SEQUENCE LISTING

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<120> Methods for Inhibiting Fibrosis in a Subject in Need Thereof

<130> MP.1.0250.PCT

<150> 62/275,025
<151> 2016-01-05

<150> 62/407,979
<151> 2016-10-13

<160> 85

<170> PatentIn version 3.5

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<213> Homo sapiens

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ctg tgt ggc tcg gtg gcc acc ccc ttg ggc ccg aag tgg cct gaa cct        101
Leu Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro
10                  15                  20                  25

gtg ttc ggg cgc ctg gca tcc ccc ggc ttt cca ggg gag tat gcc aat        149
Val Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn
                30                  35                  40

gac cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg        197
Asp Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu
            45                  50                  55

cgc ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag        245
Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu
        60                  65                  70

tac gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg        293
Tyr Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu
    75                  80                  85

tgc ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act        341
Cys Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr
90                  95                  100                 105

ttc tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac        389
Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
                110                 115                 120

tcc aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat gca gcc gag        437
Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu
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            125                 130                 135

gac att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac        485
Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp
        140                 145                 150

cac cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc tgc cgc gca        533
His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala
    155                 160                 165

ggc tac gtc ctg cac cgt aac aag cgc acc tgc tca gag cag agc ctc        581
Gly Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
170                 175                 180                 185

tag cctcccctgg agctccggcc tgcccagcag gtcagaagcc agagccagcc             634

tgctggcctc agctccgggt tgggctgaga tggctgtgcc ccaactccca ttcacccacc      694

atggacccaa taataaacct ggccccaccc c                                     725


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<213>  Homo sapiens

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


Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
    50                  55                  60


Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65                  70                  75                  80


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


Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
            100                 105                 110


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


Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
    130                 135                 140


Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145                 150                 155                 160
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Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
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Lys Arg Thr Cys Ser Glu Gln Ser Leu
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Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

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

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
85 90 95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
115 120 125

Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
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Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
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Asn Lys Arg Thr Cys Ser Glu Gln Ser Leu
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tgt ggc tcg gtg gcc acc ccc ttg ggc ccg aag tgg cct gaa cct gtg          99
Cys Gly Ser Val Ala Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val
                15                  20                  25

ttc ggg cgc ctg gca tcc ccc ggc ttt cca ggg gag tat gcc aat gac         147
Phe Gly Arg Leu Ala Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp
            30                  35                  40

cag gag cgg cgc tgg acc ctg act gca ccc ccc ggc tac cgc ctg cgc         195
Gln Glu Arg Arg Trp Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg
        45                  50                  55

ctc tac ttc acc cac ttc gac ctg gag ctc tcc cac ctc tgc gag tac         243
Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr
    60                  65                  70

gac ttc gtc aag ctg agc tcg ggg gcc aag gtg ctg gcc acg ctg tgc         291
Asp Phe Val Lys Leu Ser Ser Gly Ala Lys Val Leu Ala Thr Leu Cys
75                  80                  85                  90

ggg cag gag agc aca gac acg gag cgg gcc cct ggc aag gac act ttc         339
Gly Gln Glu Ser Thr Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe
                95                  100                 105

tac tcg ctg ggc tcc agc ctg gac att acc ttc cgc tcc gac tac tcc         387
Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser
            110                 115                 120

aac gag aag ccg ttc acg ggg ttc gag gcc ttc tat gca gcc gag gac         435
Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp
        125                 130                 135

att gac gag tgc cag gtg gcc ccg gga gag gcg ccc acc tgc gac cac         483
Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His
    140                 145                 150

cac tgc cac aac cac ctg ggc ggt ttc tac tgc tcc tgc cgc gca ggc         531
His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly
155                 160                 165                 170

tac gtc ctg cac cgt aac aag cgc acc tgc tca gcc ctg tgc tcc ggc         579
Tyr Val Leu His Arg Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly
                175                 180                 185

cag gtc ttc acc cag agg tct ggg gag ctc agc agc cct gaa tac cca         627
Gln Val Phe Thr Gln Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro
            190                 195                 200

cgg ccg tat ccc aaa ctc tcc agt tgc act tac agc atc agc ctg gag         675
Arg Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu
        205                 210                 215

gag ggg ttc agt gtc att ctg gac ttt gtg gag tcc ttc gat gtg gag         723
Glu Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu
    220                 225                 230

aca cac cct gaa acc ctg tgt ccc tac gac ttt ctc aag att caa aca         771
Thr His Pro Glu Thr Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr
235                 240                 245                 250

gac aga gaa gaa cat ggc cca ttc tgt ggg aag aca ttg ccc cac agg         819
Asp Arg Glu Glu His Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg
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                255                 260                 265

att gaa aca aaa agc aac acg gtg acc atc acc ttt gtc aca gat gaa        867
Ile Glu Thr Lys Ser Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu
            270                 275                 280

tca gga gac cac aca ggc tgg aag atc cac tac acg agc aca gcg cag        915
Ser Gly Asp His Thr Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln
        285                 290                 295

cct tgc cct tat ccg atg gcg cca cct aat ggc cac gtt tca cct gtg        963
Pro Cys Pro Tyr Pro Met Ala Pro Pro Asn Gly His Val Ser Pro Val
    300                 305                 310

caa gcc aaa tac atc ctg aaa gac agc ttc tcc atc ttt tgc gag act       1011
Gln Ala Lys Tyr Ile Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr
315                 320                 325                 330

ggc tat gag ctt ctg caa ggt cac ttg ccc ctg aaa tcc ttt act gca       1059
Gly Tyr Glu Leu Leu Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala
                335                 340                 345

gtt tgt cag aaa gat gga tct tgg gac cgg cca atg ccc gcg tgc agc       1107
Val Cys Gln Lys Asp Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser
            350                 355                 360

att gtt gac tgt ggc cct cct gat gat cta ccc agt ggc cga gtg gag       1155
Ile Val Asp Cys Gly Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu
        365                 370                 375

tac atc aca ggt cct gga gtg acc acc tac aaa gct gtg att cag tac       1203
Tyr Ile Thr Gly Pro Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr
    380                 385                 390

agc tgt gaa gag acc ttc tac aca atg aaa gtg aat gat ggt aaa tat       1251
Ser Cys Glu Glu Thr Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr
395                 400                 405                 410

gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa aaa tca       1299
Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser
                415                 420                 425

ctc cca gtc tgt gag cct gtt tgt gga cta tca gcc cgc aca aca gga       1347
Leu Pro Val Cys Glu Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly
            430                 435                 440

ggg cgt ata tat gga ggg caa aag gca aaa cct ggt gat ttt cct tgg       1395
Gly Arg Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp
        445                 450                 455

caa gtc ctg ata tta ggt gga acc aca gca gca ggt gca ctt tta tat       1443
Gln Val Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr
    460                 465                 470

gac aac tgg gtc cta aca gct gct cat gcc gtc tat gag caa aaa cat       1491
Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His
475                 480                 485                 490

gat gca tcc gcc ctg gac att cga atg ggc acc ctg aaa aga cta tca       1539
Asp Ala Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser
                495                 500                 505

cct cat tat aca caa gcc tgg tct gaa gct gtt ttt ata cat gaa ggt       1587
Pro His Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly
            510                 515                 520

tat act cat gat gct ggc ttt gac aat gac ata gca ctg att aaa ttg       1635
Tyr Thr His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu
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        525                 530                 535

aat aac aaa gtt gta atc aat agc aac atc acg cct att tgt ctg cca       1683
Asn Asn Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro
    540                 545                 550

aga aaa gaa gct gaa tcc ttt atg agg aca gat gac att gga act gca       1731
Arg Lys Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala
555                 560                 565                 570

tct gga tgg gga tta acc caa agg ggt ttt ctt gct aga aat cta atg       1779
Ser Gly Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met
                575                 580                 585

tat gtc gac ata ccg att gtt gac cat caa aaa tgt act gct gca tat       1827
Tyr Val Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr
            590                 595                 600

gaa aag cca ccc tat cca agg gga agt gta act gct aac atg ctt tgt       1875
Glu Lys Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys
        605                 610                 615

gct ggc tta gaa agt ggg ggc aag gac agc tgc aga ggt gac agc gga       1923
Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly
    620                 625                 630

ggg gca ctg gtg ttt cta gat agt gaa aca gag agg tgg ttt gtg gga       1971
Gly Ala Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly
635                 640                 645                 650

gga ata gtg tcc tgg ggt tcc atg aat tgt ggg gaa gca ggt cag tat       2019
Gly Ile Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr
                655                 660                 665

gga gtc tac aca aaa gtt att aac tat att ccc tgg atc gag aac ata       2067
Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile
            670                 675                 680

att agt gat ttt taa cttgcgtgtc tgcagtcaag gattcttcat ttttagaaat       2122
Ile Ser Asp Phe
        685

gcctgtgaag accttggcag cgacgtggct cgagaagcat tcatcattac tgtggacatg     2182

gcagttgttg ctccacccaa aaaaacagac tccaggtgag gctgctgtca tttctccact     2242

tgccagttta attccagcct tacccattga ctcaagggga cataaaccac gagagtgaca     2302

gtcatctttg cccacccagt gtaatgtcac tgctcaaatt acatttcatt accttaaaaa     2362

gccagtctct tttcatactg gctgttggca tttctgtaaa ctgcctgtcc atgctctttg     2422

tttttaaact tgttcttatt gaaaaaaaaa aaaaaaaa                             2460


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<213>  Homo sapiens

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Met Arg Leu Leu Thr Leu Leu Gly Leu Leu Cys Gly Ser Val Ala Thr
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Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
            20                  25                  30
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Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
        35                  40                  45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
    50                  55                  60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65                  70                  75                  80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
            100                 105                 110

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

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
    130                 135                 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145                 150                 155                 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
                165                 170                 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
            180                 185                 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
        195                 200                 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
    210                 215                 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
225                 230                 235                 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
                245                 250                 255

Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
            260                 265                 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
        275                 280                 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro Met
    290                 295                 300
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Ala Pro Pro Asn Gly His Val Ser Pro Val Gln Ala Lys Tyr Ile Leu
305                 310                 315                 320

Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu Gln
                325                 330                 335

Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
            340                 345                 350

Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly Pro
        355                 360                 365

Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro Gly
    370                 375                 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385                 390                 395                 400

Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp Gly
                405                 410                 415

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu Pro
            420                 425                 430

Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly Gly
        435                 440                 445

Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu Gly
    450                 455                 460

Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu Thr
465                 470                 475                 480

Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu Asp
                485                 490                 495

Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
            500                 505                 510

Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala Gly
        515                 520                 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val Ile
    530                 535                 540

Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu Ser
545                 550                 555                 560

Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu Thr
                565                 570                 575
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Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro Ile
            580                 585                 590

Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr Pro
        595                 600                 605

Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly
    610                 615                 620

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
625                 630                 635                 640

Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
                645                 650                 655

Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
            660                 665                 670

Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser Asp Phe
        675                 680                 685
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Ser Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp
            20                  25                  30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
        35                  40                  45

Phe Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu
    50                  55                  60

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

Asp Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser
                85                  90                  95

Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr Ser Asn Glu Lys Pro Phe
            100                 105                 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln
        115                 120                 125
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```
Val Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His
    130                 135                 140

Leu Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg
145                 150                 155                 160

Asn Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln
                165                 170                 175

Arg Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys
            180                 185                 190

Leu Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val
        195                 200                 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr
    210                 215                 220

Leu Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His
225                 230                 235                 240

Gly Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser
                245                 250                 255

Asn Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr
            260                 265                 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Tyr Pro
        275                 280                 285

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

Leu Lys Asp Ser Phe Ser Ile Phe Cys Glu Thr Gly Tyr Glu Leu Leu
305                 310                 315                 320

Gln Gly His Leu Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
                325                 330                 335

Gly Ser Trp Asp Arg Pro Met Pro Ala Cys Ser Ile Val Asp Cys Gly
            340                 345                 350

Pro Pro Asp Asp Leu Pro Ser Gly Arg Val Glu Tyr Ile Thr Gly Pro
        355                 360                 365

Gly Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
    370                 375                 380

Phe Tyr Thr Met Lys Val Asn Asp Gly Lys Tyr Val Cys Glu Ala Asp
385                 390                 395                 400
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Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Glu
                405                 410                 415

Pro Val Cys Gly Leu Ser Ala Arg Thr Thr Gly Gly Arg Ile Tyr Gly
            420                 425                 430

Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Ile Leu
        435                 440                 445

Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn Trp Val Leu
    450                 455                 460

Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala Ser Ala Leu
465                 470                 475                 480

Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
                485                 490                 495

Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Asp Ala
            500                 505                 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn Lys Val Val
        515                 520                 525

Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys Glu Ala Glu
    530                 535                 540

Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly Trp Gly Leu
545                 550                 555                 560

Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val Asp Ile Pro
                565                 570                 575

Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys Pro Pro Tyr
            580                 585                 590

Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly Leu Glu Ser
        595                 600                 605

Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
    610                 615                 620

Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile Val Ser Trp
625                 630                 635                 640

Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val Tyr Thr Lys
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            660                 665                 670
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ccagcgtagg actgcagacc aggccaggcc agctggacgg gcacaccatg aggtaggtgg 180

gcgccacagc ctccctgcag ggtgtggggt gggagcacag gcctgggcct caccgccct 240

gccctgccca taggctgctg accctcctgg gccttctgtg tggctcggtg gccaccccct 300

taggcccgaa gtggcctgaa cctgtgttcg ggcgcctggc atcccccggc tttccagggg 360

agtatgccaa tgaccaggag cggcgctgga ccctgactgc acccccggc taccgcctgc 420

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cagggttcag ggacacctgg gagcaggggc caggcttggc caggagggag atcaggcctg 600

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tggccacgct gtgcgggcag gagagcacag acacggagcg ggcccctggc aaggacactt 720

tctactcgct gggctccagc ctggacatta ccttccgctc cgactactcc aacgagaagc 780

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gcaaagacca aaacagccgt gacctccatt cacatgggct gagtgccaac tctgagccag 1020

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caaggccagc cagggcaaca cggtgaaact ctatctccac taaaactaca aaaattagct 1200

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ccccaacgca ccctctcctg ggatacccgg ggctcctcag ggccattgct gctctgccca 2040

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tccttcgatg tggagacaca ccctgaaacc ctgtgtccct acgactttct caaggtctgg 4020

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tggaagcgca gagctgcctc tctctggagt gcaaggagct gtagagtgta gggctcttct 4560

gggcaggact aggaagggac accaggttta gtggtgctga ggtctgaggc agcagcttct 4620

aaggggaagc acccgtgccc tcctcagcag cacccagcat cttcaccact cattcttcaa 4680

ccacccattc acccatcact catcttttac ccacccaccc tttgccactc atccttctgt 4740

ccctcatcct tccaaccatt catcaatcac ccacccatcc atcctttgcc acacaaccat 4800

ccacccattc ttctacctac ccatcctatc catccatcct tctatcagca tccttctacc 4860

acccatcctt cgttcggtca tccatcatca tccatccatc 4900

<210> 8
<211> 136
<212> PRT
<213> Homo sapiens

<400> 8

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

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser

100 105 110

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

Gly Phe Glu Ala Phe Tyr Ala Ala
130 135

<210> 9
<211> 181
<212> PRT
<213> Homo sapiens

<400> 9

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

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
20 25 30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
35 40 45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
50 55 60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65 70 75 80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
100 105 110

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

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
130 135 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145 150 155 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
165 170 175

Lys Arg Thr Cys Ser
180

<210> 10
<211> 293

<212> PRT
<213> Homo sapiens

<400> 10

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

Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Ala Ser
            20                  25                  30

Pro Gly Phe Pro Gly Glu Tyr Ala Asn Asp Gln Glu Arg Arg Trp Thr
        35                  40                  45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
    50                  55                  60

Asp Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser
65                  70                  75                  80

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

Thr Glu Arg Ala Pro Gly Lys Asp Thr Phe Tyr Ser Leu Gly Ser Ser
            100                 105                 110

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

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Ile Asp Glu Cys Gln Val
    130                 135                 140

Ala Pro Gly Glu Ala Pro Thr Cys Asp His His Cys His Asn His Leu
145                 150                 155                 160

Gly Gly Phe Tyr Cys Ser Cys Arg Ala Gly Tyr Val Leu His Arg Asn
                165                 170                 175

Lys Arg Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gln Arg
            180                 185                 190

Ser Gly Glu Leu Ser Ser Pro Glu Tyr Pro Arg Pro Tyr Pro Lys Leu
        195                 200                 205

Ser Ser Cys Thr Tyr Ser Ile Ser Leu Glu Glu Gly Phe Ser Val Ile
    210                 215                 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Thr Leu
225                 230                 235                 240

Cys Pro Tyr Asp Phe Leu Lys Ile Gln Thr Asp Arg Glu Glu His Gly
                245                 250                 255
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Pro Phe Cys Gly Lys Thr Leu Pro His Arg Ile Glu Thr Lys Ser Asn
            260                 265                 270

Thr Val Thr Ile Thr Phe Val Thr Asp Glu Ser Gly Asp His Thr Gly
        275                 280                 285

Trp Lys Ile His Tyr
    290
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<210> 11
<211> 41
<212> PRT
<213> Homo sapiens

<400> 11

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Glu Asp Ile Asp Glu Cys Gln Val Ala Pro Gly Glu Ala Pro Thr Cys
1               5                   10                  15

Asp His His Cys His Asn His Leu Gly Gly Phe Tyr Cys Ser Cys Arg
            20                  25                  30

Ala Gly Tyr Val Leu His Arg Asn Lys
        35                  40
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<210> 12
<211> 242
<212> PRT
<213> Homo sapiens

<400> 12

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Ile Tyr Gly Gly Gln Lys Ala Lys Pro Gly Asp Phe Pro Trp Gln Val
1               5                   10                  15

Leu Ile Leu Gly Gly Thr Thr Ala Ala Gly Ala Leu Leu Tyr Asp Asn
            20                  25                  30

Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu Gln Lys His Asp Ala
        35                  40                  45

Ser Ala Leu Asp Ile Arg Met Gly Thr Leu Lys Arg Leu Ser Pro His
    50                  55                  60

Tyr Thr Gln Ala Trp Ser Glu Ala Val Phe Ile His Glu Gly Tyr Thr
65                  70                  75                  80

His Asp Ala Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Asn Asn
                85                  90                  95

Lys Val Val Ile Asn Ser Asn Ile Thr Pro Ile Cys Leu Pro Arg Lys
            100                 105                 110

Glu Ala Glu Ser Phe Met Arg Thr Asp Asp Ile Gly Thr Ala Ser Gly
```

115 120 125

Trp Gly Leu Thr Gln Arg Gly Phe Leu Ala Arg Asn Leu Met Tyr Val
130 135 140

Asp Ile Pro Ile Val Asp His Gln Lys Cys Thr Ala Ala Tyr Glu Lys
145 150 155 160

Pro Pro Tyr Pro Arg Gly Ser Val Thr Ala Asn Met Leu Cys Ala Gly
165 170 175

Leu Glu Ser Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala
180 185 190

Leu Val Phe Leu Asp Ser Glu Thr Glu Arg Trp Phe Val Gly Gly Ile
195 200 205

Val Ser Trp Gly Ser Met Asn Cys Gly Glu Ala Gly Gln Tyr Gly Val
210 215 220

Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Ser
225 230 235 240

Asp Phe

<210> 13
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13

Gly Lys Asp Ser Cys Arg Gly Asp Ala Gly Gly Ala Leu Val Phe Leu
1 5 10 15

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Thr Pro Leu Gly Pro Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
1 5 10 15

<210> 15
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe Asp
1 5 10 15

Leu Glu Leu Ser His Leu Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser
20 25 30

Gly Ala Lys Val Leu Ala Thr Leu Cys Gly Gln
35 40

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

<220>
<223> Synthetic

<400> 16

Thr Phe Arg Ser Asp Tyr Ser Asn
1 5

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17

Phe Tyr Ser Leu Gly Ser Ser Leu Asp Ile Thr Phe Arg Ser Asp Tyr
1 5 10 15

Ser Asn Glu Lys Pro Phe Thr Gly Phe
20 25

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18

Ile Asp Glu Cys Gln Val Ala Pro Gly
1 5

<210> 19
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 19

Ala Asn Met Leu Cys Ala Gly Leu Glu Ser Gly Gly Lys Asp Ser Cys
1 5 10 15

Arg Gly Asp Ser Gly Gly Ala Leu Val
20 25

<210> 20
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (51)..(797)

<400> 20
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Met Ser
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ctg ttt cca tca ctc cct ctc ctt ctc ctg agt atg gtg gca gcg tct 104
Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala Ala Ser
5 10 15

tac tca gaa act gtg acc tgt gag gat gcc caa aag acc tgc cct gca 152
Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys Pro Ala
20 25 30

gtg att gcc tgt agc tct cca ggc atc aac ggc ttc cca ggc aaa gat 200
Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly Lys Asp
35 40 45 50

ggg cgt gat ggc acc aag gga gaa aag ggg gaa cca ggc caa ggg ctc 248
Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln Gly Leu
55 60 65

aga ggc tta cag ggc ccc cct gga aag ttg ggg cct cca gga aat cca 296
Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly Asn Pro
70 75 80

ggg cct tct ggg tca cca gga cca aag ggc caa aaa gga gac cct gga 344
Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp Pro Gly
85 90 95

aaa agt ccg gat ggt gat agt agc ctg gct gcc tca gaa aga aaa gct 392
Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg Lys Ala
100 105 110

ctg caa aca gaa atg gca cgt atc aaa aag tgg ctc acc ttc tct ctg 440
Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe Ser Leu
115 120 125 130

ggc aaa caa gtt ggg aac aag ttc ttc ctg acc aat ggt gaa ata atg 488
Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu Ile Met
135 140 145

acc ttt gaa aaa gtg aag gcc ttg tgt gtc aag ttc cag gcc tct gtg 536
Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala Ser Val
150 155 160

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gcc acc ccc agg aat gct gca gag aat gga gcc att cag aat ctc atc        584
Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn Leu Ile
        165                 170                 175

aag gag gaa gcc ttc ctg ggc atc act gat gag aag aca gaa ggg cag        632
Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu Gly Gln
    180                 185                 190

ttt gtg gat ctg aca gga aat aga ctg acc tac aca aac tgg aac gag        680
Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp Asn Glu
195                 200                 205                 210

ggt gaa ccc aac aat gct ggt tct gat gaa gat tgt gta ttg cta ctg        728
Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu Leu Leu
                215                 220                 225

aaa aat ggc cag tgg aat gac gtc ccc tgc tcc acc tcc cat ctg gcc        776
Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His Leu Ala
            230                 235                 240

gtc tgt gag ttc cct atc tga agggtcatat cactcaggcc ctccttgtct          827
Val Cys Glu Phe Pro Ile
        245

ttttactgca acccacaggc ccacagtatg cttgaaaaga taaattatat caatttcctc      887

atatccagta ttgttccttt tgtgggcaat cactaaaaat gatcactaac agcaccaaca      947

aagcaataat agt                                                        960
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<210> 21
<211> 248
<212> PRT
<213> Homo sapiens

<400> 21

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Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
1               5                   10                  15

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

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
        35                  40                  45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
    50                  55                  60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
65                  70                  75                  80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
                85                  90                  95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
            100                 105                 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
        115                 120                 125
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Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
245

<210> 22
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X at position 1 represents hydroxyproline

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Wherein X at position 4 represents hydrophobic residue

<400> 22

Xaa Gly Lys Xaa Gly Pro
1 5

<210> 23
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Wherein X represents hydroxyproline

<400> 23

Xaa Gly Lys Leu Gly
1 5

<210> 24
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (9)..(15)
<223> Wherein X at positions 9 and 15 represents hydroxyproline

<400> 24

Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa Gly
1 5 10 15

<210> 25
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(27)
<223> Wherein X at positions 3, 6, 15, 21, 24, 27 represents hydroxyproline

<400> 25

Gly Pro Xaa Gly Pro Xaa Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly
1 5 10 15

Lys Leu Gly Pro Xaa Gly Pro Xaa Gly Pro Xaa
20 25

<210> 26
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (26)..(26)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (32)..(32)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (35)..(35)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (41)..(41)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (50)..(50)
<223> Xaa can be any naturally occurring amino acid

<400> 26

Gly Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly
1 5 10 15

Gln Gly Leu Arg Gly Leu Gln Gly Pro Xaa Gly Lys Leu Gly Pro Xaa
20 25 30

Gly Asn Xaa Gly Pro Ser Gly Ser Xaa Gly Pro Lys Gly Gln Lys Gly
35 40 45

Asp Xaa Gly Lys Ser
50

<210> 27
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(33)
<223> Wherein X at positions 3, 6, 12, 18, 21, 30, 33 represents hydroxyproline

<400> 27

Gly Ala Xaa Gly Ser Xaa Gly Glu Lys Gly Ala Xaa Gly Pro Gln Gly
1 5 10 15

Pro Xaa Gly Pro Xaa Gly Lys Met Gly Pro Lys Gly Glu Xaa Gly Asp
20 25 30

Xaa

<210> 28
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (3)..(45)
<223> Wherein X at positions 3, 6, 9, 27, 30, 36, 42, 45 represents hydroxyproline

<400> 28

Gly Cys Xaa Gly Leu Xaa Gly Ala Xaa Gly Asp Lys Gly Glu Ala Gly
1 5 10 15

Thr Asn Gly Lys Arg Gly Glu Arg Gly Pro Xaa Gly Pro Xaa Gly Lys
20 25 30

Ala Gly Pro Xaa Gly Pro Asn Gly Ala Xaa Gly Glu Xaa
35 40 45

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29

Leu Gln Arg Ala Leu Glu Ile Leu Pro Asn Arg Val Thr Ile Lys Ala
1 5 10 15

Asn Arg Pro Phe Leu Val Phe Ile
20

<210> 30
<211> 559
<212> DNA
<213> Homo sapiens

<400> 30
atgaggctgc tgaccctcct gggccttctg tgtggctcgg tggccacccc cttgggcccg 60

aagtggcctg aacctgtgtt cgggcgcctg gcatcccccg gctttccagg ggagtatgcc 120

aatgaccagg agcggcgctg gaccctgact gcacccccg gctaccgcct gcgcctctac 180

ttcacccact tcgacctgga gctctcccac ctctgcgagt acgacttcgt caagctgagc 240

tcgggggcca aggtgctggc cacgctgtgc gggcaggaga gcacagacac ggagcgggcc 300

cctggcaagg acactttcta ctcgctgggc tccagcctgg acattacctt ccgctccgac 360

tactccaacg agaagccgtt cacggggttc gaggccttct atgcagccga ggacattgac 420

gagtgccagg tggccccggg agaggcgccc acctgcgacc accactgcca caaccacctg 480

ggcggtttct actgctcctg ccgcgcaggc tacgtcctgc accgtaacaa gcgcacctgc 540

tcagccctgt gctccggcc 559

<210> 31
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31
cgggcacacc atgaggctgc tgaccctcct gggc 34

<210> 32
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32
gacattacct tccgctccga ctccaacgag aag 33

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<400> 50

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                                    Met Arg Leu Leu Ile Phe Leu
                                    1               5

ggt ctg ctg tgg agt ttg gtg gcc aca ctt ctg ggt tca aag tgg cct         101
Gly Leu Leu Trp Ser Leu Val Ala Thr Leu Leu Gly Ser Lys Trp Pro
        10                  15                  20

gaa cct gta ttc ggg cgc ctg gtg tcc cct ggc ttc cca gag aag tat         149
Glu Pro Val Phe Gly Arg Leu Val Ser Pro Gly Phe Pro Glu Lys Tyr
    25                  30                  35

gct gac cat caa gat cga tcc tgg aca ctg act gca ccc cct ggc tac         197
Ala Asp His Gln Asp Arg Ser Trp Thr Leu Thr Ala Pro Pro Gly Tyr
40                  45                  50                  55

cgc ctg cgc ctc tac ttc acc cac ttt gac ctg gaa ctc tct tac cgc         245
Arg Leu Arg Leu Tyr Phe Thr His Phe Asp Leu Glu Leu Ser Tyr Arg
                60                  65                  70

tgc gag tat gac ttt gtc aag ttg agc tca ggg acc aag gtg ctg gcc         293
Cys Glu Tyr Asp Phe Val Lys Leu Ser Ser Gly Thr Lys Val Leu Ala
            75                  80                  85

aca ctg tgt ggg cag gag agt aca gac act gag cag gca cct ggc aat         341
Thr Leu Cys Gly Gln Glu Ser Thr Asp Thr Glu Gln Ala Pro Gly Asn
        90                  95                  100

gac acc ttc tac tca ctg ggt ccc agc cta aag gtc acc ttc cac tcc         389
Asp Thr Phe Tyr Ser Leu Gly Pro Ser Leu Lys Val Thr Phe His Ser
    105                 110                 115

gac tac tcc aat gag aag ccg ttc aca ggg ttt gag gcc ttc tat gca         437
Asp Tyr Ser Asn Glu Lys Pro Phe Thr Gly Phe Glu Ala Phe Tyr Ala
120                 125                 130                 135

gcg gag gat gtg gat gaa tgc aga gtg tct ctg gga gac tca gtc cct         485
Ala Glu Asp Val Asp Glu Cys Arg Val Ser Leu Gly Asp Ser Val Pro
                140                 145                 150

tgt gac cat tat tgc cac aac tac ttg ggc ggc tac tat tgc tcc tgc         533
Cys Asp His Tyr Cys His Asn Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys
            155                 160                 165

aga gcg ggc tac att ctc cac cag aac aag cac acg tgc tca gcc ctt         581
Arg Ala Gly Tyr Ile Leu His Gln Asn Lys His Thr Cys Ser Ala Leu
        170                 175                 180

tgt tca ggc cag gtg ttc aca gga aga tct ggg tat ctc agt agc cct         629
Cys Ser Gly Gln Val Phe Thr Gly Arg Ser Gly Tyr Leu Ser Ser Pro
    185                 190                 195

gag tac ccg cag cca tac ccc aag ctc tcc agc tgc acc tac agc atc         677
Glu Tyr Pro Gln Pro Tyr Pro Lys Leu Ser Ser Cys Thr Tyr Ser Ile
200                 205                 210                 215

cgc ctg gag gac ggc ttc agt gtc atc ctg gac ttc gtg gag tcc ttc         725
Arg Leu Glu Asp Gly Phe Ser Val Ile Leu Asp Phe Val Glu Ser Phe
                220                 225                 230

gat gtg gag acg cac cct gaa gcc cag tgc ccc tat gac tcc ctc aag         773
Asp Val Glu Thr His Pro Glu Ala Gln Cys Pro Tyr Asp Ser Leu Lys
            235                 240                 245

att caa aca gac aag ggg gaa cac ggc cca ttt tgt ggg aag acg ctg         821
Ile Gln Thr Asp Lys Gly Glu His Gly Pro Phe Cys Gly Lys Thr Leu
        250                 255                 260
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cct ccc agg att gaa act gac agc cac aag gtg acc atc acc ttt gcc        869
Pro Pro Arg Ile Glu Thr Asp Ser His Lys Val Thr Ile Thr Phe Ala
    265                 270                 275

act gac gag tcg ggg aac cac aca ggc tgg aag ata cac tac aca agc        917
Thr Asp Glu Ser Gly Asn His Thr Gly Trp Lys Ile His Tyr Thr Ser
280                 285                 290                 295

aca gca cgg ccc tgc cct gat cca acg gcg cca cct aat ggc agc att        965
Thr Ala Arg Pro Cys Pro Asp Pro Thr Ala Pro Pro Asn Gly Ser Ile
                300                 305                 310

tca cct gtg caa gcc acg tat gtc ctg aag gac agg ttt tct gtc ttc       1013
Ser Pro Val Gln Ala Thr Tyr Val Leu Lys Asp Arg Phe Ser Val Phe
            315                 320                 325

tgc aag aca ggc ttc gag ctt ctg caa ggt tct gtc ccc ctg aaa tca       1061
Cys Lys Thr Gly Phe Glu Leu Leu Gln Gly Ser Val Pro Leu Lys Ser
        330                 335                 340

ttc act gct gtc tgt cag aaa gat gga tct tgg gac cgg ccg atg cca       1109
Phe Thr Ala Val Cys Gln Lys Asp Gly Ser Trp Asp Arg Pro Met Pro
    345                 350                 355

gag tgc agc att att gat tgt ggc cct ccc gat gac cta ccc aat ggc       1157
Glu Cys Ser Ile Ile Asp Cys Gly Pro Pro Asp Asp Leu Pro Asn Gly
360                 365                 370                 375

cat gtg gac tat atc aca ggc cct caa gtg act acc tac aaa gct gtg       1205
His Val Asp Tyr Ile Thr Gly Pro Gln Val Thr Thr Tyr Lys Ala Val
                380                 385                 390

att cag tac agc tgt gaa gag act ttc tac aca atg agc agc aat ggt       1253
Ile Gln Tyr Ser Cys Glu Glu Thr Phe Tyr Thr Met Ser Ser Asn Gly
            395                 400                 405

aaa tat gtg tgt gag gct gat gga ttc tgg acg agc tcc aaa gga gaa       1301
Lys Tyr Val Cys Glu Ala Asp Gly Phe Trp Thr Ser Ser Lys Gly Glu
        410                 415                 420

aaa ctc ccc ccg gtt tgt gag cct gtt tgt ggg ctg tcc aca cac act       1349
Lys Leu Pro Pro Val Cys Glu Pro Val Cys Gly Leu Ser Thr His Thr
    425                 430                 435

ata gga gga cgc ata gtt gga ggg cag cct gca aag cct ggt gac ttt       1397
Ile Gly Gly Arg Ile Val Gly Gly Gln Pro Ala Lys Pro Gly Asp Phe
440                 445                 450                 455

cct tgg caa gtc ttg ttg ctg ggt caa act aca gca gca gca ggt gca       1445
Pro Trp Gln Val Leu Leu Leu Gly Gln Thr Thr Ala Ala Ala Gly Ala
                460                 465                 470

ctt ata cat gac aat tgg gtc cta aca gcc gct cat gct gta tat gag       1493
Leu Ile His Asp Asn Trp Val Leu Thr Ala Ala His Ala Val Tyr Glu
            475                 480                 485

aaa aga atg gca gcg tcc tcc ctg aac atc cga atg ggc atc ctc aaa       1541
Lys Arg Met Ala Ala Ser Ser Leu Asn Ile Arg Met Gly Ile Leu Lys
        490                 495                 500

agg ctc tca cct cat tac act caa gcc tgg ccc gag gaa atc ttt ata       1589
Arg Leu Ser Pro His Tyr Thr Gln Ala Trp Pro Glu Glu Ile Phe Ile
    505                 510                 515

cat gaa ggc tac act cac ggt gct ggt ttt gac aat gat ata gca ttg       1637
His Glu Gly Tyr Thr His Gly Ala Gly Phe Asp Asn Asp Ile Ala Leu
520                 525                 530                 535
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att aaa ctc aag aac aaa gtc aca atc aac gga agc atc atg cct gtt       1685
Ile Lys Leu Lys Asn Lys Val Thr Ile Asn Gly Ser Ile Met Pro Val
                540                 545                 550

tgc cta ccg cga aaa gaa gct gca tcc tta atg aga aca gac ttc act       1733
Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu Met Arg Thr Asp Phe Thr
            555                 560                 565

gga act gtg gct ggc tgg ggg tta acc cag aag ggg ctt ctt gct aga       1781
Gly Thr Val Ala Gly Trp Gly Leu Thr Gln Lys Gly Leu Leu Ala Arg
        570                 575                 580

aac cta atg ttt gtg gac ata cca att gct gac cac caa aaa tgt acc       1829
Asn Leu Met Phe Val Asp Ile Pro Ile Ala Asp His Gln Lys Cys Thr
    585                 590                 595

acc gtg tat gaa aag ctc tat cca gga gta aga gta agc gct aac atg       1877
Thr Val Tyr Glu Lys Leu Tyr Pro Gly Val Arg Val Ser Ala Asn Met
600                 605                 610                 615

ctc tgt gct ggc tta gag act ggt ggc aag gac agc tgc aga ggt gac       1925
Leu Cys Ala Gly Leu Glu Thr Gly Gly Lys Asp Ser Cys Arg Gly Asp
                620                 625                 630

agt ggg ggg gca tta gtg ttt cta gat aat gag aca cag cga tgg ttt       1973
Ser Gly Gly Ala Leu Val Phe Leu Asp Asn Glu Thr Gln Arg Trp Phe
            635                 640                 645

gtg gga gga ata gtt tcc tgg ggt tcc att aat tgt ggg gcg gca ggc       2021
Val Gly Gly Ile Val Ser Trp Gly Ser Ile Asn Cys Gly Ala Ala Gly
        650                 655                 660

cag tat ggg gtc tac aca aaa gtc atc aac tat att ccc tgg aat gag       2069
Gln Tyr Gly Val Tyr Thr Lys Val Ile Asn Tyr Ile Pro Trp Asn Glu
    665                 670                 675

aac ata ata agt aat ttc taa                                          2090
Asn Ile Ile Ser Asn Phe
680                 685
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Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val Ser
            20                  25                  30

Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp Thr
        35                  40                  45

Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His Phe
    50                  55                  60

Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu Ser
65                  70                  75                  80
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Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
                85                  90                  95

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

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
        115                 120                 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Val
    130                 135                 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145                 150                 155                 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln Asn
                165                 170                 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
            180                 185                 190

Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
        195                 200                 205

Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val Ile
    210                 215                 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala Gln
225                 230                 235                 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His Gly
                245                 250                 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser His
            260                 265                 270

Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr Gly
        275                 280                 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro Thr
    290                 295                 300

Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305                 310                 315                 320

Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu Gln
                325                 330                 335

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
            340                 345                 350
```

```
Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
        355                 360                 365

Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Gln
    370                 375                 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385                 390                 395                 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
                405                 410                 415

Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro Val
            420                 425                 430

Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly Gln
        435                 440                 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly Gln
    450                 455                 460

Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu Thr
465                 470                 475                 480

Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu Asn
                485                 490                 495

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln Ala
            500                 505                 510

Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
        515                 520                 525

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
    530                 535                 540

Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala Ser
545                 550                 555                 560

Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu Thr
                565                 570                 575

Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
            580                 585                 590

Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro Gly
        595                 600                 605

Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly Gly
    610                 615                 620
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Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625                 630                 635                 640

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
                645                 650                 655

Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val Ile
            660                 665                 670

Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
        675                 680                 685
```

<210> 52
<211> 670
<212> PRT
<213> Murine

<400> 52

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Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1               5                   10                  15

Ser Pro Gly Phe Pro Glu Lys Tyr Ala Asp His Gln Asp Arg Ser Trp
            20                  25                  30

Thr Leu Thr Ala Pro Pro Gly Tyr Arg Leu Arg Leu Tyr Phe Thr His
        35                  40                  45

Phe Asp Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
    50                  55                  60

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

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

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
            100                 105                 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
        115                 120                 125

Val Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
    130                 135                 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Ala Gly Tyr Ile Leu His Gln
145                 150                 155                 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
                165                 170                 175
```

```
Arg Ser Gly Tyr Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
            180                 185                 190

Leu Ser Ser Cys Thr Tyr Ser Ile Arg Leu Glu Asp Gly Phe Ser Val
        195                 200                 205

Ile Leu Asp Phe Val Glu Ser Phe Asp Val Glu Thr His Pro Glu Ala
    210                 215                 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Gly Glu His
225                 230                 235                 240

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

His Lys Val Thr Ile Thr Phe Ala Thr Asp Glu Ser Gly Asn His Thr
            260                 265                 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Arg Pro Cys Pro Asp Pro
        275                 280                 285

Thr Ala Pro Pro Asn Gly Ser Ile Ser Pro Val Gln Ala Thr Tyr Val
    290                 295                 300

Leu Lys Asp Arg Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu Leu
305                 310                 315                 320

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
                325                 330                 335

Gly Ser Trp Asp Arg Pro Met Pro Glu Cys Ser Ile Ile Asp Cys Gly
            340                 345                 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
        355                 360                 365

Gln Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
    370                 375                 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385                 390                 395                 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Leu Pro Pro Val Cys Glu Pro
                405                 410                 415

Val Cys Gly Leu Ser Thr His Thr Ile Gly Gly Arg Ile Val Gly Gly
            420                 425                 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
        435                 440                 445
```

```
Gln Thr Thr Ala Ala Ala Gly Ala Leu Ile His Asp Asn Trp Val Leu
    450                 455                 460

Thr Ala Ala His Ala Val Tyr Glu Lys Arg Met Ala Ala Ser Ser Leu
465                 470                 475                 480

Asn Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Pro His Tyr Thr Gln
                485                 490                 495

Ala Trp Pro Glu Glu Ile Phe Ile His Glu Gly Tyr Thr His Gly Ala
            500                 505                 510

Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr
        515                 520                 525

Ile Asn Gly Ser Ile Met Pro Val Cys Leu Pro Arg Lys Glu Ala Ala
    530                 535                 540

Ser Leu Met Arg Thr Asp Phe Thr Gly Thr Val Ala Gly Trp Gly Leu
545                 550                 555                 560

Thr Gln Lys Gly Leu Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro
                565                 570                 575

Ile Ala Asp His Gln Lys Cys Thr Thr Val Tyr Glu Lys Leu Tyr Pro
            580                 585                 590

Gly Val Arg Val Ser Ala Asn Met Leu Cys Ala Gly Leu Glu Thr Gly
        595                 600                 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
    610                 615                 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625                 630                 635                 640

Ser Ile Asn Cys Gly Ala Ala Gly Gln Tyr Gly Val Tyr Thr Lys Val
                645                 650                 655

Ile Asn Tyr Ile Pro Trp Asn Glu Asn Ile Ile Ser Asn Phe
            660                 665                 670
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<210> 53
<211> 2091
<212> DNA
<213> Rat

<220>
<221> CDS
<222> (10)..(2067)

<400> 53
tggcacaca atg agg cta ctg atc gtc ctg ggt ctg ctt tgg agt ttg gtg 51

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          Met Arg Leu Leu Ile Val Leu Gly Leu Leu Trp Ser Leu Val
          1               5                   10

gcc aca ctt ttg ggc tcc aag tgg cct gag cct gta ttc ggg cgc ctg          99
Ala Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu
15                  20                  25                  30

gtg tcc ctg gcc ttc cca gag aag tat ggc aac cat cag gat cga tcc         147
Val Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser
                35                  40                  45

tgg acg ctg act gca ccc cct ggc ttc cgc ctg cgc ctc tac ttc acc         195
Trp Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr
            50                  55                  60

cac ttc aac ctg gaa ctc tct tac cgc tgc gag tat gac ttt gtc aag         243
His Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys
        65                  70                  75

ttg acc tca ggg acc aag gtg cta gcc acg ctg tgt ggg cag gag agt         291
Leu Thr Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser
    80                  85                  90

aca gat act gag cgg gca cct ggc aat gac acc ttc tac tca ctg ggt         339
Thr Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly
95                  100                 105                 110

ccc agc cta aag gtc acc ttc cac tcc gac tac tcc aat gag aag cca         387
Pro Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro
                115                 120                 125

ttc aca gga ttt gag gcc ttc tat gca gcg gag gat gtg gat gaa tgc         435
Phe Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys
            130                 135                 140

aga aca tcc ctg gga gac tca gtc cct tgt gac cat tat tgc cac aac         483
Arg Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn
        145                 150                 155

tac ctg ggc ggc tac tac tgc tcc tgc cga gtg ggc tac att ctg cac         531
Tyr Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His
    160                 165                 170

cag aac aag cat acc tgc tca gcc ctt tgt tca ggc cag gtg ttc act         579
Gln Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr
175                 180                 185                 190

ggg agg tct ggc ttt ctc agt agc cct gag tac cca cag cca tac ccc         627
Gly Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro
                195                 200                 205

aaa ctc tcc agc tgc gcc tac aac atc cgc ctg gag gaa ggc ttc agt         675
Lys Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser
            210                 215                 220

atc acc ctg gac ttc gtg gag tcc ttt gat gtg gag atg cac cct gaa         723
Ile Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu
        225                 230                 235

gcc cag tgc ccc tac gac tcc ctc aag att caa aca gac aag agg gaa         771
Ala Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu
    240                 245                 250

tac ggc ccg ttt tgt ggg aag acg ctg ccc ccc agg att gaa act gac         819
Tyr Gly Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp
255                 260                 265                 270

agc aac aag gtg acc att acc ttt acc acc gac gag tca ggg aac cac         867
```

```
Ser Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His
                275                 280                 285

aca ggc tgg aag ata cac tac aca agc aca gca cag ccc tgc cct gat        915
Thr Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp
            290                 295                 300

cca acg gcg cca cct aat ggt cac att tca cct gtg caa gcc acg tat        963
Pro Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr
        305                 310                 315

gtc ctg aag gac agc ttt tct gtc ttc tgc aag act ggc ttc gag ctt       1011
Val Leu Lys Asp Ser Phe Ser Val Phe Cys Lys Thr Gly Phe Glu Leu
    320                 325                 330

ctg caa ggt tct gtc ccc ctg aag tca ttc act gct gtc tgt cag aaa       1059
Leu Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys
335                 340                 345                 350

gat gga tct tgg gac cgg ccg ata cca gag tgc agc att att gac tgt       1107
Asp Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys
                355                 360                 365

ggc cct ccc gat gac cta ccc aat ggc cac gtg gac tat atc aca ggc       1155
Gly Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly
            370                 375                 380

cct gaa gtg acc acc tac aaa gct gtg att cag tac agc tgt gaa gag       1203
Pro Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu
        385                 390                 395

act ttc tac aca atg agc agc aat ggt aaa tat gtg tgt gag gct gat       1251
Thr Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp
    400                 405                 410

gga ttc tgg acg agc tcc aaa gga gaa aaa tcc ctc ccg gtt tgc aag       1299
Gly Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys
415                 420                 425                 430

cct gtc tgt gga ctg tcc aca cac act tca gga ggc cgt ata att gga       1347
Pro Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly
                435                 440                 445

gga cag cct gca aag cct ggt gac ttt cct tgg caa gtc ttg tta ctg       1395
Gly Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu
            450                 455                 460

ggt gaa act aca gca gca ggt gct ctt ata cat gac gac tgg gtc cta       1443
Gly Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu
        465                 470                 475

aca gcg gct cat gct gta tat ggg aaa aca gag gcg atg tcc tcc ctg       1491
Thr Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu
    480                 485                 490

gac atc cgc atg ggc atc ctc aaa agg ctc tcc ctc att tac act caa       1539
Asp Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln
495                 500                 505                 510

gcc tgg cca gag gct gtc ttt atc cat gaa ggc tac act cac gga gct       1587
Ala Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala
                515                 520                 525

ggt ttt gac aat gat ata gca ctg att aaa ctc aag aac aaa gtc aca       1635
Gly Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr
            530                 535                 540

atc aac aga aac atc atg ccg att tgt cta cca aga aaa gaa gct gca       1683
```

```
Ile Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala
        545                 550                 555

tcc tta atg aaa aca gac ttc gtt gga act gtg gct ggc tgg ggg tta       1731
Ser Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu
    560                 565                 570

acc cag aag ggg ttt ctt gct aga aac cta atg ttt gtg gac ata cca       1779
Thr Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro
575                 580                 585                 590

att gtt gac cac caa aaa tgt gct act gcg tat aca aag cag ccc tac       1827
Ile Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr
                595                 600                 605

cca gga gca aaa gtg act gtt aac atg ctc tgt gct ggc cta gac cgc       1875
Pro Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg
            610                 615                 620

ggt ggc aag gac agc tgc aga ggt gac agc gga ggg gca tta gtg ttt       1923
Gly Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe
        625                 630                 635

cta gac aat gaa aca cag aga tgg ttt gtg gga gga ata gtt tcc tgg       1971
Leu Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp
    640                 645                 650

ggt tct att aac tgt ggg ggg tca gaa cag tat ggg gtc tac acg aaa       2019
Gly Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys
655                 660                 665                 670

gtc acg aac tat att ccc tgg att gag aac ata ata aat aat ttc taa       2067
Val Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
                675                 680                 685

tttgcaaaaa aaaaaaaaaa aaaa                                           2091


<210>  54
<211>  685
<212>  PRT
<213>  Rat

<400>  54

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


Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val Ser
            20                  25                  30


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


Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His Phe
    50                  55                  60


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


Ser Gly Thr Lys Val Leu Ala Thr Leu Cys Gly Gln Glu Ser Thr Asp
                85                  90                  95
```

```
Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro Ser
            100                 105                 110

Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe Thr
        115                 120                 125

Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg Thr
    130                 135                 140

Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr Leu
145                 150                 155                 160

Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln Asn
                165                 170                 175

Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly Arg
            180                 185                 190

Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys Leu
        195                 200                 205

Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile Thr
    210                 215                 220

Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala Gln
225                 230                 235                 240

Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr Gly
                245                 250                 255

Pro Phe Cys Gly Lys Thr Leu Pro Pro Arg Ile Glu Thr Asp Ser Asn
            260                 265                 270

Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr Gly
        275                 280                 285

Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro Thr
    290                 295                 300

Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val Leu
305                 310                 315                 320

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

Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp Gly
            340                 345                 350

Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly Pro
        355                 360                 365
```

```
Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro Glu
    370                 375                 380

Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr Phe
385                 390                 395                 400

Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly Phe
                405                 410                 415

Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro Val
            420                 425                 430

Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly Gln
        435                 440                 445

Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Gly Glu
    450                 455                 460

Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr Ala
465                 470                 475                 480

Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp Ile
                485                 490                 495

Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala Trp
            500                 505                 510

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

Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile Asn
    530                 535                 540

Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser Leu
545                 550                 555                 560

Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr Gln
                565                 570                 575

Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile Val
            580                 585                 590

Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro Gly
        595                 600                 605

Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly Gly
    610                 615                 620

Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu Asp
625                 630                 635                 640
```

Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly Ser
645 650 655

Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val Thr
660 665 670

Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
675 680 685

<210> 55
<211> 670
<212> PRT
<213> Rat

<400> 55

Thr Leu Leu Gly Ser Lys Trp Pro Glu Pro Val Phe Gly Arg Leu Val
1 5 10 15

Ser Leu Ala Phe Pro Glu Lys Tyr Gly Asn His Gln Asp Arg Ser Trp
20 25 30

Thr Leu Thr Ala Pro Pro Gly Phe Arg Leu Arg Leu Tyr Phe Thr His
35 40 45

Phe Asn Leu Glu Leu Ser Tyr Arg Cys Glu Tyr Asp Phe Val Lys Leu
50 55 60

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

Asp Thr Glu Arg Ala Pro Gly Asn Asp Thr Phe Tyr Ser Leu Gly Pro
85 90 95

Ser Leu Lys Val Thr Phe His Ser Asp Tyr Ser Asn Glu Lys Pro Phe
100 105 110

Thr Gly Phe Glu Ala Phe Tyr Ala Ala Glu Asp Val Asp Glu Cys Arg
115 120 125

Thr Ser Leu Gly Asp Ser Val Pro Cys Asp His Tyr Cys His Asn Tyr
130 135 140

Leu Gly Gly Tyr Tyr Cys Ser Cys Arg Val Gly Tyr Ile Leu His Gln
145 150 155 160

Asn Lys His Thr Cys Ser Ala Leu Cys Ser Gly Gln Val Phe Thr Gly
165 170 175

Arg Ser Gly Phe Leu Ser Ser Pro Glu Tyr Pro Gln Pro Tyr Pro Lys
180 185 190

```
Leu Ser Ser Cys Ala Tyr Asn Ile Arg Leu Glu Glu Gly Phe Ser Ile
        195                 200                 205

Thr Leu Asp Phe Val Glu Ser Phe Asp Val Glu Met His Pro Glu Ala
    210                 215                 220

Gln Cys Pro Tyr Asp Ser Leu Lys Ile Gln Thr Asp Lys Arg Glu Tyr
225                 230                 235                 240

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

Asn Lys Val Thr Ile Thr Phe Thr Thr Asp Glu Ser Gly Asn His Thr
            260                 265                 270

Gly Trp Lys Ile His Tyr Thr Ser Thr Ala Gln Pro Cys Pro Asp Pro
        275                 280                 285

Thr Ala Pro Pro Asn Gly His Ile Ser Pro Val Gln Ala Thr Tyr Val
    290                 295                 300

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

Gln Gly Ser Val Pro Leu Lys Ser Phe Thr Ala Val Cys Gln Lys Asp
                325                 330                 335

Gly Ser Trp Asp Arg Pro Ile Pro Glu Cys Ser Ile Ile Asp Cys Gly
            340                 345                 350

Pro Pro Asp Asp Leu Pro Asn Gly His Val Asp Tyr Ile Thr Gly Pro
        355                 360                 365

Glu Val Thr Thr Tyr Lys Ala Val Ile Gln Tyr Ser Cys Glu Glu Thr
    370                 375                 380

Phe Tyr Thr Met Ser Ser Asn Gly Lys Tyr Val Cys Glu Ala Asp Gly
385                 390                 395                 400

Phe Trp Thr Ser Ser Lys Gly Glu Lys Ser Leu Pro Val Cys Lys Pro
                405                 410                 415

Val Cys Gly Leu Ser Thr His Thr Ser Gly Gly Arg Ile Ile Gly Gly
            420                 425                 430

Gln Pro Ala Lys Pro Gly Asp Phe Pro Trp Gln Val Leu Leu Leu Gly
        435                 440                 445

Glu Thr Thr Ala Ala Gly Ala Leu Ile His Asp Asp Trp Val Leu Thr
    450                 455                 460
```

Ala Ala His Ala Val Tyr Gly Lys Thr Glu Ala Met Ser Ser Leu Asp
465 470 475 480

Ile Arg Met Gly Ile Leu Lys Arg Leu Ser Leu Ile Tyr Thr Gln Ala
485 490 495

Trp Pro Glu Ala Val Phe Ile His Glu Gly Tyr Thr His Gly Ala Gly
500 505 510

Phe Asp Asn Asp Ile Ala Leu Ile Lys Leu Lys Asn Lys Val Thr Ile
515 520 525

Asn Arg Asn Ile Met Pro Ile Cys Leu Pro Arg Lys Glu Ala Ala Ser
530 535 540

Leu Met Lys Thr Asp Phe Val Gly Thr Val Ala Gly Trp Gly Leu Thr
545 550 555 560

Gln Lys Gly Phe Leu Ala Arg Asn Leu Met Phe Val Asp Ile Pro Ile
565 570 575

Val Asp His Gln Lys Cys Ala Thr Ala Tyr Thr Lys Gln Pro Tyr Pro
580 585 590

Gly Ala Lys Val Thr Val Asn Met Leu Cys Ala Gly Leu Asp Arg Gly
595 600 605

Gly Lys Asp Ser Cys Arg Gly Asp Ser Gly Gly Ala Leu Val Phe Leu
610 615 620

Asp Asn Glu Thr Gln Arg Trp Phe Val Gly Gly Ile Val Ser Trp Gly
625 630 635 640

Ser Ile Asn Cys Gly Gly Ser Glu Gln Tyr Gly Val Tyr Thr Lys Val
645 650 655

Thr Asn Tyr Ile Pro Trp Ile Glu Asn Ile Ile Asn Asn Phe
660 665 670

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 56
atgaggctgc tgaccctcct gggccttc 28

<210> 57
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 57
gtgcccctcc tgcgtcacct ctg 23

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 58
cagaggtgac gcaggagggg cac 23

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Homo Sapiens

<400> 59
ttaaaatcac taattatgtt ctcgatc 27

<210> 60
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 60
atgaggctac tcatcttcct gg 22

<210> 61
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 61
ctgcagaggt gacgcagggg ggg 23

<210> 62
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 62
ccccccctgc gtcacctctg cag 23

<210> 63
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Murine

<400> 63
ttagaaatta cttattatgt tctcaatcc 29

<210> 64
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat

<400> 64
gaggtgacgc aggaggggca ttagtgttt 29

<210> 65
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Rat

<400> 65
ctagaaacac taatgcccct cctgcgtcac ctctgca 37

<210> 66
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 66
caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg 60

acctgcaccg tctctgggtt ctcactcagc aggggtaaaa tgggtgtgag ctggatccgt 120

cagcccccag ggaaggccct ggagtggctt gcacacattt tttcgagtga cgaaaaatcc 180

tacaggacat cgctgaagag caggctcacc atctccaagg acacctccaa aaaccaggtg 240

gtccttacaa tgaccaacat ggaccctgtg gacacagcca cgtattactg tgcacggata 300

cgacgtggag gaattgacta ctggggccag ggaaccctgg tcactgtctc ctca 354

<210> 67
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 67

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

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

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

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
    50                  55                  60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 68
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 68

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

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

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

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

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

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

Tyr Tyr Cys Ala Arg Asp Pro Phe Gly Val Pro Phe Asp Ile Trp Gly
            100                 105                 110
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Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 69
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 69

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
20 25 30

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

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

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

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

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 70
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 70
tcctatgagc tgatacagcc accctcggtg tcagtggccc caggacagac ggccaccatt 60

acctgtgcgg gagacaacct tgggaagaaa cgtgtgcact ggtaccagca gaggccaggc 120

caggcccctg tgttggtcat ctatgatgat agcgaccggc cctcagggat ccctgaccga 180

ttctctgcct ccaactctgg gaacacggcc accctgacca tcactagggg cgaagccggg 240

gatgaggccg actattattg tcaggtgtgg gacattgcta ctgatcatgt ggtcttcggc 300

ggagggacca agctcaccgt ccta 324

<210> 71
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 71

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

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

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

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

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

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ile Ala Thr Asp His
85 90 95

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

Ser Glu Gln Lys Leu Ile Ser Glu
115 120

<210> 72
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 72

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln
35

<210> 73
<211> 33
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 73

Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn Thr Cys Arg
1 5 10 15

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

Gln

<210> 74
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 74

Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys Thr Lys Leu
1 5 10 15

Trp Cys Asn Gln
20

<210> 75
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 75

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Val
35 40 45

Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu Thr Leu
50 55 60

Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Gly Lys Met
65 70 75 80

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu
85 90 95

```
Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser Leu Lys
            100                 105                 110

Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val Leu
        115                 120                 125

Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
    130                 135                 140

Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
145                 150                 155                 160

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                165                 170                 175

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
            180                 185                 190

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
        195                 200                 205

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
    210                 215                 220

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
225                 230                 235                 240

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
                245                 250                 255

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
            260                 265                 270

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
        275                 280                 285

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
    290                 295                 300

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
305                 310                 315                 320

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
                325                 330                 335

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
            340                 345                 350

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
        355                 360                 365
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Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
370 375 380

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
385 390 395 400

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
405 410 415

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
420 425 430

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
435 440 445

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
450 455 460

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
465 470 475 480

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
485 490

<210> 76
<211> 491
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 76

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

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

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

Trp Leu Ala His Ile Phe Ser Ser Asp Glu Lys Ser Tyr Arg Thr Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Arg Arg Gly Gly Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

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

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

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

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

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

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

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

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

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

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

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

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380
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Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

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

Gly Ser Gly Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp
450 455 460

Lys Cys Asn Thr Cys Arg Cys Gly Ser Asp Gly Lys Ser Ala Val Cys
465 470 475 480

Thr Lys Leu Trp Cys Asn Gln Gly Ser Gly Ala
485 490

<210> 77
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 77

Leu Glu Val Thr Cys Glu Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn
1 5 10 15

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

Trp Cys Asn Gln Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser Gln Pro
35 40 45

Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln Thr Ala
50 55 60

Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala Tyr Trp
65 70 75 80

Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Met Tyr Gln Asp
85 90 95

Lys Gln Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
100 105 110

Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu
115 120 125

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser Thr Ala Val Phe Gly
130 135 140

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

Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
165 170 175

Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
180 185 190

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
195 200 205

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
210 215 220

Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln
225 230 235 240

Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu
245 250 255

Cys Ser

<210> 78
<211> 258
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78

Gln Pro Val Leu Thr Gln Pro Pro Ser Leu Ser Val Ser Pro Gly Gln
1 5 10 15

Thr Ala Ser Ile Thr Cys Ser Gly Glu Lys Leu Gly Asp Lys Tyr Ala
20 25 30

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

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

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

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

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
100 105 110

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
115 120 125

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
130 135 140

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
145 150 155 160

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
165 170 175

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
180 185 190

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

Thr Glu Cys Ser Ala Ala Gly Gly Ser Gly Leu Glu Val Thr Cys Glu
210 215 220

Pro Gly Thr Thr Phe Lys Asp Lys Cys Asn Thr Cys Arg Cys Gly Ser
225 230 235 240

Asp Gly Lys Ser Ala Val Cys Thr Lys Leu Trp Cys Asn Gln Gly Ser
245 250 255

Gly Ala

<210> 79
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79

Gly Thr Gly Gly Gly Ser Gly Ser Ser Ser
1 5 10

<210> 80
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 80

Ala Ala Gly Gly Ser Gly
1 5

<210> 81
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 81

Gly Ser Gly Ala
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<210> 82
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
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gaagtgacgt gtgagcccgg aacgacattc aaagacaagt gcaatacttg tcggtgcggt 120

tcagatggga aatcggcggt ctgcacaaag ctctggtgta accagggcac cggtggaggg 180

tcgggatcca gctcacaggt caccttgaag gagtctggtc ctgtgctggt gaaacccaca 240

gagaccctca cgctgacctg caccgtctct gggttctcac tcagcagggg taaaatgggt 300

gtgagctgga tccgtcagcc cccagggaag gccctggagt ggcttgcaca catttttcg 360

agtgacgaaa aatcctacag gacatcgctg aagagcaggc tcaccatctc caaggacacc 420

tccaaaaacc aggtggtcct tacaatgacc aacatggacc ctgtggacac agccacgtat 480

tactgtgcac ggatacgacg tggaggaatt gactactggg gccagggaac cctggtcact 540

gtctcctcag cctccaccaa gggcccatcc gtcttccccc tggcgccctg ctccaggagc 600

acctccgaga gcacagccgc cctgggctgc ctggtcaagg actacttccc cgaaccggtg 660

acggtgtcgt ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta 720

cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 780

acgaagacct acacctgcaa cgtagatcac aagcccagca acaccaaggt ggacaagaga 840

gttgagtcca aatatggtcc cccatgccca ccatgcccag cacctgagtt cctgggggga 900

ccatcagtct tcctgttccc cccaaaaccc aaggacactc tcatgatctc ccggacccct 960

gaggtcacgt gcgtggtggt ggacgtgagc caggaagacc ccgaggtcca gttcaactgg 1020

tacgtggatg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagttcaac 1080

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaacggcaag 1140

gagtacaagt gcaaggtctc caacaaaggc ctcccgtcct ccatcgagaa aaccatctcc 1200

aaagccaaag ggcagccccg agagccacag gtgtacaccc tgcccccatc ccaggaggag 1260

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1320

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1380

ctggactccg acggctcctt cttcctctac agcaggctaa ccgtggacaa gagcaggtgg 1440

caggagggga atgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1500

cagaagagcc tctccctgtc tctcgggaaa tga 1533

<210> 83
<211> 1533
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83
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gtcaccttga aggagtctgg tcctgtgctg gtgaaaccca cagagaccct cacgctgacc 120

tgcaccgtct ctgggttctc actcagcagg ggtaaaatgg gtgtgagctg gatccgtcag 180

cccccaggga aggccctgga gtggcttgca cacatttttt cgagtgacga aaaatcctac 240

aggacatcgc tgaagagcag gctcaccatc tccaaggaca cctccaaaaa ccaggtggtc 300

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc acggatacga 360

cgtggaggaa ttgactactg gggccaggga accctggtca ctgtctcctc agcctccacc 420

aagggcccat ccgtcttccc cctggcgccc tgctccagga gcacctccga gagcacagcc 480

gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaactca 540

ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac 600

tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacgaagac ctacacctgc 660

aacgtagatc acaagcccag caacaccaag gtggacaaga gagttgagtc caaatatggt 720

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cccccaaaac ccaaggacac tctcatgatc tcccggaccc ctgaggtcac gtgcgtggtg 840

gtggacgtga gccaggaaga ccccgaggtc agttcaact ggtacgtgga tggcgtggag 900

gtgcataatg ccaagacaaa gccgcgggag gagcagttca acagcacgta ccgtgtggtc 960

agcgtcctca ccgtcctgca ccaggactgg ctgaacggca aggagtacaa gtgcaaggtc 1020

tccaacaaag gcctcccgtc ctccatcgag aaaaccatct ccaaagccaa agggcagccc 1080

cgagagccac aggtgtacac cctgccccca tcccaggagg agatgaccaa gaaccaggtc 1140

agcctgacct gcctggtcaa aggcttctac cccagcgaca tcgccgtgga gtgggagagc 1200

aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1260

ttcttcctct acagcaggct aaccgtggac aagagcaggt ggcaggaggg gaatgtcttc 1320

tcatgctccg tgatgcatga ggctctgcac aaccactaca cacagaagag cctctccctg 1380

tctctcggga aagccgctgg tggtagtggt ttggaagtga cgtgtgagcc cggaacgaca 1440

ttcaaagaca agtgcaatac ttgtcggtgc ggttcagatg ggaaatcggc ggtctgcaca 1500

aagctctggt gtaaccaggg tagtggtgct tga 1533

<210> 84
<211> 834
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84
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gaagtgacgt gtgagcccgg aacgacattc aaagacaagt gcaatacttg tcggtgcggt 120

tcagatggga aatcggcggt ctgcacaaag ctctggtgta accagggcac cggtggaggg 180

tcgggatcca gctcacagcc agtgctgact cagcccccct cactgtccgt gtccccagga 240

cagacagcca gcatcacctg ctctggagag aaattggggg ataaatatgc ttactggtat 300

cagcagaagc caggccagtc ccctgtgttg gtcatgtatc aagataaaca gcggccctca 360

gggatccctg agcgattctc tggctccaac tctgggaaca cagccactct gaccatcagc 420

gggacccagg ctatggatga ggctgactat tactgtcagg cgtgggacag cagcactgcg 480

gtattcggcg gagggaccaa gctgaccgtc ctaggccagc ctaaggcggc gccctcggtc 540

accctgttcc cgccctcctc tgaggagctt caagccaaca aggccacact ggtgtgtctc 600

ataagtgact tctacccggg agccgtgaca gtggcctgga aggcagatag cagccccgtc 660

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc 720

agctatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggtc 780

acgcatgaag ggagcaccgt ggagaagaca gtggccccta cagaatgttc atag 834

<210> 85
<211> 834
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85
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ccagtgctga ctcagccccc ctcactgtcc gtgtccccag gacagacagc cagcatcacc 120

tgctctggag agaaattggg ggataaatat gcttactggt atcagcagaa gccaggccag 180

tcccctgtgt tggtcatgta tcaagataaa cagcggccct cagggatccc tgagcgattc 240

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aagctgaccg tcctaggcca gcctaaggcg gcgccctcgg tcaccctgtt cccgccctcc 420

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cctgagcagt ggaagtccca cagaagctac agctgccagg tcacgcatga agggagcacc 660

gtggagaaga cagtggcccc tacagaatgt tcagccgctg gtggtagtgg tttggaagtg 720

acgtgtgagc ccggaacgac attcaaagac aagtgcaata cttgtcggtg cggttcagat 780

gggaaatcgg cggtctgcac aaagctctgg tgtaaccagg gtagtggtgc ttag 834