
435 440 445

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455 460

<210> 146

<211> 711
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(711)

<400> 146

```
atg gac atg agg gct cct gca cag att ttt ggc ttc ttg ttg ctc ttg      48
Met Asp Met Arg Ala Pro Ala Gln Ile Phe Gly Phe Leu Leu Leu Leu
1               5                  10                  15

ttt cca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc      96
Phe Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30

tta tct gcc tct ctg gga gaa aga gtc agt ctc act tgt cgg gca agt     144
Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser
        35                  40                  45

cag gac att ggt aat agc tta aac tgg ctt cag cag gaa cca gat gga     192
Gln Asp Ile Gly Asn Ser Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly
    50                  55                  60

act att aaa cgc ctg atc tac gcc aca tcc aat tta gat tct ggt gtc     240
Thr Ile Lys Arg Leu Ile Tyr Ala Thr Ser Asn Leu Asp Ser Gly Val
65                  70                  75                  80

tcc aaa agg ttc agt ggc agt agg tct ggg tca gat tat tct ctc acc     288
Ser Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr
                85                  90                  95
```

```
atc agc agc ctt gag tct gaa gat ttt gta gac tat tac tgt cta caa      336
Ile Ser Ser Leu Glu Ser Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln
            100                 105                 110

tat gct agt tct ccg tgg acg ttc ggt gga ggc acc aag ctg gaa atc      384
Tyr Ala Ser Ser Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
        115                 120                 125

aag cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      432
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac      480
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc      528
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac      576
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180                 185                 190

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac      624
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc      672
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210                 215                 220

tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga                  711
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 147
<211> 236
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 147

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

Phe Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

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

Gln Asp Ile Gly Asn Ser Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly
50 55 60

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

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

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

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

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

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

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

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

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

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

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

<210> 148
<211> 486
<212> DNA
<213> Mus musculus

<400> 148
atggagacgc tccctgcctc ttgggtcttg acgctgcttt gtctaggttc ccaccttcta 60

caggcagtta tcagcacaac cgtgatccca tcatgcatcc caggagaatc cgaggataac 120

tgtaccgcct tagttcagat ggaagacgat ccccgtgtgg ctcaagtgca gattacaaag 180

tgtagttctg acatggacgg ctactgcttg catggccagt gcatctacct ggtggacatg 240

agagagaaat tctgcagatg tgaagtgggc tacactggtc tgcgatgtga gcacttcttt 300

ctaactgttc accaacccct gagcaaagaa tacgttgcgt tgacagtgat tctcattttc 360

ctgtttctca tcataaccgc tggatgcata tactatttct gcagatggta caaaaatcga 420

aaaagtaaaa aatcgaggga ggaatatgag agagtgacct caggggaccc agtgctgcca 480

caggtc 486

<210> 149
<211> 492
<212> DNA
<213> Macaca fascicularis

<400> 149
atggagatgc tctctgccgg aagggtccct gcgctgctgc tctgcctggg tttccatctt 60

ctacaggcag tcctcagtac aactgtgatt ccatcatgta tcccaggaga gtccagtgat 120

aactgcacag ctttagttca gacagaagac aatccacgtg tggctcaagt gtcaataaca 180

aagtgtaact ctgacatgaa tggctactgt ttgcatggac agtgcatcta cctggtggac 240

atgagtcaaa attactgcag gtgtgaagtg ggttatactg gtgtccgatg tgaacatttc 300

tatttaaccg tccaccaacc tttaagcaaa gaatatgtgg ctttgaccgt gattcttatt 360

attttgtttc ttatcatagt tgtcggttcc acatattatt tctgcagatg gtacaggaat 420

cgaaaaagta aagaaccaaa gaaggaatat gagagagtta cctcagggga tccagagttg 480

ccgcaagtct ga 492

<210> 150
<211> 342
<212> PRT
<213> Mus musculus

<400> 150

Met Glu Thr Leu Pro Ala Ser Trp Val Leu Thr Leu Leu Cys Leu Gly
1 5 10 15

Ser His Leu Leu Gln Ala Val Ile Ser Thr Thr Val Ile Pro Ser Cys
20 25 30

Ile Pro Gly Glu Ser Glu Asp Asn Cys Thr Ala Leu Val Gln Met Glu
35 40 45

Asp Asp Pro Arg Val Ala Gln Val Gln Ile Thr Lys Cys Ser Ser Asp
50 55 60

Met Asp Gly Tyr Cys Leu His Gly Gln Cys Ile Tyr Leu Val Asp Met
65 70 75 80

Arg Glu Lys Phe Cys Arg Cys Glu Val Gly Tyr Thr Gly Leu Arg Cys
85 90 95

Glu His Phe Phe Leu Thr Val His Gln Pro Leu Ser Lys Glu Tyr Val
100 105 110

Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn
115 120 125

Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp
130 135 140

Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp
145 150 155 160

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

Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn
180 185 190

Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp
195 200 205

Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro
210 215 220

Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala
225 230 235 240

Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys
245 250 255

Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile
260 265 270

Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn
275 280 285

Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys
290 295 300

Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys
305 310 315 320

Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe
325 330 335

Ser Arg Thr Pro Gly Lys
340

<210> 151
<211> 343
<212> PRT
<213> Macaca fascicularis

<400> 151

Met Glu Met Leu Ser Ala Gly Arg Val Pro Ala Leu Leu Leu Cys Leu
1 5 10 15

Gly Phe His Leu Leu Gln Ala Val Leu Ser Thr Thr Val Ile Pro Ser
20 25 30

Cys Ile Pro Gly Glu Ser Ser Asp Asn Cys Thr Ala Leu Val Gln Thr
35 40 45

Glu Asp Asn Pro Arg Val Ala Gln Val Ser Ile Thr Lys Cys Asn Ser
50 55 60

Asp Met Asn Gly Tyr Cys Leu His Gly Gln Cys Ile Tyr Leu Val Asp
65 70 75 80

Met Ser Gln Asn Tyr Cys Arg Cys Glu Val Gly Tyr Thr Gly Val Arg
85 90 95

Cys Glu His Phe Tyr Leu Thr Val His Gln Pro Leu Ser Lys Glu Tyr
100 105 110

Val Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
115 120 125

Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
130 135 140

Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val
145 150 155 160

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

Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr
180 185 190

Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
195 200 205

Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
210 215 220

Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg
225 230 235 240

Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys
245 250 255

Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp
260 265 270

Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys
275 280 285

Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
290 295 300

Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser
305 310 315 320

Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
325 330 335

Phe Ser Arg Thr Pro Gly Lys
340

<210> 152
<211> 275
<212> PRT
<213> Artificial

<220>
<223> An artificially synthesized peptide sequence

<400> 152

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220

Gly Ser Ala Val Leu Ser Thr Thr Val Ile Pro Ser Cys Ile Pro Gly
225 230 235 240

Glu Ser Ser Asp Asn Cys Thr Ala Leu Val Gln Thr Glu Asp Asn Pro
245 250 255

Arg Val Ala Gln Val Ser Ile Thr Lys Cys Gly Ser Thr His His His
260 265 270

His His His
275