SEQUENCE LISTING

<110> Kyoto University
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
JAPAN BIOLOGICAL INFORMATICS CONSORTIUM

<120> Novel Nuclear Reprogramming Substance

<130> 091497

<150> US 61/208,853
<151> 2009-02-27

<150> US 61/276,123
<151> 2009-09-08

<160> 19

<170> PatentIn version 3.5

<210> 1
<211> 2337
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (534)..(1874)

<400> 1
gggtcagggt ttttgacgtt cctcgccagc tgcacaaacc tcccggagca agtgtgagtg 60

tgggtgagag tgcgcgcgcg cgcacgggct ggctgcgctt ggcacgcttg gtggcccagg 120

gtcccggggc ccggggtccc gtctggcggc ccgggattac cgtgacgtca cattgagcct 180

ctggccacct tggactggga cacctccgga gcctcacagc cccgcgccgc gccgcgcctc 240

acctcgccac cacgcgcctt tgggaacccg catcttcttc cttcccctgc ccatccatgg 300

gcccttctgt cttccggacc ccacgggccg gaggggcgcc ttccggagcg cagggctcgg 360

cagccgggct gccctcggct ctgcctccac tggggccaac caggcgaagg aaccggcgct 420

gggcatccgc agcggtgtaa ggaactgaga cacctcactg ctgggggcgc ggaacagctg 480

ggctgagacg ggaactcgac agggaagaga gagacgggcc agggacagcc acc atg 536
Met
1

tcc ttc cca cac ttt gga cac ccg tac cgc ggc gct tcc cag ttt ctg 584
Ser Phe Pro His Phe Gly His Pro Tyr Arg Gly Ala Ser Gln Phe Leu
5 10 15

gcg tcg gca agt tcc agc acc aca tgc tgc gaa tct acc caa cgc tct 632
Ala Ser Ala Ser Ser Ser Thr Thr Cys Cys Glu Ser Thr Gln Arg Ser
20 25 30

gtc tca gat gtg gca tca ggc tcc acc cca gcg ccc gct ctc tgc tgc 680
Val Ser Asp Val Ala Ser Gly Ser Thr Pro Ala Pro Ala Leu Cys Cys
35 40 45

gca ccc tac gat agt cga ctg ctg ggc agt gcg cga ccg gag ctg ggc 728
Ala Pro Tyr Asp Ser Arg Leu Leu Gly Ser Ala Arg Pro Glu Leu Gly
50 55 60 65

gcc gcc ttg ggc atc tat gga gca ccc tat gcg gcc gct gca gct gcc 776
Ala Ala Leu Gly Ile Tyr Gly Ala Pro Tyr Ala Ala Ala Ala Ala Ala

70 75 80

cag agc tac cct ggc tac ctg ccc tat agc cca gag ccc ccc tca ctg 824
Gln Ser Tyr Pro Gly Tyr Leu Pro Tyr Ser Pro Glu Pro Pro Ser Leu
85 90 95

tat ggg gca ctg aat cca cag tat gaa ttt aag gag gct gca ggg agt 872
Tyr Gly Ala Leu Asn Pro Gln Tyr Glu Phe Lys Glu Ala Ala Gly Ser
100 105 110

ttt aca tcc agc ctg gca caa cca gga gcc tat tat ccc tat gag cgg 920
Phe Thr Ser Ser Leu Ala Gln Pro Gly Ala Tyr Tyr Pro Tyr Glu Arg
115 120 125

act ctg ggg cag tac caa tat gaa cgg tat ggc gca gtg gaa ttg agt 968
Thr Leu Gly Gln Tyr Gln Tyr Glu Arg Tyr Gly Ala Val Glu Leu Ser
130 135 140 145

ggc gcc ggt cgc cga aag aac gcg acc cgg gag acc acc agt aca ctc 1016
Gly Ala Gly Arg Arg Lys Asn Ala Thr Arg Glu Thr Thr Ser Thr Leu
150 155 160

aag gcc tgg ctc aac gag cac cgc aaa aac ccc tac ccc act aag ggt 1064
Lys Ala Trp Leu Asn Glu His Arg Lys Asn Pro Tyr Pro Thr Lys Gly
165 170 175

gag aag atc atg ctg gcc atc atc acc aag atg acc ctc acc cag gtg 1112
Glu Lys Ile Met Leu Ala Ile Ile Thr Lys Met Thr Leu Thr Gln Val
180 185 190

tcc acc tgg ttc gcc aac gca cgc cgg cgc ctc aag aaa gag aac aaa 1160
Ser Thr Trp Phe Ala Asn Ala Arg Arg Arg Leu Lys Lys Glu Asn Lys
195 200 205

atg aca tgg gcg ccc aag aac aaa ggt ggg gag gag agg aag gca gag 1208

Met Thr Trp Ala Pro Lys Asn Lys Gly Gly Glu Glu Arg Lys Ala Glu
210 215 220 225

gga gga gag gag gac tca cta ggc tgc cta act gct gac acc aaa gaa 1256
Gly Gly Glu Glu Asp Ser Leu Gly Cys Leu Thr Ala Asp Thr Lys Glu
230 235 240

gtt act gct agc cag gag gcc cgg ggg ctc cgg ctg agt gac ctg gaa 1304
Val Thr Ala Ser Gln Glu Ala Arg Gly Leu Arg Leu Ser Asp Leu Glu
245 250 255

gac ctg gag gaa gag gag gag gag gag gag gag gaa gct gaa gac gag gag 1352
Asp Leu Glu Glu Glu Glu Glu Glu Glu Glu Glu Ala Glu Asp Glu Glu
260 265 270

gta gtg gcc aca gct ggg gac agg ctg acg gag ttc cga aag ggc gcg 1400
Val Val Ala Thr Ala Gly Asp Arg Leu Thr Glu Phe Arg Lys Gly Ala
275 280 285

cag tca ctg cct ggg ccg tgc gct gca gct cga gag ggc cga ttg gag 1448
Gln Ser Leu Pro Gly Pro Cys Ala Ala Ala Arg Glu Gly Arg Leu Glu
290 295 300 305

cgc agg gag tgc ggc ctg gct gcg ccc cgc ttc tcc ttc aat gac cct 1496
Arg Arg Glu Cys Gly Leu Ala Ala Pro Arg Phe Ser Phe Asn Asp Pro
310 315 320

tcc gga tcg gaa gaa gct gac ttc ctc tcg gcg gag aca ggc agc cct 1544
Ser Gly Ser Glu Glu Ala Asp Phe Leu Ser Ala Glu Thr Gly Ser Pro
325 330 335

agg ttg acc atg cac tac cca tgc ttg gag aaa ccg cgc atc tgg tct 1592
Arg Leu Thr Met His Tyr Pro Cys Leu Glu Lys Pro Arg Ile Trp Ser
340 345 350

ctg gcg cac acc gcg aca gcc agc gct gtt gaa ggt gca ccc cca gcc 1640
Leu Ala His Thr Ala Thr Ala Ser Ala Val Glu Gly Ala Pro Pro Ala
355 360 365

cgg cct agg cca cga agt cct gag tgc cgt atg att cct gga cag cct 1688
Arg Pro Arg Pro Arg Ser Pro Glu Cys Arg Met Ile Pro Gly Gln Pro
370 375 380 385

cct gcc tct gcc cgg cga ctc tca gtc ccc aga gac tcc gcg tgc gac 1736
Pro Ala Ser Ala Arg Arg Leu Ser Val Pro Arg Asp Ser Ala Cys Asp
390 395 400

gag tct tcc tgc ata ccc aaa gcc ttt gga aac ccc aag ttt gcc ctg 1784
Glu Ser Ser Cys Ile Pro Lys Ala Phe Gly Asn Pro Lys Phe Ala Leu
405 410 415

cag gga cta ccg ctg aac tgt gcg ccg tgc ccg cgg agg agc gag cct 1832
Gln Gly Leu Pro Leu Asn Cys Ala Pro Cys Pro Arg Arg Ser Glu Pro
420 425 430

gta gtg cag tgc cag tac ccg tct gga gca gaa gca ggt tag 1874
Val Val Gln Cys Gln Tyr Pro Ser Gly Ala Glu Ala Gly
435 440 445

cgcaatggct gcgatttgcg aaagaatctt ggaaatgggc cccacgtttc gaattcatct 1934

ccaggttaag aagctgccag accttgccag ggaccaggag ctctcacttt gcctaagaga 1994

cagacacaca gaaaccctcc tagcagctgt ccttgcacgc agagctgggg tggtgggccg 2054

acttgaacct tagcagtccc cacgggagat ggcagggcac cttggggaag gccaagtggg 2114

aggctgggag gctgccccac ccaccgactc taccaagtct ctcttcctcc tgtggattca 2174

gcaaggcttc ctctcctgct caccccctgtc tctcacctcc accaacccca ctcactttgt 2234

aacttcatca ctgacccggc caataaggac cctgtgcgtc ttctcccccc cctaagccct 2294

tgtgtcctta aaaataatca gtccgaaccc atgtaaaaaa aaa 2337

<210> 2
<211> 446
<212> PRT
<213> Homo sapiens

<400> 2

Met Ser Phe Pro His Phe Gly His Pro Tyr Arg Gly Ala Ser Gln Phe
1 5 10 15

Leu Ala Ser Ala Ser Ser Ser Thr Thr Cys Cys Glu Ser Thr Gln Arg
20 25 30

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

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

Gly Ala Ala Leu Gly Ile Tyr Gly Ala Pro Tyr Ala Ala Ala Ala Ala
65 70 75 80

Ala Gln Ser Tyr Pro Gly Tyr Leu Pro Tyr Ser Pro Glu Pro Pro Ser
85 90 95

Leu Tyr Gly Ala Leu Asn Pro Gln Tyr Glu Phe Lys Glu Ala Ala Gly
100 105 110

Ser Phe Thr Ser Ser Leu Ala Gln Pro Gly Ala Tyr Tyr Pro Tyr Glu
115 120 125

Arg Thr Leu Gly Gln Tyr Gln Tyr Glu Arg Tyr Gly Ala Val Glu Leu
130 135 140

Ser Gly Ala Gly Arg Arg Lys Asn Ala Thr Arg Glu Thr Thr Ser Thr
145 150 155 160

Leu Lys Ala Trp Leu Asn Glu His Arg Lys Asn Pro Tyr Pro Thr Lys
165 170 175

Gly Glu Lys Ile Met Leu Ala Ile Ile Thr Lys Met Thr Leu Thr Gln
180 185 190

Val Ser Thr Trp Phe Ala Asn Ala Arg Arg Arg Leu Lys Lys Glu Asn
195 200 205

Lys Met Thr Trp Ala Pro Lys Asn Lys Gly Gly Glu Glu Arg Lys Ala
210 215 220

Glu Gly Gly Glu Glu Asp Ser Leu Gly Cys Leu Thr Ala Asp Thr Lys

225 230 235 240

Glu Val Thr Ala Ser Gln Glu Ala Arg Gly Leu Arg Leu Ser Asp Leu
245 250 255

Glu Asp Leu Glu Glu Glu Glu Glu Glu Glu Glu Glu Ala Glu Asp Glu
260 265 270

Glu Val Val Ala Thr Ala Gly Asp Arg Leu Thr Glu Phe Arg Lys Gly
275 280 285

Ala Gln Ser Leu Pro Gly Pro Cys Ala Ala Ala Arg Glu Gly Arg Leu
290 295 300

Glu Arg Arg Glu Cys Gly Leu Ala Ala Pro Arg Phe Ser Phe Asn Asp
305 310 315 320

Pro Ser Gly Ser Glu Glu Ala Asp Phe Leu Ser Ala Glu Thr Gly Ser
325 330 335

Pro Arg Leu Thr Met His Tyr Pro Cys Leu Glu Lys Pro Arg Ile Trp
340 345 350

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

Ala Arg Pro Arg Pro Arg Ser Pro Glu Cys Arg Met Ile Pro Gly Gln
370 375 380

Pro Pro Ala Ser Ala Arg Arg Leu Ser Val Pro Arg Asp Ser Ala Cys
385 390 395 400

Asp Glu Ser Ser Cys Ile Pro Lys Ala Phe Gly Asn Pro Lys Phe Ala
405 410 415

Leu Gln Gly Leu Pro Leu Asn Cys Ala Pro Cys Pro Arg Arg Ser Glu
420 425 430

Pro Val Val Gln Cys Gln Tyr Pro Ser Gly Ala Glu Ala Gly
435 440 445

<210> 3
<211> 2380
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (634)..(1953)

<400> 3
acttctcccg gggaatttgg agagggtctg tgtgcgcgcg cgcgcgtgag ctgcaggcga 60

aagagggtag gatctagcgg cgagtcgagg gtcagggtct ttgacgtttc tcgcccgttg 120

cacaaacctc gcagagcaag aacgagtgta tccgagagtg cgtgcatgta cacgggctgg 180

ctgcccttgg cacactcggt ggcccggggc cccggggccc gcggtcccct ctggcggccg 240

gggattaccg tgacgtcacg ttgagcctct ggccaccttg gactgggaca cctcgggaac 300

ctcacagccc gacgctgcgc tgtacctcac cttgccccctg cgcgcctttg gcaccctact 360

ccttcttcct aattctgccg ccgatccatg ggcccctctg ccttctggaa cccacaggcc 420

gtaggggtgc cttaccaatc gcagaactcg gcagcccctc tgcctttgat tctgcctccc 480

gtctctcccc tcctgccaac gaactggcgg ccagctcctg cagccctgta agaaaaccag 540

acgctgcgct gcgctgctgg ggtcatcgaa tcacagagct gagcaaggga ctcgaaagga 600

aagagggact caagtccctg aagacgccct gct atg gcc ttt tca cct ttt gga 654
Met Ala Phe Ser Pro Phe Gly
1 5

cac ccg tat ggc agc aca tcc cag ttt ctg gtg tct gca agt tcc agt 702
His Pro Tyr Gly Ser Thr Ser Gln Phe Leu Val Ser Ala Ser Ser Ser
10 15 20

gcc act tgc tgc gaa acg gcc cct cgg cca gtg tca gat gtg gcc tca 750
Ala Thr Cys Cys Glu Thr Ala Pro Arg Pro Val Ser Asp Val Ala Ser
25 30 35

gcc tcc acc tct gcc tct act ctt tgc tgt aca ccc tat gac agt cgg 798
Ala Ser Thr Ser Ala Ser Thr Leu Cys Cys Thr Pro Tyr Asp Ser Arg
40 45 50 55

ctg ctg ggc agt gct cgg cca gag ctg gga gct gcc ttg ggc atc tat 846
Leu Leu Gly Ser Ala Arg Pro Glu Leu Gly Ala Ala Leu Gly Ile Tyr
60 65 70

```
gga gca ccc tat gca gct gcc cag agt tac cct ggg tac ctg acc tat      894
Gly Ala Pro Tyr Ala Ala Ala Gln Ser Tyr Pro Gly Tyr Leu Thr Tyr
            75                  80                  85

ggc cca gag cca ccc aca ctg tgt ggc gca ctg aat cct cag tat gag      942
Gly Pro Glu Pro Pro Thr Leu Cys Gly Ala Leu Asn Pro Gln Tyr Glu
        90                  95                  100

ttc aag gat gct gca gga agc ttt gcc ccc agc ctg acc cag cca ggg      990
Phe Lys Asp Ala Ala Gly Ser Phe Ala Pro Ser Leu Thr Gln Pro Gly
    105                 110                 115

gcc tac tac ccc tat gaa aca act ctg ggg cag tat caa tac gac agg     1038
Ala Tyr Tyr Pro Tyr Glu Thr Thr Leu Gly Gln Tyr Gln Tyr Asp Arg
120                 125                 130                 135

tat ggc gga gtg gaa ttg agc agt gct ggc cgc agg aag aat gcc aca     1086
Tyr Gly Gly Val Glu Leu Ser Ser Ala Gly Arg Arg Lys Asn Ala Thr
                140                 145                 150

agg gag agc acc agc gca ctg aag gcc tgg ctc cac gag cac cgc aag     1134
Arg Glu Ser Thr Ser Ala Leu Lys Ala Trp Leu His Glu His Arg Lys
            155                 160                 165

aac ccg tac ccc acc aag ggc gag aag atc atg ctg gcc atc atc acc     1182
Asn Pro Tyr Pro Thr Lys Gly Glu Lys Ile Met Leu Ala Ile Ile Thr
        170                 175                 180

aag atg acc ctc acc cag gtg tcc acc tgg ttc gcc aac gcg cgc cgg     1230
Lys Met Thr Leu Thr Gln Val Ser Thr Trp Phe Ala Asn Ala Arg Arg
    185                 190                 195

cgc ctc aag aag gag aac aag atg aca tgg gcg ccc aag aac aag gga     1278
Arg Leu Lys Lys Glu Asn Lys Met Thr Trp Ala Pro Lys Asn Lys Gly
```

200 205 210 215

ggg gag gag agg aaa gca gac agt gga gaa gac tct ctg gga tgc ctg 1326
Gly Glu Glu Arg Lys Ala Asp Ser Gly Glu Asp Ser Leu Gly Cys Leu
220 225 230

aat ggt gac acc aaa gat gct act gcc agc cag gaa gcc cgg ggg ctg 1374
Asn Gly Asp Thr Lys Asp Ala Thr Ala Ser Gln Glu Ala Arg Gly Leu
235 240 245

agg ctg agt gac ctg gaa gac ctg gag gaa gag gag gaa gag gaa gaa 1422
Arg Leu Ser Asp Leu Glu Asp Leu Glu Glu Glu Glu Glu Glu Glu Glu
250 255 260

gca gag gag gag gca gcg gtc tca gca gca cgc agg ctg gcg gat ttt 1470
Ala Glu Glu Glu Ala Ala Val Ser Ala Ala Arg Arg Leu Ala Asp Phe
265 270 275

cag aag agc acg caa ccc ctg cct gct ccc tgc gcc gcc gcc cag gag 1518
Gln Lys Ser Thr Gln Pro Leu Pro Ala Pro Cys Ala Ala Ala Gln Glu
280 285 290 295

aga tgc ttg gag agc aga gag tgc ggc ctg ggg cta ccc cgt ttc tct 1566
Arg Cys Leu Glu Ser Arg Glu Cys Gly Leu Gly Leu Pro Arg Phe Ser
300 305 310

ttt act gag gcc cca caa tca ggg gaa gct gac ttc atc aca gca gag 1614
Phe Thr Glu Ala Pro Gln Ser Gly Glu Ala Asp Phe Ile Thr Ala Glu
315 320 325

cca ggc ggc ccc acg atg atc tta cac tac cca agt ggc cac aaa ccc 1662
Pro Gly Gly Pro Thr Met Ile Leu His Tyr Pro Ser Gly His Lys Pro
330 335 340

cgc att tgg tcc tta gct cac act gcg gca gcc agc gct gtc gaa agt 1710

```
Arg Ile Trp Ser Leu Ala His Thr Ala Ala Ala Ser Ala Val Glu Ser
    345                 350                 355

gct ccc tca act ccg ccc agg gca caa agt cca gag tgc cac atg att      1758
Ala Pro Ser Thr Pro Pro Arg Ala Gln Ser Pro Glu Cys His Met Ile
360                 365                 370                 375

ccc aga cag ccc agt tct atc agg cga ctc ctg gta ccc aga gac tcc      1806
Pro Arg Gln Pro Ser Ser Ile Arg Arg Leu Leu Val Pro Arg Asp Ser
                380                 385                 390

gaa ggc gaa gag gat tct cct gca gcc aaa gct ttt gga aac tcc acg      1854
Glu Gly Glu Glu Asp Ser Pro Ala Ala Lys Ala Phe Gly Asn Ser Thr
            395                 400                 405

ttc acc ctg cag ggg ctg cca ctg aac tgt gca cca tac ccg agg cgg      1902
Phe Thr Leu Gln Gly Leu Pro Leu Asn Cys Ala Pro Tyr Pro Arg Arg
        410                 415                 420

aga gag cct gaa gtg cgg ttc cag tac cca tct gga gca gaa gca ggt      1950
Arg Glu Pro Glu Val Arg Phe Gln Tyr Pro Ser Gly Ala Glu Ala Gly
    425                 430                 435

tag tgcaatggct gcggtttgca gaagactttt ggaaatggct gcttccggat          2003

ccacattcat attaagaagt ttccagacct tggcatggac tgggagctct cactttgcct   2063

gtgacaaaca cacagaacca tcctagctgt atcttgcacg caggactggg gacaggccag   2123

atgacacaca cctcatcaga cttggaggag agaaggtggg agaccttggg ggaaagccct   2183

gtgtgtgctc acaggatact ttgaccaagt ctctcttcct cccatgaatg gaggccctga   2243

gcagcatctc ctcctgctca cccacccctg cccagcccac tcactgtgta actttcttgc   2303
```

tgaaatggtc tccaaggact gtctgtgtct ccttcctctt ccccggctct accttcaaaa 2363

ataacttagc tgagtcc 2380

<210> 4
<211> 439
<212> PRT
<213> Mus musculus

<400> 4

Met Ala Phe Ser Pro Phe Gly His Pro Tyr Gly Ser Thr Ser Gln Phe
1 5 10 15

Leu Val Ser Ala Ser Ser Ser Ala Thr Cys Cys Glu Thr Ala Pro Arg
20 25 30

Pro Val Ser Asp Val Ala Ser Ala Ser Thr Ser Ala Ser Thr Leu Cys
35 40 45

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

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

Tyr Pro Gly Tyr Leu Thr Tyr Gly Pro Glu Pro Pro Thr Leu Cys Gly
85 90 95

Ala Leu Asn Pro Gln Tyr Glu Phe Lys Asp Ala Ala Gly Ser Phe Ala
100 105 110

Pro Ser Leu Thr Gln Pro Gly Ala Tyr Tyr Pro Tyr Glu Thr Thr Leu
115 120 125

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

Gly Arg Arg Lys Asn Ala Thr Arg Glu Ser Thr Ser Ala Leu Lys Ala
145 150 155 160

Trp Leu His Glu His Arg Lys Asn Pro Tyr Pro Thr Lys Gly Glu Lys
165 170 175

Ile Met Leu Ala Ile Ile Thr Lys Met Thr Leu Thr Gln Val Ser Thr
180 185 190

Trp Phe Ala Asn Ala Arg Arg Arg Leu Lys Lys Glu Asn Lys Met Thr
195 200 205

Trp Ala Pro Lys Asn Lys Gly Gly Glu Glu Arg Lys Ala Asp Ser Gly
210 215 220

Glu Asp Ser Leu Gly Cys Leu Asn Gly Asp Thr Lys Asp Ala Thr Ala
225 230 235 240

Ser Gln Glu Ala Arg Gly Leu Arg Leu Ser Asp Leu Glu Asp Leu Glu
245 250 255

Glu Glu Glu Glu Glu Glu Glu Ala Glu Glu Glu Ala Ala Val Ser Ala
260 265 270

Ala Arg Arg Leu Ala Asp Phe Gln Lys Ser Thr Gln Pro Leu Pro Ala
275 280 285

Pro Cys Ala Ala Ala Gln Glu Arg Cys Leu Glu Ser Arg Glu Cys Gly
290 295 300

Leu Gly Leu Pro Arg Phe Ser Phe Thr Glu Ala Pro Gln Ser Gly Glu
305 310 315 320

Ala Asp Phe Ile Thr Ala Glu Pro Gly Gly Pro Thr Met Ile Leu His
325 330 335

Tyr Pro Ser Gly His Lys Pro Arg Ile Trp Ser Leu Ala His Thr Ala
340 345 350

Ala Ala Ser Ala Val Glu Ser Ala Pro Ser Thr Pro Pro Arg Ala Gln
355 360 365

Ser Pro Glu Cys His Met Ile Pro Arg Gln Pro Ser Ser Ile Arg Arg

370 375 380

Leu Leu Val Pro Arg Asp Ser Glu Gly Glu Glu Asp Ser Pro Ala Ala
385 390 395 400

Lys Ala Phe Gly Asn Ser Thr Phe Thr Leu Gln Gly Leu Pro Leu Asn
405 410 415

Cys Ala Pro Tyr Pro Arg Arg Arg Glu Pro Glu Val Arg Phe Gln Tyr
420 425 430

Pro Ser Gly Ala Glu Ala Gly
435

<210> 5
<211> 2816
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (568)..(2430)

<400> 5
cactgtgtac tgagactgga tgcatccttg caataaaaaa gaggttgatc acgacaaatg 60

tgaaccccgc cgttataaaa acagccatca tggctgtaaa tgccaaaaag cagtcagtct 120

tgtaacttga aaaaaaaaaa aaaggaattg tagattgtgc gcatggactc ggagtggggg 180

cggtggacag taagtcatga tgttttggtg gtaccacctg gttgaatttc ttcatctgaa 240

taagaagctc ctgtgatgtt ctggggaggc cttggaaggc tagcgcatcc ctcatagaaa 300

gtgaatggga gctacggaca ccgtaccccg ggctcagaga agagcctgct ggacctggac 360

cttgctgagg gccctggccc cacctgctgc cagggcctgt ttctccctgc aggaagccca 420

ccgccccggg ctcaccccca agcttgtgag aggctgctgc atttccccca ccctgacagg 480

tcacctagac cccaggccac gtatgtgaac ggcagcctcc caaccacaca acacatcaaa 540

caggagtcct tgcccgacta ccaagcc atg gca gag gcc cgc aca tcc ctg tct 594
Met Ala Glu Ala Arg Thr Ser Leu Ser
1 5

gcc cac tgt cgg ggc ccg ctg gcc act ggc ctg cac cca gac ctg gac 642
Ala His Cys Arg Gly Pro Leu Ala Thr Gly Leu His Pro Asp Leu Asp
10 15 20 25

ctc ccg ggc cga agc ctc gcc acc cct gcg cct tcc tgc tac ctt ctg 690
Leu Pro Gly Arg Ser Leu Ala Thr Pro Ala Pro Ser Cys Tyr Leu Leu
30 35 40

ggc agc gaa ccc agc tct ggc ctg ggc ctc cag ccc gag acc cac ctc 738
Gly Ser Glu Pro Ser Ser Gly Leu Gly Leu Gln Pro Glu Thr His Leu
45 50 55

ccc gag ggc agc ctg aag cgg tgc tgc gtc ttg ggc cta ccc ccc acc 786
Pro Glu Gly Ser Leu Lys Arg Cys Cys Val Leu Gly Leu Pro Pro Thr
60 65 70

tcc cca gcc tcc tcc tca ccc tgt gcc tcc tcc gac gtc acc tcc atc 834
Ser Pro Ala Ser Ser Ser Pro Cys Ala Ser Ser Asp Val Thr Ser Ile

75 80 85

atc cgc tcc tcc cag acg tct ctg gtc acc tgt gta aat gga ctc cgg 882
Ile Arg Ser Ser Gln Thr Ser Leu Val Thr Cys Val Asn Gly Leu Arg
90 95 100 105

agc ccc cct ctg acg gga gat ctg ggg ggc cct tcc aag cgg gcc cgg 930
Ser Pro Pro Leu Thr Gly Asp Leu Gly Gly Pro Ser Lys Arg Ala Arg
110 115 120

cct ggc cct gca tcg acg gac agc cat gag ggc agc ttg caa ctt gaa 978
Pro Gly Pro Ala Ser Thr Asp Ser His Glu Gly Ser Leu Gln Leu Glu
125 130 135

gcc tgc cgg aag gcg agc ttc ctg aag cag gaa ccc gcg gat gag ttt 1026
Ala Cys Arg Lys Ala Ser Phe Leu Lys Gln Glu Pro Ala Asp Glu Phe
140 145 150

tca gag ctc ttt ggg cct cac cag cag ggc ctg ccg ccc ccc tat ccc 1074
Ser Glu Leu Phe Gly Pro His Gln Gln Gly Leu Pro Pro Pro Tyr Pro
155 160 165

ctg tct cag ttg ccg cct ggc cca agc ctt gga ggc ctg ggg ctg ggc 1122
Leu Ser Gln Leu Pro Pro Gly Pro Ser Leu Gly Gly Leu Gly Leu Gly
170 175 180 185

ctg gca ggc agg gtg gtg gcc ggg cgg cag gcg tgc cgc tgg gtg gac 1170
Leu Ala Gly Arg Val Val Ala Gly Arg Gln Ala Cys Arg Trp Val Asp
190 195 200

tgc tgt gca gcc tat gag cag cag gag gag ctg gtg cgg cac atc gag 1218
Cys Cys Ala Ala Tyr Glu Gln Gln Glu Glu Leu Val Arg His Ile Glu
205 210 215

aag agc cac atc gac cag cgc aag ggc gag gac ttc acc tgc ttc tgg 1266

```
Lys Ser His Ile Asp Gln Arg Lys Gly Glu Asp Phe Thr Cys Phe Trp
        220                 225                 230

gct ggc tgc gtg cgc cgc tac aag ccc ttc aac gcc cgc tac aag ctg      1314
Ala Gly Cys Val Arg Arg Tyr Lys Pro Phe Asn Ala Arg Tyr Lys Leu
    235                 240                 245

ctc atc cac atg cga gtg cac tcg ggc gag aag ccc aac aag tgc atg      1362
Leu Ile His Met Arg Val His Ser Gly Glu Lys Pro Asn Lys Cys Met
250                 255                 260                 265

ttt gaa ggc tgc agc aag gcc ttc tca cgg ctg gag aac ctc aag atc      1410
Phe Glu Gly Cys Ser Lys Ala Phe Ser Arg Leu Glu Asn Leu Lys Ile
                270                 275                 280

cac ctg agg agc cac acg ggc gag aag ccg tac ctg tgc cag cac ccg      1458
His Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Leu Cys Gln His Pro
            285                 290                 295

ggt tgc cag aag gcc ttc agc aac tcc agc gac cgc gcc aag cac cag      1506
Gly Cys Gln Lys Ala Phe Ser Asn Ser Ser Asp Arg Ala Lys His Gln
        300                 305                 310

cgc acc cac cta gac acg aag ccg tac gcc tgt cag atc cct ggc tgc      1554
Arg Thr His Leu Asp Thr Lys Pro Tyr Ala Cys Gln Ile Pro Gly Cys
    315                 320                 325

tcc aag cgc tac aca gac ccc agc tcc ctc cgc aag cac gtc aag gcc      1602
Ser Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys His Val Lys Ala
330                 335                 340                 345

cat tca gcc aaa gag cag cag gtg cgt aag aag ctg cat gcg ggc cct      1650
His Ser Ala Lys Glu Gln Gln Val Arg Lys Lys Leu His Ala Gly Pro
                350                 355                 360
```

```
gac acc gag gcc gac gtc ctg acc gag tgt ctg gtc ctg cag cag ctc      1698
Asp Thr Glu Ala Asp Val Leu Thr Glu Cys Leu Val Leu Gln Gln Leu
            365                 370                 375

cac acg tcc aca cag ctg gct gcc agc gac ggc aag ggt ggc tgt ggc      1746
His Thr Ser Thr Gln Leu Ala Ala Ser Asp Gly Lys Gly Gly Cys Gly
        380                 385                 390

ctg ggc cag gag ctg ctc cca ggt gtg tat cct ggc tcc atc acc ccc      1794
Leu Gly Gln Glu Leu Leu Pro Gly Val Tyr Pro Gly Ser Ile Thr Pro
    395                 400                 405

cat aac gga ctt gca tcg ggc ctc ctg ccc cca gcg cac gac gta cct      1842
His Asn Gly Leu Ala Ser Gly Leu Leu Pro Pro Ala His Asp Val Pro
410                 415                 420                 425

tcc agg cac cac ccg ctg gat gcc acc acc agt tcc cac cac cat ctg      1890
Ser Arg His His Pro Leu Asp Ala Thr Thr Ser Ser His His His Leu
                430                 435                 440

tcc cct ctg ccc atg gct gag agc acc cgg gat ggg ttg ggg ccc ggc      1938
Ser Pro Leu Pro Met Ala Glu Ser Thr Arg Asp Gly Leu Gly Pro Gly
            445                 450                 455

ctc ctc tca cca ata gtc agc ccc ctg aag ggg ctg ggg cca ccg ccg      1986
Leu Leu Ser Pro Ile Val Ser Pro Leu Lys Gly Leu Gly Pro Pro Pro
        460                 465                 470

ctg ccc cca tcc tct cag agc cat tct ccg ggg ggc cag ccc ttc ccc      2034
Leu Pro Pro Ser Ser Gln Ser His Ser Pro Gly Gly Gln Pro Phe Pro
    475                 480                 485

aca ctc ccc agc aag ccg tcc tac cca ccc ttc cag agc cct cca ccc      2082
Thr Leu Pro Ser Lys Pro Ser Tyr Pro Pro Phe Gln Ser Pro Pro Pro
490                 495                 500                 505
```

ccg cct ctg ccc agc cca caa ggt tac cag ggc agt ttc cac tcc atc 2130
Pro Pro Leu Pro Ser Pro Gln Gly Tyr Gln Gly Ser Phe His Ser Ile
510 515 520

cag agt tgc ttc ccc tat ggc gac tgc tac cgg atg gct gaa cca gca 2178
Gln Ser Cys Phe Pro Tyr Gly Asp Cys Tyr Arg Met Ala Glu Pro Ala
525 530 535

gcc ggt ggg gac gga ctg gtc ggg gag acc cac ggt ttc aac ccc ctg 2226
Ala Gly Gly Asp Gly Leu Val Gly Glu Thr His Gly Phe Asn Pro Leu
540 545 550

cgg ccc aat ggc tac cac agc ctc agc acg ccc ttg cct gcc aca ggc 2274
Arg Pro Asn Gly Tyr His Ser Leu Ser Thr Pro Leu Pro Ala Thr Gly
555 560 565

tat gag gcc ctg gct gag gcc tca tgc ccc aca gcg ctg cca cag cag 2322
Tyr Glu Ala Leu Ala Glu Ala Ser Cys Pro Thr Ala Leu Pro Gln Gln
570 575 580 585

cca tct gaa gat gtg gtg tcc agc ggc ccc gag gac tgt ggc ttc ttc 2370
Pro Ser Glu Asp Val Val Ser Ser Gly Pro Glu Asp Cys Gly Phe Phe
590 595 600

ccc aat gga gcc ttt gac cac tgc ctg ggc cac atc ccc tcc atc tac 2418
Pro Asn Gly Ala Phe Asp His Cys Leu Gly His Ile Pro Ser Ile Tyr
605 610 615

aca gac acc tga aggagccccc acatgcgcct gcccatccag cactgcagat 2470
Thr Asp Thr
620

gccacctcgc ccacctgctg tcgctcccac cctccgtgca cctagcagga gtgccaggcc 2530

acagccggaa cagccaggcc atgacccagg ggagccagcg ctgccacccc acccagcgct 2590

gccagggagc cgccatccga gcttgagctg ggcgcacaga ggtgcccgcc aggatctgtg 2650

gccctgtaac attccctcga tcttgtcttc ccgttcctcc ccgcagtggt tttgaaatca 2710

cagacctcgt gtatataaaa tatgcagaac ttgttttccg ttcccctgcc agttttatat 2770

ttttggtttt acaagaaaaa acattaaaaa ctggaaagga gatgtg 2816

<210> 6
<211> 620
<212> PRT
<213> Homo sapiens

<400> 6

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

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

Thr Pro Ala Pro Ser Cys Tyr Leu Leu Gly Ser Glu Pro Ser Ser Gly
35 40 45

Leu Gly Leu Gln Pro Glu Thr His Leu Pro Glu Gly Ser Leu Lys Arg
50 55 60

Cys Cys Val Leu Gly Leu Pro Pro Thr Ser Pro Ala Ser Ser Ser Pro

65 70 75 80

Cys Ala Ser Ser Asp Val Thr Ser Ile Ile Arg Ser Ser Gln Thr Ser
85 90 95

Leu Val Thr Cys Val Asn Gly Leu Arg Ser Pro Pro Leu Thr Gly Asp
100 105 110

Leu Gly Gly Pro Ser Lys Arg Ala Arg Pro Gly Pro Ala Ser Thr Asp
115 120 125

Ser His Glu Gly Ser Leu Gln Leu Glu Ala Cys Arg Lys Ala Ser Phe
130 135 140

Leu Lys Gln Glu Pro Ala Asp Glu Phe Ser Glu Leu Phe Gly Pro His
145 150 155 160

Gln Gln Gly Leu Pro Pro Pro Tyr Pro Leu Ser Gln Leu Pro Pro Gly
165 170 175

Pro Ser Leu Gly Gly Leu Gly Leu Gly Leu Ala Gly Arg Val Val Ala
180 185 190

Gly Arg Gln Ala Cys Arg Trp Val Asp Cys Cys Ala Ala Tyr Glu Gln
195 200 205

Gln Glu Glu Leu Val Arg His Ile Glu Lys Ser His Ile Asp Gln Arg
210 215 220

Lys Gly Glu Asp Phe Thr Cys Phe Trp Ala Gly Cys Val Arg Arg Tyr
225 230 235 240

Lys Pro Phe Asn Ala Arg Tyr Lys Leu Leu Ile His Met Arg Val His
245 250 255

Ser Gly Glu Lys Pro Asn Lys Cys Met Phe Glu Gly Cys Ser Lys Ala
260 265 270

Phe Ser Arg Leu Glu Asn Leu Lys Ile His Leu Arg Ser His Thr Gly
275 280 285

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

Asn Ser Ser Asp Arg Ala Lys His Gln Arg Thr His Leu Asp Thr Lys
305 310 315 320

Pro Tyr Ala Cys Gln Ile Pro Gly Cys Ser Lys Arg Tyr Thr Asp Pro
325 330 335

Ser Ser Leu Arg Lys His Val Lys Ala His Ser Ala Lys Glu Gln Gln
340 345 350

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

Thr Glu Cys Leu Val Leu Gln Gln Leu His Thr Ser Thr Gln Leu Ala
370 375 380

Ala Ser Asp Gly Lys Gly Gly Cys Gly Leu Gly Gln Glu Leu Leu Pro
385 390 395 400

Gly Val Tyr Pro Gly Ser Ile Thr Pro His Asn Gly Leu Ala Ser Gly
405 410 415

Leu Leu Pro Pro Ala His Asp Val Pro Ser Arg His His Pro Leu Asp
420 425 430

Ala Thr Thr Ser Ser His His His Leu Ser Pro Leu Pro Met Ala Glu
435 440 445

Ser Thr Arg Asp Gly Leu Gly Pro Gly Leu Leu Ser Pro Ile Val Ser
450 455 460

Pro Leu Lys Gly Leu Gly Pro Pro Pro Leu Pro Pro Ser Ser Gln Ser
465 470 475 480

His Ser Pro Gly Gly Gln Pro Phe Pro Thr Leu Pro Ser Lys Pro Ser
485 490 495

Tyr Pro Pro Phe Gln Ser Pro Pro Pro Pro Pro Leu Pro Ser Pro Gln
500 505 510

Gly Tyr Gln Gly Ser Phe His Ser Ile Gln Ser Cys Phe Pro Tyr Gly
515 520 525

Asp Cys Tyr Arg Met Ala Glu Pro Ala Ala Gly Gly Asp Gly Leu Val
530 535 540

Gly Glu Thr His Gly Phe Asn Pro Leu Arg Pro Asn Gly Tyr His Ser
545 550 555 560

Leu Ser Thr Pro Leu Pro Ala Thr Gly Tyr Glu Ala Leu Ala Glu Ala
565 570 575

Ser Cys Pro Thr Ala Leu Pro Gln Gln Pro Ser Glu Asp Val Val Ser
580 585 590

Ser Gly Pro Glu Asp Cys Gly Phe Phe Pro Asn Gly Ala Phe Asp His
595 600 605

Cys Leu Gly His Ile Pro Ser Ile Tyr Thr Asp Thr
610 615 620

<210> 7

<211> 2904

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (222)..(2591)

<400> 7

ggggacccag tggcgtccga atccgggagc tctggggtgg cgcggggctc gccgaggggc 60

gaggcgaatt tgggggccct gaggcctcgc tctcgcggga atgatgctgg aaatgatgct 120

gaggctccgg cgtgagactt gcggctgccg gcggagcgga gtgtgagccg gtgaatgggg 180

agcctggcgc gacccccagc cgtgcgcccc gccccggcgc c atg cat tgc gag gtg 236
Met His Cys Glu Val
1 5

gcc gag gca ctt tcg gac aag agg cca aag gag gcc cct ggt gct cct 284
Ala Glu Ala Leu Ser Asp Lys Arg Pro Lys Glu Ala Pro Gly Ala Pro
10 15 20

ggc cag ggc cgc ggg cct gtc agc ctg gga gcg cac atg gcc ttc agg 332
Gly Gln Gly Arg Gly Pro Val Ser Leu Gly Ala His Met Ala Phe Arg
25 30 35

att gct gtg agt ggt ggc ggc tgc ggg gac ggg aac ccg cta gac ctg 380
Ile Ala Val Ser Gly Gly Gly Cys Gly Asp Gly Asn Pro Leu Asp Leu
40 45 50

ctg cct cgg cta ccg gtg cca cca cca cgt gcc cac gat ctc ctt cgg 428
Leu Pro Arg Leu Pro Val Pro Pro Pro Arg Ala His Asp Leu Leu Arg
55 60 65

```
ccc cgg agc cct cga gac tat ggt gtg tcc aag acc ggc agc ggg aag        476
Pro Arg Ser Pro Arg Asp Tyr Gly Val Ser Lys Thr Gly Ser Gly Lys
70                  75                  80                  85

gtg aac ggg agc tac ggg cac agc tca gag aag agc ctg ctg gac ctg        524
Val Asn Gly Ser Tyr Gly His Ser Ser Glu Lys Ser Leu Leu Asp Leu
                90                  95                  100

gac ctg gcc gag ggt ccc agc ccc tcc tgc cac cag ggt ctg ttt ctt        572
Asp Leu Ala Glu Gly Pro Ser Pro Ser Cys His Gln Gly Leu Phe Leu
            105                 110                 115

cct gca ggg acc cca cca ccc cgg ggt cac ccc cct gtc tgt gag aag        620
Pro Ala Gly Thr Pro Pro Pro Arg Gly His Pro Pro Val Cys Glu Lys
        120                 125                 130

ctg ctg cac ttc ccc cac cca aac agg tca ccc aga cct cag gct acg        668
Leu Leu His Phe Pro His Pro Asn Arg Ser Pro Arg Pro Gln Ala Thr
    135                 140                 145

ttt gtg aac ggc agc ctc cca gcc gct cag cac atc aag caa gaa gcc        716
Phe Val Asn Gly Ser Leu Pro Ala Ala Gln His Ile Lys Gln Glu Ala
150                 155                 160                 165

cta ccg gac tac cag gcc atg gtc agc gcc cac aca ccc ctg ccc acc        764
Leu Pro Asp Tyr Gln Ala Met Val Ser Ala His Thr Pro Leu Pro Thr
                170                 175                 180

cac tgc cga gcc cca tcg tcc atg ggt ctg ccc tca gac ctg gac ttt        812
His Cys Arg Ala Pro Ser Ser Met Gly Leu Pro Ser Asp Leu Asp Phe
            185                 190                 195

cca gac cga ggc ctc acc aac cct gca cct tcc tgc tac ctt ctg ggc        860
Pro Asp Arg Gly Leu Thr Asn Pro Ala Pro Ser Cys Tyr Leu Leu Gly
```

```
        200                 205                 210

aat gaa ccc atc tca gac ctg ggt ccc caa ccc gag gcc cac ctc ccc      908
Asn Glu Pro Ile Ser Asp Leu Gly Pro Gln Pro Glu Ala His Leu Pro
    215                 220                 225

gag ggc agc ctg aaa cgc tgc tgc ctc ctg ggc ctg ccc ccc acc tct      956
Glu Gly Ser Leu Lys Arg Cys Cys Leu Leu Gly Leu Pro Pro Thr Ser
230                 235                 240                 245

tca gcc tcc tcc tca ccc tgt gcc tcc tca gat atc aat cct gtc atc      1004
Ser Ala Ser Ser Ser Pro Cys Ala Ser Ser Asp Ile Asn Pro Val Ile
                250                 255                 260

cac tcc tcc cag aca gct cta gtt agc tgt gta aat gga ctc cga agc      1052
His Ser Ser Gln Thr Ala Leu Val Ser Cys Val Asn Gly Leu Arg Ser
            265                 270                 275

cca cct ctg ccg gga gac ctg ggg ggc cct ccc aag cgg tca cgg ccc      1100
Pro Pro Leu Pro Gly Asp Leu Gly Gly Pro Pro Lys Arg Ser Arg Pro
        280                 285                 290

ggg cct gca tcc agt gac ggc cag gag ggc agc ttg cag ctt gaa gca      1148
Gly Pro Ala Ser Ser Asp Gly Gln Glu Gly Ser Leu Gln Leu Glu Ala
    295                 300                 305

tgc cgg aag tca ggc ttc ctg aag cag gag ccc atg gac gag ttt tca      1196
Cys Arg Lys Ser Gly Phe Leu Lys Gln Glu Pro Met Asp Glu Phe Ser
310                 315                 320                 325

gag ctt ttt gct cca cac cac cag ggt ttg cca ccc cct tac ccc ttg      1244
Glu Leu Phe Ala Pro His His Gln Gly Leu Pro Pro Pro Tyr Pro Leu
                330                 335                 340

cct cag ttg cca act ggc ccc ggc ctc gga ggc cta ggg ctg ggc ctg      1292
```

```
Pro Gln Leu Pro Thr Gly Pro Gly Leu Gly Gly Leu Gly Leu Gly Leu
            345                 350                 355

gca ggt agg atg gtt gcc ggt cgg cag gca tgc cgc tgg gtg gac tgc      1340
Ala Gly Arg Met Val Ala Gly Arg Gln Ala Cys Arg Trp Val Asp Cys
        360                 365                 370

tgc gca gcc tac gag cag cag gag gag ctg gtg cgg cac atc gag aag      1388
Cys Ala Ala Tyr Glu Gln Gln Glu Glu Leu Val Arg His Ile Glu Lys
    375                 380                 385

agc cac atc gac cag cgc aag ggc gaa gac ttc acc tgc ttc tgg gcc      1436
Ser His Ile Asp Gln Arg Lys Gly Glu Asp Phe Thr Cys Phe Trp Ala
390                 395                 400                 405

ggg tgt gtg cgg cgc tac aag ccc ttc aat gcc cgc tac aag ctg ctc      1484
Gly Cys Val Arg Arg Tyr Lys Pro Phe Asn Ala Arg Tyr Lys Leu Leu
                410                 415                 420

atc cac atg agg gta cac tca ggc gag aag ccc aac aag tgc atg ttc      1532
Ile His Met Arg Val His Ser Gly Glu Lys Pro Asn Lys Cys Met Phe
            425                 430                 435

gaa ggc tgc agt aaa gcc ttt tcc cgt ctg gag aac ctg aag atc cat      1580
Glu Gly Cys Ser Lys Ala Phe Ser Arg Leu Glu Asn Leu Lys Ile His
        440                 445                 450

ctg cgg agc cac aca ggc gag aaa cca tac ctg tgc cag cac cca ggc      1628
Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Leu Cys Gln His Pro Gly
    455                 460                 465

tgc cag aag gcc ttc agc aac tcc agc gac cgt gcc aag cac caa cgc      1676
Cys Gln Lys Ala Phe Ser Asn Ser Ser Asp Arg Ala Lys His Gln Arg
470                 475                 480                 485
```

```
acc cac ctc gac acg aag cca tat gct tgt cag atc cct ggc tgc tcc      1724
Thr His Leu Asp Thr Lys Pro Tyr Ala Cys Gln Ile Pro Gly Cys Ser
                490                 495                 500

aag cgc tac acg gac ccc agc tcc ctc cgc aag cac gtg aag gcc cac      1772
Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys His Val Lys Ala His
            505                 510                 515

tca gcc aaa gag cag cag gtg cgt aag aag ctg cac aca ggt gcc gac      1820
Ser Ala Lys Glu Gln Gln Val Arg Lys Lys Leu His Thr Gly Ala Asp
        520                 525                 530

cca gag gct gat gtt ctg tcc gag tgt ctg tcc ctg cag cag ctc caa      1868
Pro Glu Ala Asp Val Leu Ser Glu Cys Leu Ser Leu Gln Gln Leu Gln
    535                 540                 545

gca tcc aca ctg ttg ccg gcc agc aga ggg aag ggc agc caa acc ctg      1916
Ala Ser Thr Leu Leu Pro Ala Ser Arg Gly Lys Gly Ser Gln Thr Leu
550                 555                 560                 565

agc cag gag ctc ctc cca ggt gtg tat cct ggc tcc gtc acc cca caa      1964
Ser Gln Glu Leu Leu Pro Gly Val Tyr Pro Gly Ser Val Thr Pro Gln
                570                 575                 580

aac ggg ctt gct tca ggc atc ctg tcc ccc tcc cac gat gtc cct tcc      2012
Asn Gly Leu Ala Ser Gly Ile Leu Ser Pro Ser His Asp Val Pro Ser
            585                 590                 595

agg cac cac cca ctg gag gtc ccc act ggt tcc cac cac cac ctg tcc      2060
Arg His His Pro Leu Glu Val Pro Thr Gly Ser His His His Leu Ser
        600                 605                 610

cct ctg ccc aca gct gag agc acc agg gat ggc ctg ggg ccc agt ctc      2108
Pro Leu Pro Thr Ala Glu Ser Thr Arg Asp Gly Leu Gly Pro Ser Leu
    615                 620                 625
```

ctt tca ccc atg gtc agc cca ctg aag ggg ctt ggt ccc cca ccg cta 2156
Leu Ser Pro Met Val Ser Pro Leu Lys Gly Leu Gly Pro Pro Pro Leu
630 635 640 645

cca cca gcc tcc cag agt cag tct cca ggg gga cag tca ttc tct aca 2204
Pro Pro Ala Ser Gln Ser Gln Ser Pro Gly Gly Gln Ser Phe Ser Thr
650 655 660

gtc ccc agc aag cct acc tac cca tcc ttc caa agc cca cca cct ctg 2252
Val Pro Ser Lys Pro Thr Tyr Pro Ser Phe Gln Ser Pro Pro Pro Leu
665 670 675

ccc agc ccc caa ggc tac caa ggc agt ttc cat tcc atc cag aac tgc 2300
Pro Ser Pro Gln Gly Tyr Gln Gly Ser Phe His Ser Ile Gln Asn Cys
680 685 690

ttc ccc tac gct gac tgc tac cgg gcc act gag cca gca gcc tcc agg 2348
Phe Pro Tyr Ala Asp Cys Tyr Arg Ala Thr Glu Pro Ala Ala Ser Arg
695 700 705

gat gga ctg gtg ggt gat gcc cac ggt ttc aac ccc ttg cga ccc agc 2396
Asp Gly Leu Val Gly Asp Ala His Gly Phe Asn Pro Leu Arg Pro Ser
710 715 720 725

aca tac tcc agc ctc agc aca cct tta tcc gca cca ggc tac gag acc 2444
Thr Tyr Ser Ser Leu Ser Thr Pro Leu Ser Ala Pro Gly Tyr Glu Thr
730 735 740

ctg gca gaa acg ccg tgt ccc cca gcg ctg cag cca cag cca gct gaa 2492
Leu Ala Glu Thr Pro Cys Pro Pro Ala Leu Gln Pro Gln Pro Ala Glu
745 750 755

gac ctg gta cct agt ggt cct gag gac tgt ggc ttc ttc ccc aat ggg 2540
Asp Leu Val Pro Ser Gly Pro Glu Asp Cys Gly Phe Phe Pro Asn Gly

760 765 770

gcc ttt gac cac tgt ctg agt cac atc ccg tcc atc tac act gac acc 2588
Ala Phe Asp His Cys Leu Ser His Ile Pro Ser Ile Tyr Thr Asp Thr
775 780 785

tga aggaaggggc gctgctctgc ctgcctgcct ggctcctgag ctacttcacc 2641

tacctgccat ctgctggtgc ttcccacacg gggcagcaag gccacaccac agggtacttc 2701

cctacctgga gggctgtctg gtccagagct gcctgccagg agctatggcc ctctgacagc 2761

cccatggctg tgtcttcctc tctctccata aggttctcaa atcacagacc tcgtgtatat 2821

acaatgtaca ggacctcttt tccgccgccc tgcaagtttt atatttttgg ttttacaaga 2881

aaaacattaa aaactggaaa cta 2904

<210> 8
<211> 789
<212> PRT
<213> Mus musculus

<400> 8

Met His Cys Glu Val Ala Glu Ala Leu Ser Asp Lys Arg Pro Lys Glu
1 5 10 15

Ala Pro Gly Ala Pro Gly Gln Gly Arg Gly Pro Val Ser Leu Gly Ala
20 25 30

His Met Ala Phe Arg Ile Ala Val Ser Gly Gly Gly Cys Gly Asp Gly

35 40 45

Asn Pro Leu Asp Leu Leu Pro Arg Leu Pro Val Pro Pro Pro Arg Ala
50 55 60

His Asp Leu Leu Arg Pro Arg Ser Pro Arg Asp Tyr Gly Val Ser Lys
65 70 75 80

Thr Gly Ser Gly Lys Val Asn Gly Ser Tyr Gly His Ser Ser Glu Lys
85 90 95

Ser Leu Leu Asp Leu Asp Leu Ala Glu Gly Pro Ser Pro Ser Cys His
100 105 110

Gln Gly Leu Phe Leu Pro Ala Gly Thr Pro Pro Pro Arg Gly His Pro
115 120 125

Pro Val Cys Glu Lys Leu Leu His Phe Pro His Pro Asn Arg Ser Pro
130 135 140

Arg Pro Gln Ala Thr Phe Val Asn Gly Ser Leu Pro Ala Ala Gln His
145 150 155 160

Ile Lys Gln Glu Ala Leu Pro Asp Tyr Gln Ala Met Val Ser Ala His
165 170 175

Thr Pro Leu Pro Thr His Cys Arg Ala Pro Ser Ser Met Gly Leu Pro
180 185 190

Ser Asp Leu Asp Phe Pro Asp Arg Gly Leu Thr Asn Pro Ala Pro Ser
195 200 205

Cys Tyr Leu Leu Gly Asn Glu Pro Ile Ser Asp Leu Gly Pro Gln Pro
210 215 220

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

Leu Pro Pro Thr Ser Ser Ala Ser Ser Ser Pro Cys Ala Ser Ser Asp
245 250 255

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

Asn Gly Leu Arg Ser Pro Pro Leu Pro Gly Asp Leu Gly Gly Pro Pro
275 280 285

Lys Arg Ser Arg Pro Gly Pro Ala Ser Ser Asp Gly Gln Glu Gly Ser
290 295 300

Leu Gln Leu Glu Ala Cys Arg Lys Ser Gly Phe Leu Lys Gln Glu Pro
305 310 315 320

Met Asp Glu Phe Ser Glu Leu Phe Ala Pro His His Gln Gly Leu Pro
325 330 335

Pro Pro Tyr Pro Leu Pro Gln Leu Pro Thr Gly Pro Gly Leu Gly Gly
340 345 350

Leu Gly Leu Gly Leu Ala Gly Arg Met Val Ala Gly Arg Gln Ala Cys
355 360 365

Arg Trp Val Asp Cys Cys Ala Ala Tyr Glu Gln Gln Glu Glu Leu Val
370 375 380

Arg His Ile Glu Lys Ser His Ile Asp Gln Arg Lys Gly Glu Asp Phe
385 390 395 400

Thr Cys Phe Trp Ala Gly Cys Val Arg Arg Tyr Lys Pro Phe Asn Ala
405 410 415

Arg Tyr Lys Leu Leu Ile His Met Arg Val His Ser Gly Glu Lys Pro
420 425 430

Asn Lys Cys Met Phe Glu Gly Cys Ser Lys Ala Phe Ser Arg Leu Glu
435 440 445

Asn Leu Lys Ile His Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Leu
450 455 460

Cys Gln His Pro Gly Cys Gln Lys Ala Phe Ser Asn Ser Ser Asp Arg
465 470 475 480

Ala Lys His Gln Arg Thr His Leu Asp Thr Lys Pro Tyr Ala Cys Gln
485 490 495

Ile Pro Gly Cys Ser Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys
500 505 510

His Val Lys Ala His Ser Ala Lys Glu Gln Gln Val Arg Lys Lys Leu
515 520 525

His Thr Gly Ala Asp Pro Glu Ala Asp Val Leu Ser Glu Cys Leu Ser
530 535 540

Leu Gln Gln Leu Gln Ala Ser Thr Leu Leu Pro Ala Ser Arg Gly Lys
545 550 555 560

Gly Ser Gln Thr Leu Ser Gln Glu Leu Leu Pro Gly Val Tyr Pro Gly
565 570 575

Ser Val Thr Pro Gln Asn Gly Leu Ala Ser Gly Ile Leu Ser Pro Ser
580 585 590

His Asp Val Pro Ser Arg His His Pro Leu Glu Val Pro Thr Gly Ser

595 600 605

His His His Leu Ser Pro Leu Pro Thr Ala Glu Ser Thr Arg Asp Gly
610 615 620

Leu Gly Pro Ser Leu Leu Ser Pro Met Val Ser Pro Leu Lys Gly Leu
625 630 635 640

Gly Pro Pro Pro Leu Pro Pro Ala Ser Gln Ser Gln Ser Pro Gly Gly
645 650 655

Gln Ser Phe Ser Thr Val Pro Ser Lys Pro Thr Tyr Pro Ser Phe Gln
660 665 670

Ser Pro Pro Pro Leu Pro Ser Pro Gln Gly Tyr Gln Gly Ser Phe His
675 680 685

Ser Ile Gln Asn Cys Phe Pro Tyr Ala Asp Cys Tyr Arg Ala Thr Glu
690 695 700

Pro Ala Ala Ser Arg Asp Gly Leu Val Gly Asp Ala His Gly Phe Asn
705 710 715 720

Pro Leu Arg Pro Ser Thr Tyr Ser Ser Leu Ser Thr Pro Leu Ser Ala
725 730 735

Pro Gly Tyr Glu Thr Leu Ala Glu Thr Pro Cys Pro Pro Ala Leu Gln
740 745 750

Pro Gln Pro Ala Glu Asp Leu Val Pro Ser Gly Pro Glu Asp Cys Gly
755 760 765

Phe Phe Pro Asn Gly Ala Phe Asp His Cys Leu Ser His Ile Pro Ser
770 775 780

Ile Tyr Thr Asp Thr
785

<210> 9
<211> 2250
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (583)..(1536)

<400> 9
tgggagtccg tgctcctgct cctcggttgg ctcctaagtg ccccgccagg tcccctctcc 60

tttcgctctc ccggctccgg ctcccgactc ttcggcccgc tggcatctgc ttccctcccc 120

tgcctcgttt ctcgtcgccc ctgctcgctc ccccccggcgc tcgcccgggc gctgtgctcg 180

ctcctggatc gccagccgcg cagccgggct cggccggccg cccgcgcgcc actgtgcagt 240

ggagtttggt ggaatctctg ctgacgtcac gtcactcccc acacggagta ggagcagagg 300

gaagagagag ggatgagagg gagggagagg agagagagtg cgagaccgag cgagaaagct 360

ggagaggagc agaaagaaac tgccagtggc ggctagattt cggaggcccc agtgcacccg 420

tggactcctt cggaacttgg caccctcagg agccctgcag tcctctcagg cccggctttc 480

gggcgcttgc cgtgcagccg gaggctcggc tcgctggaaa tcgccccggg aagcagtggg 540

acgcggagac agcagctctc tcccggtagc cgataacggg ga atg gag acc aac 594
Met Glu Thr Asn
1

tgc cgc aaa ctg gtg tcg gcg tgt gtg caa tta ggc gtg cag ccg gcg 642
Cys Arg Lys Leu Val Ser Ala Cys Val Gln Leu Gly Val Gln Pro Ala
5 10 15 20

gcc gtt gaa tgt ctc ttc tcc aaa gac tcc gaa atc aaa aag gtc gag 690
Ala Val Glu Cys Leu Phe Ser Lys Asp Ser Glu Ile Lys Lys Val Glu
25 30 35

ttc acg gac tct cct gag agc cga aaa gag gca gcc agc agc aag ttc 738
Phe Thr Asp Ser Pro Glu Ser Arg Lys Glu Ala Ala Ser Ser Lys Phe
40 45 50

ttc ccg cgg cag cat cct ggc gcc aat gag aaa gat aaa agc cag cag 786
Phe Pro Arg Gln His Pro Gly Ala Asn Glu Lys Asp Lys Ser Gln Gln
55 60 65

ggg aag aat gag gac gtg ggc gcc gag gac ccg tct aag aag aag cgg 834
Gly Lys Asn Glu Asp Val Gly Ala Glu Asp Pro Ser Lys Lys Lys Arg
70 75 80

caa agg cgg cag cgg act cac ttt acc agc cag cag ctc cag gag ctg 882

```
Gln Arg Arg Gln Arg Thr His Phe Thr Ser Gln Gln Leu Gln Glu Leu
85                  90                  95                  100

gag gcc act ttc cag agg aac cgc tac ccg gac atg tcc aca cgc gaa      930
Glu Ala Thr Phe Gln Arg Asn Arg Tyr Pro Asp Met Ser Thr Arg Glu
                105                 110                 115

gaa atc gct gtg tgg acc aac ctt acg gaa gcc cga gtc cgg gtt tgg      978
Glu Ile Ala Val Trp Thr Asn Leu Thr Glu Ala Arg Val Arg Val Trp
            120                 125                 130

ttc aag aat cgt cgg gcc aaa tgg aga aag agg gag cgc aac cag cag     1026
Phe Lys Asn Arg Arg Ala Lys Trp Arg Lys Arg Glu Arg Asn Gln Gln
        135                 140                 145

gcc gag cta tgc aag aat ggc ttc ggg ccg cag ttc aat ggg ctc atg     1074
Ala Glu Leu Cys Lys Asn Gly Phe Gly Pro Gln Phe Asn Gly Leu Met
    150                 155                 160

cag ccc tac gac gac atg tac cca ggc tat tcc tac aac aac tgg gcc     1122
Gln Pro Tyr Asp Asp Met Tyr Pro Gly Tyr Ser Tyr Asn Asn Trp Ala
165                 170                 175                 180

gcc aag ggc ctt aca tcc gcc tcc cta tcc acc aag agc ttc ccc ttc     1170
Ala Lys Gly Leu Thr Ser Ala Ser Leu Ser Thr Lys Ser Phe Pro Phe
                185                 190                 195

ttc aac tct atg aac gtc aac ccc ctg tca tca cag agc atg ttt tcc     1218
Phe Asn Ser Met Asn Val Asn Pro Leu Ser Ser Gln Ser Met Phe Ser
            200                 205                 210

cca ccc aac tct atc tcg tcc atg agc atg tcg tcc agc atg gtg ccc     1266
Pro Pro Asn Ser Ile Ser Ser Met Ser Met Ser Ser Ser Met Val Pro
        215                 220                 225
```

tca gca gtg aca ggc gtc ccg ggc tcc agt ctc aac agc ctg aat aac 1314
Ser Ala Val Thr Gly Val Pro Gly Ser Ser Leu Asn Ser Leu Asn Asn
230 235 240

ttg aac aac ctg agt agc ccg tcg ctg aat tcc gcg gtg ccg acg cct 1362
Leu Asn Asn Leu Ser Ser Pro Ser Leu Asn Ser Ala Val Pro Thr Pro
245 250 255 260

gcc tgt cct tac gcg ccg ccg act cct ccg tat gtt tat agg gac acg 1410
Ala Cys Pro Tyr Ala Pro Pro Thr Pro Pro Tyr Val Tyr Arg Asp Thr
265 270 275

tgt aac tcg agc ctg gcc agc ctg aga ctg aaa gca aag cag cac tcc 1458
Cys Asn Ser Ser Leu Ala Ser Leu Arg Leu Lys Ala Lys Gln His Ser
280 285 290

agc ttc ggc tac gcc agc gtg cag aac ccg gcc tcc aac ctg agt gct 1506
Ser Phe Gly Tyr Ala Ser Val Gln Asn Pro Ala Ser Asn Leu Ser Ala
295 300 305

tgc cag tat gca gtg gac cgg ccc gtg tga gccgcaccca cagcgccggg 1556
Cys Gln Tyr Ala Val Asp Arg Pro Val
310 315

atcctaggac cttgccggat ggggcaactc cgcccttgaa agactgggaa ttatgctaga 1616

aggtcgtggg cactaaagaa agggagagaa agagaagcta tatagagaaa aggaaaccac 1676

tgaatcaaag agagagctcc tttgatttca aagggatgtc ctcagtgtct gacatctttc 1736

actacaagta tttctaacag ttgcaaggac acatacacaa acaaatgttt gactggatat 1796

gacattttaa cattactata agcttgttat tttttaagtt tagcattgtt aacatttaaa 1856

tgactgaaag gatgtatata tatcgaaatg tcaaattaat tttataaaag cagttgttag 1916

taatatcaca acagtgtttt taaaggttag gctttaaaat aaagcatgtt atacagaagc 1976

gattaggatt tttcgcttgc gagcaaggga gtgtatatac taaatgccac actgtatgtt 2036

tctaacatat tattattatt ataaaaaatg tgtgaatatc agttttagaa tagtttctct 2096

ggtggatgca atgatgtttc tgaaactgct atgtacaacc taccctgtgt ataacatttc 2156

gtacaatatt attgttttac ttttcagcaa atatgaaaca aatgtgtttt atttcatggg 2216

agtaaaatat actgcataca aaaaaaaaaa aaaa 2250

<210> 10
<211> 317
<212> PRT
<213> Homo sapiens

<400> 10

Met Glu Thr Asn Cys Arg Lys Leu Val Ser Ala Cys Val Gln Leu Gly
1 5 10 15

Val Gln Pro Ala Ala Val Glu Cys Leu Phe Ser Lys Asp Ser Glu Ile
20 25 30

Lys Lys Val Glu Phe Thr Asp Ser Pro Glu Ser Arg Lys Glu Ala Ala
35 40 45

Ser Ser Lys Phe Phe Pro Arg Gln His Pro Gly Ala Asn Glu Lys Asp
50 55 60

Lys Ser Gln Gln Gly Lys Asn Glu Asp Val Gly Ala Glu Asp Pro Ser
65 70 75 80

Lys Lys Lys Arg Gln Arg Arg Gln Arg Thr His Phe Thr Ser Gln Gln
85 90 95

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

Ser Thr Arg Glu Glu Ile Ala Val Trp Thr Asn Leu Thr Glu Ala Arg
115 120 125

Val Arg Val Trp Phe Lys Asn Arg Arg Ala Lys Trp Arg Lys Arg Glu
130 135 140

Arg Asn Gln Gln Ala Glu Leu Cys Lys Asn Gly Phe Gly Pro Gln Phe
145 150 155 160

Asn Gly Leu Met Gln Pro Tyr Asp Asp Met Tyr Pro Gly Tyr Ser Tyr
165 170 175

Asn Asn Trp Ala Ala Lys Gly Leu Thr Ser Ala Ser Leu Ser Thr Lys
180 185 190

Ser Phe Pro Phe Phe Asn Ser Met Asn Val Asn Pro Leu Ser Ser Gln

195 200 205

Ser Met Phe Ser Pro Pro Asn Ser Ile Ser Ser Met Ser Met Ser Ser
210 215 220

Ser Met Val Pro Ser Ala Val Thr Gly Val Pro Gly Ser Ser Leu Asn
225 230 235 240

Ser Leu Asn Asn Leu Asn Asn Leu Ser Ser Pro Ser Leu Asn Ser Ala
245 250 255

Val Pro Thr Pro Ala Cys Pro Tyr Ala Pro Pro Thr Pro Pro Tyr Val
260 265 270

Tyr Arg Asp Thr Cys Asn Ser Ser Leu Ala Ser Leu Arg Leu Lys Ala
275 280 285

Lys Gln His Ser Ser Phe Gly Tyr Ala Ser Val Gln Asn Pro Ala Ser
290 295 300

Asn Leu Ser Ala Cys Gln Tyr Ala Val Asp Arg Pro Val
305 310 315

<210> 11
<211> 1903
<212> DNA
<213> Mus musculus

<220>

<221> CDS

<222> (256)..(1209)

<400> 11

gggaggggag agagagtgcg agaccgagag agaaagccgg agagcagcag acagaaactg 60

ccggcgcccg ctagctttag cagccccccg cgtggaccct ctcggaactt ggcaccctca 120

agatccccgc agttccaccc agacccgctc cacggcgctg gctgtgcagc ccgagcctcg 180

gccgcctggc agtcaccctg ggaagcggtg ggacggggag acagccgttc tctctccggt 240

agccgataac cggga atg gag acc aat tgt cgc aaa cta gtg tcg gcc tgc 291
Met Glu Thr Asn Cys Arg Lys Leu Val Ser Ala Cys
1 5 10

gtg caa tta ggc gtg cag ccg gca gcc gtt gaa tgt ctc ttc tcc aaa 339
Val Gln Leu Gly Val Gln Pro Ala Ala Val Glu Cys Leu Phe Ser Lys
15 20 25

gac tcc gaa atc aaa aag gtc gag ttc acg gac tct ccc aag agc cgg 387
Asp Ser Glu Ile Lys Lys Val Glu Phe Thr Asp Ser Pro Lys Ser Arg
30 35 40

aaa gag tcg gcc agc agc aag ctg ttc ccg cgg cag cac ccc ggc gcc 435
Lys Glu Ser Ala Ser Ser Lys Leu Phe Pro Arg Gln His Pro Gly Ala
45 50 55 60

aat gag aaa gat aag ggc cag caa gga aag aat gag gat gtg ggc gcc 483
Asn Glu Lys Asp Lys Gly Gln Gln Gly Lys Asn Glu Asp Val Gly Ala
65 70 75

gag gac ccg tcc aag aag aag cgg caa cgc cgg cag agg act cat ttc 531
Glu Asp Pro Ser Lys Lys Lys Arg Gln Arg Arg Gln Arg Thr His Phe
80 85 90

act agc cag cag ctg cag gag ctg gaa gcc act ttc cag aga aac cgc 579
Thr Ser Gln Gln Leu Gln Glu Leu Glu Ala Thr Phe Gln Arg Asn Arg
95 100 105

tac cca gac atg tcc act cgc gaa gaa atc gcc gtg tgg acc aac ctt 627
Tyr Pro Asp Met Ser Thr Arg Glu Glu Ile Ala Val Trp Thr Asn Leu
110 115 120

acg gaa gcc cga gtc cgg gtt tgg ttc aag aat cgc cgg gcc aaa tgg 675
Thr Glu Ala Arg Val Arg Val Trp Phe Lys Asn Arg Arg Ala Lys Trp
125 130 135 140

aga aag cgg gaa cgc aac cag cag gcc gag ctg tgc aag aat ggc ttt 723
Arg Lys Arg Glu Arg Asn Gln Gln Ala Glu Leu Cys Lys Asn Gly Phe
145 150 155

ggg ccg cag ttc aac ggg ctc atg cag ccc tac gat gac atg tac ccc 771
Gly Pro Gln Phe Asn Gly Leu Met Gln Pro Tyr Asp Asp Met Tyr Pro
160 165 170

ggc tat tcg tac aac aat tgg gct gcc aag ggc ctc acg tca gcg tct 819
Gly Tyr Ser Tyr Asn Asn Trp Ala Ala Lys Gly Leu Thr Ser Ala Ser
175 180 185

ctg tcc acc aag agc ttc ccc ttc ttc aac tcc atg aac gtc aat ccc 867
Leu Ser Thr Lys Ser Phe Pro Phe Phe Asn Ser Met Asn Val Asn Pro
190 195 200

ctg tcc tct cag agt atg ttt tcc ccg ccc aac tcc atc tca tct atg 915
Leu Ser Ser Gln Ser Met Phe Ser Pro Pro Asn Ser Ile Ser Ser Met
205 210 215 220

agt atg tcg tcc agc atg gtg ccc tcc gcg gtg acc ggc gtc ccg ggc 963
Ser Met Ser Ser Ser Met Val Pro Ser Ala Val Thr Gly Val Pro Gly
225 230 235

tcc agc ctc aat agc ctg aat aac ttg aac aac ctg agc agc ccg tcg 1011
Ser Ser Leu Asn Ser Leu Asn Asn Leu Asn Asn Leu Ser Ser Pro Ser
240 245 250

ctg aat tcc gcg gtg ccc acg ccc gcc tgt cct tac gcg ccg ccg act 1059
Leu Asn Ser Ala Val Pro Thr Pro Ala Cys Pro Tyr Ala Pro Pro Thr
255 260 265

cct ccg tac gtt tat agg gac aca tgt aac tcg agc ctg gcc agc ctg 1107
Pro Pro Tyr Val Tyr Arg Asp Thr Cys Asn Ser Ser Leu Ala Ser Leu
270 275 280

aga ctg aaa gca aag cag cac tcc agc ttc ggc tac gcc agc gtg cag 1155
Arg Leu Lys Ala Lys Gln His Ser Ser Phe Gly Tyr Ala Ser Val Gln
285 290 295 300

aac ccg gcc tcc aac ctg agt gct tgc cag tat gca gtc gac cgg ccg 1203
Asn Pro Ala Ser Asn Leu Ser Ala Cys Gln Tyr Ala Val Asp Arg Pro
305 310 315

gtg tga accgcgccca gggcgcgggg atccgaggac tgtcggagtg ggcaactctg 1259
Val

ccccagaaag actgagaatt gtgctagaag gtcgtgcgca ctatgggaag gaagaggggg 1319

gaaaaaagat cagaggaaaa gaaaccactg aattcaaaga gagagcgcct ttgatttcaa 1379

aggaatgtcc ccaagtgtct acgtctttcg ctaagagtat tcccaacagt tggaggacgc 1439

gtacgcccac aaatgtttga ctggatatga cattttaaca ttactataag cttgttattt 1499

tttaagttta gcattgttaa cattaaaatg actgaaagga tgtatatata tcgaaatgtc 1559

aaattaattt tataaaagca gttgttagta ctatcacgac agtgttttta aaggctaggc 1619

tttaaaataa agcatgttat acagaatcag ttaggatttt tcgcttgcga gcaaaggaat 1679

gtatatacta aatgccacac tgtatgtttc taacatatta ttattataaa aatgtgtgaa 1739

tataagtttt agagtagttt ctctggtgga tgccttgttt ctgaaactgc tatgtacgac 1799

ccatcctgtg tataacattt cgtacgatat tattgtttta cttttcagca aatatgaaaa 1859

aaaatgtgtt ttatttcttg ggagtaaaat atactgcata caaa 1903

<210> 12
<211> 317
<212> PRT
<213> Mus musculus

<400> 12

Met Glu Thr Asn Cys Arg Lys Leu Val Ser Ala Cys Val Gln Leu Gly
1 5 10 15

Val Gln Pro Ala Ala Val Glu Cys Leu Phe Ser Lys Asp Ser Glu Ile
20 25 30

Lys Lys Val Glu Phe Thr Asp Ser Pro Lys Ser Arg Lys Glu Ser Ala
35 40 45

Ser Ser Lys Leu Phe Pro Arg Gln His Pro Gly Ala Asn Glu Lys Asp
50 55 60

Lys Gly Gln Gln Gly Lys Asn Glu Asp Val Gly Ala Glu Asp Pro Ser
65 70 75 80

Lys Lys Lys Arg Gln Arg Arg Gln Arg Thr His Phe Thr Ser Gln Gln
85 90 95

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

Ser Thr Arg Glu Glu Ile Ala Val Trp Thr Asn Leu Thr Glu Ala Arg
115 120 125

Val Arg Val Trp Phe Lys Asn Arg Arg Ala Lys Trp Arg Lys Arg Glu
130 135 140

Arg Asn Gln Gln Ala Glu Leu Cys Lys Asn Gly Phe Gly Pro Gln Phe
145 150 155 160

Asn Gly Leu Met Gln Pro Tyr Asp Asp Met Tyr Pro Gly Tyr Ser Tyr
165 170 175

Asn Asn Trp Ala Ala Lys Gly Leu Thr Ser Ala Ser Leu Ser Thr Lys
180 185 190

Ser Phe Pro Phe Phe Asn Ser Met Asn Val Asn Pro Leu Ser Ser Gln
195 200 205

Ser Met Phe Ser Pro Pro Asn Ser Ile Ser Ser Met Ser Met Ser Ser
210 215 220

Ser Met Val Pro Ser Ala Val Thr Gly Val Pro Gly Ser Ser Leu Asn
225 230 235 240

Ser Leu Asn Asn Leu Asn Asn Leu Ser Ser Pro Ser Leu Asn Ser Ala
245 250 255

Val Pro Thr Pro Ala Cys Pro Tyr Ala Pro Pro Thr Pro Pro Tyr Val
260 265 270

Tyr Arg Asp Thr Cys Asn Ser Ser Leu Ala Ser Leu Arg Leu Lys Ala
275 280 285

Lys Gln His Ser Ser Phe Gly Tyr Ala Ser Val Gln Asn Pro Ala Ser
290 295 300

Asn Leu Ser Ala Cys Gln Tyr Ala Val Asp Arg Pro Val
305 310 315

<210> 13

<211> 1907

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)..(1084)

<400> 13

acttgctctg cagctcccag aggtggtggt tgtgttacga aggctgaccc tgcca atg 58
Met
1

gcc gac aaa atg gtg cgc acc ccc aag tgc tcg aga tgc agg aac cat 106
Ala Asp Lys Met Val Arg Thr Pro Lys Cys Ser Arg Cys Arg Asn His
5 10 15

ggc ttc ctg gtg ccc gtc aag gga cac gcg ggc aaa tgc cgc tgg aag 154
Gly Phe Leu Val Pro Val Lys Gly His Ala Gly Lys Cys Arg Trp Lys
20 25 30

cag tgc ctc tgc gag aag tgc tac ctg atc tcc gag cgc cag aag atc 202
Gln Cys Leu Cys Glu Lys Cys Tyr Leu Ile Ser Glu Arg Gln Lys Ile
35 40 45

atg gcc gcg cag aag gtg ctc aag acg cag gcc gcc gag gag gag cag 250
Met Ala Ala Gln Lys Val Leu Lys Thr Gln Ala Ala Glu Glu Glu Gln
50 55 60 65

gag gcg gcc ctg tgt gcg cag ggg ccc aag cag gcc tcc ggg gct gcg 298
Glu Ala Ala Leu Cys Ala Gln Gly Pro Lys Gln Ala Ser Gly Ala Ala
70 75 80

gcc gcc gcc ccc gcc ccc gtc ccc gtc ccg gcc gcg agc ctc cgc ccg 346

```
Ala Ala Ala Pro Ala Pro Val Pro Val Pro Ala Ala Ser Leu Arg Pro
            85                  90                  95

ctg tcc ccg ggg act ccc tcc gga gac gcc gac ccg gga ccc gag ggc      394
Leu Ser Pro Gly Thr Pro Ser Gly Asp Ala Asp Pro Gly Pro Glu Gly
        100                 105                 110

cgc gcg gcc gct tgc ttc ttc gag cag ccc ccg cgg ggc cgg aac ccc      442
Arg Ala Ala Ala Cys Phe Phe Glu Gln Pro Pro Arg Gly Arg Asn Pro
    115                 120                 125

ggc ccg aga gcc ctc cag ccg gtt ctg ggc ggc cgc agc cac gtg gag      490
Gly Pro Arg Ala Leu Gln Pro Val Leu Gly Gly Arg Ser His Val Glu
130                 135                 140                 145

ccg agc gag cga gcc gcc gtg gcg atg ccc agc ctt gcg gga ccc cct      538
Pro Ser Glu Arg Ala Ala Val Ala Met Pro Ser Leu Ala Gly Pro Pro
                150                 155                 160

ttt ggg gcg gag gcc gca ggc agt ggc tac cct ggc ccc cta gac ctg      586
Phe Gly Ala Glu Ala Ala Gly Ser Gly Tyr Pro Gly Pro Leu Asp Leu
            165                 170                 175

cgc agg ccg atg cgg acc gtg ccc ggc cca ctg ttc acc gac ttt gtg      634
Arg Arg Pro Met Arg Thr Val Pro Gly Pro Leu Phe Thr Asp Phe Val
        180                 185                 190

cgc cct ctg aac atc aac ccg gac cgt gca ctg ggc cct gag tac cct      682
Arg Pro Leu Asn Ile Asn Pro Asp Arg Ala Leu Gly Pro Glu Tyr Pro
    195                 200                 205

ggt ggc tcc agc atg cac ccc tac tgc ccg ttc ccg ctg ggc tac ctg      730
Gly Gly Ser Ser Met His Pro Tyr Cys Pro Phe Pro Leu Gly Tyr Leu
210                 215                 220                 225
```

gac gcc cct cct ggc gtc ccc ctg cag cag ggc ttc cgg cat gtg tcc 778
Asp Ala Pro Pro Gly Val Pro Leu Gln Gln Gly Phe Arg His Val Ser
230 235 240

cgc agc cag tac caa ggc gga ggc ttg gtg tca gaa cca gga gga gac 826
Arg Ser Gln Tyr Gln Gly Gly Gly Leu Val Ser Glu Pro Gly Gly Asp
245 250 255

ttc cag cca agc tac tac ctg ccg ccg ccg ccg ccg cca ctg ccg ccc 874
Phe Gln Pro Ser Tyr Tyr Leu Pro Pro Pro Pro Pro Pro Leu Pro Pro
260 265 270

ctt cca ccg ctt cca ccg cag ccc cag ttc ctc ccg cca ggc tac ctc 922
Leu Pro Pro Leu Pro Pro Gln Pro Gln Phe Leu Pro Pro Gly Tyr Leu
275 280 285

tct gcg ctc cac ttc ctc ccc ccg cca ccg cca cca cca cct cca tca 970
Ser Ala Leu His Phe Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser
290 295 300 305

tct ttc tca ctg acc gtc ctg ttt gat act gac aag gag aac act gat 1018
Ser Phe Ser Leu Thr Val Leu Phe Asp Thr Asp Lys Glu Asn Thr Asp
310 315 320

gac cag gat gca gag gta ctg tcg ggt gag ccc agc cag cca tcg tct 1066
Asp Gln Asp Ala Glu Val Leu Ser Gly Glu Pro Ser Gln Pro Ser Ser
325 330 335

cag gag cag tcc gac tag gccccaggcc cgccctcctg gccagcagag 1114
Gln Glu Gln Ser Asp
340

tggggcactg gggggcaaca gcaacagttt tcctgtcttc attcagtgat atgtagggag 1174

gaaggaggtt gatagcatag atggcaactg attcccagtt taagatagga ggaaggagag 1234

caatttctaa gtttcaatcc tgcgctgtac agttgaagaa gagtgtggag gaagctatta 1294

ccaggggagg gccagggctc tgaggagtgg gcgctgggag aagctcccat ttaggaatga 1354

atttaactgt ccttgggtta cactaccatt tattggaaca agccccagag gcagtatttg 1414

atttcctcag gccccactct aggacaggag gcaccatcta tttcagcctt ctgctgcctt 1474

tgcctggtcc tccaggttgc tgggggcacc acagacatca agattccagt tcatccaggt 1534

ggctggagcc agcagccagg accagggtcg ttgacagcag gttctgcagc atcctgcctt 1594

gctgctctgt cccccacatc ttcctggcca cagcccctg cccctcctct aaggggtttt 1654

actagcaagc atcctggctg ctggggctac ttcattcccc ctccataaag tttcagccat 1714

tatgggcact ggttttaaaa aatttattag tttgactatt tgatggtttt atagtgattg 1774

ccaactttaa aaagtaggct gttcataagc actgatgcag tccctaggga atagaatggt 1834

gcttctgatc acctgtgaca tgaacagttt cttctgtgag gacagttggc tattgaaata 1894

aaatgagcaa tgg 1907

<210> 14
<211> 342
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Asp Lys Met Val Arg Thr Pro Lys Cys Ser Arg Cys Arg Asn
1 5 10 15

His Gly Phe Leu Val Pro Val Lys Gly His Ala Gly Lys Cys Arg Trp
20 25 30

Lys Gln Cys Leu Cys Glu Lys Cys Tyr Leu Ile Ser Glu Arg Gln Lys
35 40 45

Ile Met Ala Ala Gln Lys Val Leu Lys Thr Gln Ala Ala Glu Glu Glu
50 55 60

Gln Glu Ala Ala Leu Cys Ala Gln Gly Pro Lys Gln Ala Ser Gly Ala
65 70 75 80

Ala Ala Ala Ala Pro Ala Pro Val Pro Val Pro Ala Ala Ser Leu Arg
85 90 95

Pro Leu Ser Pro Gly Thr Pro Ser Gly Asp Ala Asp Pro Gly Pro Glu
100 105 110

Gly Arg Ala Ala Ala Cys Phe Phe Glu Gln Pro Pro Arg Gly Arg Asn
115 120 125

Pro Gly Pro Arg Ala Leu Gln Pro Val Leu Gly Gly Arg Ser His Val
130 135 140

Glu Pro Ser Glu Arg Ala Ala Val Ala Met Pro Ser Leu Ala Gly Pro

145 150 155 160

Pro Phe Gly Ala Glu Ala Ala Gly Ser Gly Tyr Pro Gly Pro Leu Asp
165 170 175

Leu Arg Arg Pro Met Arg Thr Val Pro Gly Pro Leu Phe Thr Asp Phe
180 185 190

Val Arg Pro Leu Asn Ile Asn Pro Asp Arg Ala Leu Gly Pro Glu Tyr
195 200 205

Pro Gly Gly Ser Ser Met His Pro Tyr Cys Pro Phe Pro Leu Gly Tyr
210 215 220

Leu Asp Ala Pro Pro Gly Val Pro Leu Gln Gln Gly Phe Arg His Val
225 230 235 240

Ser Arg Ser Gln Tyr Gln Gly Gly Gly Leu Val Ser Glu Pro Gly Gly
245 250 255

Asp Phe Gln Pro Ser Tyr Tyr Leu Pro Pro Pro Pro Pro Pro Leu Pro
260 265 270

Pro Leu Pro Pro Leu Pro Pro Gln Pro Gln Phe Leu Pro Pro Gly Tyr
275 280 285

Leu Ser Ala Leu His Phe Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro
290 295 300

Ser Ser Phe Ser Leu Thr Val Leu Phe Asp Thr Asp Lys Glu Asn Thr
305 310 315 320

Asp Asp Gln Asp Ala Glu Val Leu Ser Gly Glu Pro Ser Gln Pro Ser
325 330 335

Ser Gln Glu Gln Ser Asp
340

<210> 15
<211> 1790
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1080)

<400> 15
atg ctt cgc gcc ccc aag tgc tct agg tgc cgg aac cat ggc tat ctg 48
Met Leu Arg Ala Pro Lys Cys Ser Arg Cys Arg Asn His Gly Tyr Leu
1 5 10 15

gta cca gtc aag ggc cat acg ggc aaa tgc cgc tgg aag cag tgc atc 96
Val Pro Val Lys Gly His Thr Gly Lys Cys Arg Trp Lys Gln Cys Ile
20 25 30

```
tgt gac aag tgc tac ctg atc acc gag cgc cag aag atc atg gct gcc        144
Cys Asp Lys Cys Tyr Leu Ile Thr Glu Arg Gln Lys Ile Met Ala Ala
        35                  40                  45

cag aag gtt ctc aga acc caa gct gcc gag gag cag gtg gcg acc gtg        192
Gln Lys Val Leu Arg Thr Gln Ala Ala Glu Glu Gln Val Ala Thr Val
    50                  55                  60

ggc acg cag ggt ccc cag ctg cct cct agg gct cca gca gcg gcg gcc        240
Gly Thr Gln Gly Pro Gln Leu Pro Pro Arg Ala Pro Ala Ala Ala Ala
65                  70                  75                  80

acc gcc ttg agc tcc agc att tgc cca ctg cct agg gcg gtt ccg gga        288
Thr Ala Leu Ser Ser Ser Ile Cys Pro Leu Pro Arg Ala Val Pro Gly
                85                  90                  95

ggc gtt ggg cca ggc ccc acg gcc act tgc ttc ctc gag agg ccc ccg        336
Gly Val Gly Pro Gly Pro Thr Ala Thr Cys Phe Leu Glu Arg Pro Pro
            100                 105                 110

cag gcc ccg agc cca ggc ccg agc acc ttc cag ctg ggc cca agt ggc        384
Gln Ala Pro Ser Pro Gly Pro Ser Thr Phe Gln Leu Gly Pro Ser Gly
        115                 120                 125

cgc ccg ggc ccc agc acc ttc cag cct gga cca ggg gcc ccc ggg gga        432
Arg Pro Gly Pro Ser Thr Phe Gln Pro Gly Pro Gly Ala Pro Gly Gly
    130                 135                 140

ctg cgc gac cgt tcc tcc gcg tgg ctg ccc cag ctc atg cca cag gcg        480
Leu Arg Asp Arg Ser Ser Ala Trp Leu Pro Gln Leu Met Pro Gln Ala
145                 150                 155                 160

ccc agg ccg gag ctt tgc tac ccg gat cag cac ctg cca gtg cgg ccc        528
Pro Arg Pro Glu Leu Cys Tyr Pro Asp Gln His Leu Pro Val Arg Pro
                165                 170                 175
```

```
gtg cca gtg cca ggg cca gtg cgg ccc gtg ccc cga ctg ccg ttc gcc        576
Val Pro Val Pro Gly Pro Val Arg Pro Val Pro Arg Leu Pro Phe Ala
            180                 185                 190

gac tac ggg cat cct ctg aga ttc aag tct gat cat gtg gta gga gct        624
Asp Tyr Gly His Pro Leu Arg Phe Lys Ser Asp His Val Val Gly Ala
        195                 200                 205

ggg aat cct gag aga gag ccg ttc aag cag tgc cct gcc tgc gtc cct        672
Gly Asn Pro Glu Arg Glu Pro Phe Lys Gln Cys Pro Ala Cys Val Pro
    210                 215                 220

gtt tca ccc tac cag tcc ttt cca ctt tcg gaa ggc cag gat tca tcc        720
Val Ser Pro Tyr Gln Ser Phe Pro Leu Ser Glu Gly Gln Asp Ser Ser
225                 230                 235                 240

tct gct ctg ggg gtc cct caa caa aga ggc ttc cgg cat gtc tcc tgc        768
Ser Ala Leu Gly Val Pro Gln Gln Arg Gly Phe Arg His Val Ser Cys
                245                 250                 255

agc ccc tac cat aga agc ggc ttg gtg tca gag cca gcc aga gac ctg        816
Ser Pro Tyr His Arg Ser Gly Leu Val Ser Glu Pro Ala Arg Asp Leu
            260                 265                 270

cag cca acc tac tgc tca ccg ccg ccg cca cca ccg ccg cca cct ccg        864
Gln Pro Thr Tyr Cys Ser Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro
        275                 280                 285

cca cca cta cca gca ccc cca ccc cag cca cag cag ccc cac ttc ctc        912
Pro Pro Leu Pro Ala Pro Pro Pro Gln Pro Gln Gln Pro His Phe Leu
    290                 295                 300

cca cca ggc tac ctc tct gct ctc cac ttc ctg cca ccg ccg cca ccg        960
Pro Pro Gly Tyr Leu Ser Ala Leu His Phe Leu Pro Pro Pro Pro Pro
```

305 310 315 320

cca cca tct cca cca tct ttc tcg ctg acc tac gat aca gac aag gag 1008
Pro Pro Ser Pro Pro Ser Phe Ser Leu Thr Tyr Asp Thr Asp Lys Glu
325 330 335

aat acc aat gac cag gat gca gaa gca ccc acc gag ccc agc cag gac 1056
Asn Thr Asn Asp Gln Asp Ala Glu Ala Pro Thr Glu Pro Ser Gln Asp
340 345 350

tct ccc cag gag cag tcc aac taa gctgcaggcc acctggaagg ccaccgggtg 1110
Ser Pro Gln Glu Gln Ser Asn
355

gggacgggca tagatggcgg gggttatttt ttcaccatgt tcatgttata taggagaaag 1170

gatactgata ggtgtaagaa ggcagcgaat tcctactcca ggttagaagg gcacaggtgg 1230

tttccaaggt tctctgggtc ctgggtgggt gttgaagtgg tgtacaaagg gagagaaagt 1290

ctgggatggg cagggctttt gaagagtggg ggctggtgaa acacaagttt agaaatgaat 1350

ttaaccatct gagccatgta tgaaattcac ttctagaggt ggcccctgat ttccccaagc 1410

ctcactcagg acagaaggca ccattcagtt cagccttctg ccccctttgc ctgaccccca 1470

agcctgggta ccgcaaacac caaggcctcc agacagtgca gggcaggtgc cagggcctga 1530

gatgctgaca gcaggttctg cagcatccac ctttgcccaa cactgcctct cgtcctcttc 1590

cagagagtga gcgtcctgac aactgagcca cttcacttcc ctgggaaact caagcatagg 1650

tgtcctttct catttaaaaa tgtagatttt agcatttgat gttcttatgg tggggaactc 1710

atgggcactg cagcagttct cggagcaaaa aaaatggcca tttgttctct ggggacagta 1770

ttaaataaag tgagcattag 1790

<210> 16
<211> 359
<212> PRT
<213> Mus musculus

<400> 16

Met Leu Arg Ala Pro Lys Cys Ser Arg Cys Arg Asn His Gly Tyr Leu
1 5 10 15

Val Pro Val Lys Gly His Thr Gly Lys Cys Arg Trp Lys Gln Cys Ile
20 25 30

Cys Asp Lys Cys Tyr Leu Ile Thr Glu Arg Gln Lys Ile Met Ala Ala
35 40 45

Gln Lys Val Leu Arg Thr Gln Ala Ala Glu Glu Gln Val Ala Thr Val
50 55 60

Gly Thr Gln Gly Pro Gln Leu Pro Pro Arg Ala Pro Ala Ala Ala Ala
65 70 75 80

Thr Ala Leu Ser Ser Ser Ile Cys Pro Leu Pro Arg Ala Val Pro Gly
85 90 95

Gly Val Gly Pro Gly Pro Thr Ala Thr Cys Phe Leu Glu Arg Pro Pro
100 105 110

Gln Ala Pro Ser Pro Gly Pro Ser Thr Phe Gln Leu Gly Pro Ser Gly
115 120 125

Arg Pro Gly Pro Ser Thr Phe Gln Pro Gly Pro Gly Ala Pro Gly Gly
130 135 140

Leu Arg Asp Arg Ser Ser Ala Trp Leu Pro Gln Leu Met Pro Gln Ala
145 150 155 160

Pro Arg Pro Glu Leu Cys Tyr Pro Asp Gln His Leu Pro Val Arg Pro
165 170 175

Val Pro Val Pro Gly Pro Val Arg Pro Val Pro Arg Leu Pro Phe Ala
180 185 190

Asp Tyr Gly His Pro Leu Arg Phe Lys Ser Asp His Val Val Gly Ala
195 200 205

Gly Asn Pro Glu Arg Glu Pro Phe Lys Gln Cys Pro Ala Cys Val Pro
210 215 220

Val Ser Pro Tyr Gln Ser Phe Pro Leu Ser Glu Gly Gln Asp Ser Ser
225 230 235 240

Ser Ala Leu Gly Val Pro Gln Gln Arg Gly Phe Arg His Val Ser Cys
245 250 255

Ser Pro Tyr His Arg Ser Gly Leu Val Ser Glu Pro Ala Arg Asp Leu
260 265 270

Gln Pro Thr Tyr Cys Ser Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro
275 280 285

Pro Pro Leu Pro Ala Pro Pro Pro Gln Pro Gln Gln Pro His Phe Leu
290 295 300

Pro Pro Gly Tyr Leu Ser Ala Leu His Phe Leu Pro Pro Pro Pro Pro
305 310 315 320

Pro Pro Ser Pro Pro Ser Phe Ser Leu Thr Tyr Asp Thr Asp Lys Glu
325 330 335

Asn Thr Asn Asp Gln Asp Ala Glu Ala Pro Thr Glu Pro Ser Gln Asp
340 345 350

Ser Pro Gln Glu Gln Ser Asn
355

<210> 17
<211> 34

<212> DNA

<213> Bacteriophage P1

<400> 17

ataacttcgt atagcataca ttatacgaag ttat 34

<210> 18

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> mutant loxP (lox71) sequence

<400> 18

taccgttcgt atagcataca ttatacgaag ttat 34

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> mutant loxP (lox66) sequence

<400> 19

ataacttcgt atagcataca ttatacgaac ggta 34