SEQUENCE LISTING

<110> GINKGO BIOMEDICAL RESEARCH INSTITUTE CO., LTD.

<120> Anti-ILT7 antibody

<130> G2-A0501P

<150> JP 2005-366465
<151> 2005-12-20

<160> 76

<170> PatentIn version 3.3

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Met Thr Leu Ile Leu Thr Ser Leu Leu Phe

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ttt ggg ctg agc ctg ggc ccc agg acc cgg gtg cag gca gaa aac cta      101
Phe Gly Leu Ser Leu Gly Pro Arg Thr Arg Val Gln Ala Glu Asn Leu
    -5              -1  1               5                  10

ccc aaa ccc atc ctg tgg gcc gag cca ggt ccc gtg atc acc tgg cat      149
Pro Lys Pro Ile Leu Trp Ala Glu Pro Gly Pro Val Ile Thr Trp His
                15                  20                  25

aac ccc gtg acc atc tgg tgt cag ggc acc ctg gag gcc cag ggg tac      197
Asn Pro Val Thr Ile Trp Cys Gln Gly Thr Leu Glu Ala Gln Gly Tyr
            30                  35                  40

cgt ctg gat aaa gag gga aac tca atg tcg agg cac ata tta aaa aca      245
Arg Leu Asp Lys Glu Gly Asn Ser Met Ser Arg His Ile Leu Lys Thr
        45                  50                  55

ctg gag tct gaa aac aag gtc aaa ctc tcc atc cca tcc atg atg tgg      293
Leu Glu Ser Glu Asn Lys Val Lys Leu Ser Ile Pro Ser Met Met Trp
    60                  65                  70

gaa cat gca ggg cga tat cac tgt tac tat cag agc cct gca ggc tgg      341
Glu His Ala Gly Arg Tyr His Cys Tyr Tyr Gln Ser Pro Ala Gly Trp
75                  80                  85                  90

tca gag ccc agc gac ccc ctg gag ctg gtg gtg aca gcc tac agc aga      389
Ser Glu Pro Ser Asp Pro Leu Glu Leu Val Val Thr Ala Tyr Ser Arg
                95                  100                 105

ccc acc ctg tcc gca ctg cca agc cct gtg gtg acc tca gga gtg aac      437
Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Ser Gly Val Asn
            110                 115                 120

gtg acc ctc cgg tgt gcc tca cgg ctg gga ctg ggc agg ttc act ctg      485
Val Thr Leu Arg Cys Ala Ser Arg Leu Gly Leu Gly Arg Phe Thr Leu
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        125                 130                 135

att gag gaa gga gac cac agg ctc tcc tgg acc ctg aac tca cac caa      533
Ile Glu Glu Gly Asp His Arg Leu Ser Trp Thr Leu Asn Ser His Gln
    140                 145                 150

cac aac cat gga aag ttc cag gcc ctg ttc ccc atg ggc ccc ctg acc      581
His Asn His Gly Lys Phe Gln Ala Leu Phe Pro Met Gly Pro Leu Thr
155                 160                 165                 170

ttc agc aac agg ggt aca ttc aga tgc tac ggc tat gaa aac aac acc      629
Phe Ser Asn Arg Gly Thr Phe Arg Cys Tyr Gly Tyr Glu Asn Asn Thr
                175                 180                 185

cca tac gtg tgg tcg gaa ccc agt gac ccc ctg cag cta ctg gtg tca      677
Pro Tyr Val Trp Ser Glu Pro Ser Asp Pro Leu Gln Leu Leu Val Ser
            190                 195                 200

ggc gtg tct agg aag ccc tcc ctc ctg acc ctg cag ggc cct gtc gtg      725
Gly Val Ser Arg Lys Pro Ser Leu Leu Thr Leu Gln Gly Pro Val Val
        205                 210                 215

acc ccc gga gag aat ctg acc ctc cag tgt ggc tct gat gtc ggc tac      773
Thr Pro Gly Glu Asn Leu Thr Leu Gln Cys Gly Ser Asp Val Gly Tyr
    220                 225                 230

atc aga tac act ctg tac aag gag ggg gcc gat ggc ctc ccc cag cgc      821
Ile Arg Tyr Thr Leu Tyr Lys Glu Gly Ala Asp Gly Leu Pro Gln Arg
235                 240                 245                 250

cct ggc cgg cag ccc cag gct ggg ctc tcc cag gcc aac ttc acc ctg      869
Pro Gly Arg Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu
                255                 260                 265

agc cct gtg agc cgc tcc tac ggg ggc cag tac aga tgc tac ggc gca      917
Ser Pro Val Ser Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala
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                270                 275                 280

cac aac gtc tcc tcc gag tgg tcg gcc ccc agt gac ccc ctg gac atc      965
His Asn Val Ser Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile
        285                 290                 295

ctg atc gca gga cag atc tct gac aga ccc tcc ctc tca gtg cag ccg     1013
Leu Ile Ala Gly Gln Ile Ser Asp Arg Pro Ser Leu Ser Val Gln Pro
    300                 305                 310

ggc ccc acg gtg acc tca gga gag aag gtg acc ctg ctg tgt cag tca     1061
Gly Pro Thr Val Thr Ser Gly Glu Lys Val Thr Leu Leu Cys Gln Ser
315                 320                 325                 330

tgg gac ccg atg ttc act ttc ctt ctg acc aag gag ggg gca gcc cat     1109
Trp Asp Pro Met Phe Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala His
                335                 340                 345

ccc ccg ttg cgt ctg aga tca atg tac gga gct cat aag tac cag gct     1157
Pro Pro Leu Arg Leu Arg Ser Met Tyr Gly Ala His Lys Tyr Gln Ala
            350                 355                 360

gaa ttc ccc atg agt cct gtg acc tca gcc cac gcg ggg acc tac agg     1205
Glu Phe Pro Met Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg
        365                 370                 375

tgc tac ggc tca cgc agc tcc aac ccc tac ctg ctg tct cac ccc agt     1253
Cys Tyr Gly Ser Arg Ser Ser Asn Pro Tyr Leu Leu Ser His Pro Ser
    380                 385                 390

gag ccc ctg gag ctc gtg gtc tca gga gca act gag acc ctc aat cca     1301
Glu Pro Leu Glu Leu Val Val Ser Gly Ala Thr Glu Thr Leu Asn Pro
395                 400                 405                 410

gca caa aag aag tca gat tcc aag act gcc cca cac ctc cag gat tac     1349
Ala Gln Lys Lys Ser Asp Ser Lys Thr Ala Pro His Leu Gln Asp Tyr
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415 420 425

aca gtg gag aat ctc atc cgc atg ggt gtg gct ggc ttg gtc ctg ctg 1397
Thr Val Glu Asn Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Leu
430 435 440

ttc ctc ggg att ctg tta ttt gag gct cag cac agc cag aga agc ccc 1445
Phe Leu Gly Ile Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Pro
445 450 455

cca agg tgc agc cag gag gca aac agc aga aag gac aat gca ccc ttc 1493
Pro Arg Cys Ser Gln Glu Ala Asn Ser Arg Lys Asp Asn Ala Pro Phe
460 465 470

aga gtg gtg gag cct tgg gaa cag atc tgatgatctg aggaggttct 1540
Arg Val Val Glu Pro Trp Glu Gln Ile
475 480

ggaagactgg ggcagcagtt ggggaagtgt ctgctga 1577

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<212> PRT
<213> Homo sapiens

<400> 2

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

Asn Ser Met Ser Arg His Ile Leu Lys Thr Leu Glu Ser Glu Asn Lys
50 55 60

Val Lys Leu Ser Ile Pro Ser Met Met Trp Glu His Ala Gly Arg Tyr
65 70 75 80

His Cys Tyr Tyr Gln Ser Pro Ala Gly Trp Ser Glu Pro Ser Asp Pro
85 90 95

Leu Glu Leu Val Val Thr Ala Tyr Ser Arg Pro Thr Leu Ser Ala Leu
100 105 110

Pro Ser Pro Val Val Thr Ser Gly Val Asn Val Thr Leu Arg Cys Ala
115 120 125

Ser Arg Leu Gly Leu Gly Arg Phe Thr Leu Ile Glu Glu Gly Asp His
130 135 140

Arg Leu Ser Trp Thr Leu Asn Ser His Gln His Asn His Gly Lys Phe
145 150 155 160

Gln Ala Leu Phe Pro Met Gly Pro Leu Thr Phe Ser Asn Arg Gly Thr
165 170 175

Phe Arg Cys Tyr Gly Tyr Glu Asn Asn Thr Pro Tyr Val Trp Ser Glu
180 185 190

Pro Ser Asp Pro Leu Gln Leu Leu Val Ser Gly Val Ser Arg Lys Pro
195 200 205

Ser Leu Leu Thr Leu Gln Gly Pro Val Val Thr Pro Gly Glu Asn Leu
210 215 220

Thr Leu Gln Cys Gly Ser Asp Val Gly Tyr Ile Arg Tyr Thr Leu Tyr
225 230 235 240

Lys Glu Gly Ala Asp Gly Leu Pro Gln Arg Pro Gly Arg Gln Pro Gln
245 250 255

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

Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Val Ser Ser Glu
275 280 285

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly Gln Ile
290 295 300

Ser Asp Arg Pro Ser Leu Ser Val Gln Pro Gly Pro Thr Val Thr Ser
305 310 315 320

Gly Glu Lys Val Thr Leu Leu Cys Gln Ser Trp Asp Pro Met Phe Thr
325 330 335

Phe Leu Leu Thr Lys Glu Gly Ala Ala His Pro Pro Leu Arg Leu Arg
340 345 350

Ser Met Tyr Gly Ala His Lys Tyr Gln Ala Glu Phe Pro Met Ser Pro
355 360 365

Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser Arg Ser
370 375 380

Ser Asn Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu Leu Val
385 390 395 400

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

Ser Lys Thr Ala Pro His Leu Gln Asp Tyr Thr Val Glu Asn Leu Ile
420 425 430

Arg Met Gly Val Ala Gly Leu Val Leu Leu Phe Leu Gly Ile Leu Leu
435 440 445

Phe Glu Ala Gln His Ser Gln Arg Ser Pro Pro Arg Cys Ser Gln Glu
450 455 460

Ala Asn Ser Arg Lys Asp Asn Ala Pro Phe Arg Val Val Glu Pro Trp
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Glu Gln Ile

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<220>
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<210> 4
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<400> 4
ttcccaaggc tccaccactc t 21

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cctcaatcca gcacaaaaga agt 23

<210> 6
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<213> Artificial

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cggatgagat tctccactgt gtaa 24

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ccacccatgg caaattcc 18

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tgggatttcc attgatgaca ag 22

<210> 9
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cagggccagg aggaggagat g 21

<210> 10
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tcagcagaca cttccccaac t 21

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tacaaggatg acgacgataa gcccaggacc cgggtgcagg cagaa 105

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<210> 13
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<400> 13
ccgctcgaga tgaccctcat tctcacaagc 30

<210> 14
<211> 55
<212> DNA
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<220>
<223> an artificially synthesized primer sequence

<400> 14
ctagactagt tcacttatcg tcgtcatcct tgtaatcgat ctgttcccaa ggctc 55

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<213> Homo sapiens

<220>
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caa gca gcg gcc ctg gga gag cct cag ctc tgc tat atc ctg gat gcc 96
Gln Ala Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp Ala
15 20 25 30

atc ctg ttt ctg tat gga att gtc ctc acc ctc ctc tac tgt cga ctg 144
Ile Leu Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg Leu
35 40 45

aag atc caa gtg cga aag gca gct ata acc agc tat gag aaa tca gat 192
Lys Ile Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser Asp
50 55 60

ggt gtt tac acg ggc ctg agc acc agg aac cag gag act tac gag act 240
Gly Val Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu Thr
65 70 75

ctg aag cat gag aaa cca cca cag tag ctttagaata gatgcggtca 287
Leu Lys His Glu Lys Pro Pro Gln
80 85

tattcttctt tggcttctgg ttcttc 313

<210> 16
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<212> PRT
<213> Homo sapiens

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1 5 10 15

Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp Ala Ile Leu
20 25 30

Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg Leu Lys Ile
35 40 45

Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser Asp Gly Val

50 55 60

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

His Glu Lys Pro Pro Gln
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<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 17
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<210> 18
<211> 21
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 18
ggaagaacca gaagccaaag a 21

<210> 19

<211> 30
<212> DNA
<213> Artificial

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<223> an artificially synthesized primer sequence

<400> 19
ccgctcgaga tgattccagc agtggtcttg 30

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<211> 61
<212> DNA
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<220>
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g 61

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<212> PRT
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<400> 21

Cys Ser Gln Glu Ala Asn Ser Arg Lys Asp Asn Ala Pro Phe Arg Val

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Val Glu Pro Trp Glu Gln Ile
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<210> 22
<211> 31
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

<400> 22
ccgctcgaga tgacccccat cctcacggtc c 31

<210> 23
<211> 55
<212> DNA
<213> Artificial

<220>
<223> an artificially synthesized primer sequence

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<212> DNA
<213> Homo sapiens

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<400> 24

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Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1               5                   10                  15

ccc agg acc cac gtg cag gca ggg cac ctc ccc aag ccc acc ctc tgg        96
Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
            20                  25                  30

gct gag cca ggc tct gtg atc atc cag gga agt cct gtg acc ctc agg       144
Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg
        35                  40                  45

tgt cag ggg agc ctt cag gct gag gag tac cat cta tat agg gaa aac       192
Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
    50                  55                  60

aaa tca gca tcc tgg gtt aga cgg ata caa gag cct ggg aag aat ggc       240
Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
65                  70                  75                  80

cag ttc ccc atc cca tcc atc acc tgg gaa cac gca ggg cgg tat cac       288
Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
                85                  90                  95

tgt cag tac tac agc cac aat cac tca tca gag tac agt gac ccc ctg       336
Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
            100                 105                 110

gag ctg gtg gtg aca gga gcc tac agc aaa ccc acc ctc tca gct ctg       384
Glu Leu Val Val Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu
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        115                 120                 125

ccc agc cct gtg gtg acc tta gga ggg aac gtg acc ctc cag tgt gtc      432
Pro Ser Pro Val Val Thr Leu Gly Gly Asn Val Thr Leu Gln Cys Val
    130                 135                 140

tca cag gtg gca ttt gac ggc ttc att ctg tgt aag gaa gga gaa gat      480
Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
145                 150                 155                 160

gaa cac cca caa cgc ctg aac tcc cat tcc cat gcc cgt ggg tgg tcc      528
Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
                165                 170                 175

tgg gcc atc ttc tcc gtg ggc ccc gtg agc ccg agt cgc agg tgg tcg      576
Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
            180                 185                 190

tac agg tgc tat gct tat gac tcg aac tct ccc tat gtg tgg tct cta      624
Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
        195                 200                 205

ccc agt gat ctc ctg gag ctc ctg gtc cca ggt gtt tct aag aag cca      672
Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys Pro
    210                 215                 220

tca ctc tca gtg cag cca ggt cct atg gtg gcc cct ggg gag agc ctg      720
Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
225                 230                 235                 240

acc ctc cag tgt gtc tct gat gtc ggc tac gac aga ttt gtt ctg tat      768
Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
                245                 250                 255

aag gag gga gaa cgt gac ttc ctc cag cgc cct ggt tgg cag ccc cag      816
Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
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                260                 265                 270

gct ggg ctc tcc cag gcc aac ttc acc ctg ggc cct gtg agc ccc tcc      864
Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Pro Ser
        275                 280                 285

cac ggg ggc cag tac aga tgc tac agt gca cac aac ctc tcc tcc gag      912
His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
    290                 295                 300

tgg tcg gcc ccc agt gac ccc ctg gac atc ctg atc aca gga cag ttc      960
Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305                 310                 315                 320

tat gac aga ccc tct ctc tcg gtg cag ccg gtc ccc aca gta gcc cca      1008
Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
                325                 330                 335

gga aag aac gtg acc ctg ctg tgt cag tca cgg ggg cag ttc cac act      1056
Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
            340                 345                 350

ttc ctt ctg acc aag gag ggg gca ggc cat ccc cca ctg cat ctg aga      1104
Phe Leu Leu Thr Lys Glu Gly Ala Gly His Pro Pro Leu His Leu Arg
        355                 360                 365

tca gag cac caa gct cag cag aac cag gct gaa ttc cgc atg ggt cct      1152
Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
    370                 375                 380

gtg acc tca gcc cac gtg ggg acc tac aga tgc tac agc tca ctc agc      1200
Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385                 390                 395                 400

tcc aac ccc tac ctg ctg tct ctc ccc agt gac ccc ctg gag ctc gtg      1248
Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
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405 410 415

gtc tca gca tcc cta ggc caa cac ccc cag gat tac aca gtg gag aat 1296
Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
420 425 430

ctc atc cgc atg ggt gtg gct ggc ttg gtc ctg gtg gtc ctc ggg att 1344
Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
435 440 445

ctg cta ttt gag gct cag cac agc cag aga agc cta caa gat gca gcc 1392
Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

ggg agg gat tac aag gat gac gac gat aag tga 1425
Gly Arg Asp Tyr Lys Asp Asp Asp Asp Lys
465 470

<210> 25
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<212> PRT
<213> Homo sapiens

<400> 25

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
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Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
20 25 30

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

Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn
50 55 60

Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly
65 70 75 80

Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr His
85 90 95

Cys Gln Tyr Tyr Ser His Asn His Ser Ser Glu Tyr Ser Asp Pro Leu
100 105 110

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

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

Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly Glu Asp
145 150 155 160

Glu His Pro Gln Arg Leu Asn Ser His Ser His Ala Arg Gly Trp Ser
165 170 175

Trp Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg Trp Ser
180 185 190

Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Val Trp Ser Leu
195 200 205

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

Ser Leu Ser Val Gln Pro Gly Pro Met Val Ala Pro Gly Glu Ser Leu
225 230 235 240

Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu Tyr
245 250 255

Lys Glu Gly Glu Arg Asp Phe Leu Gln Arg Pro Gly Trp Gln Pro Gln
260 265 270

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

His Gly Gly Gln Tyr Arg Cys Tyr Ser Ala His Asn Leu Ser Ser Glu
290 295 300

Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln Phe
305 310 315 320

Tyr Asp Arg Pro Ser Leu Ser Val Gln Pro Val Pro Thr Val Ala Pro
325 330 335

Gly Lys Asn Val Thr Leu Leu Cys Gln Ser Arg Gly Gln Phe His Thr
340 345 350

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

Ser Glu His Gln Ala Gln Gln Asn Gln Ala Glu Phe Arg Met Gly Pro
370 375 380

Val Thr Ser Ala His Val Gly Thr Tyr Arg Cys Tyr Ser Ser Leu Ser
385 390 395 400

Ser Asn Pro Tyr Leu Leu Ser Leu Pro Ser Asp Pro Leu Glu Leu Val
405 410 415

Val Ser Ala Ser Leu Gly Gln His Pro Gln Asp Tyr Thr Val Glu Asn
420 425 430

Leu Ile Arg Met Gly Val Ala Gly Leu Val Leu Val Val Leu Gly Ile
435 440 445

Leu Leu Phe Glu Ala Gln His Ser Gln Arg Ser Leu Gln Asp Ala Ala
450 455 460

Gly Arg Asp Tyr Lys Asp Asp Asp Asp Lys
465 470

<210> 26
<211> 1953
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<220>
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<222> (1)..(1953)

<400> 26

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1               5                  10                  15

ccc cgg acc cac gtg cag gca ggg cac ctc ccc aag ccc acc ctc tgg       96
Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
            20                  25                  30

gct gaa cca ggc tct gtg atc acc cag ggg agt cct gtg acc ctc agg      144
Ala Glu Pro Gly Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Arg
        35                  40                  45

tgt cag ggg ggc cag gag acc cag gag tac cgt cta tat aga gaa aag      192
Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
    50                  55                  60

aaa aca gca ccc tgg att aca cgg atc cca cag gag ctt gtg aag aag      240
Lys Thr Ala Pro Trp Ile Thr Arg Ile Pro Gln Glu Leu Val Lys Lys
65                  70                  75                  80

ggc cag ttc ccc atc cca tcc atc acc tgg gaa cat gca ggg cgg tat      288
Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr
                85                  90                  95
```

```
cgc tgt tac tat ggt agc gac act gca ggc cgc tca gag agc agt gac      336
Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp
            100                 105                 110

ccc ctg gag ctg gtg gtg aca gga gcc tac atc aaa ccc acc ctc tca      384
Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ile Lys Pro Thr Leu Ser
        115                 120                 125

gcc cag ccc agc ccc gtg gtg aac tca gga ggg aat gta acc ctc cag      432
Ala Gln Pro Ser Pro Val Val Asn Ser Gly Gly Asn Val Thr Leu Gln
    130                 135                 140

tgt gac tca cag gtg gca ttt gat ggc ttc att ctg tgt aag gaa gga      480
Cys Asp Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly
145                 150                 155                 160

gaa gat gaa cac cca caa tgc ctg aac tcc cag ccc cat gcc cgt ggg      528
Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly
                165                 170                 175

tcg tcc cgc gcc atc ttc tcc gtg ggc ccc gtg agc ccg agt cgc agg      576
Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg
            180                 185                 190

tgg tgg tac agg tgc tat gct tat gac tcg aac tct ccc tat gag tgg      624
Trp Trp Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Glu Trp
        195                 200                 205

tct cta ccc agt gat ctc ctg gag ctc ctg gtc cta ggt gtt tct aag      672
Ser Leu Pro Ser Asp Leu Leu Glu Leu Leu Val Leu Gly Val Ser Lys
    210                 215                 220

aag cca tca ctc tca gtg cag cca ggt cct atc gtg gcc cct gag gag      720
Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Ile Val Ala Pro Glu Glu
225                 230                 235                 240
```

acc ctg act ctg cag tgt ggc tct gat gct ggc tac aac aga ttt gtt 768
Thr Leu Thr Leu Gln Cys Gly Ser Asp Ala Gly Tyr Asn Arg Phe Val
245 250 255

ctg tat aag gac ggg gaa cgt gac ttc ctt cag ctc gct ggc gca cag 816
Leu Tyr Lys Asp Gly Glu Arg Asp Phe Leu Gln Leu Ala Gly Ala Gln
260 265 270

ccc cag gct ggg ctc tcc cag gcc aac ttc acc ctg ggc cct gtg agc 864
Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser
275 280 285

cgc tcc tac ggg ggc cag tac aga tgc tac ggt gca cac aac ctc tcc 912
Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser
290 295 300

tcc gag tgg tcg gcc ccc agc gac ccc ctg gac atc ctg atc gca gga 960
Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly
305 310 315 320

cag ttc tat gac aga gtc tcc ctc tcg gtg cag ccg ggc ccc acg gtg 1008
Gln Phe Tyr Asp Arg Val Ser Leu Ser Val Gln Pro Gly Pro Thr Val
325 330 335

gcc tca gga gag aac gtg acc ctg ctg tgt cag tca cag gga tgg atg 1056
Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Trp Met
340 345 350

caa act ttc ctt ctg acc aag gag ggg gca gct gat gac cca tgg cgt 1104
Gln Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala Asp Asp Pro Trp Arg
355 360 365

cta aga tca acg tac caa tct caa aaa tac cag gct gaa ttc ccc atg 1152
Leu Arg Ser Thr Tyr Gln Ser Gln Lys Tyr Gln Ala Glu Phe Pro Met
370 375 380

```
ggt cct gtg acc tca gcc cat gcg ggg acc tac agg tgc tac ggc tca      1200
Gly Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
385                 390                 395                 400

cag agc tcc aaa ccc tac ctg ctg act cac ccc agt gac ccc ctg gag      1248
Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp Pro Leu Glu
                405                 410                 415

ctc gtg gtc tca gga ccg tct ggg ggc ccc agc tcc ccg aca aca ggc      1296
Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly
            420                 425                 430

ccc acc tcc aca tct ggc cct gag gac cag ccc ctc acc ccc acc ggg      1344
Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
        435                 440                 445

tcg gat ccc cag agt ggt ctg gga agg cac ctg ggg gtt gtg atc ggc      1392
Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
    450                 455                 460

atc ttg gtg gcc gtc atc cta ctg ctc ctc ctc ctc ctc ctc ctc ttc      1440
Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe
465                 470                 475                 480

ctc atc ctc cga cat cga cgt cag ggc aaa cac tgg aca tcg acc cag      1488
Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
                485                 490                 495

aga aag gct gat ttc caa cat cct gca ggg gct gtg ggg cca gag ccc      1536
Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
            500                 505                 510

aca gac aga ggc ctg cag tgg agg tcc agc cca gct gcc gat gcc cag      1584
Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
        515                 520                 525
```

```
gaa gaa aac ctc tat gct gcc gtg aag cac aca cag cct gag gat ggg      1632
Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly
    530                 535                 540

gtg gag atg gac act cgg agc cca cac gat gaa gac ccc cag gca gtg      1680
Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val
545                 550                 555                 560

acg tat gcc gag gtg aaa cac tcc aga cct agg aga gaa atg gcc tct      1728
Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser
                565                 570                 575

cct cct tcc cca ctg tct ggg gaa ttc ctg gac aca aag gac aga cag      1776
Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln
            580                 585                 590

gcg gaa gag gac agg cag atg gac act gag gct gct gca tct gaa gcc      1824
Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala
        595                 600                 605

ccc cag gat gtg acc tac gcc cag ctg cac agc ttg acc ctt aga cgg      1872
Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg
    610                 615                 620

aag gca act gag cct cct cca tcc cag gaa ggg ccc tct cca gct gtg      1920
Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val
625                 630                 635                 640

ccc agc atc tac gcc act ctg gcc atc cac tag                         1953
Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
                645                 650
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<210> 27
<211> 650

<212> PRT
<213> Homo sapiens

<400> 27

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1 5 10 15

Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
20 25 30

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

Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60

Lys Thr Ala Pro Trp Ile Thr Arg Ile Pro Gln Glu Leu Val Lys Lys
65 70 75 80

Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr
85 90 95

Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp
100 105 110

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

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

Cys Asp Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly
145 150 155 160

Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly
165 170 175

Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg
180 185 190

Trp Trp Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Glu Trp
195 200 205

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

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

Thr Leu Thr Leu Gln Cys Gly Ser Asp Ala Gly Tyr Asn Arg Phe Val
245 250 255

Leu Tyr Lys Asp Gly Glu Arg Asp Phe Leu Gln Leu Ala Gly Ala Gln
260 265 270

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

Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser
290 295 300

Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly
305 310 315 320

Gln Phe Tyr Asp Arg Val Ser Leu Ser Val Gln Pro Gly Pro Thr Val
325 330 335

Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Trp Met
340 345 350

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

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

Gly Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
385 390 395 400

Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp Pro Leu Glu
405 410 415

Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly
420 425 430

Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
435 440 445

Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
450 455 460

Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Phe
465 470 475 480

Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
485 490 495

Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
500 505 510

Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
515 520 525

Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly
530 535 540

Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val
545 550 555 560

Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser
565 570 575

Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln
580 585 590

Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala
595 600 605

Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg
610 615 620

Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val
625 630 635 640

Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
645 650

<210> 28
<211> 1347
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1347)

<400> 28

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atg atc ccc acc ttc acg gct ctg ctc tgc ctc ggg ctg agt ctg ggc        48
Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly
1               5                  10                  15

ccc agg acc gac atg cag gca ggg ccc ctc ccc aaa ccc acc ctc tgg        96
Pro Arg Thr Asp Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
            20                  25                  30

gct gag cca ggc tct gtg atc agc tgg ggg aac tct gtg acc atc tgg       144
Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp
        35                  40                  45

tgt cag ggg acc ctg gag gct cgg gag tac cgt ctg gat aaa gag gaa       192
Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
    50                  55                  60

agc cca gca ccc tgg gac aga cag aac cca ctg gag ccc aag aac aag       240
Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
65                  70                  75                  80

gcc aga ttc tcc atc cca tcc atg aca gag gac tat gca ggg aga tac       288
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
                85                  90                  95

cgc tgt tac tat cgc agc cct gta ggc tgg tca cag ccc agt gac ccc       336
Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
            100                 105                 110

ctg gag ctg gtg atg aca gga gcc tac agt aaa ccc acc ctt tca gcc       384
Leu Glu Leu Val Met Thr Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala
        115                 120                 125

ctg ccg agt cct ctt gtg acc tca gga aag agc gtg acc ctg ctg tgt       432
Leu Pro Ser Pro Leu Val Thr Ser Gly Lys Ser Val Thr Leu Leu Cys
    130                 135                 140
```

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cag tca cgg agc cca atg gac act ttc ctt ctg atc aag gag cgg gca      480
Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
145                 150                 155                 160

gcc cat ccc cta ctg cat ctg aga tca gag cac gga gct cag cag cac      528
Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His
                165                 170                 175

cag gct gaa ttc ccc atg agt cct gtg acc tca gtg cac ggg ggg acc      576
Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
            180                 185                 190

tac agg tgc ttc agc tca cac ggc ttc tcc cac tac ctg ctg tca cac      624
Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
        195                 200                 205

ccc agt gac ccc ctg gag ctc ata gtc tca gga tcc ttg gag ggt ccc      672
Pro Ser Asp Pro Leu Glu Leu Ile Val Ser Gly Ser Leu Glu Gly Pro
    210                 215                 220

agg ccc tca ccc aca agg tcc gtc tca aca gct gca ggc cct gag gac      720
Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
225                 230                 235                 240

cag ccc ctc atg cct aca ggg tca gtc ccc cac agt ggt ctg aga agg      768
Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
                245                 250                 255

cac tgg gag gta ctg atc ggg gtc ttg gtg gtc tcc atc ctg ctt ctc      816
His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
            260                 265                 270

tcc ctc ctc ctc ttc ctc ctc ctc caa cac tgg cgt cag gga aaa cac      864
Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His
        275                 280                 285
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agg aca ttg gcc cag aga cag gct gat ttc caa cgt cct cca ggg gct 912
Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
290 295 300

gcc gag cca gag ccc aag gac ggg ggc cta cag agg agg tcc agc cca 960
Ala Glu Pro Glu Pro Lys Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro
305 310 315 320

gct gct gac gtc cag gga gaa aac ttc tgt gct gcc gtg aag aac aca 1008
Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asn Thr
325 330 335

cag cct gag gac ggg gtg gaa atg gac act cgg cag agc cca cac gat 1056
Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Gln Ser Pro His Asp
340 345 350

gaa gac ccc cag gca gtg acg tat gcc aag gtg aaa cac tcc aga cct 1104
Glu Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro
355 360 365

agg aga gaa atg gcc tct cct ccc tcc cca ctg tct ggg gaa ttc ctg 1152
Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu
370 375 380

gac aca aag gac aga cag gca gaa gag gac aga cag atg gac act gag 1200
Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu
385 390 395 400

gct gct gca tct gaa gcc ccc cag gat gtg acc tac gcc cgg ctg cac 1248
Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Arg Leu His
405 410 415

agc ttt acc ctc aga cag aag gca act gag cct cct cca tcc cag gaa 1296
Ser Phe Thr Leu Arg Gln Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu
420 425 430

ggg gcc tct cca gct gag ccc agt gtc tat gcc act ctg gcc atc cac 1344
Gly Ala Ser Pro Ala Glu Pro Ser Val Tyr Ala Thr Leu Ala Ile His
435 440 445

taa 1347

<210> 29
<211> 448
<212> PRT
<213> Homo sapiens

<400> 29

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

Pro Arg Thr Asp Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
20 25 30

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

Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
50 55 60

Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
65 70 75 80

Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
85 90 95

Arg Cys Tyr Tyr Arg Ser Pro Val Gly Trp Ser Gln Pro Ser Asp Pro
100 105 110

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

Leu Pro Ser Pro Leu Val Thr Ser Gly Lys Ser Val Thr Leu Leu Cys
130 135 140

Gln Ser Arg Ser Pro Met Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala
145 150 155 160

Ala His Pro Leu Leu His Leu Arg Ser Glu His Gly Ala Gln Gln His
165 170 175

Gln Ala Glu Phe Pro Met Ser Pro Val Thr Ser Val His Gly Gly Thr
180 185 190

Tyr Arg Cys Phe Ser Ser His Gly Phe Ser His Tyr Leu Leu Ser His
195 200 205

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

Arg Pro Ser Pro Thr Arg Ser Val Ser Thr Ala Ala Gly Pro Glu Asp
225 230 235 240

Gln Pro Leu Met Pro Thr Gly Ser Val Pro His Ser Gly Leu Arg Arg
245 250 255

His Trp Glu Val Leu Ile Gly Val Leu Val Val Ser Ile Leu Leu Leu
260 265 270

Ser Leu Leu Leu Phe Leu Leu Leu Gln His Trp Arg Gln Gly Lys His
275 280 285

Arg Thr Leu Ala Gln Arg Gln Ala Asp Phe Gln Arg Pro Pro Gly Ala
290 295 300

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

Ala Ala Asp Val Gln Gly Glu Asn Phe Cys Ala Ala Val Lys Asn Thr
325 330 335

Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Gln Ser Pro His Asp
340 345 350

Glu Asp Pro Gln Ala Val Thr Tyr Ala Lys Val Lys His Ser Arg Pro
355 360 365

Arg Arg Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu
370 375 380

Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu
385 390 395 400

Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Arg Leu His
405 410 415

Ser Phe Thr Leu Arg Gln Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu
420 425 430

Gly Ala Ser Pro Ala Glu Pro Ser Val Tyr Ala Thr Leu Ala Ile His
435 440 445

<210> 30
<211> 24
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 30
ccatagttcc attttacagt tacc 24

<210> 31
<211> 20
<212> DNA
<213> Artificial

<220>

<223> An artificially synthesized primer sequence

<400> 31
gggaccaagg gatagacaga 20

<210> 32
<211> 24
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 32
tccagagttc caggtcaagg tcac 24

<210> 33
<211> 20
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 33
gccagtggat agaccgatgg 20

<210> 34
<211> 36
<212> DNA
<213> Artificial

<220>

<223> An artificially synthesized primer sequence

<220>
<221> modified_base
<222> (24)..(25)
<223> I

<220>
<221> modified_base
<222> (29)..(30)
<223> I

<220>
<221> modified_base
<222> (34)..(35)
<223> I

<400> 34
ggccacgcgt cgactagtac gggnngggnn gggnng 36

<210> 35
<211> 20
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 35
ggccacgcgt cgactagtac 20

<210> 36
<211> 24

<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 36
ttcactgcca tcaatcttcc actt 24

<210> 37
<211> 21
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence

<400> 37
gatggataca gttggtgcag c 21

<210> 38
<211> 408
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(408)

<220>
<221> sig_peptide
<222> (1)..(54)

<220>
<221> mat_peptide
<222> (55)..(408)

<400> 38

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atg aga gtg ctg att ctt ttg tgg ctg ttc aca gcc ttt cct ggt atc      48
Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
            -15                 -10                 -5

ctg tct gat gtg cag ctt cag gag tcg gga cct ggc ctg gtg aaa cct      96
Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
    -1  1               5                   10

tct cag tct ctg tcc ctc acc tgc act gtc act ggc tac tca atc acc     144
Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15                  20                  25                  30

agt gat tat gcc tgg aac tgg atc cgg cag ttt cca gga aac aaa ctg     192
Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
                35                  40                  45

gag tgg atg ggc tac ata agc tac agt ggt agc act agc tac aac cca     240
Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
            50                  55                  60

tct ctc aaa agt cga atc tct atc act cga gac aca tcc aag aac cag     288
Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
        65                  70                  75

ttc ttc ctg cag ttg aat tct gtg act act gag gac aca gcc aca tat     336
Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
    80                  85                  90

tac tgt gca aga tct ccc cct tac tat gct atg gac tac tgg ggt caa     384
Tyr Cys Ala Arg Ser Pro Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
95                  100                 105                 110
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gga acc tca gtc acc gtc tcc tca 408
Gly Thr Ser Val Thr Val Ser Ser
115

<210> 39
<211> 136
<212> PRT
<213> Mus musculus

<400> 39

Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
-15 -10 -5

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

Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15 20 25 30

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

Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
50 55 60

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
65 70 75

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

Tyr Cys Ala Arg Ser Pro Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105 110

Gly Thr Ser Val Thr Val Ser Ser
115

<210> 40
<211> 381
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(381)

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

<220>
<221> mat_peptide
<222> (61)..(381)

<400> 40
atg gag aca cat tct cag gtc ttt gta tac atg ttg ctg tgg ttg tct 48
Met Glu Thr His Ser Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
-20 -15 -10 -5

```
ggt gtt gaa gga gac att gtg atg acc cag tct cac aaa ttc atg tcc      96
Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
           -1  1               5                  10

aca tca gta gga gac agg gtc agc atc acc tgc aag gcc agt cag gat     144
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp
        15                  20                  25

gtg ggt act gct gta gcc tgg tat caa cag aaa cca ggg caa tct cct     192
Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    30                  35                  40

aaa cta ctg att tac tgg gca tcc acc cgg cac act gga gtc cct gat     240
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
45                  50                  55                  60

cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc att agc     288
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                65                  70                  75

aat gtg cag tct gaa gac ttg gca gat tat ttc tgt cag caa tat agc     336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
            80                  85                  90

agc tat cct ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa         381
Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
        95                  100                 105
```

<210> 41
<211> 127
<212> PRT
<213> Mus musculus

<400> 41

Met Glu Thr His Ser Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
-20 -15 -10 -5

Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
-1 1 5 10

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

Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
30 35 40

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
45 50 55 60

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
80 85 90

Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
95 100 105

<210> 42
<211> 414
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(414)

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

<220>
<221> mat_peptide
<222> (58)..(414)

<400> 42

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atg gga tgg agc tgg gtc ttt ctc ttc ctc ctg tca gga act gca ggt      48
Met Gly Trp Ser Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
                -15                 -10                 -5

gtc cac tgc cag gtc cag ctg aag cag tct gga gct gag ctg gtg agg      96
Val His Cys Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Val Arg
        -1  1               5                   10

cct ggg gct tca gtg aag ctg tcc tgc aag act tct gga tac atc ttc     144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
    15                  20                  25

acc agc tac tgg att cac tgg gta aaa cag agg tct gga cag ggc ctt     192
Thr Ser Tyr Trp Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu
30                  35                  40                  45

gag tgg att gca agg att tat cct gga act ggt agt act tac tac aat     240
Glu Trp Ile Ala Arg Ile Tyr Pro Gly Thr Gly Ser Thr Tyr Tyr Asn
                50                  55                  60

gag aag ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc     288
```

```
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
            65                  70                  75

act gcc tac atg cag ctc agc agc ctg aaa tct gag gac tct gct gtc      336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Lys Ser Glu Asp Ser Ala Val
        80                  85                  90

tat ttc tgt gca aga tac cct acc tac gac tgg tac ttc gat gtc tgg      384
Tyr Phe Cys Ala Arg Tyr Pro Thr Tyr Asp Trp Tyr Phe Asp Val Trp
    95                  100                 105

ggc gca ggg acc acg gtc acc gtc tcc tca                              414
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
110                 115
```

<210> 43
<211> 138
<212> PRT
<213> Mus musculus

<400> 43

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

Val His Cys Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Val Arg
        -1  1               5                   10

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

Thr Ser Tyr Trp Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu
```

30 35 40 45

Glu Trp Ile Ala Arg Ile Tyr Pro Gly Thr Gly Ser Thr Tyr Tyr Asn
50 55 60

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
65 70 75

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

Tyr Phe Cys Ala Arg Tyr Pro Thr Tyr Asp Trp Tyr Phe Asp Val Trp
95 100 105

Gly Ala Gly Thr Thr Val Thr Val Ser Ser
110 115

<210> 44
<211> 381
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(381)

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

<220>
<221> mat_peptide
<222> (61)..(381)

<400> 44

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atg gtt ttc aca cct cag att ctt gga ctt atg ctt ttc tgg att tca      48
Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser
-20                 -15                 -10                 -5

gcc tcc aga ggt gat att gtg cta act cag tct cca gcc acc ctg tct      96
Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            -1  1               5                  10

gtg act cca gga gat aga gtc agt ctt tcc tgc agg gcc agt caa agt     144
Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser
        15                  20                  25

att agc aac tac cta cac tgg tat caa caa aaa tca cat gag tct cca     192
Ile Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
    30                  35                  40

agg ctt ctc atc aag tat gct tcc cag tcc atc tct ggg atc ccc tcc     240
Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
45                  50                  55                  60

agg ttc agt ggc agt gga tca ggg aca gat ttc act ctc agt atc aac     288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
                65                  70                  75

agt gtg gag act gaa gat ttt gga atg tat ttc tgt caa cag agt aac     336
Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn
            80                  85                  90

agc tgg ccg ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa         381
Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
```

95 100 105

<210> 45
<211> 127
<212> PRT
<213> Mus musculus

<400> 45

Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
-1 1 5 10

Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser
15 20 25

Ile Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
30 35 40

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
65 70 75

Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn
80 85 90

Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
95 100 105

<210> 46
<211> 408
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(408)

<220>
<221> sig_peptide
<222> (1)..(54)

<220>
<221> mat_peptide
<222> (55)..(408)

<400> 46
atg aga gtg ctg att ctt ttg tgg ctg ttc aca gcc ttt cct ggt atc 48
Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
-15 -10 -5

ctg tct gat gtg cag ctt cag gag tcg gga cct ggc ctg gtg aaa cct 96
Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
-1 1 5 10

tct cag tct ctg tcc ctc acc tgc act gtc act ggc tac tca atc acc 144
Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15 20 25 30

agt gat tat gcc tgg aac tgg atc cgg cag ttt cca gga aac aaa ctg 192
Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
35 40 45

gag tgg atg ggc tac ata agc tac agt ggt agc act agc tac aac cca 240
Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
50 55 60

tct ctc aaa agt cga atc tct atc act cga gac aca tcc aag aac cag 288
Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
65 70 75

ttc ttc ctg cag ttg aat tct gtg act act gag gac aca gcc aca tat 336
Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
80 85 90

tac tgt gca aga gcc ctc cca tta ccc tgg ttt gct tac tgg ggc caa 384
Tyr Cys Ala Arg Ala Leu Pro Leu Pro Trp Phe Ala Tyr Trp Gly Gln
95 100 105 110

ggg act ctg gtc act gtc tct gca 408
Gly Thr Leu Val Thr Val Ser Ala
115

<210> 47
<211> 136
<212> PRT
<213> Mus musculus

<400> 47

Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
-15 -10 -5

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

Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15 20 25 30

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

Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
50 55 60

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
65 70 75

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

Tyr Cys Ala Arg Ala Leu Pro Leu Pro Trp Phe Ala Tyr Trp Gly Gln
95 100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115

<210> 48
<211> 381
<212> DNA

<213> Mus musculus

<220>
<221> CDS
<222> (1)..(381)

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

<220>
<221> mat_peptide
<222> (61)..(381)

<400> 48

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atg gag aca cat tct cag gtc ttt gta tac atg ttg ctg tgg ttg tct       48
Met Glu Thr His Ser Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
-20                 -15                 -10                 -5

ggt gtt gaa gga gac att gtg atg acc cag tct cac aaa ttc atg tcc       96
Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
            -1  1               5                  10

aca tca gta gga gac agg gtc agc atc acc tgc aag gcc agt cag gat      144
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp
        15                  20                  25

gtg ggt act gct gta gcc tgg tat caa cag aaa cca ggg caa tct cct      192
Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    30                  35                  40

aaa cta ctg att tac tgg gca tcc acc cgg cac act gga gtc cct gat      240
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
45                  50                  55                  60
```

cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc att agc 288
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

aat gtg cag tct gaa gac ttg gca gat tat ttc tgt cag caa tat agc 336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
80 85 90

agc tat cct tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 381
Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

<210> 49
<211> 127
<212> PRT
<213> Mus musculus

<400> 49

Met Glu Thr His Ser Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
-20 -15 -10 -5

Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
-1 1 5 10

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

Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
30 35 40

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
45 50 55 60

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
80 85 90

Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
95 100 105

<210> 50
<211> 1401
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

<220>
<221> CDS
<222> (1)..(1398)

<220>
<221> sig_peptide
<222> (1)..(54)

<220>
<221> mat_peptide
<222> (55)..(1398)

<400> 50

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atg aga gtg ctg att ctt ttg tgg ctg ttc aca gcc ttt cct ggt atc      48
Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
            -15                 -10                 -5

ctg tct gat gtg cag ctt cag gag tcg gga cct ggc ctg gtg aaa cct      96
Leu Ser Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
    -1  1               5                   10

tct cag tct ctg tcc ctc acc tgc act gtc act ggc tac tca atc acc     144
Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15                  20                  25                  30

agt gat tat gcc tgg aac tgg atc cgg cag ttt cca gga aac aaa ctg     192
Ser Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu
                35                  40                  45

gag tgg atg ggc tac ata agc tac agt ggt agc act agc tac aac cca     240
Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
            50                  55                  60

tct ctc aaa agt cga atc tct atc act cga gac aca tcc aag aac cag     288
Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
        65                  70                  75

ttc ttc ctg cag ttg aat tct gtg act act gag gac aca gcc aca tat     336
Phe Phe Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr
    80                  85                  90

tac tgt gca aga tct ccc cct tac tat gct atg gac tac tgg ggt caa     384
Tyr Cys Ala Arg Ser Pro Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
95                  100                 105                 110

gga acc tca gtc acc gtc tcc tca gcc tcc acc aag ggc cca tcg gtc     432
Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
```

115 120 125

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
130 135 140

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
145 150 155

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
160 165 170

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
175 180 185 190

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
195 200 205

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
210 215 220

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
225 230 235

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
240 245 250

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

255 260 265 270

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
275 280 285

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
290 295 300

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
305 310 315

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
320 325 330

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
335 340 345 350

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
355 360 365

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
370 375 380

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
385 390 395

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

400 405 410

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
415 420 425 430

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
435 440 445

ggt aaa tga 1401
Gly Lys

<210> 51
<211> 466
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 51

Met Arg Val Leu Ile Leu Leu Trp Leu Phe Thr Ala Phe Pro Gly Ile
-15 -10 -5

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

Ser Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
15 20 25 30

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

Glu Trp Met Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro
50 55 60

Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln
65 70 75

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

Tyr Cys Ala Arg Ser Pro Pro Tyr Tyr Ala Met Asp Tyr Trp Gly Gln
95 100 105 110

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

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

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

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

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
175 180 185 190

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

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

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

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
255 260 265 270

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

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

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315

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

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
335 340 345 350

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

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

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

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
415 420 425 430

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

Gly Lys

<210> 52
<211> 705
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized nucleotide sequence

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

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

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

<400> 52

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atg gag aca cat tct cag gtc ttt gta tac atg ttg ctg tgg ttg tct      48
Met Glu Thr His Ser Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
-20                 -15                 -10                 -5

ggt gtt gaa gga gac att gtg atg acc cag tct cac aaa ttc atg tcc      96
Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
            -1  1               5                  10

aca tca gta gga gac agg gtc agc atc acc tgc aag gcc agt cag gat     144
Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp
        15                  20                  25

gtg ggt act gct gta gcc tgg tat caa cag aaa cca ggg caa tct cct     192
```

```
Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    30                  35                  40

aaa cta ctg att tac tgg gca tcc acc cgg cac act gga gtc cct gat      240
Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
45                  50                  55                  60

cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc att agc      288
Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                65                  70                  75

aat gtg cag tct gaa gac ttg gca gat tat ttc tgt cag caa tat agc      336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
            80                  85                  90

agc tat cct ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa cga      384
Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
        95                  100                 105

act 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
    110                 115                 120

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
125                 130                 135                 140

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
                145                 150                 155

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
            160                 165                 170

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

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
    190                 195                 200

gtc aca aag agc ttc aac agg gga gag tgc tag                         705
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205                 210
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<210> 53
<211> 234
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 53

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Met Glu Thr His Ser Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser
-20                 -15                 -10                 -5

Gly Val Glu Gly Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser
           -1  1                5                  10

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

Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro
    30                  35                  40
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Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp
45 50 55 60

Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75

Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser
80 85 90

Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
95 100 105

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

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

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

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

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210

<210> 54
<211> 1407
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<220>
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<222> (1)..(1404)

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<222> (1)..(57)

<220>
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<222> (55)..(1404)

<400> 54
atg gga tgg agc tgg gtc ttt ctc ttc ctc ctg tca gga act gca ggt 48
Met Gly Trp Ser Trp Val Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
-15 -10 -5

```
gtc cac tgc cag gtc cag ctg aag cag tct gga gct gag ctg gtg agg      96
Val His Cys Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Val Arg
 -1  1               5                  10

cct ggg gct tca gtg aag ctg tcc tgc aag act tct gga tac atc ttc     144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe
15                  20                  25                  30

acc agc tac tgg att cac tgg gta aaa cag agg tct gga cag ggc ctt     192
Thr Ser Tyr Trp Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu
                35                  40                  45

gag tgg att gca agg att tat cct gga act ggt agt act tac tac aat     240
Glu Trp Ile Ala Arg Ile Tyr Pro Gly Thr Gly Ser Thr Tyr Tyr Asn
            50                  55                  60

gag aag ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc     288
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
        65                  70                  75

act gcc tac atg cag ctc agc agc ctg aaa tct gag gac tct gct gtc     336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Lys Ser Glu Asp Ser Ala Val
    80                  85                  90

tat ttc tgt gca aga tac cct acc tac gac tgg tac ttc gat gtc tgg     384
Tyr Phe Cys Ala Arg Tyr Pro Thr Tyr Asp Trp Tyr Phe Asp Val Trp
95                  100                 105                 110

ggc gca ggg acc acg gtc acc gtc tcc tca gcc tcc acc aag ggc cca     432
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
                115                 120                 125

tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca     480
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
            130                 135                 140
```

```
gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg      528
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
        145                 150                 155

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

gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc      624
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
175                 180                 185                 190

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

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

tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg      768
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
        225                 230                 235

ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      816
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    240                 245                 250

atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc      864
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
255                 260                 265                 270

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

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

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat     1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
        305                 310                 315

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

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag     1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
335                 340                 345                 350

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

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

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct     1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        385                 390                 395

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

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg     1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
415                 420                 425                 430
```

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg 1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

tct ccg ggt aaa tga 1407
Ser Pro Gly Lys
450

<210> 55
<211> 468
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 55

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

Val His Cys Gln Val Gln Leu Lys Gln Ser Gly Ala Glu Leu Val Arg
-1 1 5 10

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

Thr Ser Tyr Trp Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu
30 35 40 45

Glu Trp Ile Ala Arg Ile Tyr Pro Gly Thr Gly Ser Thr Tyr Tyr Asn

50 55 60

Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
65 70 75

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

Tyr Phe Cys Ala Arg Tyr Pro Thr Tyr Asp Trp Tyr Phe Asp Val Trp
95 100 105

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

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

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

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

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

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

190 195 200 205

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

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
240 245 250

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
255 260 265

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315

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

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

335 340 345

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

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

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

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
415 420 425

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
430 435 440 445

Ser Pro Gly Lys

<210> 56
<211> 705
<212> DNA
<213> Artificial

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

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

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

<400> 56

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atg gtt ttc aca cct cag att ctt gga ctt atg ctt ttc tgg att tca      48
Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser
-20                 -15                 -10                 -5

gcc tcc aga ggt gat att gtg cta act cag tct cca gcc acc ctg tct      96
Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
            -1  1               5                  10

gtg act cca gga gat aga gtc agt ctt tcc tgc agg gcc agt caa agt     144
Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser
        15                  20                  25

att agc aac tac cta cac tgg tat caa caa aaa tca cat gag tct cca     192
Ile Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
    30                  35                  40

agg ctt ctc atc aag tat gct tcc cag tcc atc tct ggg atc ccc tcc     240
Arg Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser
45                  50                  55                  60
```

```
agg ttc agt ggc agt gga tca ggg aca gat ttc act ctc agt atc aac      288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
                65                  70                  75

agt gtg gag act gaa gat ttt gga atg tat ttc tgt caa cag agt aac      336
Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn
            80                  85                  90

agc tgg ccg ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa cga      384
Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
        95                  100                 105

act 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
    110                 115                 120

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
125                 130                 135                 140

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
                145                 150                 155

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
            160                 165                 170

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
        175                 180                 185

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
    190                 195                 200
```

gtc aca aag agc ttc aac agg gga gag tgc tag 705
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210

<210> 57
<211> 234
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 57

Met Val Phe Thr Pro Gln Ile Leu Gly Leu Met Leu Phe Trp Ile Ser
-20 -15 -10 -5

Ala Ser Arg Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser
-1 1 5 10

Val Thr Pro Gly Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser
15 20 25

Ile Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro
30 35 40

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
65 70 75

Ser Val Glu Thr Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Asn
80 85 90

Ser Trp Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
95 100 105

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

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

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

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

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

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

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210

<210> 58
<211> 6
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(6)
<223> CDR

<400> 58

Ser Asp Tyr Ala Trp Asn
1 5

<210> 59
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR

<400> 59

Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

Arg

<210> 60
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDR

<400> 60

Ser Pro Pro Tyr Tyr Ala Met Asp Tyr
1 5

<210> 61
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDR

<400> 61

Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala
1 5 10

<210> 62
<211> 7
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(7)
<223> CDR

<400> 62

Trp Ala Ser Thr Arg His Thr
1 5

<210> 63
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDR

<400> 63

Gln Gln Tyr Ser Ser Tyr Pro Leu Thr
1 5

<210> 64
<211> 5
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(5)
<223> CDR

<400> 64

Ser Tyr Trp Ile His
1 5

<210> 65
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> CDR

<400> 65

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

Gly

<210> 66
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> CDR

<400> 66

Tyr Pro Thr Tyr Asp Trp Tyr Phe Asp Val
1 5 10

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

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDR

<400> 67

Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu His
1 5 10

<210> 68
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDR

<400> 68

Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 69
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDR

<400> 69

Gln Gln Ser Asn Ser Trp Pro Leu Thr
1 5

<210> 70
<211> 6
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(6)
<223> CDR

<400> 70

Ser Asp Tyr Ala Trp Asn
1 5

<210> 71
<211> 17
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(17)
<223> CDR

<400> 71

Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

Arg

<210> 72
<211> 9
<212> PRT
<213> Mus musculus

<220>
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<222> (1)..(9)
<223> CDR

<400> 72

Ala Leu Pro Leu Pro Trp Phe Ala Tyr
1 5

<210> 73
<211> 11
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> CDR

<400> 73

Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala
1 5 10

<210> 74
<211> 7
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> CDR

<400> 74

Trp Ala Ser Thr Arg His Thr
1 5

<210> 75
<211> 9
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> CDR

<400> 75

Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr
1 5

<210> 76
<211> 4

<212> PRT
<213> Artificial

<220>
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<220>
<221> misc_feature
<222> (2)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 76

Tyr Xaa Xaa Leu
1