SEQUENCE LISTING

<110> NIPPI, INCORPORATED

<120> A method for producing a protein.

<130> FA1238-14040PCT

<150> JP2013-064357
<151> 2013-03-26

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<151> 2013-12-18

<160> 39

<170> PatentIn version 3.5

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Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
            20                  25                  30

atg aag gaa acg tca tat gaa gaa gcc cta gcc aac cag cgc aag gag      144
Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
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atg gcg aaa act cac cac cag aaa gtc gag aag aaa aag aag gag aaa      192
Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
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aca gtg gag aag aaa gga aag acc aag aaa aag gaa gag aaa cct aat      240
Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

ggg aag ata cct gat cat gat cca gcc ccc aat gtg act gtc ctc ctt      288
Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
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Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
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Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
        115                 120                 125

cag gag aag ctg gcc tcc tcc ccc aag gac aaa aag aag aag gag aaa      432
Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
    130                 135                 140

aaa gtg gca aaa gtg gaa cca gct gtc agc tct gta gtg aat tcc atc      480
Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
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gtg ccg atg gtg gtg gtg ccc cca gtg ggt gcc aag ggc aac aca cca      576
Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro
            180                 185                 190

gcc act ggc act act cag ggc aaa aag gcg gag ggg act cag aat caa      624
Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
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agc aaa aag gct gaa gga gcc cca aac cag ggc aga aag gca gag gga      672
Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
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acc cca aac cag ggc aaa aag aca gag gga acc cca aac caa ggg aaa      720
Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
225                 230                 235                 240

aag gca gag gga acc cca aac caa ggc aaa aag gca gaa gga acc cca      768
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gat aca acc cca aac cag ggg aaa aag gtg gag ggg gcc cca acc cag      864
Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
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ggc aga aag gcc gag ggg gct cag aac cag gcc aaa aag gta gaa ggg      912
Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly
    290                 295                 300

gcc cag aac cag ggc aaa aag gca gag ggg gcc cag aat cag ggc aaa      960
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
305                 310                 315                 320

aag gga gag ggg gcc cag aac cag ggc aag aag gcc gag ggg gcc cag     1008
Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                325                 330                 335

aat cag ggc aag aag gcc gag ggg gcc cag aat cag ggc aag aag gcc     1056
Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            340                 345                 350

gag ggg gcc cag aat cag ggc aag aag gcc gag ggg gcc cag aat cag     1104
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ggc aag aag gct gag ggg gct cag aac cag ggc aaa aag gcc gag ggg     1152
Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
    370                 375                 380

gct cag aac cag ggc aaa aaa gta gaa ggg gcc cag aac cag ggc aag     1200
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385                 390                 395                 400

aag gct gag ggt gcc cag aac cag ggc aaa aag gcc gag ggg gcc cag     1248
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                405                 410                 415

aat cag ggc aaa aag gcc gag ggg gcc cag aac cag ggc aag aag gca     1296
Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            420                 425                 430
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gag ggg gcc cag aac cag ggc aag aag gcc gag ggg gcc cag aac cag      1344
Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
        435                 440                 445

gac aag aag gcc gag ggg gcc cag aac cag ggc agg aag gcc gag ggg      1392
Asp Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly
    450                 455                 460

gcc cag aac cag ggc agg aag gcc gag ggg gcc cag aac cag ggc aag      1440
Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
465                 470                 475                 480

aag gcc gag ggg gcc cag aac cag ggc aag aag gcc gag ggg acc ccg      1488
Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
                485                 490                 495

aac cag ggc aag aag gcc gag ggg acc ccg aac cag ggc aag aag gcc      1536
Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala
            500                 505                 510

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Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
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ggc aag aag gcc gag ggg acc ccg aac cag ggc aag aag gcc gag ggg      1632
Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly
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gcc cag aac cag ggc aag aag gcc gag ggg gcc cag aac cag ggc aag      1680
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
545                 550                 555                 560

aag gcc gag ggg gcc cag aac cag ggc aag aag gcc gag ggg gcc cag      1728
Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                565                 570                 575

aac cag ggc aag aag gcc gag ggg gcc cag aac cag ggc aag aag gcc      1776
Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            580                 585                 590

gag ggt gct cag aac cag ggc aaa aaa gta gaa ggg gcc cag aac cag      1824
Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln
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ggc aag aag gct gag ggg gcc cag aac cag ggc aag aag gcc gag ggg      1872
Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
    610                 615                 620

gct cag aac cag ggc aaa aag gcc gag gga gcc cag aac cag ggc caa      1920
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln
625                 630                 635                 640

aaa gga gag gga gcc cag aat cag ggt aaa aag aca gaa ggg gct cag      1968
Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln
                645                 650                 655

ggc aaa aag gca gaa agg agt ccc aac caa ggc aaa aaa gga gag gga      2016
Gly Lys Lys Ala Glu Arg Ser Pro Asn Gln Gly Lys Lys Gly Glu Gly
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gct ccc atc cag ggc aaa aag gca gat tcg gtt gct aat cag ggc aca      2064
Ala Pro Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr
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aag gta gag ggt att aca aac cag ggg aaa aaa gca gaa ggg tcc ccc      2112
Lys Val Glu Gly Ile Thr Asn Gln Gly Lys Lys Ala Glu Gly Ser Pro
    690                 695                 700
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gac gca gct gcc aat cag ggt aaa aag aca gag tca gct tct gtc cag      2208
Asp Ala Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln
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ggc aga aat aca gat gtg gcc cag agc cca gag gca cca aag caa gag      2256
Gly Arg Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu
            740                 745                 750

gct cct gcc aag aag aag tct ggt tca aag aaa aaa ggt gag cct ggg      2304
Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly
        755                 760                 765

ccc cca gat gcc gac ggc cct ctc tac ctc ccc tac aag acg ctg gtc      2352
Pro Pro Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val
    770                 775                 780

tcc acg gtt ggg agc atg gtg ttc aac gag ggc gag gcc cag cgg ctc      2400
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785                 790                 795                 800

atc gag atc ctg tcc gag aag gct ggc atc att cag gac acc tgg cac      2448
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aag gcc act cag aag ggt gac cct gtg gcg att ctg aaa cgc cag ctg      2496
Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu
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gaa gag aag gaa aaa ctg ctg gcc aca gaa cag gaa gat gcg gct gtc      2544
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        835                 840                 845

gcc aag agc aaa ctg agg gag ctc aac aag gag atg gca gca gaa aag      2592
Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys
    850                 855                 860

gcc aaa gca gca gcc ggg gag gcc aaa gtg aaa aag cag ctg gtg gcc      2640
Ala Lys Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala
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cgg gag cag gag atc acg gct gtg cag gca cgc atg cag gcc agc tac      2688
Arg Glu Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr
                885                 890                 895

cgg gag cac gtg aag gag gtg cag cag ctg cag ggc aag atc cgg act      2736
Arg Glu His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr
            900                 905                 910

ctt cag gag cag ctg gag aat ggc ccc aac acg cag ctg gcc cgc ctg      2784
Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu
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cag cag gag aac tcc atc ctg cgg gat gcc ttg aac cag gcc acg agc      2832
Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser
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cag gtg gag agc aag cag aac gca gag ctg gcc aag ctt cgg cag gag      2880
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945                 950                 955                 960

ctc agc aag gtc agc aaa gag ctg gtg gag aag tca gag gct gtg cgg      2928
Leu Ser Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg
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caa gat gag cag cag cgg aaa gct ctg gaa gcc aag gca gct gcc ttc     2976
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            980                 985                 990

gag aag cag gtc ctg cag ctg cag  gcg tcc cac agg gag  agt gag gag   3024
Glu Lys Gln Val Leu Gln Leu Gln  Ala Ser His Arg Glu  Ser Glu Glu
        995                1000                1005

gcc ctg  cag aag cgc ctg gac  gag gtc agc cgg gag  ctg tgc cac      3069
Ala Leu  Gln Lys Arg Leu Asp  Glu Val Ser Arg Glu  Leu Cys His
    1010                1015                1020

acg cag  agc agc cac gcc agc  ctc cgg gcg gat gcc  gag aag gcc      3114
Thr Gln  Ser Ser His Ala Ser  Leu Arg Ala Asp Ala  Glu Lys Ala
    1025                1030                1035

cag gag  caa cag cag cag atg  gcc gag ctg cac agc  aag tta cag      3159
Gln Glu  Gln Gln Gln Gln Met  Ala Glu Leu His Ser  Lys Leu Gln
    1040                1045                1050

tcc tcc  gag gca gag gtg cgc  agc aaa tgc gag gag  ctg agt ggc      3204
Ser Ser  Glu Ala Glu Val Arg  Ser Lys Cys Glu Glu  Leu Ser Gly
    1055                1060                1065

ctc cac  ggg cag ctc cag gag  gcc agg gcg gag aac  tcc cag ctc      3249
Leu His  Gly Gln Leu Gln Glu  Ala Arg Ala Glu Asn  Ser Gln Leu
    1070                1075                1080

aca gag  aga atc cgt tcc att  gag gcc ctg ctg gag  gcg ggc cag      3294
Thr Glu  Arg Ile Arg Ser Ile  Glu Ala Leu Leu Glu  Ala Gly Gln
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gcg cgg  gat gcc cag gac gtc  cag gcc agc cag gcg  gag gct gac      3339
Ala Arg  Asp Ala Gln Asp Val  Gln Ala Ser Gln Ala  Glu Ala Asp
    1100                1105                1110

cag cag  cag act cgc ctc aag  gag ctg gag tcc cag  gtg tcg ggt      3384
Gln Gln  Gln Thr Arg Leu Lys  Glu Leu Glu Ser Gln  Val Ser Gly
    1115                1120                1125

ctg gag  aag gag gcc atc gag  ctc agg gag gcc gtg  gag cag cag      3429
Leu Glu  Lys Glu Ala Ile Glu  Leu Arg Glu Ala Val  Glu Gln Gln
    1130                1135                1140

aaa gtg  aag aac aat gac ctc  cgg gag aag aac tgg  aag gcc atg      3474
Lys Val  Lys Asn Asn Asp Leu  Arg Glu Lys Asn Trp  Lys Ala Met
    1145                1150                1155

gag gca  ctg gcc acg gcc gag  cag gcc tgc aag gag  aag ctg cac      3519
Glu Ala  Leu Ala Thr Ala Glu  Gln Ala Cys Lys Glu  Lys Leu His
    1160                1165                1170

tcc ctg  acc cag gcc aag gag  gaa tcg gag aag cag  ctc tgt ctg      3564
Ser Leu  Thr Gln Ala Lys Glu  Glu Ser Glu Lys Gln  Leu Cys Leu
    1175                1180                1185

att gag  gcg cag acc atg gag  gcc ctg ctg gct ctg  ctc cca gaa      3609
Ile Glu  Ala Gln Thr Met Glu  Ala Leu Leu Ala Leu  Leu Pro Glu
    1190                1195                1200

ctc tct  gtc ttg gca caa cag  aat tac acc gag tgg  ctg cag gat      3654
Leu Ser  Val Leu Ala Gln Gln  Asn Tyr Thr Glu Trp  Leu Gln Asp
    1205                1210                1215

ctc aaa  gag aaa ggc ccc acg  ctg ctg aag cac ccg  cca gct ccc      3699
Leu Lys  Glu Lys Gly Pro Thr  Leu Leu Lys His Pro  Pro Ala Pro
    1220                1225                1230
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gcg gag  cct tcc tcg gac ctg  gcc tcc aag ttg agg  gag gcc gag      3744
Ala Glu  Pro Ser Ser Asp Leu  Ala Ser Lys Leu Arg  Glu Ala Glu
    1235                 1240                 1245

gag acg  cag agc aca ctg cag  gcc gag tgt gac cag  tac cgc agc      3789
Glu Thr  Gln Ser Thr Leu Gln  Ala Glu Cys Asp Gln  Tyr Arg Ser
    1250                 1255                 1260

atc ctg  gcg gag acg gag ggc  atg ctc aga gac ctg  cag aag agc      3834
Ile Leu  Ala Glu Thr Glu Gly  Met Leu Arg Asp Leu  Gln Lys Ser
    1265                 1270                 1275

gtg gag  gag gag gag cag gtg  tgg agg gcc aag gtg  ggc gcc gca      3879
Val Glu  Glu Glu Glu Gln Val  Trp Arg Ala Lys Val  Gly Ala Ala
    1280                 1285                 1290

gag gag  gag ctc cag aag tcc  cgg gtc aca gtg aag  cat ctc gaa      3924
Glu Glu  Glu Leu Gln Lys Ser  Arg Val Thr Val Lys  His Leu Glu
    1295                 1300                 1305

gag att  gta gag aag cta aaa  gga gaa ctt gaa agt  tcg gac cag      3969
Glu Ile  Val Glu Lys Leu Lys  Gly Glu Leu Glu Ser  Ser Asp Gln
    1310                 1315                 1320

gtg agg  gag cac acg tcg cat  ttg gag gca gag ctg  gaa aag cac      4014
Val Arg  Glu His Thr Ser His  Leu Glu Ala Glu Leu  Glu Lys His
    1325                 1330                 1335

atg gcg  gcc gcc agc gcc gag  tgc cag aac tac gcc  aag gag gtg      4059
Met Ala  Ala Ala Ser Ala Glu  Cys Gln Asn Tyr Ala  Lys Glu Val
    1340                 1345                 1350

gca ggg  ctg agg caa ctt ctc  cta gaa tct caa tct  cag ctc gat      4104
Ala Gly  Leu Arg Gln Leu Leu  Leu Glu Ser Gln Ser  Gln Leu Asp
    1355                 1360                 1365

gcc gcc  aag agc gaa gcc cag  aaa cag agc gat gag  ctt gcc ctg      4149
Ala Ala  Lys Ser Glu Ala Gln  Lys Gln Ser Asp Glu  Leu Ala Leu
    1370                 1375                 1380

gtc agg  cag cag ttg agt gaa  atg aag agc cac gtg  gag gat ggt      4194
Val Arg  Gln Gln Leu Ser Glu  Met Lys Ser His Val  Glu Asp Gly
    1385                 1390                 1395

gac att  gct ggg gcc cca gct  tcc tcc cca gag gcg  ccc cca gcc      4239
Asp Ile  Ala Gly Ala Pro Ala  Ser Ser Pro Glu Ala  Pro Pro Ala
    1400                 1405                 1410

gag cag  gac ccc gtt cag ctg  aag acg cag ctg gag  tgg acg gaa      4284
Glu Gln  Asp Pro Val Gln Leu  Lys Thr Gln Leu Glu  Trp Thr Glu
    1415                 1420                 1425

gcc atc  ctg gag gat gag cag  aca cag cgg cag aag  ctc acg gcc      4329
Ala Ile  Leu Glu Asp Glu Gln  Thr Gln Arg Gln Lys  Leu Thr Ala
    1430                 1435                 1440

gag ttt  gag gag gct cag acc  tcg gca tgt cgg tta  caa gaa gaa      4374
Glu Phe  Glu Glu Ala Gln Thr  Ser Ala Cys Arg Leu  Gln Glu Glu
    1445                 1450                 1455

ttg gag  aag ctc cgc aca gcc  ggc ccc cta gag tct  tca gaa aca      4419
Leu Glu  Lys Leu Arg Thr Ala  Gly Pro Leu Glu Ser  Ser Glu Thr
    1460                 1465                 1470

gag gag  gcc tca cag ctg aag  gag aga cta gaa aaa  gag aag aag      4464
Glu Glu  Ala Ser Gln Leu Lys  Glu Arg Leu Glu Lys  Glu Lys Lys
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tta aca  agt gac ctg ggg cgc  gcc gcc acg aga ctg  cag gag ctt      4509
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    1490                 1495                 1500

ctg aag  acg acc cag gag cag  ctg gca agg gag aag  gac acg gtg      4554
Leu Lys  Thr Thr Gln Glu Gln  Leu Ala Arg Glu Lys  Asp Thr Val
    1505                 1510                 1515

aag aag  ctg cag gaa cag ctg  gaa aag gca gag gac  ggc agc agc      4599
Lys Lys  Leu Gln Glu Gln Leu  Glu Lys Ala Glu Asp  Gly Ser Ser
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    1535                 1540
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            20                  25                  30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
        35                  40                  45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
    50                  55                  60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
                85                  90                  95

Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
            100                 105                 110

Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
        115                 120                 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
    130                 135                 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145                 150                 155                 160

Gln Val Leu Thr Ser Lys Ala Ala Ile Leu Glu Thr Ala Pro Lys Glu
                165                 170                 175
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Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro
            180                 185                 190

Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
        195                 200                 205

Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
    210                 215                 220

Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
225                 230                 235                 240

Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
                245                 250                 255

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
            260                 265                 270

Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
        275                 280                 285

Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly
    290                 295                 300

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
305                 310                 315                 320

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                325                 330                 335

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            340                 345                 350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
        355                 360                 365

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
    370                 375                 380

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
385                 390                 395                 400

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                405                 410                 415

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            420                 425                 430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
        435                 440                 445
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Asp Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly
450                 455                 460

Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
465                 470                 475                 480

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
                485                 490                 495

Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala
            500                 505                 510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
        515                 520                 525

Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly
    530                 535                 540

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
545                 550                 555                 560

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
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Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            580                 585                 590

Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln
        595                 600                 605

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
    610                 615                 620

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln
625                 630                 635                 640

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln
                645                 650                 655

Gly Lys Lys Ala Glu Arg Ser Pro Asn Gln Gly Lys Lys Gly Glu Gly
            660                 665                 670

Ala Pro Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr
        675                 680                 685

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

Ser Glu Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala
705                 710                 715                 720
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Asp Ala Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln
                725                 730                 735

Gly Arg Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu
            740                 745                 750

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly
        755                 760                 765

Pro Pro Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val
    770                 775                 780

Ser Thr Val Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu
785                 790                 795                 800

Ile Glu Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His
                805                 810                 815

Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu
            820                 825                 830

Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val
        835                 840                 845

Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys
    850                 855                 860

Ala Lys Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala
865                 870                 875                 880

Arg Glu Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr
                885                 890                 895

Arg Glu His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr
            900                 905                 910

Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu
        915                 920                 925

Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser
    930                 935                 940

Gln Val Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu
945                 950                 955                 960

Leu Ser Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg
                965                 970                 975

Gln Asp Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe
            980                 985                 990
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Glu Lys Gln Val Leu Gln Leu Gln  Ala Ser His Arg Glu  Ser Glu Glu
        995                 1000                1005

Ala Leu  Gln Lys Arg Leu Asp  Glu Val Ser Arg Glu  Leu Cys His
    1010                1015                1020

Thr Gln  Ser Ser His Ala Ser  Leu Arg Ala Asp Ala  Glu Lys Ala
    1025                1030                1035

Gln Glu  Gln Gln Gln Gln Met  Ala Glu Leu His Ser  Lys Leu Gln
    1040                1045                1050

Ser Ser  Glu Ala Glu Val Arg  Ser Lys Cys Glu Glu  Leu Ser Gly
    1055                1060                1065

Leu His  Gly Gln Leu Gln Glu  Ala Arg Ala Glu Asn  Ser Gln Leu
    1070                1075                1080

Thr Glu  Arg Ile Arg Ser Ile  Glu Ala Leu Leu Glu  Ala Gly Gln
    1085                1090                1095

Ala Arg  Asp Ala Gln Asp Val  Gln Ala Ser Gln Ala  Glu Ala Asp
    1100                1105                1110

Gln Gln  Gln Thr Arg Leu Lys  Glu Leu Glu Ser Gln  Val Ser Gly
    1115                1120                1125

Leu Glu  Lys Glu Ala Ile Glu  Leu Arg Glu Ala Val  Glu Gln Gln
    1130                1135                1140

Lys Val  Lys Asn Asn Asp Leu  Arg Glu Lys Asn Trp  Lys Ala Met
    1145                1150                1155

Glu Ala  Leu Ala Thr Ala Glu  Gln Ala Cys Lys Glu  Lys Leu His
    1160                1165                1170

Ser Leu  Thr Gln Ala Lys Glu  Glu Ser Glu Lys Gln  Leu Cys Leu
    1175                1180                1185

Ile Glu  Ala Gln Thr Met Glu  Ala Leu Leu Ala Leu  Leu Pro Glu
    1190                1195                1200

Leu Ser  Val Leu Ala Gln Gln  Asn Tyr Thr Glu Trp  Leu Gln Asp
    1205                1210                1215

Leu Lys  Glu Lys Gly Pro Thr  Leu Leu Lys His Pro  Pro Ala Pro
    1220                1225                1230

Ala Glu  Pro Ser Ser Asp Leu  Ala Ser Lys Leu Arg  Glu Ala Glu
    1235                1240                1245
```

```
Glu Thr  Gln Ser Thr Leu Gln  Ala Glu Cys Asp Gln  Tyr Arg Ser
     1250                 1255                 1260

Ile Leu  Ala Glu Thr Glu Gly  Met Leu Arg Asp Leu  Gln Lys Ser
     1265                 1270                 1275

Val Glu  Glu Glu Glu Gln Val  Trp Arg Ala Lys Val  Gly Ala Ala
     1280                 1285                 1290

Glu Glu  Glu Leu Gln Lys Ser  Arg Val Thr Val Lys  His Leu Glu
     1295                 1300                 1305

Glu Ile  Val Glu Lys Leu Lys  Gly Glu Leu Glu Ser  Ser Asp Gln
     1310                 1315                 1320

Val Arg  Glu His Thr Ser His  Leu Glu Ala Glu Leu  Glu Lys His
     1325                 1330                 1335

Met Ala  Ala Ala Ser Ala Glu  Cys Gln Asn Tyr Ala  Lys Glu Val
     1340                 1345                 1350

Ala Gly  Leu Arg Gln Leu Leu  Leu Glu Ser Gln Ser  Gln Leu Asp
     1355                 1360                 1365

Ala Ala  Lys Ser Glu Ala Gln  Lys Gln Ser Asp Glu  Leu Ala Leu
     1370                 1375                 1380

Val Arg  Gln Gln Leu Ser Glu  Met Lys Ser His Val  Glu Asp Gly
     1385                 1390                 1395

Asp Ile  Ala Gly Ala Pro Ala  Ser Ser Pro Glu Ala  Pro Pro Ala
     1400                 1405                 1410

Glu Gln  Asp Pro Val Gln Leu  Lys Thr Gln Leu Glu  Trp Thr Glu
     1415                 1420                 1425

Ala Ile  Leu Glu Asp Glu Gln  Thr Gln Arg Gln Lys  Leu Thr Ala
     1430                 1435                 1440

Glu Phe  Glu Glu Ala Gln Thr  Ser Ala Cys Arg Leu  Gln Glu Glu
     1445                 1450                 1455

Leu Glu  Lys Leu Arg Thr Ala  Gly Pro Leu Glu Ser  Ser Glu Thr
     1460                 1465                 1470

Glu Glu  Ala Ser Gln Leu Lys  Glu Arg Leu Glu Lys  Glu Lys Lys
     1475                 1480                 1485

Leu Thr  Ser Asp Leu Gly Arg  Ala Ala Thr Arg Leu  Gln Glu Leu
     1490                 1495                 1500
```

```
Leu Lys  Thr Thr Gln Glu Gln  Leu Ala Arg Glu Lys  Asp Thr Val
    1505                 1510                 1515

Lys Lys  Leu Gln Glu Gln Leu  Glu Lys Ala Glu Asp  Gly Ser Ser
    1520                 1525                 1530

Ser Lys  Glu Gly Thr Ser Val
    1535                 1540
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<210> 3
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1275)

<400> 3

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atg gct gcc ggg ccg atc tcc gag cgg aat cag gat gcc act gtg tac       48
Met Ala Ala Gly Pro Ile Ser Glu Arg Asn Gln Asp Ala Thr Val Tyr
1               5                  10                  15

gtg ggg ggc ctg gat gag aag gtt agt gaa ccg ctg ctg tgg gaa ctg       96
Val Gly Gly Leu Asp Glu Lys Val Ser Glu Pro Leu Leu Trp Glu Leu
            20                  25                  30

ttt ctc cag gct gga cca gta gtc aac acc cac atg cca aag gat aga      144
Phe Leu Gln Ala Gly Pro Val Val Asn Thr His Met Pro Lys Asp Arg
        35                  40                  45

gtc act ggc cag cac caa ggc tat ggc ttt gtg gaa ttc ttg agt gag      192
Val Thr Gly Gln His Gln Gly Tyr Gly Phe Val Glu Phe Leu Ser Glu
    50                  55                  60

gaa gat gct gac tat gcc att aag atc atg aac atg atc aaa ctc tat      240
Glu Asp Ala Asp Tyr Ala Ile Lys Ile Met Asn Met Ile Lys Leu Tyr
65                  70                  75                  80

ggg aag cca ata cgg gtg aac aaa gca tca gct cac aac aaa aac ctg      288
Gly Lys Pro Ile Arg Val Asn Lys Ala Ser Ala His Asn Lys Asn Leu
                85                  90                  95

gat gta ggg gcc aac att ttc att ggg aac ctg gac cct gag att gat      336
Asp Val Gly Ala Asn Ile Phe Ile Gly Asn Leu Asp Pro Glu Ile Asp
            100                 105                 110

gag aag ttg ctt tat gat act ttc agc gcc ttt ggg gtc atc tta caa      384
Glu Lys Leu Leu Tyr Asp Thr Phe Ser Ala Phe Gly Val Ile Leu Gln
        115                 120                 125

acc ccc aaa att atg cgg gac cct gac aca ggc aac tcc aaa ggt tat      432
Thr Pro Lys Ile Met Arg Asp Pro Asp Thr Gly Asn Ser Lys Gly Tyr
    130                 135                 140

gcc ttt att aat ttt gct tca ttt gat gct tcg gat gca gca att gaa      480
Ala Phe Ile Asn Phe Ala Ser Phe Asp Ala Ser Asp Ala Ala Ile Glu
145                 150                 155                 160

gcc atg aat ggg cag tac ctc tgt aac cgt cct atc acc gta tct tat      528
Ala Met Asn Gly Gln Tyr Leu Cys Asn Arg Pro Ile Thr Val Ser Tyr
                165                 170                 175
```

```
gcc ttc aag aag gac tcc aag ggt gag cgc cat ggc tca gca gcc gaa      576
Ala Phe Lys Lys Asp Ser Lys Gly Glu Arg His Gly Ser Ala Ala Glu
            180                 185                 190

cga ctt ctg gca gct cag aac ccg ctc tcc cag gct gat cgc cct cat      624
Arg Leu Leu Ala Ala Gln Asn Pro Leu Ser Gln Ala Asp Arg Pro His
        195                 200                 205

cag ctg ttt gca gat gca cct cct cca ccc tct gct ccc aat cct gtg      672
Gln Leu Phe Ala Asp Ala Pro Pro Pro Pro Ser Ala Pro Asn Pro Val
    210                 215                 220

gta tca tca ttg ggg tct ggg ctt cct cca cca ggc atg cct cct cct      720
Val Ser Ser Leu Gly Ser Gly Leu Pro Pro Pro Gly Met Pro Pro Pro
225                 230                 235                 240

ggc tcc ttc cca ccc cca gtg cca cct cct gga gcc ctc cca cct ggg      768
Gly Ser Phe Pro Pro Pro Val Pro Pro Pro Gly Ala Leu Pro Pro Gly
                245                 250                 255

ata ccc cca gcc atg ccc cca cca cct atg cct cct ggg gct gca gga      816
Ile Pro Pro Ala Met Pro Pro Pro Pro Met Pro Pro Gly Ala Ala Gly
            260                 265                 270

cat ggc ccc cca tcg gca gga acc cca ggg gca gga cat cct ggt cat      864
His Gly Pro Pro Ser Ala Gly Thr Pro Gly Ala Gly His Pro Gly His
        275                 280                 285

gga cac tca cat cct cac cca ttc cca ccg ggt ggg atg ccc cat cca      912
Gly His Ser His Pro His Pro Phe Pro Pro Gly Gly Met Pro His Pro
    290                 295                 300

ggg atg tct cag atg cag ctt gca cac cat ggc cct cat ggc tta gga      960
Gly Met Ser Gln Met Gln Leu Ala His His Gly Pro His Gly Leu Gly
305                 310                 315                 320

cat ccc cac gct gga ccc cca ggc tct ggg ggc cag cca ccg ccc cga     1008
His Pro His Ala Gly Pro Pro Gly Ser Gly Gly Gln Pro Pro Pro Arg
                325                 330                 335

cca cca cct gga atg cct cat cct gga cct cct cca atg ggc atg ccc     1056
Pro Pro Pro Gly Met Pro His Pro Gly Pro Pro Pro Met Gly Met Pro
            340                 345                 350

ccc cga ggg cct cca ttc gga tct ccc atg ggt cac cca ggt cct atg     1104
Pro Arg Gly Pro Pro Phe Gly Ser Pro Met Gly His Pro Gly Pro Met
        355                 360                 365

cct ccg cat ggt atg cgt gga cct cct cca ctg atg ccc ccc cat gga     1152
Pro Pro His Gly Met Arg Gly Pro Pro Pro Leu Met Pro Pro His Gly
    370                 375                 380

tac act ggc cct cca cga ccc cca ccc tat ggc tac cag cgg ggg cct     1200
Tyr Thr Gly Pro Pro Arg Pro Pro Pro Tyr Gly Tyr Gln Arg Gly Pro
385                 390                 395                 400

ctc cct cca ccc aga ccc act ccc cgg cca cca gtt ccc cct cga ggc     1248
Leu Pro Pro Pro Arg Pro Thr Pro Arg Pro Pro Val Pro Pro Arg Gly
                405                 410                 415

cca ctt cga ggc cct ctc cct cag taa                                1275
Pro Leu Arg Gly Pro Leu Pro Gln
            420
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<210> 4
<211> 424
<212> PRT

<213> Homo sapiens

<400> 4

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Met Ala Ala Gly Pro Ile Ser Glu Arg Asn Gln Asp Ala Thr Val Tyr
1               5                  10                  15

Val Gly Gly Leu Asp Glu Lys Val Ser Glu Pro Leu Leu Trp Glu Leu
            20                  25                  30

Phe Leu Gln Ala Gly Pro Val Val Asn Thr His Met Pro Lys Asp Arg
        35                  40                  45

Val Thr Gly Gln His Gln Gly Tyr Gly Phe Val Glu Phe Leu Ser Glu
    50                  55                  60

Glu Asp Ala Asp Tyr Ala Ile Lys Ile Met Asn Met Ile Lys Leu Tyr
65                  70                  75                  80

Gly Lys Pro Ile Arg Val Asn Lys Ala Ser Ala His Asn Lys Asn Leu
                85                  90                  95

Asp Val Gly Ala Asn Ile Phe Ile Gly Asn Leu Asp Pro Glu Ile Asp
            100                 105                 110

Glu Lys Leu Leu Tyr Asp Thr Phe Ser Ala Phe Gly Val Ile Leu Gln
        115                 120                 125

Thr Pro Lys Ile Met Arg Asp Pro Asp Thr Gly Asn Ser Lys Gly Tyr
    130                 135                 140

Ala Phe Ile Asn Phe Ala Ser Phe Asp Ala Ser Asp Ala Ala Ile Glu
145                 150                 155                 160

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

Ala Phe Lys Lys Asp Ser Lys Gly Glu Arg His Gly Ser Ala Ala Glu
            180                 185                 190

Arg Leu Leu Ala Ala Gln Asn Pro Leu Ser Gln Ala Asp Arg Pro His
        195                 200                 205

Gln Leu Phe Ala Asp Ala Pro Pro Pro Pro Ser Ala Pro Asn Pro Val
    210                 215                 220

Val Ser Ser Leu Gly Ser Gly Leu Pro Pro Pro Gly Met Pro Pro Pro
225                 230                 235                 240

Gly Ser Phe Pro Pro Pro Val Pro Pro Pro Gly Ala Leu Pro Pro Gly
                245                 250                 255
```

```
Ile Pro Pro Ala Met Pro Pro Pro Pro Met Pro Pro Gly Ala Ala Gly
            260                 265                 270

His Gly Pro Pro Ser Ala Gly Thr Pro Gly Ala Gly His Pro Gly His
        275                 280                 285

Gly His Ser His Pro His Pro Phe Pro Pro Gly Gly Met Pro His Pro
    290                 295                 300

Gly Met Ser Gln Met Gln Leu Ala His His Gly Pro His Gly Leu Gly
305                 310                 315                 320

His Pro His Ala Gly Pro Pro Gly Ser Gly Gly Gln Pro Pro Pro Arg
                325                 330                 335

Pro Pro Pro Gly Met Pro His Pro Gly Pro Pro Pro Met Gly Met Pro
            340                 345                 350

Pro Arg Gly Pro Pro Phe Gly Ser Pro Met Gly His Pro Gly Pro Met
        355                 360                 365

Pro Pro His Gly Met Arg Gly Pro Pro Pro Leu Met Pro Pro His Gly
    370                 375                 380

Tyr Thr Gly Pro Pro Arg Pro Pro Pro Tyr Gly Tyr Gln Arg Gly Pro
385                 390                 395                 400

Leu Pro Pro Pro Arg Pro Thr Pro Arg Pro Pro Val Pro Pro Arg Gly
                405                 410                 415

Pro Leu Arg Gly Pro Leu Pro Gln
            420
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<210> 5
<211> 126
<212> DNA
<213> Homo sapiens

<400> 5
tcgtcggagc agacgggagt ttctcctcgg ggtcggagca ggaggcacgc ggagtgtgag 60

gccacgcatg agcggacgct aacccccctcc ccagccacaa agagtctaca tgtctagggt 120

ctagac 126

<210> 6
<211> 266
<212> DNA
<213> Homo sapiens

<400> 6
gcccgcgccg gctgtgctgc acaggggggag gagagggaac cccaggcgcg agcgggaaga 60

ggggacctgc agccacaact tctctggtcc tctgcatccc ttctgtccct ccacccgtcc 120

ccttccccac cctctggccc ccaccttctt ggaggcgaca acccccggga ggcattagaa 180

ggattttttc ccgcaggttg cgaagggaag caaacttggt ggcaacttgc ctcccggtgc 240

gggcgtctct cccccaccgt ctcaac 266

<210> 7
<211> 27
<212> DNA
<213> Homo sapiens

<400> 7
tcgtcggagc agacgggagt ttctcct 27

<210> 8
<211> 32
<212> DNA
<213> Homo sapiens

<400> 8
ccaccttctt ggaggcgaca acccccggga gg 32

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #3.

<400> 9
gatcttcgtc ggagcagacg ggagtttctc cta 33

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #3.

<400> 10
agcttaggag aaactcccgt ctgctccgac gaa 33

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #4.

<400> 11
gatcttctgc atcccttctg tccctccaca 30

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #4.

<400> 12
agcttgtgga gggacagaag ggatgcagaa 30

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #2.

<400> 13
aaaaaaagat ctgcccgcgc cggctgt 27

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #2.

<400> 14
aaaaaaaagc ttgttgagac ggtgggggga 29

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #1.

<400> 15
aaaaaaagat cttcgtcgga gcagacg 27

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #1.

<400> 16
aaaaaaaagc ttgtctagac cctagac 27

<210> 17
<211> 9
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (4)..(6)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> "v" is a or g or c.

<400> 17
gagnnnacv 9

<210> 18
<211> 10
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)..(7)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> "v" is a or g or c.

<400> 18
gagnnnnacv 10

<210> 19
<211> 11
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (4)..(8)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> "v" is a or g or c.

<400> 19
gagnnnnnac v 11

<210> 20
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (4)..(9)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> "r" is a or g

<220>
<221> misc_feature
<222> (12)..(12)
<223> "v" is a or g or c.

<400> 20
gagnnnnnna cv 12

<210> 21
<211> 60
<212> DNA
<213> Homo sapiens

<400> 21
tcgtcggagc agacgggagt ttctcctcgg ggtcggagca ggaggcacgc ggagtgtgag 60

<210> 22
<211> 66
<212> DNA
<213> Homo sapiens

<400> 22
gccacgcatg agcggacgct aacccccctcc ccagccacaa agagtctaca tgtctagggt 60

ctagac 66

<210> 23
<211> 181
<212> DNA
<213> Homo sapiens

<400> 23
aacgggcgcc gcggcgggga gaagacgcag agcgctgctg ggctgccggg tctcccgctt 60

ccccctcctg ctccaagggc ctcctgcatg agggcgcggt agagacccgg acccgcgccg 120

tgctcctgcc gtttcgctgc gctccgcccg ggcccggctc agccaggccc cgcggtgagc 180

c 181

<210> 24
<211> 30
<212> DNA
<213> Homo sapiens

<400> 24
caggggggagg agagggaacc ccaggcgcga 30

<210> 25
<211> 32
<212> DNA
<213> Homo sapiens

<400> 25
gagcgggaag aggggacctg cagccacaac tt 32

<210> 26
<211> 60
<212> DNA
<213> Homo sapiens

<400> 26

caggggggagg agagggaacc ccaggcgcga gcgggaagag gggacctgca gccacaactt 60

<210> 27
<211> 113
<212> DNA
<213> Homo sapiens

<400> 27
tcgtcggagc agacgggagt ttctcctcgg ggtcggagca ggaggcacgc ggagtgtgag 60

gccacgcatg agcggacgct aacccccctcc ccagccacaa agagtctaca tgt 113

<210> 28
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #5.

<400> 28
aaaaaaagat cttcgtcgga gcagacggga gt 32

<210> 29
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #5.

<400> 29
aaaaaaaagc ttctcacact ccgcgtgcct cc 32

<210> 30
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #6.

<400> 30
aaaaaaagat ctgccacgca tgagcggacg ct 32

<210> 31
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #6.

<400> 31
aaaaaaaagc ttgtctagac cctagacatg ta 32

<210> 32
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #8.

<400> 32
gatctcaggg ggaggagagg gaaccccagg cgcgaa 36

<210> 33
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #8.

<400> 33
agctttcgcg cctggggttc cctcctcctcc ccctga 36

<210> 34
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #9.

<400> 34
gatctgagcg ggaagagggg acctgcagcc acaactta 38

<210> 35
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #9.

<400> 35
agcttaagtt gtggctgcag gtcccctctt cccgctca 38

<210> 36
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #10.

<400> 36
gatctcaggg ggaggagagg gaaccccagg cgcgagcggg aagaggggac ctgcagccac 60

aactta 66

<210> 37
<211> 66
<212> DNA

<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #10.

<400> 37
agcttaagtt gtggctgcag gtcccctctt cccgctcgcg cctggggttc cctctcctcc 60

ccctga 66

<210> 38
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #11.

<400> 38
aaaaaaagat cttcgtcgga gcagacggga gt 32

<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #11.

<400> 39
aaaaaaaagc ttacatgtag actctttgtg gc 32

CLAIMS

1. A recombinant cell having enhanced intracellular expression of the full length or a portion of p180 protein, or a protein promoting mRNA localization to an endoplasmic reticulum (ER), or both of said proteins, and having enhanced intracellular synthetic or secretory capacity of a protein as a product of interest.

2. The recombinant cell according to claim 1, wherein the p180 protein is selected from the group consisting of:

(a) a protein that consists of an amino acid sequence with at least 70% sequence identity to the amino acid sequence (SEQ ID NO: 2) of human-derived p180 protein, and which has a capability of promoting polysome formation on an intracellular endoplasmic reticulum membrane;

(b) a protein that consists of an amino acid sequence derived from the amino acid sequence (SEQ ID NO: 2) of the human-derived p180 protein by deletion, substitution, or addition of one or more amino acids, and which has a capability of promoting polysome formation on the intracellular endoplasmic reticulum membrane;

(c) a protein that consists of an amino acid sequence specified by a nucleotide sequence with at least 70% sequence identity to the nucleotide sequence (SEQ ID NO: 1) of a gene encoding the human-derived p180 protein, and which has a capability of promoting polysome formation on the intracellular endoplasmic reticulum membrane;

(d) a protein that consists of an amino acid sequence specified by a nucleotide sequence derived from the nucleotide sequence (SEQ ID NO: 1) of the gene encoding the human-derived p180 protein by deletion, substitution, or addition of one or more nucleotides, and which has a capability of promoting polysome formation on the intracellular endoplasmic reticulum membrane; and

(e) a protein that consists of an amino acid sequence specified by a nucleotide sequence hybridizable under stringent conditions with a nucleotide sequence complementary to the nucleotide sequence (SEQ ID NO: 1) of the gene encoding the human-derived p180

protein, and which has a capability of promoting polysome formation on the intracellular endoplasmic reticulum membrane.

3. The recombinant cell according to claim 1 or 2, wherein the p180 protein is derived from a mammalian animal.

4. The recombinant cell according to claim 3, wherein the full length or the portion of the mammalian p180 protein is the human p180 protein (SEQ ID NO: 2), murine p180 protein (GenBank Accession No. NP_077243), rat p180 protein (GenBank Accession No. XP_230637), Chinese hamster p180 protein (GenBank Accession No. XM_003496471), canine p180 protein (GenBank Accession No. NP_001003179), equine p180 protein (GenBank Accession No. XP_001915027), simian p180 protein (GenBank Accession No. XP_002798281), chimpanzee p180 protein (GenBank Accession No. XP_514527), porcine p180 protein (GenBank Accession No. XP_001926148), or a portion thereof.

5. The recombinant cell according to any one of claims 1 to 4, wherein the portion of the p180 protein is selected from: a portion comprising an amino acid sequence corresponding to a region consisting of the amino acids at positions 27 to 157 of a protein having the amino acid sequence of SEQ ID NO: 2 (human p180 protein); a portion comprising an amino acid sequence corresponding to a region consisting of the amino acids at positions 623 to 737 of said protein; an amino acid sequence corresponding to a region consisting of the amino acids at positions 738 to 944 of said protein; and a portion comprising an amino acid sequence corresponding to a region consisting of the amino acids at positions 945 to 1540 of said protein.

6. The recombinant cell according to any one of claims 1 to 5, wherein the protein promoting mRNA localization to the endoplasmic reticulum (ER) is selected from the group consisting of the full length or a portion of splicing factor 3B subunit 4 (SF3b4) protein (the full-length amino acid sequence 424 AA of SEQ ID NO: 4; RRM1 consisting of 13 to 91 AA of SEQ ID NO: 4; and RRM2 consisting of 100 of SEQ ID NO: 4).

7. The recombinant cell according to claim 6, wherein the SF3b4 protein is selected from the group consisting of:

(i) a protein that consists of an amino acid sequence with at least 70% sequence identity to the amino acid sequence (SEQ ID NO: 4) of human-derived SF3b4 protein, and which has a capability of promoting mRNA localization to the endoplasmic reticulum;

(ii) a protein that consists of an amino acid sequence derived from the amino acid sequence (SEQ ID NO: 4) of the human-derived SF3b4 protein by deletion, substitution, or addition of one or more amino acids, and which has a capability of promoting mRNA localization to the endoplasmic reticulum;

(iii) a protein that consists of an amino acid sequence specified by a nucleotide sequence with at least 70% sequence identity to the nucleotide sequence (SEQ ID NO: 3) of a gene encoding the human-derived SF3b4 protein, and which has a capability of promoting mRNA localization to the endoplasmic reticulum;

(iv) a protein that consists of an amino acid sequence specified by a nucleotide sequence derived from the nucleotide sequence (SEQ ID NO: 3) of the gene encoding the human-derived SF3b4 protein by deletion, substitution, or addition of one or more nucleotides, and which has a capability of promoting mRNA localization to the endoplasmic reticulum; and

(v) a protein that consists of an amino acid sequence specified by a nucleotide sequence hybridizable under stringent conditions with a nucleotide sequence complementary to the nucleotide sequence (SEQ ID NO: 3) of the gene encoding the human-derived SF3b4 protein, and which has a capability of promoting mRNA localization to the endoplasmic reticulum.

8. The recombinant cell according to claim 6 or 7, wherein the SF3b4 protein is derived from a mammalian animal.

9. The recombinant cell according to claim 8, wherein the full length or the portion of mammalian SF3b4 protein is the human SF3b4 protein (SEQ ID NO: 4), murine SF3b4 protein (GenBank Accession No. NP_694693.1), rat SF3b4 protein (GenBank Accession No. NP_001011951.1), Chinese hamster SF3b4 protein (GenBank Accession No. XP_003498680.1), canine SF3b4 protein (GenBank Accession No. XP_540295.3),

equine SF3b4 protein (GenBank Accession No. XP_001488649.2), simian SF3b4 protein (GenBank Accession No. NP_001097793.1), chimpanzee SF3b4 protein (GenBank Accession No. XP_513768.2), porcine SF3b4 protein (GenBank Accession No. XP_001926524.1), or a portion thereof.

10. The recombinant cell according to any one of claims 1 to 9, wherein the synthetic or secretory capacity of the protein as a product of interest is enhanced by transforming a nucleic acid molecule encoding the protein as a product of interest or increasing production of the protein as a product of interest.

11. A cell line designated by Accession No. NITE BP-01753 (CHO 3D5), Accession No. NITE BP-1535 (CHO YA7), or Accession No. NITE ABP-01811 (CHO 1B2).

12. A method for producing a protein as a product of interest, wherein, in a recombinant cell having enhanced expression of the full length or a portion of p180 protein, a protein promoting mRNA localization to an endoplasmic reticulum (ER), or both of said proteins, a nucleic acid molecule encoding the protein as a product of interest is transformed or production of the protein as a product of interest is increased, whereby the protein as a product of interest is produced.

13. The method according to claim 12, wherein the p180 protein is derived from a mammalian animal.

14. The method according to claim 13, wherein the full length or the portion of the mammalian p180 protein is human p180 protein (SEQ ID NO: 2), murine p180 protein (GenBank Accession No. NP_077243), rat p180 protein (GenBank Accession No. XP_230637), Chinese hamster p180 protein (GenBank Accession No. XM_003496471), canine p180 protein (GenBank Accession No. NP_001003179), equine p180 protein (GenBank Accession No. XP_001915027), simian p180 protein (GenBank Accession No. XP_002798281), chimpanzee p180 protein (GenBank Accession No. XP_514527), porcine p180 protein (GenBank Accession No. XP_001926148), or a portion thereof.

15. The method according to claim 13 or 14, wherein the portion of the mammalian p180 protein is selected from: a portion comprising a region consisting of the amino acids at

positions 27 to 157 of a protein having the amino acid sequence of SEQ ID NO: 2 (human p180 protein); a portion comprising a region consisting of the amino acids at positions 623 to 737 of said protein; a portion comprising a region consisting of the amino acids at positions 738 to 944 of said protein; and a portion comprising a region consisting of the amino acids at positions 945 to 1540 of said protein.

16. The method according to any one of claims 12 to 15, wherein the protein promoting mRNA localization to the endoplasmic reticulum (ER) is selected from the group consisting of the full length or a portion of splicing factor 3B subunit 4 (SF3b4) protein (the full-length amino acid sequence 424 AA of SEQ ID NO: 4; RRM1 consisting of 13 to 91 AA of SEQ ID NO: 4; and RRM2 consisting of 100 of SEQ ID NO: 4).

17. The method according to claim 16, wherein the SF3b4 protein is derived from a mammalian animal.

18. The method according to claim 17, wherein the full length or the portion of mammalian SF3b4 protein is the human SF3b4 protein (SEQ ID NO: 4), murine SF3b4 protein (GenBank Accession No. NP_694693.1), rat SF3b4 protein (GenBank Accession No. NP_001011951.1), Chinese hamster SF3b4 protein (GenBank Accession No. XP_003498680.1), canine SF3b4 protein (GenBank Accession No. XP_540295.3), equine SF3b4 protein (GenBank Accession No. XP_001488649.2), simian SF3b4 protein (GenBank Accession No. NP_001097793.1), chimpanzee SF3b4 protein (GenBank Accession No. XP_515768.2), porcine SF3b4 protein (GenBank Accession No. XP_001926524.1), or a portion thereof.

19. The method according to any one of claims 12 to 18, wherein the recombinant cell is a cell line designated by Accession No. NITE BP-01753 (CHO 3D5), Accession No. NITE BP-1538 (CHO YA7), or Accession No. NITE ABP-01811 (CHO 1B2).

20. The method according to any one of claims 12 to 19, wherein the protein as a product of interest is a glycoprotein.

21. The method according to claim 20, wherein the protein as a product of interest is a collagen, a fibronectin, or an antibody.

22. A method for increasing an amount of a protein as a product of interest to be expressed in a cell as an expression system, wherein, in an expression unit for expressing the protein as a product of interest, a cic-element to be recognized/bound (or interacted with) by an RNA-binding protein is inserted, downstream of a promoter and upstream of the start codon in the nucleotide sequence of a DNA encoding the protein as a product of interest, whereby the amount of the protein as a product of interest to be expressed in the cell as an expression system is increased.

23. The method according to claim 22, wherein the cis-element is to be recognized/bound (or interacted with) by an RNA recognition motif (RRM)-type RNA-binding protein.

24. The method according to claim 23, wherein the cis-element is to be recognized/bound (or interacted with) by an RNA recognition motif (RRM) of the SF3b4 protein.

25. The method according to any one of claims 22 to 24, wherein the cis-element has a nucleotide sequence containing one or more 9mer to 12mer sequence motifs GAN_1-$(X)_n$-ACN_2 (n = 3 to 6) (N_1 and N_2 can be independently any of the nucleotides A, T, C and G).

26. The method according to claim 25, wherein the cis-element has a nucleotide sequence containing one or more 9mer to 12mer sequence motifs GAG-$(X)_n$-ACV (n = 3 to 6) (V represents A, G or C), SEQ ID NOs: 17 to 20.

27. The method according to any one of claims 22 to 26, wherein the nucleotide sequence of the cis-element is a sequence selected from the group consisting of: a sequence derived from the nucleotide sequence of the 5' untranslated region of a type I collagen gene; a sequence derived from the nucleotide sequence of the 5' untranslated region of a fibronectin gene; a sequence derived from the nucleotide sequence of the 5' untranslated region of the matrix metalloproteinase 14 (MMP14) gene; a sequence derived from the nucleotide sequence of the 5' untranslated region of the prolyl 4-hydroxylase A2 (P4HA2) gene; and a sequence derived from the nucleotide sequence of the 5' untranslated region of the prolyl 4-hydroxylase A1 (P4HA1) gene.

28. The method according to any one of claims 22 to 27, wherein the nucleotide sequence of the cis-element is any sequence selected from the group consisting of the full length of SEQ ID NO: 5 or the full length of SEQ ID NO: 7, and the nucleotides at positions 1 to 102, positions 1 to 78, positions 1 to 60, positions 61 to 126, positions 16 to 57, positions 79 to 126, positions 103 to 126, positions 58 to 78, positions 51 to 78, positions 1 to 27, and positions 70 to 78 of SEQ ID NO: 5.

29. The method according to any one of claims 22 to 28, wherein the cell as an expression system is an intact host cell, a cell having enhanced expression of the full length or a portion of p180 protein, a cell having enhanced expression of the full length or a portion of SF3b4 protein, or a cell having enhanced expression of both of said proteins.

30. A medicinal composition for suppressing collagen synthesis and preventing the alveolar epithelium and aggravation of fibrosis due to abnormal collagen through functional inhibition or expression suppression of SF3b4.

SEQUENCE LISTING

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            20                  25                  30

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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

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Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
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Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
            100                 105                 110

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

gtg ccg atg gtg gtg gtg ccc cca gtg ggt gcc aag ggc aac aca cca          576
Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro
            180                 185                 190

gcc act ggc act act cag ggc aaa aag gcg gag ggg act cag aat caa          624
Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
        195                 200                 205

agc aaa aag gct gaa gga gcc cca aac cag ggc aga aag gca gag gga          672
Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
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acc cca aac cag ggc aaa aag aca gag gga acc cca aac caa ggg aaa          720
Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
225                 230                 235                 240

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Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
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Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
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Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly
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gcc cag aac cag ggc aaa aag gca gag ggg gcc cag aat cag ggc aaa          960
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
305                 310                 315                 320

aag gga gag ggg gcc cag aac cag ggc aag aag gcc gag ggg gcc cag         1008
Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                325                 330                 335

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Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            340                 345                 350

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Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
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Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
385                 390                 395                 400

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Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
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gag ggg gcc cag aac cag ggc aag aag gcc gag ggg gcc cag aac cag        1344
Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
        435                 440                 445

gac aag aag gcc gag ggg gcc cag aac cag ggc agg aag gcc gag ggg        1392
Asp Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly
    450                 455                 460

gcc cag aac cag ggc agg aag gcc gag ggg gcc cag aac cag ggc aag        1440
Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
465                 470                 475                 480

aag gcc gag ggg gcc cag aac cag ggc aag aag gcc gag ggg acc ccg        1488
Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
                485                 490                 495

aac cag ggc aag aag gcc gag ggg acc ccg aac cag ggc aag aag gcc        1536
Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala
            500                 505                 510

gag ggg gcc cag aac cag ggc aag aag gcc gag ggg gcc cag aac cag        1584
Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
        515                 520                 525

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Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly
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gcc cag aac cag ggc aag aag gcc gag ggg gcc cag aac cag ggc aag        1680
Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
545                 550                 555                 560

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Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
                565                 570                 575

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Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
            580                 585                 590

gag ggt gct cag aac cag ggc aaa aaa gta gaa ggg gcc cag aac cag        1824
Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln
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Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
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Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln
625                 630                 635                 640

aaa gga gag gga gcc cag aat cag ggt aaa aag aca gaa ggg gct cag        1968
Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln
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Ser Glu Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala
705                 710                 715                 720

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Asp Ala Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln
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Gly Arg Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu
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Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly
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Pro Pro Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val
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785                 790                 795                 800

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Ile Glu Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His
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gaa gag aag gaa aaa ctg ctg gcc aca gaa cag gaa gat gcg gct gtc        2544
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Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys
    850                 855                 860

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Gln Asp Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe
            980                 985                 990

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Thr Gln  Ser Ser His Ala Ser  Leu Arg Ala Asp Ala  Glu Lys Ala
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ctc aaa  gag aaa ggc ccc acg  ctg ctg aag cac ccg  cca gct ccc        3699
Leu Lys  Glu Lys Gly Pro Thr  Leu Leu Lys His Pro  Pro Ala Pro
    1220                 1225                 1230

gcg gag  cct tcc tcg gac ctg  gcc tcc aag ttg agg  gag gcc gag        3744
Ala Glu  Pro Ser Ser Asp Leu  Ala Ser Lys Leu Arg  Glu Ala Glu
    1235                 1240                 1245

gag acg  cag agc aca ctg cag  gcc gag tgt gac cag  tac cgc agc        3789
Glu Thr  Gln Ser Thr Leu Gln  Ala Glu Cys Asp Gln  Tyr Arg Ser
    1250                 1255                 1260

atc ctg  gcg gag acg gag ggc  atg ctc aga gac ctg  cag aag agc        3834
Ile Leu  Ala Glu Thr Glu Gly  Met Leu Arg Asp Leu  Gln Lys Ser
    1265                 1270                 1275

gtg gag  gag gag gag cag gtg  tgg agg gcc aag gtg  ggc gcc gca        3879
Val Glu  Glu Glu Glu Gln Val  Trp Arg Ala Lys Val  Gly Ala Ala
    1280                 1285                 1290

gag gag  gag ctc cag aag tcc  cgg gtc aca gtg aag  cat ctc gaa        3924
Glu Glu  Glu Leu Gln Lys Ser  Arg Val Thr Val Lys  His Leu Glu
    1295                 1300                 1305

gag att  gta gag aag cta aaa  gga gaa ctt gaa agt  tcg gac cag        3969
Glu Ile  Val Glu Lys Leu Lys  Gly Glu Leu Glu Ser  Ser Asp Gln
    1310                 1315                 1320

gtg agg  gag cac acg tcg cat  ttg gag gca gag ctg  gaa aag cac        4014
Val Arg  Glu His Thr Ser His  Leu Glu Ala Glu Leu  Glu Lys His
    1325                 1330                 1335

atg gcg  gcc gcc agc gcc gag  tgc cag aac tac gcc  aag gag gtg        4059
Met Ala  Ala Ala Ser Ala Glu  Cys Gln Asn Tyr Ala  Lys Glu Val
    1340                 1345                 1350

gca ggg  ctg agg caa ctt ctc  cta gaa tct caa tct  cag ctc gat        4104
Ala Gly  Leu Arg Gln Leu Leu  Leu Glu Ser Gln Ser  Gln Leu Asp
    1355                 1360                 1365

gcc gcc  aag agc gaa gcc cag  aaa cag agc gat gag  ctt gcc ctg        4149
Ala Ala  Lys Ser Glu Ala Gln  Lys Gln Ser Asp Glu  Leu Ala Leu
    1370                 1375                 1380

gtc agg  cag cag ttg agt gaa  atg aag agc cac gta  gag gat ggt        4194
Val Arg  Gln Gln Leu Ser Glu  Met Lys Ser His Val  Glu Asp Gly
    1385                 1390                 1395

gac att  gct ggg gcc cca gct  tcc tcc cca gag gcg  ccc cca gcc        4239
Asp Ile  Ala Gly Ala Pro Ala  Ser Ser Pro Glu Ala  Pro Pro Ala
    1400                 1405                 1410

gag cag  gac ccc gtt cag ctg  aag acg cag ctg gag  tgg aca gaa        4284
Glu Gln  Asp Pro Val Gln Leu  Lys Thr Gln Leu Glu  Trp Thr Glu
    1415                 1420                 1425

gcc atc  ctg gag gat gag cag  aca cag cgg cag aag  ctc acg gcc        4329
Ala Ile  Leu Glu Asp Glu Gln  Thr Gln Arg Gln Lys  Leu Thr Ala
    1430                 1435                 1440

gag ttt  gag gag gct cag acc  tcg gca tgt cgg tta  caa gaa gaa        4374
Glu Phe  Glu Glu Ala Gln Thr  Ser Ala Cys Arg Leu  Gln Glu Glu
    1445                 1450                 1455

ttg gag  aag ctc cgc aca gcc  ggc ccc cta gag tct  tca gaa aca        4419
Leu Glu  Lys Leu Arg Thr Ala  Gly Pro Leu Glu Ser  Ser Glu Thr
    1460                 1465                 1470
```

```
gag gag  gcc tca cag ctg aag  gag aga cta gaa aaa  gag aag aag        4464
Glu Glu  Ala Ser Gln Leu Lys  Glu Arg Leu Glu Lys  Glu Lys Lys
    1475                 1480                 1485

tta aca  agt gac ctg ggg cgc  gcc gcc acg aga ctg  cag gag ctt        4509
Leu Thr  Ser Asp Leu Gly Arg  Ala Ala Thr Arg Leu  Gln Glu Leu
    1490                 1495                 1500

ctg aag  acg acc cag gag cag  ctg gca agg gag aag  gac acg gtg        4554
Leu Lys  Thr Thr Gln Glu Gln  Leu Ala Arg Glu Lys  Asp Thr Val
    1505                 1510                 1515

aag aag  ctg cag gaa cag ctg  gaa aag gca gag gac  ggc agc agc        4599
Lys Lys  Leu Gln Glu Gln Leu  Glu Lys Ala Glu Asp  Gly Ser Ser
    1520                 1525                 1530

tca aag  gag ggc acc tct gtc  tga                                   4623
Ser Lys  Glu Gly Thr Ser Val
    1535                 1540
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<210> 2
<211> 1540
<212> PRT
<213> Homo sapiens

<400> 2

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Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1               5                  10                  15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
            20                  25                  30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
        35                  40                  45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
    50                  55                  60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
                85                  90                  95

Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
            100                 105                 110

Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
        115                 120                 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
    130                 135                 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145                 150                 155                 160
```

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

Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Gly Asn Thr Pro
180 185 190

Ala Thr Gly Thr Thr Gln Gly Lys Lys Ala Glu Gly Thr Gln Asn Gln
195 200 205

Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
210 215 220

Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly Lys
225 230 235 240

Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
245 250 255

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
260 265 270

Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr Gln
275 280 285

Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu Gly
290 295 300

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
305 310 315 320

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
325 330 335

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
340 345 350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
355 360 365

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
370 375 380

Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
385 390 395 400

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
405 410 415

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
420 425 430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
435 440 445

Asp Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly
450 455 460

Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
465 470 475 480

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
485 490 495

Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala
500 505 510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
515 520 525

Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly
530 535 540

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
545 550 555 560

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
565 570 575

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
580 585 590

Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln
595 600 605

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
610 615 620

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln
625 630 635 640

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln
645 650 655

Gly Lys Lys Ala Glu Arg Ser Pro Asn Gln Gly Lys Lys Gly Glu Gly
660 665 670

Ala Pro Ile Gln Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr
675 680 685

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

Ser Glu Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala
705 710 715 720

Asp Ala Ala Ala Asn Gln Gly Lys Lys Thr Glu Ser Ala Ser Val Gln
725 730 735

Gly Arg Asn Thr Asp Val Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu
740 745 750

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu Pro Gly
755 760 765

Pro Pro Asp Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val
770 775 780

Ser Thr Val Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu
785 790 795 800

Ile Glu Ile Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His
805 810 815

Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu
820 825 830

Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val
835 840 845

Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys
850 855 860

Ala Lys Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala
865 870 875 880

Arg Glu Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr
885 890 895

Arg Glu His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr
900 905 910

Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu
915 920 925

Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser
930 935 940

Gln Val Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu
945 950 955 960

Leu Ser Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg
965 970 975

```
Gln Asp Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe
            980                 985                 990

Glu Lys Gln Val Leu Gln Leu Gln  Ala Ser His Arg Glu  Ser Glu Glu
        995                 1000                1005

Ala Leu  Gln Lys Arg Leu Asp  Glu Val Ser Arg Glu  Leu Cys His
    1010                1015                1020

Thr Gln  Ser Ser His Ala Ser  Leu Arg Ala Asp Ala  Glu Lys Ala
    1025                1030                1035

Gln Glu  Gln Gln Gln Gln Met  Ala Glu Leu His Ser  Lys Leu Gln
    1040                1045                1050

Ser Ser  Glu Ala Glu Val Arg  Ser Lys Cys Glu Glu  Leu Ser Gly
    1055                1060                1065

Leu His  Gly Gln Leu Gln Glu  Ala Arg Ala Glu Asn  Ser Gln Leu
    1070                1075                1080

Thr Glu  Arg Ile Arg Ser Ile  Glu Ala Leu Leu Glu  Ala Gly Gln
    1085                1090                1095

Ala Arg  Asp Ala Gln Asp Val  Gln Ala Ser Gln Ala  Glu Ala Asp
    1100                1105                1110

Gln Gln  Gln Thr Arg Leu Lys  Glu Leu Glu Ser Gln  Val Ser Gly
    1115                1120                1125

Leu Glu  Lys Glu Ala Ile Glu  Leu Arg Glu Ala Val  Glu Gln Gln
    1130                1135                1140

Lys Val  Lys Asn Asn Asp Leu  Arg Glu Lys Asn Trp  Lys Ala Met
    1145                1150                1155

Glu Ala  Leu Ala Thr Ala Glu  Gln Ala Cys Lys Glu  Lys Leu His
    1160                1165                1170

Ser Leu  Thr Gln Ala Lys Glu  Glu Ser Glu Lys Gln  Leu Cys Leu
    1175                1180                1185

Ile Glu  Ala Gln Thr Met Glu  Ala Leu Leu Ala Leu  Leu Pro Glu
    1190                1195                1200

Leu Ser  Val Leu Ala Gln Gln  Asn Tyr Thr Glu Trp  Leu Gln Asp
    1205                1210                1215

Leu Lys  Glu Lys Gly Pro Thr  Leu Leu Lys His Pro  Pro Ala Pro
    1220                1225                1230
```

```
Ala Glu  Pro Ser Ser Asp Leu  Ala Ser Lys Leu Arg  Glu Ala Glu
    1235                1240                1245

Glu Thr  Gln Ser Thr Leu Gln  Ala Glu Cys Asp Gln  Tyr Arg Ser
    1250                1255                1260

Ile Leu  Ala Glu Thr Glu Gly  Met Leu Arg Asp Leu  Gln Lys Ser
    1265                1270                1275

Val Glu  Glu Glu Glu Gln Val  Trp Arg Ala Lys Val  Gly Ala Ala
    1280                1285                1290

Glu Glu  Glu Leu Gln Lys Ser  Arg Val Thr Val Lys  His Leu Glu
    1295                1300                1305

Glu Ile  Val Glu Lys Leu Lys  Gly Glu Leu Glu Ser  Ser Asp Gln
    1310                1315                1320

Val Arg  Glu His Thr Ser His  Leu Glu Ala Glu Leu  Glu Lys His
    1325                1330                1335

Met Ala  Ala Ala Ser Ala Glu  Cys Gln Asn Tyr Ala  Lys Glu Val
    1340                1345                1350

Ala Gly  Leu Arg Gln Leu Leu  Leu Glu Ser Gln Ser  Gln Leu Asp
    1355                1360                1365

Ala Ala  Lys Ser Glu Ala Gln  Lys Gln Ser Asp Glu  Leu Ala Leu
    1370                1375                1380

Val Arg  Gln Gln Leu Ser Glu  Met Lys Ser His Val  Glu Asp Gly
    1385                1390                1395

Asp Ile  Ala Gly Ala Pro Ala  Ser Ser Pro Glu Ala  Pro Pro Ala
    1400                1405                1410

Glu Gln  Asp Pro Val Gln Leu  Lys Thr Gln Leu Glu  Trp Thr Glu
    1415                1420                1425

Ala Ile  Leu Glu Asp Glu Gln  Thr Gln Arg Gln Lys  Leu Thr Ala
    1430                1435                1440

Glu Phe  Glu Glu Ala Gln Thr  Ser Ala Cys Arg Leu  Gln Glu Glu
    1445                1450                1455

Leu Glu  Lys Leu Arg Thr Ala  Gly Pro Leu Glu Ser  Ser Glu Thr
    1460                1465                1470

Glu Glu  Ala Ser Gln Leu Lys  Glu Arg Leu Glu Lys  Glu Lys Lys
    1475                1480                1485
```

```
Leu Thr  Ser Asp Leu Gly Arg  Ala Ala Thr Arg Leu  Gln Glu Leu
    1490                 1495                 1500

Leu Lys  Thr Thr Gln Glu Gln  Leu Ala Arg Glu Lys  Asp Thr Val
    1505                 1510                 1515

Lys Lys  Leu Gln Glu Gln Leu  Glu Lys Ala Glu Asp  Gly Ser Ser
    1520                 1525                 1530

Ser Lys  Glu Gly Thr Ser Val
    1535                 1540
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<210> 3
<211> 1275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1275)

<400> 3

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atg gct gcc ggg ccg atc tcc gag cgg aat cag gat gcc act gtg tac          48
Met Ala Ala Gly Pro Ile Ser Glu Arg Asn Gln Asp Ala Thr Val Tyr
1               5                  10                  15

gtg ggg ggc ctg gat gag aag gtt agt gaa ccg ctg ctg tgg gaa ctg          96
Val Gly Gly Leu Asp Glu Lys Val Ser Glu Pro Leu Leu Trp Glu Leu
            20                  25                  30

ttt ctc cag gct gga cca gta gtc aac acc cac atg cca aag gat aga         144
Phe Leu Gln Ala Gly Pro Val Val Asn Thr His Met Pro Lys Asp Arg
        35                  40                  45

gtc act ggc cag cac caa ggc tat ggc ttt gtg gaa ttc ttg agt gag         192
Val Thr Gly Gln His Gln Gly Tyr Gly Phe Val Glu Phe Leu Ser Glu
    50                  55                  60

gaa gat gct gac tat gcc att aag atc atg aac atg atc aaa ctc tat         240
Glu Asp Ala Asp Tyr Ala Ile Lys Ile Met Asn Met Ile Lys Leu Tyr
65                  70                  75                  80

ggg aag cca ata cgg gtg aac aaa gca tca gct cac aac aaa aac ctg         288
Gly Lys Pro Ile Arg Val Asn Lys Ala Ser Ala His Asn Lys Asn Leu
                85                  90                  95

gat gta ggg gcc aac att ttc att ggg aac ctg gac cct gag att gat         336
Asp Val Gly Ala Asn Ile Phe Ile Gly Asn Leu Asp Pro Glu Ile Asp
            100                 105                 110

gag aag ttg ctt tat gat act ttc agc gcc ttt ggg gtc atc tta caa         384
Glu Lys Leu Leu Tyr Asp Thr Phe Ser Ala Phe Gly Val Ile Leu Gln
        115                 120                 125

acc ccc aaa att atg cgg gac cct gac aca ggc aac tcc aaa ggt tat         432
Thr Pro Lys Ile Met Arg Asp Pro Asp Thr Gly Asn Ser Lys Gly Tyr
    130                 135                 140

gcc ttt att aat ttt gct tca ttt gat gct tcg gat gca gca att gaa         480
Ala Phe Ile Asn Phe Ala Ser Phe Asp Ala Ser Asp Ala Ala Ile Glu
145                 150                 155                 160

gcc atg aat ggg cag tac ctc tgt aac cgt cct atc acc gta tct tat         528
```

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

gcc ttc aag aag gac tcc aag ggt gag cgc cat ggc tca gca gcc gaa  576
Ala Phe Lys Lys Asp Ser Lys Gly Glu Arg His Gly Ser Ala Ala Glu
            180                 185                 190

cga ctt ctg gca gct cag aac ccg ctc tcc cag gct gat cgc cct cat  624
Arg Leu Leu Ala Ala Gln Asn Pro Leu Ser Gln Ala Asp Arg Pro His
        195                 200                 205

cag ctg ttt gca gat gca cct cct cca ccc tct gct ccc aat cct gtg  672
Gln Leu Phe Ala Asp Ala Pro Pro Pro Pro Ser Ala Pro Asn Pro Val
    210                 215                 220

gta tca tca ttg ggg tct ggg ctt cct cca cca ggc atg cct cct cct  720
Val Ser Ser Leu Gly Ser Gly Leu Pro Pro Pro Gly Met Pro Pro Pro
225                 230                 235                 240

ggc tcc ttc cca ccc cca gtg cca cct cct gga gcc ctc cca cct ggg  768
Gly Ser Phe Pro Pro Pro Val Pro Pro Pro Gly Ala Leu Pro Pro Gly
                245                 250                 255

ata ccc cca gcc atg ccc cca cca cct atg cct cct ggg gct gca gga  816
Ile Pro Pro Ala Met Pro Pro Pro Pro Met Pro Pro Gly Ala Ala Gly
            260                 265                 270

cat ggc ccc cca tcg gca gga acc cca ggg gca gga cat cct ggt cat  864
His Gly Pro Pro Ser Ala Gly Thr Pro Gly Ala Gly His Pro Gly His
        275                 280                 285

gga cac tca cat cct cac cca ttc cca ccg ggt ggg atg ccc cat cca  912
Gly His Ser His Pro His Pro Phe Pro Pro Gly Gly Met Pro His Pro
    290                 295                 300

ggg atg tct cag atg cag ctt gca cac cat ggc cct cat ggc tta gga  960
Gly Met Ser Gln Met Gln Leu Ala His His Gly Pro His Gly Leu Gly
305                 310                 315                 320

cat ccc cac gct gga ccc cca ggc tct ggg ggc cag cca ccg ccc cga 1008
His Pro His Ala Gly Pro Pro Gly Ser Gly Gly Gln Pro Pro Pro Arg
                325                 330                 335

cca cca cct gga atg cct cat cct gga cct cct cca atg ggc atg ccc 1056
Pro Pro Pro Gly Met Pro His Pro Gly Pro Pro Pro Met Gly Met Pro
            340                 345                 350

ccc cga ggg cct cca ttc gga tct ccc atg ggt cac cca ggt cct atg 1104
Pro Arg Gly Pro Pro Phe Gly Ser Pro Met Gly His Pro Gly Pro Met
        355                 360                 365

cct ccg cat ggt atg cgt gga cct cct cca ctg atg ccc ccc cat gga 1152
Pro Pro His Gly Met Arg Gly Pro Pro Pro Leu Met Pro Pro His Gly
    370                 375                 380

tac act ggc cct cca cga ccc cca ccc tat ggc tac cag cgg ggg cct 1200
Tyr Thr Gly Pro Pro Arg Pro Pro Pro Tyr Gly Tyr Gln Arg Gly Pro
385                 390                 395                 400

ctc cct cca ccc aga ccc act ccc cgg cca cca gtt ccc cct cga ggc 1248
Leu Pro Pro Pro Arg Pro Thr Pro Arg Pro Pro Val Pro Pro Arg Gly
                405                 410                 415

cca ctt cga ggc cct ctc cct cag taa                             1275
Pro Leu Arg Gly Pro Leu Pro Gln
            420
```

<210> 4
<211> 424
<212> PRT
<213> Homo sapiens

<400> 4

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Met Ala Ala Gly Pro Ile Ser Glu Arg Asn Gln Asp Ala Thr Val Tyr
1               5                  10                  15

Val Gly Gly Leu Asp Glu Lys Val Ser Glu Pro Leu Leu Trp Glu Leu
            20                  25                  30

Phe Leu Gln Ala Gly Pro Val Val Asn Thr His Met Pro Lys Asp Arg
        35                  40                  45

Val Thr Gly Gln His Gln Gly Tyr Gly Phe Val Glu Phe Leu Ser Glu
    50                  55                  60

Glu Asp Ala Asp Tyr Ala Ile Lys Ile Met Asn Met Ile Lys Leu Tyr
65                  70                  75                  80

Gly Lys Pro Ile Arg Val Asn Lys Ala Ser Ala His Asn Lys Asn Leu
                85                  90                  95

Asp Val Gly Ala Asn Ile Phe Ile Gly Asn Leu Asp Pro Glu Ile Asp
            100                 105                 110

Glu Lys Leu Leu Tyr Asp Thr Phe Ser Ala Phe Gly Val Ile Leu Gln
        115                 120                 125

Thr Pro Lys Ile Met Arg Asp Pro Asp Thr Gly Asn Ser Lys Gly Tyr
    130                 135                 140

Ala Phe Ile Asn Phe Ala Ser Phe Asp Ala Ser Asp Ala Ala Ile Glu
145                 150                 155                 160

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

Ala Phe Lys Lys Asp Ser Lys Gly Glu Arg His Gly Ser Ala Ala Glu
            180                 185                 190

Arg Leu Leu Ala Ala Gln Asn Pro Leu Ser Gln Ala Asp Arg Pro His
        195                 200                 205

Gln Leu Phe Ala Asp Ala Pro Pro Pro Pro Ser Ala Pro Asn Pro Val
    210                 215                 220

Val Ser Ser Leu Gly Ser Gly Leu Pro Pro Pro Gly Met Pro Pro Pro
225                 230                 235                 240

Gly Ser Phe Pro Pro Pro Val Pro Pro Pro Gly Ala Leu Pro Pro Gly
```

245 250 255

Ile Pro Pro Ala Met Pro Pro Pro Pro Met Pro Pro Gly Ala Ala Gly
260 265 270

His Gly Pro Pro Ser Ala Gly Thr Pro Gly Ala Gly His Pro Gly His
275 280 285

Gly His Ser His Pro His Pro Phe Pro Pro Gly Gly Met Pro His Pro
290 295 300

Gly Met Ser Gln Met Gln Leu Ala His His Gly Pro His Gly Leu Gly
305 310 315 320

His Pro His Ala Gly Pro Pro Gly Ser Gly Gly Gln Pro Pro Pro Arg
325 330 335

Pro Pro Pro Gly Met Pro His Pro Gly Pro Pro Pro Met Gly Met Pro
340 345 350

Pro Arg Gly Pro Pro Phe Gly Ser Pro Met Gly His Pro Gly Pro Met
355 360 365

Pro Pro His Gly Met Arg Gly Pro Pro Pro Leu Met Pro Pro His Gly
370 375 380

Tyr Thr Gly Pro Pro Arg Pro Pro Pro Tyr Gly Tyr Gln Arg Gly Pro
385 390 395 400

Leu Pro Pro Pro Arg Pro Thr Pro Arg Pro Pro Val Pro Pro Arg Gly
405 410 415

Pro Leu Arg Gly Pro Leu Pro Gln
420

<210> 5
<211> 126
<212> DNA
<213> Homo sapiens

<400> 5
tcgtcggagc agacgggagt ttctcctcgg ggtcggagca ggaggcacgc ggagtgtgag 60

gccacgcatg agcggacgct aacccccctcc ccagccacaa agagtctaca tgtctagggt 120

ctagac 126

<210> 6
<211> 266
<212> DNA
<213> Homo sapiens

<400> 6
gcccgcgccg gctgtgctgc acaggggggag gagagggaac cccaggcgcg agcgggaaga 60

ggggacctgc agccacaact tctctggtcc tctgcatccc ttctgtccct ccacccgtcc 120

ccttccccac cctctggccc ccaccttctt ggaggcgaca acccccggga ggcattagaa 180

gggatttttc ccgcaggttg cgaagggaag caaacttggt ggcaacttgc ctcccggtgc 240

gggcgtctct cccccaccgt ctcaac 266

<210> 7
<211> 27
<212> DNA
<213> Homo sapiens

<400> 7
tcgtcggagc agacgggagt ttctcct 27

<210> 8
<211> 32
<212> DNA
<213> Homo sapiens

<400> 8
ccaccttctt ggaggcgaca acccccggga gg 32

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #3.

<400> 9
gatcttcgtc ggagcagacg ggagtttctc cta 33

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #3.

<400> 10
agcttaggag aaactcccgt ctgctccgac gaa 33

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #4.

<400> 11
gatcttctgc atcccttctg tccctccaca 30

<210> 12
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #4.

<400> 12
agcttgtgga gggacagaag ggatgcagaa 30

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #2.

<400> 13
aaaaaaagat ctgcccgcgc cggctgt 27

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #2.

<400> 14
aaaaaaaagc ttgttgagac ggtgggggga 29

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #1.

<400> 15
aaaaaaagat cttcgtcgga gcagacg 27

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #1.

<400> 16
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<210> 17
<211> 9
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (4)..(6)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> "v" is a or g or c.

<400> 17
gagnnnacv 9

<210> 18
<211> 10
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (4)..(7)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> "v" is a or g or c.

<400> 18
gagnnnnacv 10

<210> 19
<211> 11
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (4)..(8)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> "v" is a or g or c.

<400> 19
gagnnnnnac v 11

<210> 20
<211> 12
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (4)..(9)
<223> "n" is a, c, g, or t

<220>
<221> misc_feature

<222> (12)..(12)
<223> "r" is a or g

<220>
<221> misc_feature
<222> (12)..(12)
<223> "v" is a or g or c.

<400> 20
gagnnnnnna cv 12

<210> 21
<211> 60
<212> DNA
<213> Homo sapiens

<400> 21
tcgtcggagc agacgggagt ttctcctcgg ggtcggagca ggaggcacgc ggagtgtgag 60

<210> 22
<211> 66
<212> DNA
<213> Homo sapiens

<400> 22
gccacgcatg agcggacgct aacccccctcc ccagccacaa agagtctaca tgtctagggt 60

ctagac 66

<210> 23
<211> 181
<212> DNA
<213> Homo sapiens

<400> 23
aacgggcgcc gcggcgggga gaagacgcag agcgctgctg ggctgccggg tctcccgctt 60

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c 181

<210> 24
<211> 30
<212> DNA
<213> Homo sapiens

<400> 24
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<210> 25
<211> 32
<212> DNA
<213> Homo sapiens

<400> 25
gagcgggaag aggggacctg cagccacaac tt 32

<210> 26
<211> 60
<212> DNA

<213> Homo sapiens

<400> 26
caggggagg agagggaacc ccaggcgcga gcgggaagag gggacctgca gccacaactt 60

<210> 27
<211> 113
<212> DNA
<213> Homo sapiens

<400> 27
tcgtcggagc agacgggagt ttctcctcgg ggtcggagca ggaggcacgc ggagtgtgag 60

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<210> 28
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #5.

<400> 28
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<210> 29
<211> 32
<212> DNA
<213> Artificial Sequence

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<210> 30
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #6.

<400> 30
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<210> 31
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #6.

<400> 31
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<210> 32
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #8.

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<210> 33
<211> 36
<212> DNA
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<210> 34
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<220>
<223> A primer for amprifying the portion of cis-element of cis-element #9.

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<210> 35
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #9.

<400> 35
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<210> 36
<211> 66
<212> DNA
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<220>
<223> A primer for amprifying the portion of cis-element of cis-element #10.

<400> 36
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aactta 66

<210> 37
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ccctga 66

<210> 38
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #11.

<400> 38
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<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> A primer for amprifying the portion of cis-element of cis-element #11.

<400> 39
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<210> 40
<211> 2907
<212> DNA
<213> Pan paniscus

<400> 40
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aagacgctgg tctccacggt tgggagcatg gtgttcaacg agggcgaggc ccagcggctc 180

atcgagatcc tgtctgagaa ggctggcatc attcaggaca cctggcacaa ggccactcag 240

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aaggaggtgc agcagctgca gggcaagatc cggactcttc aggagcagct ggagaatggc 540

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35 40 45

Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser Lys Leu
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Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys Ala Ala Ala
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Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln Glu Ile
85 90 95

Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His Val Lys
100 105 110

Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu Gln Leu
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Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser
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Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu Ser Lys
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Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys Val Ser
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Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg Gln Asp Glu Gln Gln
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Leu Asp Glu Val Ser Arg Glu Leu Cys His Thr Gln Ser Ser His Ala
225 230 235 240

Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln Gln Met
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Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu Val Arg Ser
260 265 270

Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln Glu Ala Arg
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Leu Glu Ala Gly Gln Val Arg Asp Ala Gln Asp Ala Gln Ala Ser Gln
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Ala Glu Ala Asp Gln Gln Gln Thr Arg Leu Lys Glu Leu Glu Ser Gln
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Val Ser Gly Leu Glu Lys Glu Ala Ile Glu Leu Arg Glu Ala Val Glu
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Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Lys Ala
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Met Glu Ala Leu Thr Thr Ala Glu Gln Ala Cys Lys Glu Lys Leu His
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Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu Cys Leu Ile
385 390 395 400

Glu Ala Gln Thr Met Glu Ala Leu Leu Ala Leu Leu Pro Glu Leu Ser
405 410 415

Val Leu Ala Gln Gln Ser Tyr Thr Glu Trp Leu Gln Asp Leu Lys Glu
420 425 430

Lys Gly Pro Thr Leu Leu Lys His Pro Pro Ala Pro Ala Glu Pro Ser
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Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu Thr Gln Ser Thr
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Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala Glu Thr Glu
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Gly Met Leu Arg Asp Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val
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Trp Arg Ala Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys Ser Arg
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Leu Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu Glu Ala
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Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln Asn Tyr
545                 550                 555                 560

Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser Gln Ser
                565                 570                 575

Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp Glu Leu
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Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val Glu Asp
        595                 600                 605

Gly Asp Ile Ala Gly Ala Pro Ala Ser Ser Pro Glu Ala Pro Pro Ala
    610                 615                 620

Glu Gln Asp Pro Val Gln Leu Lys Thr Gln Leu Glu Arg Thr Glu Ala
625                 630                 635                 640

Ile Leu Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala Glu Phe
                645                 650                 655

Glu Glu Ala Gln Thr Ser Ala Cys Arg Leu Gln Glu Glu Leu Glu Lys
            660                 665                 670

Leu Arg Thr Ala Gly Pro Leu Glu Ser Ser Glu Thr Glu Glu Ala Ser
        675                 680                 685

Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser Asp Leu
    690                 695                 700

Gly Arg Ala Ala Ile Lys Leu Gln Glu Leu Leu Lys Thr Thr Gln Glu
705                 710                 715                 720

Gln Leu Ala Arg Glu Lys Asp Thr Val Lys Lys Leu Gln Glu Gln Leu
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Glu Lys Thr Glu Asp Gly Ser Ser Ser Lys Glu Gly Thr Ser Val
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gctgacagac cagggtgtgc tgggagtcca ggactctcgg ggtttatgtc aatcagtgca 4980

attgtctgta tttctcagtg gggccaggtt gggaagcaac aggccaggtg gtgagttctc 5040

agaggctgct gagcagactg gagggcctca gcccagccca gcaaggctgc agcccatcac 5100

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Met Ala Lys Thr His His Gln Lys Gly Glu Lys Lys Lys Lys Glu Lys
50 55 60

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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
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Gly Lys Ile Pro Glu His Asp Leu Asp Pro Asn Val Thr Ile Ile Leu
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Lys Glu Pro Val Arg Val Ser Ala Val Ala Val Ala Pro Thr Ser Val
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His Ser Ser Val Gly His Thr Pro Ile Ala Thr Val Pro Ala Met Pro
        115                 120                 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Arg Lys Lys Lys Glu Lys
    130                 135                 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Ile Val Asn Ser Ile
145                 150                 155                 160

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

Ala Thr Ser Ser Gln Gly Lys Lys Gly Gln Gly Ala Gln Asn Gln Ala
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Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala
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Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys
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Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn
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Gln Ala Lys Lys Gly Glu Gly Gly Gln Asn Gln Ala Lys Lys Gly Glu
            260                 265                 270

Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly
        275                 280                 285

Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala
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Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys
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Gly Glu Gly Ala Gln Asn Gln Ser Lys Lys Gly Glu Gly Ala Gln Asn
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Gln Ala Lys Lys Gly Glu Gly Gly Gln Asn Gln Ala Lys Lys Gly Glu
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Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala
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Lys Lys Gly Glu Gly Val Gln Asn Gln Ala Lys Lys Gly Val Glu Gly
370 375 380

Ala Gln Asn Gln Gly Lys Lys Gly Glu Ala Asn Gln Asn Gln Ala Lys
385 390 395 400

Lys Gly Glu Gly Gly Gln Asn Gln Thr Lys Lys Gly Glu Gly Pro Gln
405 410 415

Asn Gln Gly Lys Lys Gly Glu Ala Ala Gln Lys Gln Asp Lys Lys Ile
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Glu Gly Ala Gln Asn Gln Gly Lys Lys Pro Glu Gly Thr Ser Asn Gln
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Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly
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Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys
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Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln
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Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly
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Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Pro Gln Asn Gln
515 520 525

Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly
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Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys
545 550 555 560

Lys Ala Glu Gly Val Gln Ser Gln Ser Lys Lys Gly Glu Gly Thr Gln
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Asn Gln Gly Lys Lys Gly Asp Gly Asn Pro Asn Gln Gly Lys Lys Gly
580 585 590

Glu Gly Ala Ser Asn Gln Asn Arg Lys Thr Asp Thr Val Ala Asn Gln
595 600 605

Gly Thr Lys Gln Glu Gly Val Ser Asn Gln Val Lys Lys Ser Glu Gly
610 615 620

Ser Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys
625 630 635 640

Lys Lys Asp Gly Ser Pro Ser Gln Ala Lys Lys Val Asp Ala Ala Ala
645 650 655

Asn Gln Gly Lys Lys Ser Glu Met Ala Pro Ala Gln Gly Gln Lys Ala
660 665 670

Ser Met Val Gln Ser Gln Glu Ala Pro Lys Gln Asp Ala Pro Ala Lys
675 680 685

Lys Lys Ser Gly Ser Arg Lys Lys Gly Glu Pro Gly Pro Pro Asp Cys
690 695 700

Asp Gly Pro Leu Phe Leu Pro Tyr Lys Thr Leu Val Ser Thr Val Gly
705 710 715 720

Ser Met Val Phe Ser Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile Leu
725 730 735

Ser Glu Lys Thr Gly Val Ile Gln Asp Thr Trp His Lys Ala Thr Gln
740 745 750

Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys Glu
755 760 765

Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser Lys
770 775 780

Leu Arg Glu Leu Asn Lys Glu Met Ala Ser Glu Lys Ala Lys Ala Ala
785 790 795 800

Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln Glu
805 810 815

Ile Ala Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Asp His Val
820 825 830

Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu Gln
835 840 845

Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu Asn
850 855 860

Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu Ser
865 870 875 880

Lys Gln Asn Thr Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys Val
885 890 895

Asn Lys Glu Leu Val Glu Lys Ser Glu Ala Ser Arg Gln Glu Glu Gln
900 905 910

Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Thr Phe Glu Lys Gln Val
915 920 925

Leu Gln Leu Gln Ala Ser His Lys Glu Ser Glu Glu Ala Leu Gln Lys
930 935 940

Arg Leu Glu Glu Val Thr Arg Glu Leu Cys Arg Ala Gln Thr Ser His
945 950 955 960

Ala Asn Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln Arg
965 970 975

Val Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Val Glu Val Lys
980 985 990

Ser Lys Cys Glu Glu Leu Ser Ser Leu His Gly Gln Leu Lys Glu Ala
995 1000 1005

Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
1010 1015 1020

Ala Leu Leu Glu Ala Gly Gln Ala Gln Asp Thr Gln Ala Ser His
1025 1030 1035

Ala Glu Ala Asn Gln Gln Gln Thr Arg Leu Lys Glu Leu Glu Ser
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Gln Val Ser Cys Leu Glu Lys Glu Thr Ser Glu Leu Lys Glu Ala
1055 1060 1065

Met Glu Gln Gln Lys Gly Lys Asn Asn Asp Leu Arg Glu Lys Asn
1070 1075 1080

Trp Lys Ala Met Glu Ala Leu Ala Leu Ala Glu Arg Ala Cys Glu
1085 1090 1095

Glu Lys Leu Arg Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys
1100 1105 1110

Gln Leu His Leu Ala Glu Ala Gln Thr Lys Glu Thr Leu Leu Ala
1115 1120 1125

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

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Trp Leu Gln Glu Phe Lys Glu Lys Gly Ser Glu Leu Leu Lys Lys
1145                1150                1155

Pro Pro Thr Leu Glu Pro Ser Met Asp Ile Val Leu Lys Leu Arg
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Glu Ala Glu Glu Thr Gln Asn Ser Leu Gln Ala Glu Cys Asp Gln
1175                1180                1185

Tyr Arg Thr Ile Leu Ala Glu Thr Glu Gly Met Leu Lys Asp Leu
1190                1195                1200

Gln Lys Ser Val Glu Glu Glu Glu Arg Val Trp Lys Ala Lys Val
1205                1210                1215

Gly Ala Ala Glu Glu Glu Leu His Lys Ser Arg Val Thr Val Lys
1220                1225                1230

His Leu Glu Asp Ile Val Glu Lys Leu Lys Gly Glu Leu Glu Ser
1235                1240                1245

Ser Asp Gln Val Arg Glu His Thr Ser His Leu Glu Ala Glu Leu
1250                1255                1260

Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln Asn Tyr Ala
1265                1270                1275

Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser Gln Ser
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Gln Leu Asp Glu Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp Glu
1295                1300                1305

Leu Ala Leu Val Arg Gln Gln Leu Ser Asp Met Arg Ser His Val
1310                1315                1320

Glu Asp Gly Asp Val Ala Gly Ser Pro Ala Val Pro Pro Ala Glu
1325                1330                1335

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

Met Ala Lys Thr Asn His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
    50                  55                  60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

Gly Lys Ile Pro Asp His Glu Pro Thr Pro Gly Val Thr Ile Leu Pro
                85                  90                  95

Lys Asp Pro Val Trp Ala Pro Ala Val Ala Val Ala Pro Thr Ser Val
            100                 105                 110

Gln Ser Pro Val Val Thr Ala Pro Val Ala Thr Val Ser Ala Met Pro
        115                 120                 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
    130                 135                 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145                 150                 155                 160

Gln Val Leu Ala Ser Lys Ala Ala Ile Leu Glu Ala Ala Pro Lys Glu
                165                 170                 175

Val Pro Met Val Val Val Ser Pro Val Gly Ala Lys Gly Ser Ala Pro
            180                 185                 190

Ala Thr Ser Ser Thr Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln
        195                 200                 205
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Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly
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Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys
225 230 235 240

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
245 250 255

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
260 265 270

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
275 280 285

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ser Glu Gly
290 295 300

Ala Gln Asn Gln Gly Lys Lys Ser Glu Gly Ala Gln Asn Gln Gly Lys
305 310 315 320

Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln
325 330 335

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
340 345 350

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
355 360 365

Gly Lys Lys Ser Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly
370 375 380

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
385 390 395 400

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

Asn Gln Ser Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr
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Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
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Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
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Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
465 470 475 480

Lys Ser Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro
485 490 495

Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val
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Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Asn Gln Asn Gln
515 520 525

Gly Lys Lys Ser Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly
530 535 540

Gly Gln Asn Gln Gly Lys Lys Ser Glu Gly Ala Gln Asn Gln Gly Arg
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Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
565 570 575

Asn Gln Gly Lys Lys Ala Glu Gly Asn Gln Asn Gln Gly Lys Lys Ala
580 585 590

Glu Gly Asn Gln Asn Gln Gly Arg Lys Glu Gln Ser Thr Leu Asp Gln
595 600 605

Gly Lys Met Val Glu Val Val Gln Asn Gln Ser Lys Lys Ala Asp Gly
610 615 620

Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Arg
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Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
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Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
660 665 670

Glu Gly Ala Gln Asn Gln Gly Arg Lys Val Glu Ala Gly Gln Asn Gln
675 680 685

Gly Lys Lys Ala Asp Ser Val Ala Asn Gln Gly Thr Lys Val Glu Gly
690 695 700

Ile Ala Asn Gln Gly Lys Lys Ala Asp Gly Thr Pro Asn Gln Gly Lys
705 710 715 720

Lys Ala Glu Gly Thr Ser Asn Gln Gly Lys Lys Ser Glu Gly Ser Pro
725 730 735

Asn Gln Gly Lys Lys Val Asp Ala Ser Ala Asn Gln Gly Lys Lys Ala
740 745 750

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Glu Ser Ala Pro Thr Gln Gly Lys Asn Ala Asp Met Val Gln Ser Gln
        755                 760                 765

Glu Ala Pro Lys Gln Glu Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys
    770                 775                 780

Lys Lys Gly Glu Pro Gly Pro Pro Asp Ala Asn Gly Thr Leu His Leu
785                 790                 795                 800

Pro Tyr Lys Thr Leu Val Ser Ala Val Gly Ser Met Val Leu Ser Glu
                805                 810                 815

Gly Glu Ala Gln Arg Leu Met Glu Ile Leu Ala Asp Lys Ala Gly Ile
            820                 825                 830

Val Gln Asp Thr Trp His Lys Ala Thr Gln Lys Gly Asp Pro Val Val
        835                 840                 845

Ile Leu Lys Arg Gln Leu Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu
    850                 855                 860

Gln Glu Asp Ala Ala Val Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys
865                 870                 875                 880

Glu Leu Ala Ala Glu Lys Ala Lys Ala Ala Ala Gly Glu Ala Lys Val
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Lys Lys Gln Leu Val Ala Arg Glu Gln Glu Ile Thr Ala Val Gln Ala
            900                 905                 910

Arg Met Gln Ala Ser Tyr Arg Glu His Val Lys Glu Val Gln Gln Leu
        915                 920                 925

Gln Gly Lys Ile Arg Thr Leu Gln Glu Gln Leu Glu Asn Gly Pro Ser
    930                 935                 940

Ala Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala
945                 950                 955                 960

Leu Asn Gln Ala Thr Ser Gln Val Glu Ser Lys Gln Asn Thr Glu Leu
                965                 970                 975

Ala Lys Leu Arg Gln Glu Leu Gly Lys Val Ser Lys Glu Leu Val Glu
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Lys Ser Glu Ala Val Arg Gln Glu  Glu Gln Gln Arg Lys  Ala Leu Glu
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Ala Lys  Ala Ala Ala Val Glu  Lys Gln Val Leu Gln  Leu Gln Ala
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Val Ser Arg Glu Leu Cys Arg Ala Gln Ser Ser His Ala Ser Leu
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Arg Ala Asp Ala Glu Lys Ala Arg Glu Gln Gln Gln Gln Met Ala
1055 1060 1065

Glu Leu His Gly Lys Leu Gln Ser Ser Glu Ala Glu Val Arg Gly
1070 1075 1080

Lys Cys Glu Glu Leu Arg Gly Leu His Gly Gln Leu Asp Glu Ala
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Arg Ala Gln Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
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Ala Leu Leu Glu Ala Ser Gln Ala Gln Asp Ala Gln Ala Ser Arg
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Val Glu Ala Asp Gln Gln Gln Ala Arg Leu Met Glu Leu Glu Ser
1130 1135 1140

Gln Val Trp Cys Leu Glu Lys Glu Ala Thr Glu Leu Arg Glu Ala
1145 1150 1155

Val Glu Gln Gln Lys Ala Lys Asn Asn Asp Leu Arg Glu Lys Asn
1160 1165 1170

Trp Lys Ala Met Glu Ala Leu Ala Ser Ala Glu Lys Ser Cys Glu
1175 1180 1185

Glu Lys Leu Arg Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys
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Gln Leu Ser Leu Thr Glu Ala Gln Thr Lys Glu Ala Leu Leu Ala
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Leu Leu Pro Gly Leu Pro Thr Ser Thr Asn Gln Ser Tyr Ala Glu
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Trp Leu Gln Glu Leu Lys Glu Asn Ala Cys Leu Glu Leu Ser Lys
1235 1240 1245

Arg Pro Gln Ala Ser Pro Glu Pro Ser Asp Leu Ala Ala Lys Leu
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Arg Glu Ala Glu Glu Thr Gln Ser Gly Leu Gln Ala Glu Cys Asp
1265 1270 1275

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Gln Tyr  Arg Ser Ile Leu Ala  Glu Thr Glu Ala Met  Leu Lys Ala
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Leu Gln  Lys Ser Val Glu Glu  Glu Glu Gln Val Trp  Lys Ala Arg
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Val Ser  Ala Ala Glu Glu Glu  Leu Gln Glu Ser Arg  Val Thr Val
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Lys His  Leu Glu Glu Val Val  Glu Lys Leu Lys Gly  Glu Leu Glu
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Ser Ser  Asp Gln Val Arg Glu  His Thr Trp Arg Leu  Glu Ala Glu
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Leu Glu  Lys His Val Ala Ala  Ala Ser Ala Glu Cys  Gln Ser Tyr
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Ala Gln  Glu Val Ala Gly Leu  Arg Gln Leu Leu Leu  Glu Ser Gln
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Phe Ser  Trp Met Arg Xaa Xaa  Xaa Xaa Xaa Xaa Xaa  Xaa Xaa Xaa
    1385                 1390                 1395

Xaa Xaa  Xaa Xaa Xaa Xaa Xaa  Ser Gln Leu Gln Gly  Glu Leu Glu
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Lys Leu  Arg Cys Thr Ala Pro  Leu Arg Ser Ser Glu  Asn Xaa Glu
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Ala Ala  Gln Leu Lys Glu Arg  Leu Glu Lys Glu Lys  Lys Leu Thr
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Gly Asp  Leu Gly Arg Ala Ala  Thr Lys Leu Gln Glu  Leu Leu Lys
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Thr Thr  Gln Glu Gln Leu Ala  Lys Glu Lys Asp Thr  Val Gln Lys
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Gly Thr  Ser Val
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ctccatcctg ccgtcgagcc ggcaccgctc cttgggtctg aagttggaga agaaaagttg 180

gcccaggttc tatctgggcg gactccaact ccagcagatt ctgatggccc tctctatctc 240

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tgtctcattg aaatattatc cgagaaagct ggcgtggttc aggatacctg gcataaggct 360

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<212> PRT
<213> Monodelphis domestica

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Leu Ser Pro Ala Arg Val Phe Leu Leu His Pro Ala Val Glu Pro Ala
35 40 45

Pro Leu Leu Gly Ser Glu Val Gly Glu Glu Lys Leu Ala Gln Val Leu
50 55 60

Ser Gly Arg Thr Pro Thr Pro Ala Asp Ser Asp Gly Pro Leu Tyr Leu
65 70 75 80

Pro Tyr Lys Thr Leu Val Ser Thr Leu Arg Ser Thr Val Phe Asn Glu
85 90 95

Gly Glu Ala His Cys Leu Ile Glu Ile Leu Ser Glu Lys Ala Gly Val
100 105 110

Val Gln Asp Thr Trp His Lys Ala Thr Gln Lys Gly Asp Pro Val Ala
115 120 125

Val Leu Lys Arg Gln Leu Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu
130 135 140

Gln Gln Asp Ala Ala Ala Ala Lys Asn Arg Leu Arg Glu Leu Asn Lys
145 150 155 160

Glu Leu Ala Ser Glu Lys Ser Lys Ala Ala Ala Gly Glu Ala Asn Val
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Lys Lys Gln Leu Leu Ala Arg Glu Gln Glu Ile Val Ala Val Gln Ala
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Arg Met Lys Ala Ser Tyr Arg Asp His Val Asn Glu Val Gln Gln Leu
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Gln Gly Lys Ile Arg Ser Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn
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Thr Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala
225                 230                 235                 240

Leu Asn Gln Ala Thr Ser Gln Thr Glu Ser Lys Gln Asn Thr Glu Leu
                245                 250                 255

Ala Lys Leu Arg Gln Glu Cys Ser Lys Leu Thr Lys Glu Val Ala Glu
            260                 265                 270

Lys Ser Glu Ala Val Gln Gln Glu Glu Gln Gln Lys Lys Ser Leu Glu
        275                 280                 285

Ile Lys Ala Ala Thr Leu Glu Lys Gln Val Gln Gln Leu Gln Val Ser
    290                 295                 300

Gln Lys Glu Lys Glu Asp Ser Leu Gln Lys Arg Leu Asp Glu Val Ser
305                 310                 315                 320

Gly Glu Leu Arg Lys Ser Gln Ser Ser Asn Lys Asn Leu Leu Ala Asp
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Leu Glu Lys Ala Lys Gly Asp Arg Gln Asn Ile Ala Glu Leu Arg Thr
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Lys Leu Gln Ser Ser Glu Thr Glu Val Lys Ser Lys Ser Glu Glu Leu
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Asn Lys Leu Lys Gly Lys Leu Ser Glu Ser Ser Ser Glu Asn Val Gln
    370                 375                 380

Leu Thr Glu Arg Ile Lys Ser Ile Glu Ala Leu Leu Glu Ala Gly Gln
385                 390                 395                 400

Val Lys Glu Ala Lys Asp Ala Gln Ala Ser Gln Ala Glu Val Asp Gln
                405                 410                 415

Leu Gln Ala Arg Leu Lys Asp Arg Glu Ala Arg Val Thr Ser Leu Glu
            420                 425                 430

Lys Glu Ala Thr Glu Leu Lys Glu Ala Val Glu Gln Gln Lys Leu Lys
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Asn Asn Asp Leu Arg Glu Lys Asn Trp Arg Ala Met Glu Ala Leu Ala
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Ser Ala Glu Lys Gly Cys Glu Glu Lys Leu Ser Ser Leu Thr Lys Ala
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Lys Glu Glu Ala Glu Lys Gln Phe Ser Ile Thr Gln Thr Lys Thr Lys
485 490 495

Glu Thr Leu Leu Ser Leu Phe Pro Asp Ile Ser Ile Ala Thr Gln Gln
500 505 510

Ser Tyr Asp Gly Trp Leu Glu Glu Phe Lys Glu Lys Arg Met Glu Ala
515 520 525

Val Lys Gln Lys Ala Pro Ala Gly Val Ser Leu Asp Leu Ala Ser Lys
530 535 540

Leu Lys Glu Ala Glu Glu Ala Gln Ser Thr Leu Gln Ser Glu Cys Asp
545 550 555 560

Gln Tyr Arg Asn Ile Leu Ala Glu Thr Glu Gly Met Leu Lys Asp Leu
565 570 575

Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala Lys Leu Thr
580 585 590

Val Ser Glu Glu Glu Leu Gln Lys Ser Gln Ile Lys Val Lys His Leu
595 600 605

Glu Glu Thr Met Glu Lys Leu Lys Gly Asp Leu Gln Asn Val Asp Gln
610 615 620

Val Lys Glu Tyr Ala Ala Leu Leu Glu Ala Arg Leu Glu Glu His Met
625 630 635 640

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Leu Arg Asp Leu Leu Thr Glu Ala Arg Glu Gln Met Asp Ala Ala Asn
660 665 670

Ser Glu Ala Gln Lys Gln Ser Lys Glu Leu Ala Leu Val Arg Gln Gln
675 680 685

Leu Ser Glu Met Glu Asn His Val Gln Asp Gly Glu Val Val Gly Ser
690 695 700

Gln Ala Asp Leu Thr Glu Gln Glu Pro Leu Glu Leu Lys Thr Gln Leu
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Glu Arg Thr Glu Thr Ile Leu Glu Lys Glu Gln Ile Gln Arg Gln Lys
725 730 735

Leu Thr Thr Glu Phe Glu Glu Ala Gln Asn Ser Val Phe Asn Leu Gln
740 745 750

Ala Glu Leu Glu Lys Leu Arg Ala Ser Ile Gly Val Glu Ser Ser Glu
755 760 765

Thr Glu Glu Ala Val His Leu Lys Glu Arg Leu Glu Lys Glu Lys Met
770 775 780

Met Thr Thr Ser Leu Gly Gln Ala Ala Thr Lys Leu Gln Gly Leu Leu
785 790 795 800

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

Ala Arg Gly Arg Arg Asp Pro Asn Leu Ser Ala Ser Arg Leu Arg Gln
65                  70                  75                  80

Ser Arg Ile Leu Val Arg Asp Cys Trp Glu Arg Arg Gly Pro Arg Val
                85                  90                  95

Gly Gly Ala Gly Arg Arg Pro Pro Pro Arg Asp Arg Gln Ser Gly Gly
            100                 105                 110

Val Arg Thr Asn Gly Lys Arg Arg Leu Asp Glu Trp Leu Ala Arg Val
        115                 120                 125

Gly Lys Ala Gly Gly Gly Asp Pro Gly Gly Gly Gly Arg Ser Pro Ala
    130                 135                 140

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

Ala Ala Gly Ala Asp Gly Arg Arg Gly Gly Arg Arg Gln Gly Arg Ser
                165                 170                 175

Val Tyr Ser Cys Ser Gly Ala Val Ser Trp Arg Arg Leu Gly Arg Leu
            180                 185                 190

Leu Ser Pro Gly Ser Ala Ala Ala Ala Lys Ala Ala Ser Pro Ala Leu
        195                 200                 205

Ser Leu Ser Phe Ser Arg Leu Trp Leu Gln Val Lys Gly Lys Gln Ala
    210                 215                 220

Arg Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly
225                 230                 235                 240

Gly Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe
                245                 250                 255

Ser Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys
            260                 265                 270

Glu Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu
        275                 280                 285

Lys Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro
    290                 295                 300
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Asn Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu
305                 310                 315                 320

Leu Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro
                325                 330                 335

Val Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met
            340                 345                 350

Pro Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu
        355                 360                 365

Lys Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser
    370                 375                 380

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

Glu Val Pro Met Val Ala Val Pro Pro Val Gly Ala Lys Gly Asn Thr
                405                 410                 415

Pro Ala Thr Gly Thr Ala Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn
            420                 425                 430

Gln Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu
        435                 440                 445

Gly Thr Pro Asn Gln Gly Lys Lys Thr Glu Gly Thr Pro Asn Gln Gly
    450                 455                 460

Lys Lys Ala Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Thr
465                 470                 475                 480

Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys
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Val Asp Thr Thr Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Pro Thr
            500                 505                 510

Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Ala Lys Lys Val Glu
        515                 520                 525

Gly Ala Gln Asn Gln Gly Lys Lys Ala Asp Gly Ala Gln Asn Gln Gly
    530                 535                 540

Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala
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Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Gln Lys Glu Gly Lys Lys
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Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Xaa Xaa Gly
595 600 605

Ala Gln Asn Gln Gly Lys Ser Arg Arg Gly Pro Glu Pro Gly Gln Glu
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Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Pro Arg Xaa
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Ser Gly Gln Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu
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Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly
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Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala
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Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys
690 695 700

Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn
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Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Val Glu
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Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly
740 745 750

Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala
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Gln Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys Lys
770 775 780

Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn
785 790 795 800

Gln Gly Arg Lys Ala Glu Gly Ala Gln Asn Gln Gly Gln Lys Gly Glu
805 810 815

Gly Ala Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Pro Asn Gln Gly
820 825 830

Lys Lys Gly Glu Gly Ala Pro Asn Gln Gly Lys Lys Ala Asp Ser Ala
835 840 845

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Ala Glu Gly Ser Pro Ser Gln Gly Lys Lys Ala Glu Gly Ser Pro Asn
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Gln Gly Lys Lys Ala Asp Ala Ala Ala Asn Gln Gly Lys Lys Thr Glu
                885                 890                 895

Ser Ala Ser Val Gln Gly Arg Asn Thr Asp Val Ala Gln Ser Pro Glu
            900                 905                 910

Ala Pro Lys Gln Glu Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys
        915                 920                 925

Lys Gly Glu Pro Gly Pro Pro Asp Ala Asp Gly Pro Leu Tyr Leu Pro
    930                 935                 940

Tyr Lys Thr Leu Val Ser Thr Val Gly Ser Met Val Phe Asn Glu Gly
945                 950                 955                 960

Glu Ala Gln Arg Leu Ile Glu Ile Leu Ser Glu Lys Ala Gly Ile Ile
                965                 970                 975

Gln Asp Thr Trp His Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile
            980                 985                 990

Leu Lys Arg Gln Leu Glu Glu Lys  Glu Lys Leu Leu Ala  Thr Glu Gln
        995                 1000                1005

Glu Asp  Ala Ala Val Ala Lys  Ser Lys Leu Arg Glu  Leu Asn Lys
    1010                1015                1020

Glu Met  Ala Ala Glu Lys Ala  Lys Ala Ala Ala Gly  Glu Ala Lys
    1025                1030                1035

Val Lys  Lys Gln Leu Val Ala  Arg Glu Gln Glu Ile  Thr Ala Val
    1040                1045                1050

Gln Ala  Arg Met Gln Ala Ser  Tyr Arg Glu His Val  Lys Glu Val
    1055                1060                1065

Gln Gln  Leu Gln Gly Lys Ile  Arg Thr Leu Gln Glu  Gln Leu Glu
    1070                1075                1080

Asn Gly  Pro Asn Thr Gln Leu  Ala Arg Leu Gln Gln  Glu Asn Ser
    1085                1090                1095

Ile Leu  Arg Asp Ala Leu Asn  Gln Ala Thr Ser Gln  Val Glu Ser
    1100                1105                1110
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Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu
1145 1150 1155

Lys Gln Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu
1160 1165 1170

Ala Leu Gln Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys His
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Ala Gln Ser Ser His Ala Ser Leu Arg Ala Asp Val Glu Lys Ala
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Gln Glu Gln Gln Gln Gln Met Ala Glu Leu His Ser Lys Leu Gln
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Ser Ser Glu Ala Glu Val Arg Ser Lys Cys Glu Glu Leu Ser Gly
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Leu His Gly Gln Leu Gln Glu Ala Arg Ala Glu Asn Ser Gln Leu
1235 1240 1245

Thr Glu Arg Ile Arg Ser Ile Glu Ala Leu Leu Glu Ala Gly Gln
1250 1255 1260

Ala Arg Asp Ala Gln Asp Ala Gln Ala Ser Gln Ala Glu Ala Asp
1265 1270 1275

Gln Gln Gln Thr Arg Leu Lys Glu Leu Glu Ser Gln Val Ser Gly
1280 1285 1290

Leu Glu Lys Glu Ala Ile Glu Leu Arg Glu Ala Val Glu Gln Gln
1295 1300 1305

Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Lys Ala Met
1310 1315 1320

Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys Lys Glu Lys Leu His
1325 1330 1335

Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu Cys Leu
1340 1345 1350

Ile Glu Ala Gln Thr Met Glu Ala Leu Leu Ala Leu Leu Pro Glu
1355 1360 1365

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Leu Ser  Val Leu Ala Gln Gln  Asn Tyr Thr Glu Trp  Leu Gln Asp
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Leu Lys  Glu Lys Gly Pro Thr  Leu Leu Lys His Pro  Pro Ala Pro
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Thr Glu  Pro Ser Ser Asp Leu  Ala Ser Lys Leu Arg  Glu Ala Glu
    1400                 1405                 1410

Glu Thr  Gln Ser Thr Leu Gln  Ala Glu Cys Asp Gln  Tyr Arg Ser
    1415                 1420                 1425

Ile Leu  Ala Glu Thr Glu Gly  Met Leu Arg Asp Leu  Gln Lys Ser
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Val Glu  Glu Glu Glu Gln Val  Trp Arg Ala Lys Val  Gly Ala Ala
    1445                 1450                 1455

Glu Glu  Glu Leu Gln Lys Ser  Arg Val Thr Val Lys  His Leu Glu
    1460                 1465                 1470

Glu Ile  Val Glu Lys Leu Lys  Gly Glu Leu Glu Ser  Ser Asp Gln
    1475                 1480                 1485

Val Arg  Glu His Thr Ser His  Leu Glu Ala Glu Leu  Glu Lys His
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Met Ala  Ala Ala Ser Ala Glu  Cys Gln Asn Tyr Ala  Lys Glu Val
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Ala Gly  Leu Arg Gln Leu Leu  Leu Glu Ser Gln Ser  Gln Leu Asp
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Ala Ala  Lys Ser Glu Ala Gln  Lys Gln Ser Asp Glu  Leu Ala Leu
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Val Arg  Gln Gln Leu Ser Glu  Met Lys Ser His Val  Glu Asp Gly
    1550                 1555                 1560

Asp Ile  Ala Gly Ala Pro Ala  Ser Ser Pro Glu Ala  Pro Gln Ala
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Glu Gln  Asp Pro Val Gln Leu  Glu Thr Gln Leu Glu  Arg Thr Glu
    1580                 1585                 1590

Ala Ile  Leu Glu Asp Glu Gln  Thr Gln Arg Gln Lys  Leu Thr Ala
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Glu Phe  Glu Glu Ala Gln Thr  Ser Ala Cys Arg Leu  Gln Glu Glu
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Leu Thr Ser Asp Leu Gly Arg Ala Ala Thr Lys Leu Gln Glu Leu
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Leu Lys Thr Thr Gln Glu Gln Leu Ala Arg Glu Lys Asp Thr Val
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Met Ala Lys Thr Ser His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
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Gly Lys Ile Pro Asp His Glu Pro Thr Pro Gly Val Thr Ile Val Pro
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Lys Asp Pro Val Trp Ala Pro Ala Val Ala Val Gly Ala Thr Pro Val
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Glu Phe Pro Pro Pro Xaa Leu Ala Asp Tyr Ala Pro Pro Pro Ala Thr
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Pro Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu
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Val Gly Ser Met Val Leu Ser Glu Gly Glu Ala Gln Arg Leu Met Glu
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Ile Leu Ala Asp Lys Ala Gly Ile Met Gln Asp Thr Trp His Lys Ala
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Thr Gln Lys Gly Asp Pro Val Val Ile Leu Lys Arg Gln Leu Glu Glu
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Gln Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu
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Pro Glu Pro Leu Asp Leu Ala Ala Lys Leu Arg Glu Ala Glu Glu Thr
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Gln Ser Gly Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala
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Glu Thr Arg Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala Arg Val
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Leu Glu Glu Val Val Glu Lys Leu Lys Gly Glu Leu Glu Ser Ser Asp
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Gln Val Arg Glu His Thr Trp Arg Leu Glu Ala Glu Leu Glu Lys His
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Val Ala Ala Ala Ser Ala Glu Cys Gln Ser Tyr Ala Gln Glu Val Ala
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Gly Leu Arg Gln Leu Leu Leu Glu Ser Gln Ser Gln Leu Asp Ala Ala
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Lys Ser Glu Ala Gln Lys Gln Ser Asp Glu Leu Ala Leu Val Arg Gln
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Gln Leu Ser Glu Met Lys Ser His Val Glu Asp Gly Asp Val Ala Glu
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Ala Pro Arg Ala Glu Gln Asp Pro Ala Glu Leu Lys Thr Gln Leu Glu
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Cys Thr Ser Ala Leu Gly Ser Ser Glu Val Glu Glu Ala Ala Gln Leu
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Ala Ala Thr Lys Leu Gln Glu Leu Leu Lys Thr Thr Gln Glu Gln Leu
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Leu Glu Lys Thr Gln Gln Gln Lys Leu Glu Lys Lys Lys Lys Asp Lys
50 55 60

Pro Val Glu Lys Lys Gly Lys Ala Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Glu Gln Gln Leu Thr Gln Glu Val Thr Asp Pro Pro
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Lys Glu Val Leu Pro Glu Pro Ala Ala Val Pro Glu Pro Val Arg Val
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Glu Thr Pro Val Ala Ala Val Ala Val Val Pro Gln Glu Lys Glu Lys
115 120 125

Pro Ala Pro Lys Ser Pro Lys Glu Lys Arg Lys Lys Glu Lys Lys Val
130 135 140

Ala Lys Val Glu Pro Ala Pro Ser Pro Val Leu Ala Pro Pro Pro Val
145 150 155 160

Ser Val Pro Lys Ser Ser Pro Val Arg Glu Val Ala Pro Lys Glu Val
165 170 175

Pro Val Val Ala Val Pro Pro Val Gly Thr Gln Gln Ser Ala Pro Val
180 185 190

Ile Ser Ser Val Thr Val Lys Lys Thr Glu Ala Leu Pro Ala Gln Glu
195 200 205

Asp Gln Lys His Asp Ala Pro Ala Lys Lys Lys Ala Ala Ser Lys Lys
210 215 220

Lys Ser Glu Pro Ala Pro Thr Asp Ser Asp Gly Ala Leu Tyr Leu Pro
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Tyr Lys Thr Leu Val Ser Thr Val Arg Ser Met Val Phe Ser Glu Gly
245 250 255

Glu Ala Gln Gln Leu Ile Glu Ile Leu Thr Glu Lys Ala Gly Ile Ile
260 265 270

Gln Asp Thr Trp His Thr Ala Thr Gln Lys Gly Asp Pro Val Ala Val
275 280 285

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Glu Asp Ala Ala Ala Ala Arg Ser Lys Leu Arg Glu Leu Ser Lys Glu
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325 330 335

Glu Gln Leu Leu Ala Arg Glu Arg Glu Ile Val Ala Val Gln Ala Arg
340 345 350

Met Gln Ala Ser Tyr Gln Asp His Val Ser Glu Thr Gln Gln Leu Gln
355 360 365

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Gly Lys Ile Arg Thr Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr
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Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu
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Asn Gln Ala Thr Ser Gln Met Glu Ser Lys Gln Asn Ala Glu Leu Ala
                405                 410                 415

Lys Leu Arg Gln Glu Cys Ser Lys Leu Met Lys Glu Leu Ser Glu Lys
            420                 425                 430

Ser Glu Val Leu Gln Gln Glu Glu Gln Gln Arg Lys Ser Trp Glu Ile
        435                 440                 445

Lys Ala Thr Ala Ser Glu Lys Arg Ile Glu Gln Leu Gln Ala Tyr Gln
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Arg Glu Ala Glu Val Met Leu Gln Lys Arg Leu Asp Glu Val Ser Asp
465                 470                 475                 480

Glu Leu Arg Lys Thr Gln Ser Ser Tyr Lys Ser Leu Leu Ala Asp Ala
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Glu Lys Thr Lys Gly Gln Gln Gln Ser Ile Ala Glu Leu Gln Ala Lys
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Leu Leu Ser Ser Glu Ala Glu Val Lys Ser Lys Leu Leu Glu Leu Asp
        515                 520                 525

Ser Val Lys Gly Lys Leu Gln Asp Ala Ser Ser Glu Asn Ala Lys Leu
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Leu Glu Arg Ile Lys Ser Ile Glu Ala Leu Leu Glu Ala Gly Arg Met
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Arg Glu Ala Glu Lys Asp Arg Asp Leu Gln Ala Ala Asn Glu Ala Glu
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Met Lys Gln Leu Gln Ser Arg Leu Gln Glu Lys Thr Asn Gln Leu Ser
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Ala Leu Glu Arg Glu Ala Thr Gln Leu Arg Glu Ala Val Glu Gln Gln
        595                 600                 605

Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Lys Ala Met Glu
    610                 615                 620

Ala Val Thr Thr Val Glu Lys Ala Cys Glu Glu Lys Leu Leu Ala Ala
625                 630                 635                 640
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Thr Lys Ala Lys Glu Glu Leu Ala Gln Gln Leu Asp Ala Val Gln Thr
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Arg Thr Lys Gln Met Leu Leu Ser Ala Leu Pro Gly Val Thr Met Ser
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Ser Gln Gln Asp Tyr Asp Thr Trp Leu Gln Glu Phe Lys Glu Lys Thr
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Val Ala Val Leu Lys Gln Gln Met Ile Thr Ala Glu Ser Pro Asp Ser
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Ala Leu Lys Leu Lys Glu Ala Glu Glu Ala Gln Ser Thr Leu Gln Ala
705                 710                 715                 720

Glu Cys Glu Gln Tyr Arg Thr Ile Leu Ala Glu Thr Glu Gly Met Leu
                725                 730                 735

Arg Asn Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala
            740                 745                 750

Lys Leu Thr Ala Ser Glu Glu Glu Leu Gln Lys Ser His Leu Gln Leu
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Lys Ser Leu Glu Gly Val Val Glu Lys Leu Lys Ala Asp Leu Gln Ser
    770                 775                 780

Thr Asp Gln Leu Lys Glu Tyr Thr Ser Leu Leu Glu Thr Gln Leu Glu
785                 790                 795                 800

Asn His Leu Glu Thr Ala Ser Ser Glu Arg Gln Asn Tyr Thr Lys Glu
                805                 810                 815

Val Glu Ala Leu Arg Gln Leu Leu Ser Glu Ser Gln Glu Gln Leu Glu
            820                 825                 830

Ala Ala Lys Thr Glu Thr Gln Lys Gln Ser Lys Glu Leu Ala Leu Val
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Arg Gln Gln Leu Ser Glu Ala Lys Thr His Val Gln Glu Gly Glu Val
    850                 855                 860

Val Gly Leu Gln Ala Glu Pro Ser Glu Pro Ala Ala Leu Glu Leu Lys
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Thr Gln Leu Glu Gln Asn Glu Thr Leu Ala Glu Lys Glu Gln Met Leu
                885                 890                 895

Arg Gln Lys Leu Ala Arg Glu Leu Glu Glu Ala Gln Ser Leu Ala Arg
            900                 905                 910
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Ser Leu Gln Ala Glu Leu Glu Lys Leu Arg Leu Ala Glu His Ala Ala
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Ala Ser Asp Lys Glu Glu Ala Gln His Leu Lys Glu Arg Leu Glu Lys
930 935 940

Glu Lys Lys Leu Thr Lys Asp Leu Gly Gln Ala Ala Thr Lys Leu Gln
945 950 955 960

Glu Leu Leu Lys Val Ser Gln Asp Gln Val Ala Lys Glu Arg Glu Val
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Ser Lys Glu Gly Thr Ser Val
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<400> 55

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35 40 45

Leu Glu Lys Thr Asn Gln His Lys Ile Glu Lys Lys Lys Lys Glu Lys
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Pro Val Glu Lys Lys Gly Lys Ala Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Glu Gln Gln Val Thr Gln Glu Val Thr Asp Ser Ser
85 90 95

Lys Asp Val Val Val Glu Pro Ala Val Val Pro Glu Pro Val Ala Val
100 105 110

Glu Ser Pro Ile Ala Ala Val Ser Val Pro Pro Gln Glu Lys Glu Lys
115 120 125

Pro Ala Leu Ser Pro Lys Glu Lys Arg Lys Lys Glu Lys Lys Val Ala
130 135 140

Lys Val Glu Pro Ala Pro Ser Pro Ala Leu Ala Ser Pro Pro Ala Ser
145 150 155 160

Val Pro Lys Gly Ser Pro Val Leu Glu Val Thr Pro Lys Glu Val Pro
165 170 175

Val Val Ala Val Pro Pro Val Gly Thr Gln Gln Ser Ala Pro Val Val
180 185 190

Ser Ser Val Pro Ile Lys Lys Pro Glu Ala Leu Pro Thr His Glu Glu
195 200 205

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Gln Lys His Asp Gly Pro Val Lys Lys Lys Ser Ala Ser Lys Lys Lys
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Ala Glu Pro Ala Pro Ala Asp Ser Asp Gly Pro Leu Tyr Leu Pro Tyr
225                 230                 235                 240

Lys Thr Leu Val Ser Thr Ile Ser Ser Met Ala Phe Ser Glu Gly Glu
                245                 250                 255

Ala Gln Gln Leu Ile Glu Ile Leu Thr Glu Arg Ala Gly Ile Val Gln
            260                 265                 270

Asp Thr Trp His Thr Ala Thr Gln Lys Gly Asp Pro Val Ala Val Leu
        275                 280                 285

Lys Arg Gln Leu Glu Glu Lys Glu Lys Gln Leu Thr Ala Glu Gln Glu
    290                 295                 300

Asp Ala Ala Ala Ala Arg Asn Lys Leu Arg Glu Leu Ser Lys Glu Leu
305                 310                 315                 320

Ala Ala Glu Lys Ala Lys Ala Ala Ala Ser Glu Ser Lys Leu Lys Glu
                325                 330                 335

Gln Leu Val Thr Arg Glu Arg Glu Ile Thr Ala Val Gln Ala Arg Met
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Gln Ala Ser Tyr Gln Asp His Val Asn Glu Thr Gln Gln Leu Gln Gly
        355                 360                 365

Lys Ile Arg Ala Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln
    370                 375                 380

Leu Ala Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn
385                 390                 395                 400

Gln Ala Thr Ser Gln Thr Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys
                405                 410                 415

Leu Arg Gln Glu Cys Asn Lys Leu Met Lys Glu Leu Ser Glu Lys Ser
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Glu Val Leu Gln Gln Glu Glu Gln Gln Lys Lys Ser Trp Glu Ile Lys
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Ala Ala Ala Ser Glu Lys Gln Ile Glu Gln Leu Gln Thr Ser Gln Arg
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Glu Met Glu Ala Thr Leu Gln Lys Arg Leu Asp Glu Val Ser Asp Glu
465                 470                 475                 480
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Lys Ala Lys Gly Gln Gln Gln Ser Ile Ala Glu Leu Gln Ala Lys Leu
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515 520 525

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Glu Arg Ile Lys Ser Ile Glu Ala Leu Leu Glu Ala Gly Arg Met Arg
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Glu Ala Glu Glu Asp Arg Asp Leu Gln Ala Ala Asn Glu Ala Glu Met
565 570 575

Lys Gln Leu Gln Leu Arg Leu Gln Glu Lys Thr Asp Gln Leu Leu Ser
580 585 590

Leu Glu Arg Glu Ala Ala Glu Leu Arg Glu Ala Met Glu Gln Gln Lys
595 600 605

Thr Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Lys Ala Val Glu Ala
610 615 620

Leu Thr Thr Val Glu Lys Ala Cys Glu Glu Lys Leu Leu Ala Ala Thr
625 630 635 640

Lys Ala Lys Glu Glu Leu Ala His Gln Leu Asp Val Leu Gln Thr Arg
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Thr Lys Glu Thr Leu Leu Ser Ala Leu Pro Glu Val Thr Val Ser Gln
660 665 670

Gln Asp Tyr Glu Ala Trp Leu Gln Glu Phe Lys Glu Lys Ala Val Asn
675 680 685

Val Leu Lys Gln His Thr Val Met Thr Glu Pro Val Asp Ser Ala Leu
690 695 700

Lys Leu Lys Glu Ala Glu Glu Ala Gln Ser Thr Leu Gln Ala Glu Cys
705 710 715 720

Glu Gln Tyr Arg Ala Ile Leu Ala Glu Thr Glu Gly Met Leu Arg Asp
725 730 735

Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala Lys Leu
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Thr Val Ser Glu Glu Glu Leu Gln Lys Ser Gln Leu Gln Leu Lys Ser
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Leu Glu Asp Met Ile Glu Lys Leu Lys Ala Glu Leu Gln Ser Thr Asp
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Gln Leu Lys Glu Tyr Ile Ser Leu Leu Glu Ala Gln Leu Glu Asn His
785                 790                 795                 800

Leu Gln Thr Ala Ser Ser Glu Arg Gln Asn Tyr Thr Lys Glu Val Glu
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Gly Leu Arg Gln Leu Leu Ser Glu Ser Gln Glu Gln Leu Glu Ala Ala
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Lys Thr Glu Thr Gln Lys Gln Ser Lys Glu Leu Ala Leu Val Arg Gln
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Gln Leu Ser Glu Met Lys Ser His Val Gln Asp Gly Glu Val Ala Gly
    850                 855                 860

Ser Gln Ala Asp Leu Gly Asp Pro Thr Pro Phe Glu Leu Lys Met Gln
865                 870                 875                 880

Leu Glu Gln Asn Glu Ala Leu Met Glu Lys Glu Gln Glu Leu Arg Gln
                885                 890                 895

Lys Leu Thr Arg Glu Leu Glu Glu Ala Gln Ser Ser Ala Cys Ser Leu
            900                 905                 910

Gln Ala Glu Leu Glu Lys Leu Arg Leu Ala Glu Asn Ala Ala Ala Ser
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Asp Met Glu Glu Ala Gln His Leu Lys Glu Arg Leu Glu Lys Glu Lys
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Lys Leu Thr Arg Asp Leu Gly Gln Ala Ala Thr Lys Leu Gln Glu Leu
945                 950                 955                 960

Leu Lys Val Thr Gln Asp Gln Leu Ala Lys Glu Arg Glu Thr Val Lys
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Glu Gly Thr Ser Val
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tctgtacgtc aatcagtgca attgttgttt gttgggggtt ggggtgggag tgactgtttc 3240

tgcagagtca ttgagaatgg ggagaaagag ccagcttgag agg 3283

<210> 57
<211> 918
<212> PRT
<213> Sarcophilus harrisii

<400> 57

Met Asp Ile Tyr Asp Pro Gln Thr Leu Gly Val Met Val Phe Gly Gly
1 5 10 15

Phe Met Val Ile Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45

Met Ala Lys Asn His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
50 55 60

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Pro Val Glu Lys Lys Gly Arg Ala Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

Gly Lys Ile Pro Glu Pro Glu Leu Phe Pro Asn Val Thr Val Ile Ser
                85                  90                  95

Lys Asp Pro Ile Pro Glu Thr Gly Val Val Val Ala Pro Ile Val Leu
            100                 105                 110

Glu Pro Ala Val Pro Val Ala Pro Val Ala Ala Val Val Ala Ser Thr
        115                 120                 125

Pro Ala Pro Leu Gln Gly Gln Pro Ala Ser Ser Pro Lys Glu Lys Arg
    130                 135                 140

Lys Lys Glu Lys Lys Val Ala Lys Val Glu Pro Ala Pro Asn Pro Val
145                 150                 155                 160

Val Ser Ser Ile His Val Leu Ser Ser Lys Ser Ser Val Leu Glu Ala
                165                 170                 175

Ala Pro Lys Glu Val Pro Val Val Ala Val Pro Pro Val Gly Thr Lys
            180                 185                 190

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

Ile Val Asn His Glu Glu Pro Lys Asn Glu Val Pro Ser Lys Lys Lys
    210                 215                 220

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

Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr Leu Arg Ser Thr Val
                245                 250                 255

Phe Asn Glu Gly Glu Ala His Cys Leu Ile Glu Ile Leu Ser Glu Lys
            260                 265                 270

Ala Gly Ile Val Gln Asp Thr Trp His Lys Ala Thr Gln Lys Gly Asp
        275                 280                 285

Pro Val Ala Val Leu Lys Arg Gln Leu Glu Glu Lys Glu Lys Leu Leu
    290                 295                 300

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

Leu Asn Lys Glu Leu Ala Ser Glu Lys Ser Lys Ala Ala Ala Gly Glu
                325                 330                 335
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Ala Asn Val Lys Lys Gln Leu Leu Ala Arg Glu Gln Glu Ile Val Ala
            340                 345                 350

Val Gln Ala Arg Met Lys Ala Ser Tyr Arg Asp His Val Asn Glu Val
        355                 360                 365

Gln Gln Leu Gln Gly Lys Ile Arg Ser Leu Gln Glu Gln Leu Glu Asn
    370                 375                 380

Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser Ile Leu
385                 390                 395                 400

Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Thr Glu Ser Lys Gln Asn
                405                 410                 415

Ala Glu Leu Ala Lys Leu Arg Gln Glu Cys Cys Lys Leu Thr Lys Glu
            420                 425                 430

Val Ala Glu Lys Ser Glu Ala Val Gln Gln Glu Glu Glu Gln Lys Lys
        435                 440                 445

Ser Leu Glu Val Lys Thr Ala Ala Leu Glu Lys Gln Val His Gln Leu
    450                 455                 460

Gln Val Ser Gln Lys Glu Lys Glu Asp Thr Leu Gln Lys Arg Leu Asp
465                 470                 475                 480

Glu Val Ser Gly Glu Leu Arg Lys Ser Gln Ser Ile Tyr Lys Asn Leu
                485                 490                 495

Leu Ala Asp Leu Glu Lys Ala Lys Gly Asp Gln Gln Asn Ile Thr Glu
            500                 505                 510

Leu Arg Ser Lys Leu Gln Ser Ser Glu Thr Glu Val Lys Ser Lys Ser
        515                 520                 525

Glu Glu Leu Asn Lys Leu Lys Gly Lys Leu Leu Glu Ser Ser Ala Glu
    530                 535                 540

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

Ala Gly Gln Ala Lys Glu Ala Lys Asp Ala Gln Ala Asn Gln Ala Glu
                565                 570                 575

Val Asp Gln Leu Gln Ala Arg Leu Lys Glu Arg Glu Val Gln Val Ala
            580                 585                 590

Ser Leu Glu Lys Glu Ala Thr Glu Leu Lys Glu Ala Val Glu Gln Gln
        595                 600                 605
```

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Lys Leu Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Arg Ala Met Glu
    610                 615                 620

Ala Leu Ala Ser Ala Glu Lys Gly Cys Glu Glu Lys Leu Ser Ser Leu
625                 630                 635                 640

Ser Lys Ala Lys Glu Glu Val Glu Lys Gln Tyr Ser Ile Ser Gln Arg
                645                 650                 655

Lys Thr Lys Glu Thr Leu Leu Ser Leu Phe Pro Asp Ile Ser Ile Ala
            660                 665                 670

Thr Gln Gln Ser Tyr Asp Glu Trp Leu Gln Glu Phe Lys Glu Lys Ser
        675                 680                 685

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

Ala Ser Lys Leu Lys Asp Ala Glu Glu Ala Gln Asn Thr Leu Gln Ser
705                 710                 715                 720

Glu Cys Asp Gln Tyr Arg Thr Ile Leu Ala Glu Thr Glu Gly Met Leu
                725                 730                 735

Lys Asp Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala
            740                 745                 750

Lys Leu Thr Val Ser Glu Glu Glu Leu Gln Lys Ser Gln Ile Lys Val
        755                 760                 765

Lys His Leu Glu Glu Thr Met Glu Lys Leu Lys Gly Asp Leu Gln Asn
    770                 775                 780

Thr Ala Gln Val Lys Glu His Ala Ala Leu Leu Glu Ala Arg Leu Glu
785                 790                 795                 800

Glu His Met Ser Ala Ser Thr Ala Glu Cys Gln Lys Tyr Ala Lys Glu
                805                 810                 815

Val Glu Leu Leu Arg Asp Leu Leu Thr Glu Ala Arg Glu Gln Met Asp
            820                 825                 830

Ala Thr Asn Ser Glu Ala Gln Lys Gln Ser Lys Glu Leu Ala Leu Val
        835                 840                 845

Arg Lys Gln Leu Ser Glu Met Lys Asn His Val Gln Asp Gly Glu Val
    850                 855                 860

Val Gly Ser Gln Ala Asp Leu Thr Glu Gln Glu Pro Leu Glu Leu Lys
865                 870                 875                 880
```

Thr Gln Leu Glu Gln Thr Glu Ile Leu Leu Glu Lys Glu Gln Ile Gln
885 890 895

Arg Gln Lys Leu Thr Val Glu Phe Glu Glu Asp Ala Gly Ser Ala
900 905 910

Lys Glu Gly Thr Ser Val
915

<210> 58
<211> 3667
<212> DNA
<213> Xenopus (Silurana) tropicalis

<400> 58
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cgtcatggtg tttggtggct ttatgttggt ttctgctctt ggaatctttc ttgtgtcaac 120

cttttcaatg aaagagacat cctatgaaga agcattggcc aagcagcgca aagaaactga 180

gaagaaccag cccaaagttg ataagaagaa gaaagaaaag ctcccagttc aaaaaggaaa 240

agctaaaaag aaggatgaaa agcccaatgg aaaaatacct gaacatgaat ctaaccagga 300

acctacagac ccaaaaaaaa aagctgaatc tggacatgag ctaattctgg agaagacacc 360

agtgcctgtt gtaccagttg tacctgtgga agttccaatt gtgcctgtgg tagcaccagt 420

tcctaagaaa tctgctccag gttctgtaaa atctgctcca gtttccgaaa aacctgctcc 480

cgtttctcaa aagcctgctc ccgtttctca aaagcctgct cccgtttctc aaaagcctgc 540

tccggtttcc caaaagcctg ctccggtttc ccaaaagcct gctccggttt ctcaaaagcc 600

tgctccggtt tcccaaaagc ctgctccggt ttcccaaaag cctgctccgg tttcccaaaa 660

gcctgctccg gtttcccaaa agcctgctcc ggtttctcaa aagcctgctc ccgtttctca 720

aaagcctgct cccgttcccg aaaagcccgc tcctgcttcc gaaaagcctg ctccagttca 780

agaaaaatct gctccatctc ctaaagacaa aaagaaaaag ccggaaaaga aggtccttaa 840

ggttgaacca tctccaagtc cagctgtaac tttcacccag gctgtgtcct ctaagcatgt 900

gccagtgtta gatgcaccta tcaaagaagt gcctgtcgtt gcagtatctc ctgttggatc 960

tcagcctgca tcctccactc aacccccctaa aaaagctgaa gccatagtta atcaagaaga 1020

ctccaaacag gagaatgtgc caaagaaaaa gagtgctcct aagaaaaaaa ctgaaccaag 1080

tgcagaggaa tgtgaaggtg cagtttatat tccatacaag accctggttc ctaccatcca 1140

atcaatgtgt ttcagcaaag gagaagctca gaagctgatt gaaatactgg cagaaaaata 1200

tggcatcatg caggatactt ggcaaacggc aactcaaaaa ggagatccag tggcagctct 1260

taaacgggtg gtggaggaga aggagaagtt actgttggcc cagcatgaaa agaccaactc 1320

ttataaggaa aagttcatgg aagttaacaa ggaactgcag agtgagaagt ccagggctaa 1380

aacggagcag accaaattta aggagcagct ggtgactcgc gaacaggaga tcaatgcatt 1440

gcaagcacgc atgcaggcca gctatcagga ccatgtaaat gagactcagc agctgcaaac 1500

caaggttcgg tccctgcaag aggaaataga gaatggcccc aaggcacagc ttactcgcct 1560

gcagcaggag aattctatcc ttagggatgc cttaaaccag gccacaagcc agacagagag 1620

caaacaaaat gctgagttgg caaaactgcg tcaagagtgc agcaaactct ctaaggaact 1680

tagtgacaag tctgagtcct tgcagcaaga ggaacaacgt agaaagtccc ttgatggtaa 1740

agtagtgaca tacgagaagc agatcactca gctgcagaca ttacagcagg agggtgaaac 1800

cacattacaa aagagattag atgaagttaa tgaagaactg cgcaagtctc agagcactta 1860

ccagaaccta ctggcagaca cagaaaaggc caaggcagaa cagaagaacc atgcagatct 1920

tcaaactaaa ctgcagtcct atgaagcaga aagcaagcag aaatcagaag agctggataa 1980

attgaacaaa cagcttcaag gggtttcagg agaaaattcc cagcttatgg aaaggataaa 2040

atccatagag gcactgctgg aggcaggaca gaataaagac actgataaag aaaagcagca 2100

gcaggaagta agagaagctg aaactgcaca actacaaatc aggcttcaag aaaaagattc 2160

acatattgca tctctagaaa aggaaacttc tgaattaaaa gaagcggttg aacaacagaa 2220

aaataaaaat aatgatttaa gggagaagaa ttggcaagcc atggaagcac tgggcttgtc 2280

agaaaagacc agtgaggaga agctgaactc tgaaaagaag gcaaaggaag aaatggtaca 2340

acaactcaat gcagtacaga tacagacaaa agaaacgctg cagttactat atccacagat 2400

cactattgag ccacaacagt catatagtga gtggttacag gagttcagac agaggacgac 2460

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agaagcggaa gatacacaga gtgctctaca gactgaatgt gagcagtaca gaaccatcct 2580

tggagaaaca gaagcaatgc ttaaagctct tcagaagagt gttgaagaag aggagcaagt 2640

atggaaggca aaattagcag catcagagga agatctctca aagtcacatt cccaggtgaa 2700

aacactagaa gaaactgtgg aaaaattaag gtcagatctt caaagcacag aacagctaaa 2760

agagtgtata tctctgatgg aggcacagct ggagacccag atgaatgcaa aaagtacaga 2820

atgccagact tactcaaacg aaatagagag tttgcagcag cttttatcag aatctcagga 2880

acacctaaat gctaccaaag ctgaagcaag gaagcaaagc gtagaactct ctgtgctccg 2940

gcaacaactt agtgaaatgc aaaatcatgt aaatgatact gaacaccaga cttcaaagat 3000

catggaagta ccaatggtaa atcttgagag cactttagca gaaacacaag agcagaaatc 3060

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catgaattct tcctctatta cccaaatgcc ttaaacattc ctttcttgaa attaaaatag 3240

taataacatt ctagtgagcc aaaacacttc agaaacacaa gtgagaagta acgttatata 3300

ctttttttata tgaacaaagt actttacata ttaaataaaa aaaaaccaga ccaaaagagc 3360

acaagaatct gtgtgagcaa gccaattcca ctaacccact cctctagcct acggagagca 3420

gggagcgtgg gtgttatgca aagggaaaga ctctatgctg tgtacaggaa acagtgcaat 3480

ttctttattg tttgtctttt gagtgatgat ggatgaacgg aagccaagaa gtgattatga 3540

agatgcctaa tgtattggaa ctggtctcca gtataaaacc atgtgaattg ttaagattcc 3600

aaaatgccat taaaatgaag atgtgtccaa atggaaaaaa aaaaaaaaaa caaaaaaaaa 3660

aaaaaaa 3667

<210> 59
<211> 1037
<212> PRT
<213> Xenopus (Silurana) tropicalis

<400> 59

Met Val Phe Gly Gly Phe Met Leu Val Ser Ala Leu Gly Ile Phe Leu
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Val Ser Thr Phe Ser Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala
20 25 30

Lys Gln Arg Lys Glu Thr Glu Lys Asn Gln Pro Lys Val Asp Lys Lys
35 40 45

Lys Lys Glu Lys Leu Pro Val Gln Lys Gly Lys Ala Lys Lys Lys Asp
50 55 60

Glu Lys Pro Asn Gly Lys Ile Pro Glu His Glu Ser Asn Gln Glu Pro
65 70 75 80

Thr Asp Pro Lys Lys Lys Ala Glu Ser Gly His Glu Leu Ile Leu Glu
85 90 95

Lys Thr Pro Val Pro Val Val Pro Val Val Pro Val Glu Val Pro Ile
100 105 110

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

Lys Ser Ala Pro Val Ser Glu Lys Pro Ala Pro Val Ser Gln Lys Pro
130 135 140

Ala Pro Val Ser Gln Lys Pro Ala Pro Val Ser Gln Lys Pro Ala Pro
145 150 155 160

Val Ser Gln Lys Pro Ala Pro Val Ser Gln Lys Pro Ala Pro Val Ser
165 170 175

Gln Lys Pro Ala Pro Val Ser Gln Lys Pro Ala Pro Val Ser Gln Lys
180 185 190

Pro Ala Pro Val Ser Gln Lys Pro Ala Pro Val Ser Gln Lys Pro Ala
195 200 205

Pro Val Ser Gln Lys Pro Ala Pro Val Ser Gln Lys Pro Ala Pro Val
210 215 220

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Pro Glu Lys Pro Ala Pro Ala Ser Glu Lys Pro Ala Pro Val Gln Glu
225                 230                 235                 240

Lys Ser Ala Pro Ser Pro Lys Asp Lys Lys Lys Lys Pro Glu Lys Lys
                245                 250                 255

Val Leu Lys Val Glu Pro Ser Pro Ser Pro Ala Val Thr Phe Thr Gln
            260                 265                 270

Ala Val Ser Ser Lys His Val Pro Val Leu Asp Ala Pro Ile Lys Glu
        275                 280                 285

Val Pro Val Val Ala Val Ser Pro Val Gly Ser Gln Pro Ala Ser Ser
    290                 295                 300

Thr Gln Pro Pro Lys Lys Ala Glu Ala Ile Val Asn Gln Glu Asp Ser
305                 310                 315                 320

Lys Gln Glu Asn Val Pro Lys Lys Lys Ser Ala Pro Lys Lys Lys Thr
                325                 330                 335

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

Thr Leu Val Pro Thr Ile Gln Ser Met Cys Phe Ser Lys Gly Glu Ala
        355                 360                 365

Gln Lys Leu Ile Glu Ile Leu Ala Glu Lys Tyr Gly Ile Met Gln Asp
    370                 375                 380

Thr Trp Gln Thr Ala Thr Gln Lys Gly Asp Pro Val Ala Ala Leu Lys
385                 390                 395                 400

Arg Val Val Glu Glu Lys Glu Lys Leu Leu Leu Ala Gln His Glu Lys
                405                 410                 415

Thr Asn Ser Tyr Lys Glu Lys Phe Met Glu Val Asn Lys Glu Leu Gln
            420                 425                 430

Ser Glu Lys Ser Arg Ala Lys Thr Glu Gln Thr Lys Phe Lys Glu Gln
        435                 440                 445

Leu Val Thr Arg Glu Gln Glu Ile Asn Ala Leu Gln Ala Arg Met Gln
    450                 455                 460

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

Val Arg Ser Leu Gln Glu Glu Ile Glu Asn Gly Pro Lys Ala Gln Leu
                485                 490                 495
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Thr Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln
500 505 510

Ala Thr Ser Gln Thr Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu
515 520 525

Arg Gln Glu Cys Ser Lys Leu Ser Lys Glu Leu Ser Asp Lys Ser Glu
530 535 540

Ser Leu Gln Gln Glu Glu Gln Arg Arg Lys Ser Leu Asp Gly Lys Val
545 550 555 560

Val Thr Tyr Glu Lys Gln Ile Thr Gln Leu Gln Thr Leu Gln Gln Glu
565 570 575

Gly Glu Thr Thr Leu Gln Lys Arg Leu Asp Glu Val Asn Glu Glu Leu
580 585 590

Arg Lys Ser Gln Ser Thr Tyr Gln Asn Leu Leu Ala Asp Thr Glu Lys
595 600 605

Ala Lys Ala Glu Gln Lys Asn His Ala Asp Leu Gln Thr Lys Leu Gln
610 615 620

Ser Tyr Glu Ala Glu Ser Lys Gln Lys Ser Glu Glu Leu Asp Lys Leu
625 630 635 640

Asn Lys Gln Leu Gln Gly Val Ser Gly Glu Asn Ser Gln Leu Met Glu
645 650 655

Arg Ile Lys Ser Ile Glu Ala Leu Leu Glu Ala Gly Gln Asn Lys Asp
660 665 670

Thr Asp Lys Glu Lys Gln Gln Gln Glu Val Arg Glu Ala Glu Thr Ala
675 680 685

Gln Leu Gln Ile Arg Leu Gln Glu Lys Asp Ser His Ile Ala Ser Leu
690 695 700

Glu Lys Glu Thr Ser Glu Leu Lys Glu Ala Val Glu Gln Gln Lys Asn
705 710 715 720

Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Gln Ala Met Glu Ala Leu
725 730 735

Gly Leu Ser Glu Lys Thr Ser Glu Glu Lys Leu Asn Ser Glu Lys Lys
740 745 750

Ala Lys Glu Glu Met Val Gln Gln Leu Asn Ala Val Gln Ile Gln Thr
755 760 765

```
Lys Glu Thr Leu Gln Leu Leu Tyr Pro Gln Ile Thr Ile Glu Pro Gln
    770                 775                 780

Gln Ser Tyr Ser Glu Trp Leu Gln Glu Phe Arg Gln Arg Thr Thr Glu
785                 790                 795                 800

Phe Leu Ser Gln Pro Thr Glu Lys Gly Gly Ser Ser Glu Ser Gln Leu
                805                 810                 815

Lys Leu Lys Glu Ala Glu Asp Thr Gln Ser Ala Leu Gln Thr Glu Cys
            820                 825                 830

Glu Gln Tyr Arg Thr Ile Leu Gly Glu Thr Glu Ala Met Leu Lys Ala
        835                 840                 845

Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala Lys Leu
    850                 855                 860

Ala Ala Ser Glu Glu Asp Leu Ser Lys Ser His Ser Gln Val Lys Thr
865                 870                 875                 880

Leu Glu Glu Thr Val Glu Lys Leu Arg Ser Asp Leu Gln Ser Thr Glu
                885                 890                 895

Gln Leu Lys Glu Cys Ile Ser Leu Met Glu Ala Gln Leu Glu Thr Gln
            900                 905                 910

Met Asn Ala Lys Ser Thr Glu Cys Gln Thr Tyr Ser Asn Glu Ile Glu
        915                 920                 925

Ser Leu Gln Gln Leu Leu Ser Glu Ser Gln Glu His Leu Asn Ala Thr
    930                 935                 940

Lys Ala Glu Ala Arg Lys Gln Ser Val Glu Leu Ser Val Leu Arg Gln
945                 950                 955                 960

Gln Leu Ser Glu Met Gln Asn His Val Asn Asp Thr Glu His Gln Thr
                965                 970                 975

Ser Lys Ile Met Glu Val Pro Met Val Asn Leu Glu Ser Thr Leu Ala
            980                 985                 990

Glu Thr Gln Glu Gln Lys Ser Val  Arg Ser Leu Gln Glu  Glu Leu Glu
        995                 1000                1005

Lys Leu  Lys Ser Thr Glu Glu  Pro Asp Thr Glu Glu  Val Gln Gln
    1010                1015                1020

Ile Lys  Gly Glu Glu Asn Asp  Ser Asn Asn Gly Thr  Ser Val
    1025                1030                1035
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<210> 60
<211> 3689
<212> DNA
<213> Xenopus laevis

<400> 60
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gatccgcaga ccttgggcgt catggtgttt ggtggcttta tgttggtttc tgctcttgga 120

atctttcttg tgtcaacctt ttcaatgaaa gagacatcct atgaagaagc attggccaag 180

cagcgcaagg aaagtgagaa gaaccagcag cccaaagttg ataagaaaaa gaaagaaaag 240

ctccccgaga aaaaagggaa agctaaaaag aaggatgaaa agcccaatgg aacaatacct 300

gaacatgaac ctaatcagga atctacagac tcaacaaaag ctgaatctgc acgtgagcta 360

attctggaga agacaccagt tccggtagta ccagttgtac ctgtggaagt acctattgtg 420

cctgtggtag ctccagttcc taagaaatct gcttcaggtt ctgaaaaagc tgccttggct 480

ccacaaaaag ctgctccggc tccacaaaaa gctgctccgg ctccacaaaa agctgctccg 540

gctccacaaa aagctgctcc ggctccacaa aaagctgccc cggctccaca aaaagctgcc 600

ccggctccac aaaaagctgc cccggctcca caaaaagctg ccccggctcc acaaaaagct 660

gccccggctc cacaaaaagc tgccccggct ccacaaaaag ctgccccagt ttctgtcaaa 720

tctgttccag tttccgaaaa acctgctccc gttccagaaa aatctgctcc agtttctgaa 780

aaatctgctc cagtttctga aaaatctgct ccatctccta aagacaaaaa gaaaaagaca 840

gagaagaagg tccttaaggt cgaaccatcc ccaattccag ctgtggcttt tacccaggct 900

gtgccctcta agcacgtgcc agtgttggct gcacctacca aagaagtgcc tgtcattgcc 960

gtatctcctg tcggatccca gcctttatcc tccactcaac ctcctaagaa agctgaagcc 1020

accgtaaacc aggaagactc caaacaggaa gcagttccaa agaaaaagag cgcacctaag 1080

aaaaaaactg aaccaagtgc agaggaatgt gaaggtgctg tttatattcc atacaagacc 1140

ctggttccta ccatccaagc aatgtgcttt agcaaaggag aagctcagaa gctgattgaa 1200

atactggccg ataaatatgg catcatgcag gatacctggc aaacggcaac tcaaaaagga 1260

gatccaatga ctgctcttaa acgggtggtg gaggagaagg aaaagttact gttggcccag 1320

catgaaaaga ccaactctta taaggaaaag tttgtggaaa tcaacaagga attgcagagt 1380

gagaagtcca agagtgttaa agagcagtcc aagtttaagg agcagctggt gacacgggaa 1440

caggaaaacc atgcattgca agcccgcatg caggccagct atcaggacca tgtaaatgag 1500

actcagcagc tgcaagccaa ggttcggtcc ctgcaagagg aaatcgagaa tggccccaag 1560

gcacagctta ctcgcctcca gcaggagaat tctatcctta gagatgcctt aaaccaggcc 1620

acaagccaaa ccgagagcaa acaaaatgca gaattggcta aactacgcca agagtgcagc 1680

aagctctcta aggaacttac tgagaagtct gagtccttgc agcaagagga acaacgtagg 1740

aagtcccttg atggtaaaat atcatcctat gagaagcaaa tcactcagct gcagacatta 1800

cagcaggagg gtgatgccac attacaaaag agattagatg aagtgaatga agaactgcgc 1860

aagtctcaga acagttacca gaacctactg gcagacacag aaaaggccaa ggcagaacag 1920

aagaaccatg cagatcttca aaccaaactg cagtcctatg aagcagaagg caagcagaaa 1980

tcagaaaagc tggatgattt gaacaaacag cttcaggaga ctacaggaga aaatgcccag 2040

ctgatggata ggataaaatc tatagaggca cttttggaag caggacataa taaagatgct 2100

gataacgaaa agcagcagca gcaggaagca aaagaaggtg aaattgcact agcacaacta 2160

caggccaggc ttcaagaaaa agattcacag attgcatctt tagaaaagga agctgctgaa 2220

ttaaaagaag cggttgagca acagaaaaat aaaaataatg atttacggga aaagaactgg 2280

caagccatgg aagcactggg cctggcggaa aagacctgtg aggagaagct taactcggaa 2340

aagaaggcaa aggaagagat gatacaacaa ctcaatgcag tacagacaca gactaaagaa 2400

acactgcagt cactacttcc acagaccact atagtctccc aacagtcata cagtgaatgg 2460

ttacaggagt tccgacagag tacgtcagaa ttactcagcc agcagaccga gaaagacagt 2520

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ctcaaaaagt cacattctca ggtcaaaaca ctagaagaaa ctgtggaaaa attaaggtca 2760

gatattcaaa gcacagaaca gctaaaagag tgtatatcgt tgatggaggc tcagctggag 2820

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caaagtatag aactgtctct gctccggcaa cagctcggtg aaattcaaaa tcatgtaaat 3000

gatacggaaa aacatggttc acagaacatg gaagtaccaa aggcaaattc tgaagatcag 3060

agcactttag cagaaatgca agagcagaaa tcagtgcaca gtttgcagga agaactggaa 3120

aagttaaaat caacagaaga gccatcttct ggcacagacg aagtgcaaca gatcaaggga 3180

gaagaaaatg actctaacaa tgggacatca gtttgacaca tgaatttttc ttttcttttt 3240

ttttttttta cccaaatgcc ttaaacattc cttccttgaa attaaaatag taataacctt 3300

ctagtgagcc aaaacacttc agaagtaacg ttatatacct tttttttat atgaacaaaa 3360

tacatgacat gttgaattaa aaaaacagac caaaagagca caagaatgtg tgtgtgtgag 3420

ccaattccac aaacccactc ctctacccta tggagagcag ggaacgtggg cgttgtgcaa 3480

agggaacgac tctatgctgt gtaaaggaaa cagtgcaatc tctttattgt ttgtcttttg 3540

agtgatgatg gatgaacgga agccaagaag tgattatgaa gatgcctaat gtattggaac 3600

tggtctccag tataaaacca tgtgaattgt ttgattccta aatgccatta aaatgaagat 3660

gtgtccaaat ggaaaaaaaa aaaaaaaaa 3689

<210> 61
<211> 1055
<212> PRT

<213> Xenopus laevis

<400> 61

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Met Asp Leu Tyr Asp Pro Gln Thr Leu Gly Val Met Val Phe Gly Gly
1               5                  10                  15

Phe Met Leu Val Ser Ala Leu Gly Ile Phe Leu Val Ser Thr Phe Ser
            20                  25                  30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Lys Gln Arg Lys Glu
        35                  40                  45

Ser Glu Lys Asn Gln Gln Pro Lys Val Asp Lys Lys Lys Lys Glu Lys
    50                  55                  60

Leu Pro Glu Lys Lys Gly Lys Ala Lys Lys Lys Asp Glu Lys Pro Asn
65                  70                  75                  80

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

Lys Ala Glu Ser Ala Arg Glu Leu Ile Leu Glu Lys Thr Pro Val Pro
            100                 105                 110

Val Val Pro Val Val Pro Val Glu Val Pro Ile Val Pro Val Val Ala
        115                 120                 125

Pro Val Pro Lys Lys Ser Ala Ser Gly Ser Glu Lys Ala Ala Leu Ala
    130                 135                 140

Pro Gln Lys Ala Ala Pro Ala Pro Gln Lys Ala Ala Pro Ala Pro Gln
145                 150                 155                 160

Lys Ala Ala Pro Ala Pro Gln Lys Ala Ala Pro Ala Pro Gln Lys Ala
                165                 170                 175

Ala Pro Ala Pro Gln Lys Ala Ala Pro Ala Pro Gln Lys Ala Ala Pro
            180                 185                 190

Ala Pro Gln Lys Ala Ala Pro Ala Pro Gln Lys Ala Ala Pro Ala Pro
        195                 200                 205

Gln Lys Ala Ala Pro Ala Pro Gln Lys Ala Ala Pro Val Ser Val Lys
    210                 215                 220

Ser Val Pro Val Ser Glu Lys Pro Ala Pro Val Pro Glu Lys Ser Ala
225                 230                 235                 240

Pro Val Ser Glu Lys Ser Ala Pro Val Ser Glu Lys Ser Ala Pro Ser
                245                 250                 255
```

Pro Lys Asp Lys Lys Lys Lys Thr Glu Lys Lys Val Leu Lys Val Glu
260 265 270

Pro Ser Pro Ile Pro Ala Val Ala Phe Thr Gln Ala Val Pro Ser Lys
275 280 285

His Val Pro Val Leu Ala Ala Pro Thr Lys Glu Val Pro Val Ile Ala
290 295 300

Val Ser Pro Val Gly Ser Gln Pro Leu Ser Ser Thr Gln Pro Pro Lys
305 310 315 320

Lys Ala Glu Ala Thr Val Asn Gln Glu Asp Ser Lys Gln Glu Ala Val
325 330 335

Pro Lys Lys Lys Ser Ala Pro Lys Lys Lys Thr Glu Pro Ser Ala Glu
340 345 350

Glu Cys Glu Gly Ala Val Tyr Ile Pro Tyr Lys Thr Leu Val Pro Thr
355 360 365

Ile Gln Ala Met Cys Phe Ser Lys Gly Glu Ala Gln Lys Leu Ile Glu
370 375 380

Ile Leu Ala Asp Lys Tyr Gly Ile Met Gln Asp Thr Trp Gln Thr Ala
385 390 395 400

Thr Gln Lys Gly Asp Pro Met Thr Ala Leu Lys Arg Val Val Glu Glu
405 410 415

Lys Glu Lys Leu Leu Leu Ala Gln His Glu Lys Thr Asn Ser Tyr Lys
420 425 430

Glu Lys Phe Val Glu Ile Asn Lys Glu Leu Gln Ser Glu Lys Ser Lys
435 440 445

Ser Val Lys Glu Gln Ser Lys Phe Lys Glu Gln Leu Val Thr Arg Glu
450 455 460

Gln Glu Asn His Ala Leu Gln Ala Arg Met Gln Ala Ser Tyr Gln Asp
465 470 475 480

His Val Asn Glu Thr Gln Gln Leu Gln Ala Lys Val Arg Ser Leu Gln
485 490 495

Glu Glu Ile Glu Asn Gly Pro Lys Ala Gln Leu Thr Arg Leu Gln Gln
500 505 510

Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Thr
515 520 525

```
Glu Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Cys Ser
    530                 535                 540

Lys Leu Ser Lys Glu Leu Thr Glu Lys Ser Glu Ser Leu Gln Gln Glu
545                 550                 555                 560

Glu Gln Arg Arg Lys Ser Leu Asp Gly Lys Ile Ser Ser Tyr Glu Lys
                565                 570                 575

Gln Ile Thr Gln Leu Gln Thr Leu Gln Gln Glu Gly Asp Ala Thr Leu
            580                 585                 590

Gln Lys Arg Leu Asp Glu Val Asn Glu Glu Leu Arg Lys Ser Gln Asn
        595                 600                 605

Ser Tyr Gln Asn Leu Leu Ala Asp Thr Glu Lys Ala Lys Ala Glu Gln
    610                 615                 620

Lys Asn His Ala Asp Leu Gln Thr Lys Leu Gln Ser Tyr Glu Ala Glu
625                 630                 635                 640

Gly Lys Gln Lys Ser Glu Lys Leu Asp Asp Leu Asn Lys Gln Leu Gln
                645                 650                 655

Glu Thr Thr Gly Glu Asn Ala Gln Leu Met Asp Arg Ile Lys Ser Ile
            660                 665                 670

Glu Ala Leu Leu Glu Ala Gly His Asn Lys Asp Ala Asp Asn Glu Lys
        675                 680                 685

Gln Gln Gln Gln Glu Ala Lys Glu Gly Glu Ile Ala Leu Ala Gln Leu
    690                 695                 700

Gln Ala Arg Leu Gln Glu Lys Asp Ser Gln Ile Ala Ser Leu Glu Lys
705                 710                 715                 720

Glu Ala Ala Glu Leu Lys Glu Ala Val Glu Gln Gln Lys Asn Lys Asn
                725                 730                 735

Asn Asp Leu Arg Glu Lys Asn Trp Gln Ala Met Glu Ala Leu Gly Leu
            740                 745                 750

Ala Glu Lys Thr Cys Glu Glu Lys Leu Asn Ser Glu Lys Lys Ala Lys
        755                 760                 765

Glu Glu Met Ile Gln Gln Leu Asn Ala Val Gln Thr Gln Thr Lys Glu
    770                 775                 780

Thr Leu Gln Ser Leu Leu Pro Gln Thr Thr Ile Val Ser Gln Gln Ser
785                 790                 795                 800
```

```
Tyr Ser Glu Trp Leu Gln Glu Phe Arg Gln Ser Thr Ser Glu Leu Leu
                805                 810                 815

Ser Gln Gln Thr Glu Lys Asp Ser Ser Ser Glu Leu Gln Phe Lys Leu
            820                 825                 830

Lys Glu Ala Glu Asp Ala Gln Ser Ala Leu Gln Ala Glu Cys Glu Gln
        835                 840                 845

Tyr Arg Thr Ile Leu Gly Glu Thr Glu Ala Met Leu Lys Ala Leu Gln
    850                 855                 860

Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys Ala Lys Leu Thr Ala
865                 870                 875                 880

Ser Glu Glu Asp Leu Lys Lys Ser His Ser Gln Val Lys Thr Leu Glu
                885                 890                 895

Glu Thr Val Glu Lys Leu Arg Ser Asp Ile Gln Ser Thr Glu Gln Leu
            900                 905                 910

Lys Glu Cys Ile Ser Leu Met Glu Ala Gln Leu Glu Ser Gln Met Asn
        915                 920                 925

Ala Lys Ser Thr Glu Cys Gln Thr Tyr Ser Lys Glu Ile Glu Ser Leu
    930                 935                 940

Gln Gln Leu Leu Ser Glu Ser Gln Glu His Leu Asp Ala Thr Lys Ala
945                 950                 955                 960

Glu Ala Arg Lys Gln Ser Ile Glu Leu Ser Leu Leu Arg Gln Gln Leu
                965                 970                 975

Gly Glu Ile Gln Asn His Val Asn Asp Thr Glu Lys His Gly Ser Gln
            980                 985                 990

Asn Met Glu Val Pro Lys Ala Asn  Ser Glu Asp Gln Ser  Thr Leu Ala
        995                 1000                1005

Glu Met  Gln Glu Gln Lys Ser  Val His Ser Leu Gln  Glu Glu Leu
    1010                1015                1020

Glu Lys  Leu Lys Ser Thr Glu  Glu Pro Ser Ser Gly  Thr Asp Glu
    1025                1030                1035

Val Gln  Gln Ile Lys Gly Glu  Glu Asn Asp Ser Asn  Asn Gly Thr
    1040                1045                1050

Ser Val
    1055
```

<210> 62
<211> 1740
<212> DNA
<213> Perca flavescens

<400> 62
gccatcaccg ccatgacgct cagcgaccac gagatgcaca aactcaccga ggtcctgaac 60

cagaaggctg gagtccgcca cgaatcctgg cagctggcct gtcagaaagg agacccgctg 120

tccaatctga agaaacagct ggaggagaaa gagaagctgc tgaccgtcga gcaggagagc 180

tccgccgccg ccaagactcg cctccgagac atcagcaagg aacttggtgc agagaaatcc 240

aagacggcgt ctttggatgc ccgtctgaag gcggagctga gtgctcaggt tcagaaggtc 300

gacgccatgc gggccaaaat ggagacagct aaccaggaac acctcaaaca tacgcagcag 360

ctcaaccaga agatcgggag tctgcaggaa cagctggaga acggtcccaa cgctcagctg 420

gcccgactgc agcaggagaa ctccatcctc cgagatgcct tgaaccaggc aaccagccag 480

gccgagggca ggcagaatgc ggagctggcc cgtctcaggc aggactgcgt ccgtctgggt 540

cgagagttgg ccgagcgtac cgacgcgctg cgggccgacg aagatcgcag gaagggcctg 600

gaggccaaga tggccgccgc cgagcaagaa ctagccaaag cccagctggc ccgcaaggac 660

actgagcgtg ctctgcagaa gcaactggag gaagcacgtt tggagctgaa cgcatcaaag 720

caggaagctg ctgccgttag cgagctgcag ggggcgctgg agtccagaga ggctgaactg 780

caggagctca aggtccagct ggagaaccag gctgcagtcc aggtggagcg atcgtctgac 840

gtggagcagc tgaagaacag tgtgcagcgc agagacgagc aggttgtctc tctggaggcg 900

gagctcactc agctgagggc ggagctacag ctgctgacat catcacagtc acagagagtg 960

aaggaggaag aagaagaaga agaagcagcc ggtgagcaga cgcagaaaga ccgatcagga 1020

agcgagacgg agtccgagca gccgtttgaa agtctggagg aagactctca gctgctgcgt 1080

ctggaggaag aactgcacac gctcagagag gagctgcagc aggctcataa ccacggcgac 1140

gagctacagg acaaaatggc gacgctttcg gcggcggagc gtcagagcga gcagcgagag 1200

gcggagctta aagcagcgct ggctgaagcc gagtccaggt ttgcgtctct gcgtcaggac 1260

ttccaggcgt cgctgcaggt tctgtttccc ggcatctctg tggagacgga gaagagcgac 1320

tggctcgagc ttcttactca gaaagttcag gagagaaaag gtgaaacaga gagcgctcag 1380

tctgagctgc agtcgaggct gatggaggcc gacaggagac agactgaact gcagacggag 1440

ttggatcaga accggaagct gctgcgggaa acggaggcgg agcttcacgc tctgcagcga 1500

cgctctgaag aagaagaaaa cgtctggaag aacaaactgt ccgataccga acagcagaaa 1560

caaacggttc tggatcagct gacgctgctg caggacgaag tgcagtcgaa gacgtcggag 1620

acagaaaaca ctcagcagct gaaggaacag ctgatgttgc tggaggctca gctggagaaa 1680

cagctggagg acgccagcgt ctcgcagagc tgctgcgagg agctcgctca gttgcggtct 1740

<210> 63
<211> 580
<212> PRT

<213> Perca flavescens

<400> 63

```
Ala Ile Thr Ala Met Thr Leu Ser Asp His Glu Met His Lys Leu Thr
1               5                  10                  15

Glu Val Leu Asn Gln Lys Ala Gly Val Arg His Glu Ser Trp Gln Leu
            20                  25                  30

Ala Cys Gln Lys Gly Asp Pro Leu Ser Asn Leu Lys Lys Gln Leu Glu
        35                  40                  45

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

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

Lys Thr Ala Ser Leu Asp Ala Arg Leu Lys Ala Glu Leu Ser Ala Gln
                85                  90                  95

Val Gln Lys Val Asp Ala Met Arg Ala Lys Met Glu Thr Ala Asn Gln
            100                 105                 110

Glu His Leu Lys His Thr Gln Gln Leu Asn Gln Lys Ile Gly Ser Leu
        115                 120                 125

Gln Glu Gln Leu Glu Asn Gly Pro Asn Ala Gln Leu Ala Arg Leu Gln
    130                 135                 140

Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln
145                 150                 155                 160

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

Val Arg Leu Gly Arg Glu Leu Ala Glu Arg Thr Asp Ala Leu Arg Ala
            180                 185                 190

Asp Glu Asp Arg Arg Lys Gly Leu Glu Ala Lys Met Ala Ala Ala Glu
        195                 200                 205

Gln Glu Leu Ala Lys Ala Gln Leu Ala Arg Lys Asp Thr Glu Arg Ala
    210                 215                 220

Leu Gln Lys Gln Leu Glu Glu Ala Arg Leu Glu Leu Asn Ala Ser Lys
225                 230                 235                 240

Gln Glu Ala Ala Ala Val Ser Glu Leu Gln Gly Ala Leu Glu Ser Arg
                245                 250                 255
```

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Glu Ala Glu Leu Gln Glu Leu Lys Val Gln Leu Glu Asn Gln Ala Ala
            260                 265                 270

Val Gln Val Glu Arg Ser Ser Asp Val Glu Gln Leu Lys Asn Ser Val
        275                 280                 285

Gln Arg Arg Asp Glu Gln Val Val Ser Leu Glu Ala Glu Leu Thr Gln
    290                 295                 300

Leu Arg Ala Glu Leu Gln Leu Leu Thr Ser Ser Gln Ser Gln Arg Val
305                 310                 315                 320

Lys Glu Glu Glu Glu Glu Glu Glu Ala Ala Gly Glu Gln Thr Gln Lys
                325                 330                 335

Asp Arg Ser Gly Ser Glu Thr Glu Ser Glu Gln Pro Phe Glu Ser Leu
            340                 345                 350

Glu Glu Asp Ser Gln Leu Leu Arg Leu Glu Glu Glu Leu His Thr Leu
        355                 360                 365

Arg Glu Glu Leu Gln Gln Ala His Asn His Gly Asp Glu Leu Gln Asp
    370                 375                 380

Lys Met Ala Thr Leu Ser Ala Ala Glu Arg Gln Ser Glu Gln Arg Glu
385                 390                 395                 400

Ala Glu Leu Lys Ala Ala Leu Ala Glu Ala Glu Ser Arg Phe Ala Ser
                405                 410                 415

Leu Arg Gln Asp Phe Gln Ala Ser Leu Gln Val Leu Phe Pro Gly Ile
            420                 425                 430

Ser Val Glu Thr Glu Lys Ser Asp Trp Leu Glu Leu Leu Thr Gln Lys
        435                 440                 445

Val Gln Glu Arg Lys Gly Glu Thr Glu Ser Ala Gln Ser Glu Leu Gln
    450                 455                 460

Ser Arg Leu Met Glu Ala Asp Arg Arg Gln Thr Glu Leu Gln Thr Glu
465                 470                 475                 480

Leu Asp Gln Asn Arg Lys Leu Leu Arg Glu Thr Glu Ala Glu Leu His
                485                 490                 495

Ala Leu Gln Arg Arg Ser Glu Glu Glu Glu Asn Val Trp Lys Asn Lys
            500                 505                 510

Leu Ser Asp Thr Glu Gln Gln Lys Gln Thr Val Leu Asp Gln Leu Thr
        515                 520                 525
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Leu Leu Gln Asp Glu Val Gln Ser Lys Thr Ser Glu Thr Glu Asn Thr
530 535 540

Gln Gln Leu Lys Glu Gln Leu Met Leu Leu Glu Ala Gln Leu Glu Lys
545 550 555 560

Gln Leu Glu Asp Ala Ser Val Ser Gln Ser Cys Cys Glu Glu Leu Ala
565 570 575

Gln Leu Arg Ser
580

<210> 64
<211> 1464
<212> PRT
<213> Mus musculus

<400> 64

Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1 5 10 15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45

Met Ala Lys Thr His His Gln Lys Gly Glu Lys Lys Lys Lys Glu Lys
50 55 60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Glu His Asp Leu Asp Pro Asn Val Thr Ile Ile Leu
85 90 95

Lys Glu Pro Val Arg Val Ser Ala Val Ala Val Ala Pro Thr Ser Val
100 105 110

His Ser Ser Val Gly His Thr Pro Ile Ala Thr Val Pro Ala Met Pro
115 120 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Arg Lys Lys Lys Glu Lys
130 135 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Ile Val Asn Ser Ile
145 150 155 160

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

Val Pro Met Val Ala Val Pro Pro Val Gly Ser Lys Ala Ser Ser Pro

180 185 190

Ala Thr Ser Ser Gln Gly Lys Lys Gly Gln Gly Ala Gln Asn Gln Ala
195 200 205

Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala
210 215 220

Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys
225 230 235 240

Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn
245 250 255

Gln Ala Lys Lys Gly Glu Gly Gly Gln Asn Gln Ala Lys Lys Gly Glu
260 265 270

Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly
275 280 285

Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala
290 295 300

Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys
305 310 315 320

Gly Glu Gly Ala Gln Asn Gln Ser Lys Lys Gly Glu Gly Ala Gln Asn
325 330 335

Gln Ala Lys Lys Gly Glu Gly Gly Gln Asn Gln Ala Lys Lys Gly Glu
340 345 350

Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala
355 360 365

Lys Lys Gly Glu Gly Val Gln Asn Gln Ala Lys Lys Gly Val Glu Gly
370 375 380

Ala Gln Asn Gln Gly Lys Lys Gly Glu Ala Asn Gln Asn Gln Ala Lys
385 390 395 400

Lys Gly Glu Gly Gly Gln Asn Gln Thr Lys Lys Gly Glu Gly Pro Gln
405 410 415

Asn Gln Gly Lys Lys Gly Glu Ala Ala Gln Lys Gln Asp Lys Lys Ile
420 425 430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Pro Glu Gly Thr Ser Asn Gln
435 440 445

Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly

450 455 460

Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys
465 470 475 480

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln
485 490 495

Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly
500 505 510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Pro Gln Asn Gln
515 520 525

Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly
530 535 540

Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys
545 550 555 560

Lys Ala Glu Gly Val Gln Ser Gln Ser Lys Lys Gly Glu Gly Thr Gln
565 570 575

Asn Gln Gly Lys Lys Gly Asp Gly Asn Pro Asn Gln Gly Lys Lys Gly
580 585 590

Glu Gly Ala Ser Asn Gln Asn Arg Lys Thr Asp Thr Val Ala Asn Gln
595 600 605

Gly Thr Lys Gln Glu Gly Val Ser Asn Gln Val Lys Lys Ser Glu Gly
610 615 620

Ser Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys
625 630 635 640

Lys Lys Asp Gly Ser Pro Ser Gln Ala Lys Lys Val Asp Ala Ala Ala
645 650 655

Asn Gln Gly Lys Lys Ser Glu Met Ala Pro Ala Gln Gly Gln Lys Ala
660 665 670

Ser Met Val Gln Ser Gln Glu Ala Pro Lys Gln Asp Ala Pro Ala Lys
675 680 685

Lys Lys Ser Gly Ser Arg Lys Lys Gly Glu Pro Gly Pro Pro Asp Cys
690 695 700

Asp Gly Pro Leu Phe Leu Pro Tyr Lys Thr Leu Val Ser Thr Val Gly
705 710 715 720

Ser Met Val Phe Ser Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile Leu

725 730 735

Ser Glu Lys Thr Gly Val Ile Gln Asp Thr Trp His Lys Ala Thr Gln
740 745 750

Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys Glu
755 760 765

Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser Lys
770 775 780

Leu Arg Glu Leu Asn Lys Glu Met Ala Ser Glu Lys Ala Lys Ala Ala
785 790 795 800

Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln Glu
805 810 815

Ile Ala Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Asp His Val
820 825 830

Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu Gln
835 840 845

Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu Asn
850 855 860

Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu Ser
865 870 875 880

Lys Gln Asn Thr Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys Val
885 890 895

Asn Lys Glu Leu Val Glu Lys Ser Glu Ala Ser Arg Gln Glu Glu Gln
900 905 910

Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Thr Phe Glu Lys Gln Val
915 920 925

Leu Gln Leu Gln Ala Ser His Lys Glu Ser Glu Glu Ala Leu Gln Lys
930 935 940

Arg Leu Glu Glu Val Thr Arg Glu Leu Cys Arg Ala Gln Thr Ser His
945 950 955 960

Ala Asn Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln Arg
965 970 975

Val Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Val Glu Val Lys
980 985 990

Ser Lys Cys Glu Glu Leu Ser Ser Leu His Gly Gln Leu Lys Glu Ala

995 1000 1005

Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
1010 1015 1020

Ala Leu Leu Glu Ala Gly Gln Ala Gln Asp Thr Gln Ala Ser His
1025 1030 1035

Ala Glu Ala Asn Gln Gln Gln Thr Arg Leu Lys Glu Leu Glu Ser
1040 1045 1050

Gln Val Ser Cys Leu Glu Lys Glu Thr Ser Glu Leu Lys Glu Ala
1055 1060 1065

Met Glu Gln Gln Lys Gly Lys Asn Asn Asp Leu Arg Glu Lys Asn
1070 1075 1080

Trp Lys Ala Met Glu Ala Leu Ala Leu Ala Glu Arg Ala Cys Glu
1085 1090 1095

Glu Lys Leu Arg Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys
1100 1105 1110

Gln Leu His Leu Ala Glu Ala Gln Thr Lys Glu Thr Leu Leu Ala
1115 1120 1125

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

Trp Leu Gln Glu Phe Lys Glu Lys Gly Ser Glu Leu Leu Lys Lys
1145 1150 1155

Pro Pro Thr Leu Glu Pro Ser Met Asp Ile Val Leu Lys Leu Arg
1160 1165 1170

Glu Ala Glu Glu Thr Gln Asn Ser Leu Gln Ala Glu Cys Asp Gln
1175 1180 1185

Tyr Arg Thr Ile Leu Ala Glu Thr Glu Gly Met Leu Lys Asp Leu
1190 1195 1200

Gln Lys Ser Val Glu Glu Glu Glu Arg Val Trp Lys Ala Lys Val
1205 1210 1215

Gly Ala Ala Glu Glu Glu Leu His Lys Ser Arg Val Thr Val Lys
1220 1225 1230

His Leu Glu Asp Ile Val Glu Lys Leu Lys Gly Glu Leu Glu Ser
1235 1240 1245

Ser Asp Gln Val Arg Glu His Thr Ser His Leu Glu Ala Glu Leu

1250 1255 1260

Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln Asn Tyr Ala
1265 1270 1275

Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser Gln Ser
1280 1285 1290

Gln Leu Asp Glu Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp Glu
1295 1300 1305

Leu Ala Leu Val Arg Gln Gln Leu Ser Asp Met Arg Ser His Val
1310 1315 1320

Glu Asp Gly Asp Val Ala Gly Ser Pro Ala Val Pro Pro Ala Glu
1325 1330 1335

Gln Asp Pro Met Lys Leu Lys Thr Gln Leu Glu Arg Thr Glu Ala
1340 1345 1350

Thr Leu Glu Ala Glu Gln Thr Arg Arg Gln Lys Leu Thr Ala Glu
1355 1360 1365

Phe Glu Glu Ala Gln Arg Thr Ala Cys Arg Ile Gln Glu Glu Leu
1370 1375 1380

Glu Lys Leu Arg Ala Ala Gly Pro Leu Glu Ser Ser Gly Lys Glu
1385 1390 1395

Glu Ile Thr Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Arg Leu
1400 1405 1410

Thr Ser Asp Leu Gly Arg Ala Ala Ile Lys Leu Gln Glu Leu Leu
1415 1420 1425

Lys Thr Thr Gln Glu Gln Leu Thr Lys Glu Lys Asp Thr Val Lys
1430 1435 1440

Lys Leu Gln Glu Gln Leu Gly Lys Ala Glu Asp Gly Ser Ser Ser
1445 1450 1455

Lys Glu Gly Thr Ser Val
1460

<210> 65
<211> 1453
<212> PRT
<213> Rattus norvegicus

<400> 65

Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1 5 10 15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45

Met Ala Lys Thr His His Gln Lys Gly Glu Lys Lys Lys Lys Glu Lys
50 55 60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Glu His Asp Leu Asp Pro Asn Val Thr Ile Ile Leu
85 90 95

Lys Glu Pro Met Arg Val Pro Ala Val Ala Val Ala Pro Thr Ser Val
100 105 110

His Ser Ser Val Gly Arg Thr Pro Val Ala Thr Val Pro Ala Met Pro
115 120 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Ile Val Asn Ser Ile
145 150 155 160

Gln Val Leu Ala Ser Lys Ser Ala Ile Leu Glu Ala Ser Pro Lys Glu
165 170 175

Val Pro Met Val Ala Val Pro Pro Val Gly Ser Lys Ala Ser Ala Pro
180 185 190

Ala Thr Ser Ser Gln Gly Lys Lys Gly Gln Gly Ala Gln Asn Gln Ala
195 200 205

Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Val
210 215 220

Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Val Lys Lys
225 230 235 240

Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn
245 250 255

Gln Ala Lys Lys Gly Glu Gly Thr Gln Asn Gln Ala Lys Lys Gly Glu
260 265 270

Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala
275 280 285

Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala
290 295 300

Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys
305 310 315 320

Gly Glu Gly Gly Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn
325 330 335

Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu
340 345 350

Gly Val Gln Asn Gln Ala Lys Lys Gly Val Glu Gly Ala Gln Asn Gln
355 360 365

Gly Lys Lys Gly Glu Ala Asn Gln Asn Gln Ala Lys Lys Gly Glu Gly
370 375 380

Gly Gln Asn Gln Thr Lys Lys Gly Glu Gly Leu Gln Asn Gln Gly Lys
385 390 395 400

Lys Gly Glu Ala Thr Gln Lys Gln Asp Lys Lys Ile Glu Gly Ala Gln
405 410 415

Asn Gln Gly Lys Lys Pro Glu Gly Thr Pro Asn Gln Gly Lys Lys Gly
420 425 430

Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln
435 440 445

Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly
450 455 460

Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys
465 470 475 480

Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln
485 490 495

Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly
500 505 510

Glu Gly Ser Pro Ser Gln Asn Ile Lys Val Glu Gly Met Gln Asn Gln
515 520 525

Gly Arg Lys Ala Glu Gly Thr Pro Ala Gln Gly Lys Lys Met Glu Ala
530 535 540

Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Val Gln Ser Gln Gly Lys
545 550 555 560

Lys Gly Glu Gly Ser Gln Asn Gln Gly Lys Lys Gly Asp Gly Asn Pro
565 570 575

Asn Gln Gly Lys Lys Gly Glu Gly Ala Pro Asn Gln Asn Arg Lys Thr
580 585 590

Asp Thr Val Ala Asn Gln Gly Thr Lys Thr Glu Gly Val Ser Asn Gln
595 600 605

Val Lys Lys Ser Glu Gly Ser Pro Asn Gln Gly Lys Lys Ala Glu Gly
610 615 620

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

Lys Val Asp Ala Ala Ala Gly Gln Gly Lys Lys Ser Glu Met Thr Pro
645 650 655

Ala Gln Gly Lys Asn Ala Ser Met Val Gln Ser Gln Glu Ala Pro Lys
660 665 670

Gln Glu Ala Pro Ala Lys Lys Lys Ser Lys Lys Lys Gly Glu Pro Gly
675 680 685

Pro Pro Asp Cys Asp Ser Pro Leu Phe Leu Pro Tyr Lys Thr Leu Val
690 695 700

Ser Thr Val Gly Ser Met Val Phe Ser Glu Gly Glu Ala Gln Arg Leu
705 710 715 720

Ile Glu Ile Leu Ser Glu Lys Thr Gly Val Ile Gln Asp Thr Trp His
725 730 735

Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Val Leu Lys Arg Gln Leu
740 745 750

Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val
755 760 765

Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ser Glu Lys
770 775 780

Ala Lys Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala
785 790 795 800

Arg Glu Gln Glu Ile Ala Ala Val Gln Ala Arg Met Gln Ala Ser Tyr
805 810 815

Gln Asp His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr
820 825 830

```
Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu
        835                 840                 845

Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser
    850                 855                 860

Gln Val Glu Ser Lys Gln Asn Thr Glu Leu Ala Lys Leu Arg Gln Glu
865                 870                 875                 880

Leu Ser Lys Val Asn Lys Glu Leu Val Glu Lys Ser Glu Ala Ser Arg
                885                 890                 895

Gln Glu Glu Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Thr Phe
            900                 905                 910

Glu Lys Gln Ile Leu Gln Leu Gln Ala Ser His Lys Glu Ser Glu Glu
        915                 920                 925

Ala Leu Gln Lys Arg Leu Glu Glu Val Thr Arg Glu Leu Cys Arg Ala
    930                 935                 940

Gln Thr Ser His Ala Asn Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu
945                 950                 955                 960

Gln Gln Gln Arg Val Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu
                965                 970                 975

Val Glu Val Lys Ser Lys Cys Glu Glu Leu Ser Asp Leu His Gly Gln
            980                 985                 990

Leu Lys Glu Ala Arg Ala Glu Asn  Ser Gln Leu Thr Glu  Arg Ile Arg
        995                 1000                1005

Ser Ile  Glu Ala Leu Leu Glu  Ala Gly Gln Ala Gln  Asp Ser Gln
    1010                1015                1020

Ala Ser  Arg Ala Glu Ala Asp  Gln Gln Gln Thr Arg  Leu Lys Glu
    1025                1030                1035

Leu Glu  Ser Gln Val Ser Cys  Leu Glu Lys Glu Thr  Ser Glu Leu
    1040                1045                1050

Lys Glu  Ala Met Glu Gln Gln  Lys Gly Lys Asn Asn  Asp Leu Arg
    1055                1060                1065

Glu Lys  Asn Trp Lys Ala Met  Glu Ala Leu Ala Leu  Ala Glu Arg
    1070                1075                1080

Ala Cys  Glu Glu Lys Leu Arg  Ser Leu Thr Gln Ala  Lys Glu Glu
    1085                1090                1095
```

Ser Glu Lys Gln Leu His Leu Ala Glu Ala Gln Thr Lys Glu Val
1100 1105 1110

Leu Leu Ala Leu Leu Pro Glu Leu Ser Ile Pro Ala His Gln Asn
1115 1120 1125

Tyr Ala Asp Trp Leu Gln Glu Val Lys Glu Lys Gly Ser Glu Leu
1130 1135 1140

Leu Lys Lys Pro Pro Val Ser Val Glu Pro Ser Leu Asp Ile Val
1145 1150 1155

Ser Lys Leu Arg Glu Ala Glu Glu Thr Gln Asn Ser Leu Gln Ala
1160 1165 1170

Glu Cys Asp Gln Tyr Arg Thr Ile Leu Ala Glu Thr Glu Gly Met
1175 1180 1185

Leu Lys Asp Leu Gln Lys Ser Val Glu Glu Glu Glu Arg Val Trp
1190 1195 1200

Lys Ala Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys Ser Arg
1205 1210 1215

Phe Thr Val Lys His Leu Glu Asp Leu Val Glu Lys Leu Arg Gly
1220 1225 1230

Glu Leu Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu
1235 1240 1245

Glu Ala Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys
1250 1255 1260

Gln Asn Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu
1265 1270 1275

Asp Ser Gln Ser Gln Leu Glu Glu Ala Lys Ser Glu Ala Gln Lys
1280 1285 1290

Gln Ser Asn Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Asp Met
1295 1300 1305

Arg Ser His Val Glu Asp Gly Asp Val Ala Gly Ser Pro Ala Val
1310 1315 1320

Pro Pro Ala Glu Gln Asp Pro Val Lys Leu Lys Thr Gln Leu Glu
1325 1330 1335

Arg Thr Glu Ala Thr Leu Glu Asp Glu Gln Thr Arg Arg Gln Lys
1340 1345 1350

```
Leu Thr  Ala Glu Phe Glu Glu  Ala Gln Ser Thr Ala  Cys Arg Leu
    1355                 1360                 1365

Gln Glu  Glu Leu Glu Lys Leu  Arg Ala Ala Gly Pro  Leu Glu Ser
    1370                 1375                 1380

Ser Gly  Ile Glu Glu Val Thr  Gln Leu Lys Glu Arg  Leu Glu Lys
    1385                 1390                 1395

Glu Lys  Arg Leu Thr Ser Asp  Leu Gly Arg Ala Ala  Thr Lys Leu
    1400                 1405                 1410

Gln Glu  Leu Leu Lys Thr Thr  Gln Glu Gln Leu Thr  Lys Glu Lys
    1415                 1420                 1425

Asp Thr  Val Lys Lys Leu Gln  Glu Gln Leu Gly Lys  Ala Glu Asp
    1430                 1435                 1440

Gly Ser  Ser Ser Lys Glu Gly  Thr Ser Val
    1445                 1450
```

<210> 66
<211> 1534
<212> PRT
<213> Canis lupus familiaris

<400> 66

```
Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Met Val Phe Gly Gly
1               5                  10                  15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
            20                  25                  30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
        35                  40                  45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
    50                  55                  60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65                  70                  75                  80

Gly Lys Ile Pro Asp His Glu Pro Ala Pro Asn Val Thr Ile Leu Leu
                85                  90                  95

Lys Asp Pro Val Arg Ala Pro Ala Val Pro Val Ala Pro Thr Pro Val
            100                 105                 110

Gln Pro Pro Val Val Ile Ala Pro Val Ala Thr Val Pro Ala Met Pro
        115                 120                 125
```

Gln Glu Lys Leu Ala Pro Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Val
145 150 155 160

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

Val Pro Met Val Val Val Pro Pro Val Gly Ala Lys Ala Gly Thr Pro
180 185 190

Ala Thr Ser Thr Ala Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
195 200 205

Ser Arg Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly
210 215 220

Ala Leu Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
225 230 235 240

Lys Val Glu Val Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Gly Gln
245 250 255

Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
260 265 270

Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln
275 280 285

Gly Lys Lys Thr Asp Gly Ala Pro Asn Gln Gly Lys Lys Ser Glu Gly
290 295 300

Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys
305 310 315 320

Lys Val Glu Val Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Gly Gln
325 330 335

Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala
340 345 350

Glu Gly Thr Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln
355 360 365

Gly Lys Lys Thr Asp Gly Ala Pro Asn Gln Gly Lys Lys Ser Glu Gly
370 375 380

Ala Pro Asn Gln Gly Lys Lys Val Glu Gly Ala Gln Asn Gln Gly Lys
385 390 395 400

Lys Val Glu Gly Val Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
405 410 415

Asn Gln Gly Lys Lys Ala Glu Gly Thr Ser Ser Gln Gly Arg Lys Glu
420 425 430

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

Gly Lys Lys Val Glu Val Val Gln Asn Gln Ser Lys Lys Val Glu Gly
450 455 460

Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ser Gln Asn Gln Gly Lys
465 470 475 480

Lys Thr Glu Gly Ala Ser Asn Gln Gly Lys Lys Val Asp Gly Ala Gln
485 490 495

Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys Val
500 505 510

Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Thr Pro Asn Gln
515 520 525

Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
530 535 540

Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys
545 550 555 560

Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro
565 570 575

Asn Gln Gly Lys Lys Ala Glu Ala Ala Pro Asn Gln Gly Lys Lys Ala
580 585 590

Glu Gly Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln
595 600 605

Gly Lys Lys Ala Glu Ala Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly
610 615 620

Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys
625 630 635 640

Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
645 650 655

Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys Ala
660 665 670

Asp Leu Val Ala Asn Gln Gly Thr Lys Ala Glu Gly Val Ala Gly Gln
675 680 685

Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys Gly Glu Gly
690 695 700

Thr Pro Asn Gln Gly Lys Lys Ser Glu Gly Ser Pro Asn Gln Gly Lys
705 710 715 720

Lys Val Asp Ala Ser Ala Asn Gln Ser Lys Arg Ala Glu Ser Ala Pro
725 730 735

Ile Gln Gly Lys Asn Ala Asp Met Val Gln Ser Gln Glu Ala Pro Lys
740 745 750

Gln Glu Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Glu
755 760 765

Pro Gly Pro Pro Asp Ser Asp Ser Pro Leu Tyr Leu Pro Tyr Lys Thr
770 775 780

Leu Val Ser Thr Val Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln
785 790 795 800

Arg Leu Ile Glu Ile Leu Ser Glu Lys Ala Gly Val Ile Gln Asp Thr
805 810 815

Trp His Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg
820 825 830

Gln Leu Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala
835 840 845

Ala Val Ala Lys Ser Lys Leu Arg Glu Val Asn Lys Glu Leu Ala Ala
850 855 860

Glu Lys Ala Lys Ala Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu
865 870 875 880

Val Ala Arg Glu Gln Glu Ile Thr Ala Val Gln Ala Arg Ile Glu Ala
885 890 895

Ser Tyr Arg Glu His Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile
900 905 910

Arg Thr Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala
915 920 925

Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala
930 935 940

```
Thr Ser Gln Val Glu Ser Lys Gln Asn Thr Glu Leu Ala Lys Leu Arg
945                 950                 955                 960

Gln Glu Leu Ser Lys Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala
                965                 970                 975

Ala Arg Gln Glu Glu Gln Gln Arg Lys Ala Leu Glu Thr Lys Thr Ala
            980                 985                 990

Ala Leu Glu Lys Gln Val Leu Gln  Leu Gln Ala Ser His  Lys Glu Ser
        995                 1000                1005

Glu Glu  Ala Leu Gln Lys Arg  Leu Asp Glu Val Ser  Arg Glu Leu
    1010                1015                1020

Cys Arg  Ser Gln Thr Ser His  Ala Ser Leu Arg Ala  Asp Ala Glu
    1025                1030                1035

Lys Ala  Gln Glu Gln Gln Gln  Gln Met Ala Glu Leu  His Ser Lys
    1040                1045                1050

Leu Gln  Ser Ser Glu Ala Glu  Val Lys Ser Lys Ser  Glu Glu Leu
    1055                1060                1065

Ser Gly  Leu His Gly Gln Leu  Lys Glu Ala Arg Ala  Glu Asn Ser
    1070                1075                1080

Gln Leu  Met Glu Arg Ile Arg  Ser Ile Glu Ala Leu  Leu Glu Ala
    1085                1090                1095

Gly Gln  Ala Arg Asp Thr Gln  Asp Ala Gln Ala Ser  Arg Ala Glu
    1100                1105                1110

His Gln  Ala Arg Leu Lys Glu  Leu Glu Ser Gln Val  Trp Cys Leu
    1115                1120                1125

Glu Lys  Glu Ala Thr Glu Leu  Lys Glu Ala Val Glu  Gln Gln Lys
    1130                1135                1140

Val Lys  Asn Asn Asp Leu Arg  Glu Lys Asn Trp Lys  Ala Met Glu
    1145                1150                1155

Ala Leu  Ala Ser Ala Glu Arg  Ala Cys Glu Glu Lys  Leu Arg Ser
    1160                1165                1170

Leu Thr  Gln Ala Lys Glu Glu  Ser Glu Lys Gln Leu  Ser Leu Thr
    1175                1180                1185

Glu Ala  Gln Thr Lys Glu Ala  Leu Leu Ala Leu Leu  Pro Ala Leu
    1190                1195                1200
```

Ser Ser Ser Ala Pro Gln Ser Tyr Thr Glu Trp Leu Gln Glu Leu
1205 1210 1215

Arg Glu Lys Gly Pro Glu Leu Leu Lys Gln Arg Pro Ala Asp Thr
1220 1225 1230

Asp Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu
1235 1240 1245

Thr Gln Asn Asn Leu Gln Ala Glu Cys Asp Gln Tyr Arg Thr Ile
1250 1255 1260

Leu Ala Glu Thr Glu Gly Met Leu Lys Asp Leu Gln Lys Ser Val
1265 1270 1275

Glu Glu Glu Glu Gln Val Trp Lys Ala Lys Val Ser Ala Thr Glu
1280 1285 1290

Glu Glu Leu Gln Lys Ser Arg Val Thr Val Lys His Leu Glu Asp
1295 1300 1305

Ile Val Glu Lys Leu Lys Gly Glu Leu Glu Ser Ser Glu Gln Val
1310 1315 1320

Arg Glu His Thr Ser His Leu Glu Ala Glu Leu Glu Lys His Met
1325 1330 1335

Ala Ala Ala Ser Ala Glu Cys Gln Ser Tyr Ala Lys Glu Val Ala
1340 1345 1350

Gly Leu Arg Gln Leu Leu Leu Glu Ser Gln Ser Gln Leu Asp Ala
1355 1360 1365

Ala Lys Ser Glu Ala Gln Lys Gln Ser Asn Glu Leu Ala Leu Val
1370 1375 1380

Arg Gln Gln Leu Ser Glu Met Lys Ser His Val Glu Asp Gly Asp
1385 1390 1395

Val Ala Gly Ser Pro Ala Ala Pro Pro Ala Glu Gln Asp Pro Val
1400 1405 1410

Glu Leu Lys Ala Gln Leu Glu Arg Thr Glu Ala Thr Leu Glu Asp
1415 1420 1425

Glu Gln Ala Leu Arg Arg Lys Leu Thr Ala Glu Phe Gln Glu Ala
1430 1435 1440

Gln Ser Ser Ala Cys Arg Leu Gln Ala Glu Leu Glu Lys Leu Arg
1445 1450 1455

Ser Thr Gly Pro Leu Glu Ser Ser Ala Ala Glu Glu Ala Thr Gln
1460 1465 1470

Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser Asp Leu
1475 1480 1485

Gly His Ala Ala Thr Lys Leu Gln Glu Leu Leu Lys Thr Thr Gln
1490 1495 1500

Glu Gln Leu Ala Lys Glu Arg Asp Thr Val Lys Lys Leu Gln Glu
1505 1510 1515

Gln Leu Asp Lys Thr Asp Asp Ser Ser Ser Lys Glu Gly Thr Ser
1520 1525 1530

Val

<210> 67
<211> 977
<212> PRT
<213> Macaca mulatta

<400> 67

Met Asp Ile Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1 5 10 15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Asp Lys
50 55 60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
85 90 95

Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
100 105 110

Gln Pro Pro Ile Ile Ile Ala Pro Val Ala Thr Val Pro Ala Thr Pro
115 120 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

```
Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145                 150                 155                 160

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

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

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Pro Pro Asp
        195                 200                 205

Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr Val
    210                 215                 220

Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile
225                 230                 235                 240

Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala Thr
                245                 250                 255

Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys
            260                 265                 270

Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser
        275                 280                 285

Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys Ala
    290                 295                 300

Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln
305                 310                 315                 320

Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His
                325                 330                 335

Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu
            340                 345                 350

Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu
        355                 360                 365

Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu
    370                 375                 380

Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys
385                 390                 395                 400

Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Ala Arg Gln Asp Glu
                405                 410                 415
```

Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys Gln
420 425 430

Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu Gln
435 440 445

Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys Arg Ala Gln Ser Ser
450 455 460

His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln
465 470 475 480

Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu Val
485 490 495

Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln Glu
500 505 510

Ala Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
515 520 525

Ala Leu Leu Glu Ala Gly Gln Ala Arg Asp Ala Gln Asp Ala Gln Ala
530 535 540

Ser Arg Ala Glu Ala Asp Gln Gln Gln Thr Arg Leu Lys Glu Leu Glu
545 550 555 560

Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Thr Glu Leu Arg Glu Ala
565 570 575

Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp
580 585 590

Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys Lys Glu Lys
595 600 605

Leu His Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu His
610 615 620

Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu Thr Leu Leu Pro Glu
625 630 635 640

Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr Glu Trp Leu Gln Asp Leu
645 650 655

Lys Glu Lys Gly Pro Thr Leu Leu Lys His Pro Pro Ala Pro Ala Glu
660 665 670

Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu Ala Gln
675 680 685

```
Ser Thr Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala Glu
    690                 695                 700

Thr Glu Gly Met Leu Arg Asp Leu Gln Lys Ser Val Glu Glu Glu Glu
705                 710                 715                 720

Gln Val Trp Arg Ala Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys
                725                 730                 735

Ser Arg Val Thr Val Lys His Leu Glu Glu Ile Val Glu Lys Leu Lys
            740                 745                 750

Gly Glu Leu Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu
        755                 760                 765

Glu Ala Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln
    770                 775                 780

Asn Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser
785                 790                 795                 800

Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp
                805                 810                 815

Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val
            820                 825                 830

Glu Asp Gly Asp Ile Ala Gly Ala Pro Ala Ser Ser Pro Glu Ala Pro
        835                 840                 845

Pro Ala Gln Gln Asp Pro Ala Gln Leu Lys Thr Gln Leu Glu Arg Thr
    850                 855                 860

Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala
865                 870                 875                 880

Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys Arg Leu Gln Glu Glu Leu
                885                 890                 895

Glu Lys Leu Arg Thr Ala Gly Pro Leu Glu Ser Ser Glu Thr Glu Glu
            900                 905                 910

Ala Ser Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser
        915                 920                 925

Asp Leu Gly Arg Ala Ala Thr Lys Leu Gln Glu Leu Leu Lys Thr Thr
    930                 935                 940

Gln Glu Gln Leu Ala Arg Glu Lys Asp Thr Val Lys Lys Leu Gln Glu
945                 950                 955                 960
```

Gln Leu Glu Lys Thr Glu Asp Gly Ser Ser Ser Lys Glu Gly Thr Ser
965 970 975

Val

<210> 68
<211> 977
<212> PRT
<213> Equus caballus

<400> 68

Met Asp Phe Tyr Asp Thr Gln Thr Leu Gly Val Val Val Phe Gly Gly
1 5 10 15

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45

Met Ala Lys Thr His His His Lys Val Glu Lys Lys Lys Lys Glu Lys
50 55 60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Asp His Glu Pro Ser Pro Asn Met Thr Ile Leu Leu
85 90 95

Lys Asp Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
100 105 110

Gln Pro Pro Val Val Ile Ala Pro Val Ala Thr Val Pro Ala Met Pro
115 120 125

Gln Glu Lys Pro Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145 150 155 160

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

Gly Lys Asn Ala Asp Met Val Gln Ser Gln Glu Ala Pro Lys Gln Glu
180 185 190

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Arg Gly Pro Pro Asp
195 200 205

Ser Asp Ser Pro Leu Tyr Leu Pro Tyr Lys Ser Leu Val Ser Thr Val

210 215 220

Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile
225 230 235 240

Leu Ser Glu Lys Ala Gly Val Ile Gln Asp Thr Trp His Lys Ala Thr
245 250 255

Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys
260 265 270

Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser
275 280 285

Lys Leu Arg Glu Leu Asn Lys Glu Leu Ala Ala Glu Lys Ala Lys Ala
290 295 300

Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln
305 310 315 320

Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His
325 330 335

Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu
340 345 350

Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu
355 360 365

Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu
370 375 380

Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys
385 390 395 400

Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Ala Arg Gln Glu Glu
405 410 415

Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys Gln
420 425 430

Val Leu Gln Leu Gln Val Ser His Lys Glu Ser Glu Glu Ala Leu Gln
435 440 445

Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys Arg Ser Gln Thr Ser
450 455 460

His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln
465 470 475 480

Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu Val

485 490 495

Lys Ser Lys Cys Glu Glu Leu Ser Ser Leu His Gly Gln Leu Lys Glu
500 505 510

Ala Arg Ala Glu Asn Ser Glu Leu Thr Glu Lys Ile Arg Ser Ile Glu
515 520 525

Ala Leu Leu Glu Ala Gly Gln Ala Arg Asp Gly Gln Asp Thr Gln Ala
530 535 540

Ser Gln Ala Glu Ala Asp Gln Gln Leu Ala Arg Leu Lys Glu Leu Glu
545 550 555 560

Ser Gln Val Trp Cys Leu Glu Lys Glu Ala Thr Glu Leu Lys Glu Ala
565 570 575

Val Glu Gln Gln Lys Thr Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp
580 585 590

Lys Ala Met Glu Ala Leu Ala Ser Ala Glu Arg Gly Cys Glu Glu Lys
595 600 605

Leu Arg Ser Leu Thr Arg Ala Lys Glu Glu Ser Glu Lys Gln Leu Ser
610 615 620

Leu Ala Glu Ala Gln Thr Lys Glu Ala Leu Leu Ala Leu Leu Pro Ala
625 630 635 640

Leu Ser Asp Leu Thr His Gln Asn Tyr Ala Glu Trp Leu Gln Glu Val
645 650 655

Lys Glu Lys Gly Pro Glu Leu Leu Lys Gln Pro Ser Ala His Thr Glu
660 665 670

Pro Ser Ser Asp Leu Ala Ala Lys Leu Arg Glu Ala Glu Glu Thr Gln
675 680 685

Ser Thr Leu Gln Ala Glu Cys Glu Gln Tyr Arg Thr Ile Leu Gly Glu
690 695 700

Thr Glu Gly Met Leu Lys Asp Leu Gln Lys Ser Val Glu Glu Glu Glu
705 710 715 720

Gln Val Trp Lys Ala Lys Val Ser Ala Thr Glu Glu Glu Leu Gln Lys
725 730 735

Ser Arg Val Thr Val Lys His Leu Glu Glu Ile Val Glu Lys Leu Lys
740 745 750

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

755 760 765

Glu Ala Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln
770 775 780

Ser Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser
785 790 795 800

Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp
805 810 815

Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val
820 825 830

Glu Asp Gly Asp Val Ala Gly Ser Arg Ala Ala Pro Ser Glu Ala Pro
835 840 845

Pro Ala Glu Gln Asp Pro Val Glu Leu Lys Thr Gln Leu Glu Trp Thr
850 855 860

Glu Ala Ser Leu Glu Asp Glu Gln Thr Arg Arg Gln Lys Leu Thr Ala
865 870 875 880

Glu Phe Gln Glu Ala Gln Ser Ser Ala Cys Arg Leu Gln Glu Glu Leu
885 890 895

Glu Lys Leu Arg Ser Thr Gly Pro Leu Gly Ala Ser Ala Ala Glu Glu
900 905 910

Ala Thr Glu Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser
915 920 925

Asp Leu Gly Arg Ala Ala Thr Lys Leu Gln Glu Leu Leu Lys Thr Thr
930 935 940

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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
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Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
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Met Ala Lys Thr His His Gln Lys Gly Glu Lys Lys Lys Lys Glu Lys
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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
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Gly Lys Ile Pro Asp His Asp Leu Asp Ser Asn Val Thr Ile Ile Leu
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Lys Glu Pro Val Arg Val Pro Ala Met Ala Val Ala Pro Thr Ser Val

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His Ser Ser Met Val Phe Pro Pro Val Ala Thr Val Pro Ala Met Pro
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Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
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Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Ile Val Asn Ser Ile
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Gln Val Leu Ala Ser Lys Ser Ala Ile Leu Glu Ala Thr Pro Lys Glu
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Val Pro Met Val Ala Val Pro Pro Val Gly Ser Lys Ala Ser Ala Pro
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Ala Thr Ser Ser Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala
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Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala
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Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Thr Lys Lys
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Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn
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Gln Thr Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu
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Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala
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Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn
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370 375 380

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Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn
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Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu
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Gly Ala Gln Asn Gln Ala Lys Lys Gly Glu Gly Ala Gln Asn Gln Ala
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Gly Glu Gly Ala Gln Asn Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn
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Gln Gly Lys Lys Gly Asp Gly Asn Pro Asn Gln Gly Lys Lys Gly Glu
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Gly Ala Pro Asn Gln Ser Arg Lys Thr Asp Ala Val Ala Asn Gln Gly
595 600 605

Thr Lys Thr Glu Gly Val Ser Asn Gln Gly Lys Lys Ala Glu Gly Ser
610 615 620

Pro Asn Gln Gly Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Lys Lys
625 630 635 640

Val Glu Gly Ser Pro Asn Gln Gly Lys Lys Val Asp Thr Ala Ser Asn

645 650 655

Gln Gly Asn Lys Leu Glu Ser Ala Pro Ala Gln Gly Lys Asn Ser Gly
660 665 670

Met Val Gln Ser Gln Glu Ala Pro Lys Gln Glu Ala Pro Ala Lys Lys
675 680 685

Lys Ser Gly Ser Lys Arg Lys Ala Glu Pro Gly Ser Pro Asp Cys Asp
690 695 700

Ser Pro Leu Phe Leu Pro Tyr Lys Thr Leu Val Ser Thr Val Gly Ser
705 710 715 720

Met Met Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile Leu Ser
725 730 735

Glu Lys Ile Gly Val Thr Gln Asp Thr Trp His Lys Ala Thr Gln Lys
740 745 750

Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys Glu Lys
755 760 765

Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser Lys Leu
770 775 780

Arg Glu Leu Asn Lys Glu Met Ala Ser Glu Lys Ala Lys Ala Ala Ala
785 790 795 800

Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln Glu Ile
805 810 815

Ala Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Gln Asp His Val Lys
820 825 830

Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu Gln Leu
835 840 845

Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser
850 855 860

Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu Ser Lys
865 870 875 880

Gln Asn Thr Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys Val Asn
885 890 895

Lys Glu Leu Val Glu Lys Ser Glu Ala Ser Arg Gln Glu Glu Gln Gln
900 905 910

Arg Lys Ala Leu Glu Ala Lys Ala Ala Thr Phe Glu Lys Gln Val Leu

915 920 925

Gln Leu Gln Ala Ser His Lys Glu Ser Glu Glu Ala Leu Gln Lys Arg
930 935 940

Leu Glu Glu Val Thr Arg Glu Leu Cys Arg Ala Gln Ser Ser His Ala
945 950 955 960

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

Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Val Glu Val Lys Ser
980 985 990

Lys Cys Glu Glu Leu Ser Asn Leu His Gly Gln Leu Lys Glu Ala Arg
995 1000 1005

Ala Glu Asn Glu Gln Leu Thr Glu Arg Ile His Ser Ile Glu Thr
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Leu Leu Glu Ala Gly Gln Ala Gln Asn Thr Gln Ala Ser Gln Ala
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Glu Ala Asp Gln Gln Gln Ile Arg Leu Lys Glu Leu Glu Ser Gln
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Val Leu Ser Leu Glu Lys Glu Thr Ser Glu Leu Lys Glu Ala Met
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Glu Gln Gln Lys Gly Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp
1070 1075 1080

Lys Ala Met Glu Ala Leu Ala Leu Ala Glu Arg Thr Cys Glu Glu
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Lys Leu His Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln
1100 1105 1110

Leu His Leu Ala Glu Ala Gln Thr Lys Glu Val Leu Leu Ala Leu
1115 1120 1125

Leu Pro Asp Leu Ser Ile Ser Ala His Gln Asn Tyr Ala Glu Trp
1130 1135 1140

Leu Arg Glu Val Lys Glu Lys Gly Ser Glu Leu Leu Lys Lys Pro
1145 1150 1155

Pro Ala Ser Leu Glu Pro Ser Leu Asp Val Val Ser Lys Leu Arg
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Glu Ala Glu Glu Thr Gln Asn Ser Leu Gln Ala Glu Cys Asp Gln

1175 1180 1185

Tyr Arg Ser Ile Leu Ala Glu Thr Glu Gly Met Leu Lys Asp Leu
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Gln Lys Ser Val Glu Glu Glu Glu Arg Val Trp Lys Ala Lys Val
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Gly Ala Ala Glu Glu Glu Leu Gln Lys Ser Arg Val Thr Val Lys
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His Leu Glu Asp Ile Val Glu Lys Leu Lys Gly Glu Leu Glu Ser
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Ser Asp Gln Val Arg Glu His Thr Ser Phe Leu Glu Ala Glu Leu
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Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln Asn Tyr Ala
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Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Asp Ser Gln Ser
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Leu Ala Leu Val Arg Gln Gln Leu Ser Asp Met Lys Ser His Val
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Gln Asp Pro Ile Lys Leu Lys Thr Gln Leu Glu Arg Thr Glu Ala
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Ile Leu Glu Asp Glu Gln Thr Arg Arg Gln Lys Leu Thr Ala Glu
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Phe Glu Glu Ala Gln Ser Thr Ala Cys Arg Leu Gln Glu Glu Leu
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Glu Lys Leu Arg Ala Ala Gly Gly Pro Leu Glu Ser Ser Gly Ile
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Glu Glu Val Thr Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Arg
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Leu Thr Ser Asp Leu Gly Arg Ala Ala Thr Lys Leu Gln Glu Leu
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Leu Lys Thr Thr Gln Glu Gln Leu Thr Lys Glu Lys Asp Thr Val

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Lys Lys Leu Gln Glu Gln Leu Glu Lys Ala Glu Asp Gly Ser Ser
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Ser Lys Glu Gly Thr Ser Val
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35 40 45

Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
50 55 60

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

Met Ala Lys Thr Asn His Gln Lys Val Glu Lys Lys Lys Glu Lys
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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
100 105 110

Gly Lys Ile Pro Asp His Asp Leu Ala Pro Asn Val Thr Val Leu Leu
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Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
130 135 140

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

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
180 185 190

Gln Val Leu Ala Ser Lys Thr Ala Ile Leu Glu Thr Ala Pro Lys Glu
195 200 205

Val Pro Met Val Val Val Pro Pro Val Gly Ala Arg Gly Asn Thr Pro
210 215 220

Ala Thr Gly Thr Ala Gln Gly Lys Lys Gly Glu Gly Ala Gln Asn Gln
225 230 235 240

Ser Lys Lys Ala Glu Gly Ala Pro Asn Gln Gly Arg Lys Ala Glu Gly
245 250 255

Thr Pro Asn Leu Trp Ile Met Ala Asp Xaa Thr Pro Tyr Gln Gly Lys
260 265 270

Lys Ala Glu Gly Thr Pro Tyr Gln Cys Ile Met Ala Asp Gly Ala Gln
275 280 285

Asn Gln Gly Lys Lys Val Asp Met Thr Pro Asn Gln Gly Lys Lys Ala
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Glu Gly Ser Pro Thr Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
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Gly Lys Arg Ala Glu Gly Ala Gln Asn Gln Gly Arg Lys Ala Glu Gly
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Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln
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Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Thr
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Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly Ala Gln Asn Gln
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Ser Lys Lys Ala Glu Gly Ala Gln Asn Gln Gly Lys Lys Ala Glu Gly
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Lys Ala Glu Gly Ser Gln Asn Gln Gly Lys Lys Thr Glu Gly Ala Gln
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Glu Gly Ala Gln Gly Lys Lys Ala Glu Gly Ser Pro Asn Gln Gly Lys
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Lys Ala Asp Ser Val Ala Asn Gln Gly Lys Lys Ala Glu Gly Lys Lys
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580 585 590

Gln Gly Lys Lys Ala Asp Ala Ala Ala Ser Gln Gly Lys Thr Thr Glu
595 600 605

Ala Ala Pro Val Gln Gly Arg Asn Ala Asp Val Ala Gln Ser Pro Glu
610 615 620

Ala Pro Lys Gln Glu Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys
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Lys Gly Glu Pro Gly Pro Pro Asp Ala Asp Gly Pro Leu Tyr Leu Pro
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Tyr Lys Thr Leu Val Ser Thr Val Gly Ser Met Val Phe Asn Glu Gly
660 665 670

Glu Ala Gln Arg Leu Ile Glu Ile Leu Ser Glu Lys Ala Gly Ile Ile
675 680 685

Gln Asp Thr Trp His Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile
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Leu Lys Arg Gln Leu Glu Glu Lys Glu Lys Leu Leu Ala Thr Glu Gln
705 710 715 720

Glu Asp Ala Ala Val Ala Lys Ser Lys Leu Arg Glu Leu Asn Lys Glu
725 730 735

Met Ala Ala Glu Lys Ala Lys Ala Ala Ala Gly Glu Ala Lys Val Lys
740 745 750

Lys Gln Leu Val Ala Arg Glu Gln Glu Ile Thr Ala Val Gln Ala Arg
755 760 765

Met Gln Ala Ser Tyr Arg Glu His Val Lys Glu Val Gln Gln Leu Gln
770 775 780

Gly Lys Ile Arg Thr Leu Gln Glu Gln Leu Glu Asn Gly Pro Asn Thr
785 790 795 800

Gln Leu Ala Arg Leu Gln Gln Glu Asn Ser Ile Leu Arg Asp Ala Leu
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Asn Gln Ala Thr Ser Gln Val Glu Ser Lys Gln Asn Ala Glu Leu Ala
820 825 830

Lys Leu Arg Gln Glu Leu Ser Lys Ala Ser Lys Glu Leu Ala Glu Lys
835 840 845

Ser Glu Ala Ala Arg Gln Asp Glu Gln Gln Arg Lys Ala Leu Glu Ala
850 855 860

Lys Ala Ala Ala Ile Glu Lys Gln Val Leu Gln Leu Gln Ala Ser His
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Arg Glu Ser Glu Glu Ala Leu Gln Lys Arg Leu Asp Glu Val Ser Trp
885 890 895

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Glu Lys Ala Gln Glu Gln Gln Gln Met Ala Glu Leu His Ser Lys
        915                 920                 925

Leu Gln Ser Ser Glu Ala Glu Val Arg Ser Lys Cys Glu Glu Leu Asn
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Gly Leu His Gly Gln Leu Gln Glu Ala Arg Thr Glu Asn Ser Gln Leu
945                 950                 955                 960

Thr Glu Arg Ile Arg Ser Ile Glu Ala Leu Leu Glu Ala Gly Gln Thr
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Arg Asp Ala Gln Asp Thr Gln Ala Ser Gln Val Glu Thr Asp Gln Gln
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Gln Thr Arg Thr Cys Pro Gln Ala  Arg Glu Ala Gly Pro  Gly His Arg
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Glu Val  His Ala Thr Ala Cys  Gly Gly Arg Thr Glu  Gly Val Val
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His Ser  Val Thr His Cys Gln  Met Gly Pro Arg Pro  Pro Ala Gln
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Lys Ala  Leu Leu Ser Trp Ser  Ser Ser Ser Lys Lys  His Leu Thr
    1040                1045                1050

Met Cys  Phe Ser Ala Glu Thr  Ala Pro Gln Ala Thr  Val His Val
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Leu Arg  Leu Gly Asp Trp Glu  Arg Leu Ala Gly Trp  Pro Ser Cys
    1070                1075                1080

Ser Leu  Gln Arg Leu Gln Leu  Pro Lys Glu Gly Pro  Ser Leu Gly
    1085                1090                1095

Leu Pro  Val Pro Gly Phe Ala  Arg Ala Gly Pro Arg  Ile Ser Thr
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Ser Arg  Leu Asp Leu Arg Glu  Lys Asn Trp Lys Ala  Met Glu Ala
    1115                1120                1125

Leu Ala  Thr Ala Glu Gln Ala  Cys Lys Glu Lys Leu  His Ser Leu
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Thr Gln  Ala Lys Glu Glu Ser  Glu Lys Gln Leu Arg  Leu Thr Glu
    1145                1150                1155
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Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu Thr
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Gln Ser Thr Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu
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Glu His Thr Ser His Leu Glu Ala Glu Leu Glu Lys His Met Ala
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Gln Gln Leu Ser Glu Met Lys Ser His Val Glu Asp Gly Asp Ile
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Leu Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala Glu Phe
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Lys Leu Arg Thr Ala Gly Pro Leu Glu Ser Ser Glu Thr Glu Glu
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Ser Asp Leu Gly Arg Ala Ala Ala Lys Leu Gln Glu Leu Leu Lys
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Met Thr Gln Glu Gln Leu Ala Arg Glu Lys Asp Thr Val Lys Thr
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<211> 977
<212> PRT
<213> Papio anubis

<400> 76

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Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
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Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
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Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
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Gln Pro Pro Ile Ile Ile Ala Pro Val Ala Thr Val Pro Ala Thr Pro
115 120 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
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Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile

145 150 155 160

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

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

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Pro Pro Asp
195 200 205

Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr Val
210 215 220

Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile
225 230 235 240

Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala Thr
245 250 255

Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys
260 265 270

Glu Lys Leu Leu Ala Ala Glu Gln Glu Asp Ala Ala Val Ala Lys Ser
275 280 285

Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys Ala
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Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln
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Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His
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Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu
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Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu
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Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu
370 375 380

Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys
385 390 395 400

Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Ala Arg Gln Asp Glu
405 410 415

Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys Gln

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Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu Gln
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Lys Arg Leu Asp Glu Val Gly Gln Glu Leu Cys Arg Ala Gln Ser Ser
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His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln
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Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu Val
485 490 495

Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln Glu
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515 520 525

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

Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Thr Glu Leu Arg Glu Ala
565 570 575

Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp
580 585 590

Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys Lys Glu Lys
595 600 605

Leu His Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu His
610 615 620

Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu Thr Leu Leu Pro Glu
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Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr Glu Trp Leu Gln Asp Leu
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Lys Glu Lys Gly Pro Thr Leu Leu Lys His Pro Pro Ala Pro Ala Glu
660 665 670

Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu Ala Gln
675 680 685

Ser Thr Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala Glu

690 695 700

Thr Glu Gly Met Leu Arg Asp Leu Gln Lys Ser Val Glu Glu Glu Glu
705 710 715 720

Gln Val Trp Arg Ala Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys
725 730 735

Ser Arg Val Thr Val Lys His Leu Glu Glu Ile Val Glu Lys Leu Lys
740 745 750

Gly Glu Leu Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu
755 760 765

Glu Ala Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln
770 775 780

Asn Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser
785 790 795 800

Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp
805 810 815

Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val
820 825 830

Glu Asp Gly Asp Ile Ala Gly Ala Pro Ala Ser Ser Pro Glu Ala Pro
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Pro Ala Gln Gln Asp Pro Ala Gln Leu Lys Thr Gln Leu Glu Arg Thr
850 855 860

Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala
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Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys Arg Leu Gln Glu Glu Leu
885 890 895

Glu Lys Leu Arg Thr Ala Gly Pro Leu Glu Ser Ser Glu Thr Glu Glu
900 905 910

Ala Ser Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser
915 920 925

Asp Leu Gly Arg Ala Ala Thr Lys Leu Gln Glu Leu Leu Lys Thr Thr
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g 3541

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<212> PRT
<213> Gorilla gorilla gorilla

<400> 78

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35 40 45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Asp His Asp Pro Ala Pro Asn Val Thr Val Leu Leu
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Arg Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
100 105 110

Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
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Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145 150 155 160

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

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

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Pro Pro Asp
195 200 205

Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr Val
210 215 220

Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile
225 230 235 240

Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala Thr
245 250 255

Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys
260 265 270

Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser
275 280 285

Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys Ala
290 295 300

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Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His
325 330 335

Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu
340 345 350

Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu
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Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu
370 375 380

Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys
385 390 395 400

Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Val Arg Gln Asp Glu
405 410 415

Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys Gln
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Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu Gln
435 440 445

Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys His Ala Gln Ser Ser
450 455 460

His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln
465 470 475 480

Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu Val
485 490 495

Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln Glu
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Ala Arg Ala Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
515 520 525

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

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

Val Glu Gln Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp
580 585 590

Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Ala Cys Lys Glu Lys
595 600 605

Leu His Ser Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu Cys
610 615 620

Leu Ile Glu Ala Gln Thr Met Glu Ala Leu Leu Ala Leu Leu Pro Glu
625 630 635 640

Leu Ser Val Leu Ala Gln Gln Asn Tyr Thr Glu Trp Leu Gln Asp Leu
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Lys Glu Lys Gly Pro Thr Leu Leu Lys His Pro Pro Ala Pro Ala Glu
660 665 670

Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu Thr Gln
675 680 685

Ser Thr Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala Glu
690 695 700

Thr Glu Gly Met Leu Arg Asp Leu Gln Lys Ser Val Glu Glu Glu Glu
705 710 715 720

Gln Val Trp Arg Ala Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys
725 730 735

Ser Arg Val Thr Val Lys His Leu Glu Glu Ile Val Glu Lys Leu Lys
740 745 750

Gly Glu Leu Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu
755 760 765

Glu Ala Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln
770 775 780

Asn Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser
785 790 795 800

Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp
805 810 815

Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val
820 825 830

Glu Asp Gly Asp Ile Ala Gly Ala Pro Ala Ser Ser Pro Glu Ala Pro
835 840 845

Pro Ala Glu Gln Asp Pro Val Gln Leu Lys Thr Gln Leu Glu Gln Thr
850 855 860

Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala
865 870 875 880

Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys Arg Leu Gln Glu Glu Leu
885 890 895

Glu Lys Leu Arg Thr Ala Gly Pro Leu Glu Ser Ser Glu Thr Glu Glu
900 905 910

Ala Ser Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser
915 920 925

Asp Leu Gly Arg Ala Ala Thr Lys Leu Gln Glu Leu Leu Lys Thr Thr
930 935 940

Gln Glu Gln Leu Ala Arg Glu Lys Asp Thr Val Lys Lys Leu Gln Glu
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Gln Leu Glu Lys Thr Glu Asp Gly Ser Ser Ser Lys Glu Gly Thr Ser
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Val

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<213> Saimiri boliviensis boliviensis

<400> 80

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Phe Met Val Val Ser Ala Ile Gly Ile Phe Leu Val Ser Thr Phe Ser
20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Lys Glu
35 40 45

Met Ala Lys Thr Asn His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
50 55 60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Asp His Asp Leu Ala Pro Asn Val Thr Val Leu Leu
85 90 95

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Gln Glu Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
            100                 105                 110

Gln Pro Pro Ile Ile Val Ala Pro Val Ala Thr Val Pro Ala Met Pro
        115                 120                 125

Gln Glu Lys Leu Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
    130                 135                 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145                 150                 155                 160

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

Gly Arg Asn Thr Asp Thr Ala Gln Ser Pro Glu Ala Pro Lys Gln Glu
            180                 185                 190

Ala Pro Ala Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Pro Pro Asp
        195                 200                 205

Ala Asp Gly Pro Leu Tyr Leu Pro Tyr Lys Thr Leu Val Ser Thr Val
    210                 215                 220

Gly Ser Met Val Phe Asn Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile
225                 230                 235                 240

Leu Ser Glu Lys Ala Gly Ile Ile Gln Asp Thr Trp His Lys Ala Thr
                245                 250                 255

Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys
            260                 265                 270

Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Ala Ala Val Ala Lys Ser
        275                 280                 285

Lys Leu Arg Glu Leu Asn Lys Glu Met Ala Ala Glu Lys Ala Lys Ala
    290                 295                 300

Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Gln Gln Gln
305                 310                 315                 320

Glu Ile Ala Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His
                325                 330                 335

Val Lys Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu
            340                 345                 350

Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu
        355                 360                 365
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Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu
370 375 380

Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Ser Lys
385 390 395 400

Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Ala Arg Gln Asp Glu
405 410 415

Gln Gln Arg Lys Ala Leu Glu Ala Lys Ala Ala Ala Phe Glu Lys Gln
420 425 430

Val Leu Gln Leu Gln Ala Ser His Arg Glu Ser Glu Glu Ala Leu Gln
435 440 445

Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys Arg Thr Gln Asp Ser
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His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Gln Glu Gln Gln Gln
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Gln Met Ala Glu Leu His Ser Lys Leu Gln Ser Ser Glu Ala Glu Val
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Arg Ser Lys Cys Glu Glu Leu Ser Gly Leu His Gly Gln Leu Gln Glu
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Ala Arg Thr Glu Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
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Ala Leu Leu Glu Ala Gly Gln Thr Arg Asp Ala Gln Asp Ile Gln Ala
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Ser Gln Ala Glu Ala Asp Gln Gln Gln Thr Arg Leu Lys Glu Leu Glu
545 550 555 560

Ser Gln Val Ser Gly Leu Glu Lys Glu Ala Thr Glu Leu Arg Glu Ala
565 570 575

Val Glu Gln Gln Lys Met Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp
580 585 590

Lys Ala Met Glu Ala Leu Ala Thr Ala Glu Gln Thr Cys Lys Glu Lys
595 600 605

Leu His Ser Leu Asn Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu Arg
610 615 620

Leu Thr Glu Val Gln Thr Arg Glu Ala Leu Leu Ala Leu Leu Pro Glu
625 630 635 640

Leu Ser Ile Leu Ala Gln Gln Asn Tyr Thr Glu Trp Leu Gln Glu Leu
645 650 655

Lys Glu Lys Gly Pro Thr Leu Leu Lys Gln Pro Pro Ala Pro Thr Glu
660 665 670

Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu Ala Glu Glu Thr Gln
675 680 685

Ser Thr Leu Gln Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala Glu
690 695 700

Thr Glu Gly Met Leu Arg Asp Leu Gln Lys Ser Val Glu Glu Glu Glu
705 710 715 720

Gln Val Trp Arg Ala Lys Val Gly Ala Ala Glu Glu Glu Leu Gln Lys
725 730 735

Ser Arg Val Thr Val Lys His Leu Glu Glu Met Val Glu Lys Leu Lys
740 745 750

Gly Glu Leu Glu Ser Ser Asp Gln Val Arg Glu His Thr Ser His Leu
755 760 765

Glu Ala Glu Leu Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln
770 775 780

Asn Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser
785 790 795 800

Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp
805 810 815

Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val
820 825 830

Glu Asp Gly Asp Ile Ala Gly Ala Pro Ala Ser Ser Pro Glu Ala Ser
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Pro Ala Glu Gln Asp Pro Val Gln Leu Lys Thr Gln Leu Glu Arg Thr
850 855 860

Glu Ala Ile Leu Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala
865 870 875 880

Glu Phe Glu Glu Ala Gln Thr Ser Ala Cys Arg Leu Gln Glu Glu Leu
885 890 895

Glu Lys Leu Arg Thr Ala Ser Pro Leu Glu Ser Ser Glu Thr Glu Ala
900 905 910

Ala Ser Gln Leu Lys Glu Arg Leu Glu Lys Glu Lys Lys Leu Thr Ser
915 920 925

Asp Leu Gly Arg Ala Ala Ala Lys Leu Gln Glu Leu Leu Lys Met Thr
930 935 940

Gln Glu Gln Leu Ala Arg Glu Lys Asp Thr Val Lys Thr Leu Gln Glu
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Val

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<211> 974
<212> PRT
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<400> 82

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20 25 30

Met Lys Glu Thr Ser Tyr Glu Glu Ala Leu Ala Asn Gln Arg Arg Glu
35 40 45

Met Ala Lys Thr His His Gln Lys Val Glu Lys Lys Lys Lys Glu Lys
50 55 60

Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Asp Glu Lys Pro Asn
65 70 75 80

Gly Lys Ile Pro Asp His Glu Pro Gly Pro Asn Val Thr Ile Leu Pro
85 90 95

Lys Asp Ala Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
100 105 110

Gln Ser Pro Val Val Ile Pro Pro Val Ala Thr Val Pro Ala Met Pro
115 120 125

Gln Glu Lys Pro Ala Ser Ser Pro Lys Asp Lys Lys Lys Lys Glu Lys
130 135 140

Lys Val Ala Lys Val Glu Pro Ala Val Ser Ser Val Val Asn Ser Ile
145 150 155 160

Gln Val Leu Ala Ser Lys Ala Ala Ile Leu Glu Ala Ala Pro Lys Glu
165 170 175

Gly Lys Asn Ala Asp Met Val Gln Ser Gln Glu Ala Gln Lys Gln Glu

180 185 190

Ala Pro Val Lys Lys Lys Ser Gly Ser Lys Lys Lys Gly Pro Pro Glu
195 200 205

Thr Asp Ser Pro Leu Cys Leu Pro Tyr Lys Thr Leu Val Ser Thr Val
210 215 220

Gly Ser Met Val Phe Ser Glu Gly Glu Ala Gln Arg Leu Ile Glu Ile
225 230 235 240

Leu Ser Glu Lys Ala Gly Val Val Gln Asp Thr Trp His Lys Ala Thr
245 250 255

Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg Gln Leu Glu Glu Lys
260 265 270

Glu Lys Leu Leu Ala Thr Glu Gln Glu Asp Thr Ala Ala Ala Lys Ser
275 280 285

Lys Leu Arg Glu Leu Asn Lys Glu Leu Ala Ala Glu Lys Ala Lys Ala
290 295 300

Ala Ala Gly Glu Ala Lys Val Lys Lys Gln Leu Val Ala Arg Glu Gln
305 310 315 320

Glu Ile Thr Ala Val Gln Ala Arg Met Gln Ala Ser Tyr Arg Glu His
325 330 335

Val Gln Glu Val Gln Gln Leu Gln Gly Lys Ile Arg Thr Leu Gln Glu
340 345 350

Gln Leu Glu Asn Gly Pro Asn Thr Gln Leu Ala Arg Leu Gln Gln Glu
355 360 365

Asn Ser Ile Leu Arg Asp Ala Leu Asn Gln Ala Thr Ser Gln Val Glu
370 375 380

Ser Lys Gln Asn Ala Glu Leu Ala Lys Leu Arg Gln Glu Leu Gly Lys
385 390 395 400

Val Ser Lys Glu Leu Val Glu Lys Ser Glu Ala Ala Arg Gln Glu Glu
405 410 415

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

Val Leu Gln Leu Gln Ala Ser His Lys Glu Ser Glu Glu Ala Leu Gln
435 440 445

Lys Arg Leu Asp Glu Val Ser Arg Glu Leu Cys Arg Ser Gln Thr Ser

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His Ala Ser Leu Arg Ala Asp Ala Glu Lys Ala Arg Glu Gln Gln Gln
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Gln Met Ala Glu Leu His Gly Lys Leu Gln Ser Ser Glu Ala Glu Val
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Arg Ser Arg Cys Glu Glu Leu Ser Ser Val His Gly Gln Leu Asp Glu
            500                 505                 510

Ala Lys Ala Gln Asn Ser Gln Leu Thr Glu Arg Ile Arg Ser Ile Glu
        515                 520                 525

Ala Leu Leu Glu Ala Ser Gln Ala Arg Asp Ala Gln Ala Ser Arg Glu
    530                 535                 540

Glu Ala Asn Gln Gln Gln Ala Arg Leu Met Glu Leu Glu Ser Gln Val
545                 550                 555                 560

Trp Cys Leu Glu Lys Glu Ala Thr Glu Leu Lys Glu Ala Val Glu Gln
                565                 570                 575

Gln Lys Val Lys Asn Asn Asp Leu Arg Glu Lys Asn Trp Lys Ala Met
            580                 585                 590

Glu Ala Leu Ala Ser Ala Glu Arg Gly Cys Glu Glu Lys Leu Arg Ser
        595                 600                 605

Leu Thr Gln Ala Lys Glu Glu Ser Glu Lys Gln Leu Ser Leu Thr Glu
    610                 615                 620

Ala Gln Thr Arg Glu Ala Leu Leu Ala Leu Leu Pro Gly Leu Ser Ala
625                 630                 635                 640

Pro Thr His Gln Asn Tyr Ala Asp Trp Leu Gln Glu Leu Lys Glu Lys
                645                 650                 655

Gly Pro Glu Leu Leu Lys Gln Pro Pro Ala His Thr Glu Pro Ser Asp
            660                 665                 670

Leu Ala Ala Lys Leu Arg Glu Ala Glu Glu Thr Gln Asn Ser Leu Gln
        675                 680                 685

Ala Glu Cys Asp Gln Tyr Arg Ser Ile Leu Ala Glu Thr Glu Ala Met
    690                 695                 700

Leu Lys Ala Leu Gln Lys Ser Val Glu Glu Glu Glu Gln Val Trp Lys
705                 710                 715                 720

Ala Arg Val Ser Ala Thr Glu Glu Glu Leu Gln Lys Ser Arg Val Thr
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725 730 735

Val Lys His Leu Glu Glu Thr Val Gly Lys Leu Lys Gly Glu Leu Glu
740 745 750

Ser Ala Asp Gln Val Arg Glu His Thr Ser His Leu Glu Ala Glu Leu
755 760 765

Glu Lys His Met Ala Ala Ala Ser Ala Glu Cys Gln Asn Tyr Ala Thr
770 775 780

Glu Val Ala Gly Leu Arg Gln Leu Leu Leu Glu Ser Gln Ser Gln Leu
785 790 795 800

Asp Ala Ala Lys Ser Glu Ala Gln Lys Gln Ser Asp Glu Leu Ala Leu
805 810 815

Val Arg Gln Gln Leu Ser Glu Met Lys Ser His Val Glu Asp Gly Asp
820 825 830

Val Ala Gly Ser Pro Ala Ala Pro Pro Glu Ala Pro Ser Ala Glu Gln
835 840 845

Asp Pro Ile Glu Leu Lys Met Gln Leu Glu Arg Thr Glu Ala Ile Leu
850 855 860

Glu Asp Glu Gln Thr Gln Arg Gln Lys Leu Thr Ala Glu Phe Glu Glu
865 870 875 880

Ala Gln Leu Val Ser Ser Arg Leu Gln Gly Glu Leu Glu Lys Leu Arg
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Cys Ser Ser Ala Leu Gly Ser Ser Glu Ala Glu Glu Ala Thr Arg Leu
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Thr Val Glu Lys Lys Gly Lys Thr Lys Lys Lys Glu Glu Lys Pro Asn
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Gly Lys Ile Pro Asp His Glu Pro Ala Pro Asn Val Thr Ile Leu Leu
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Lys Asp Pro Val Arg Ala Pro Ala Val Ala Val Ala Pro Thr Pro Val
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Gln Pro Pro Val Val Ile Ala Pro Val Ala Pro Val Pro Ala Val Pro
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Lys Ala Pro Pro Asp Ser Asp Ser Pro Leu Tyr Leu Pro Tyr Lys Thr
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Trp His Lys Ala Thr Gln Lys Gly Asp Pro Val Ala Ile Leu Lys Arg
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Pro Ala Ser Thr Glu Pro Ser Ser Asp Leu Ala Ser Lys Leu Arg Glu
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Glu Glu Leu Gln Lys Ser Arg Val Thr Val Thr His Leu Glu Glu Ile
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Val Glu Lys Leu Arg Gly Glu Leu Glu Ser Ser Asp Gln Val Arg Glu
755 760 765

His Thr Ser His Leu Glu Ala Glu Leu Glu Lys His Met Ala Ala Ser
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Ser Ala Glu Cys Gln Ser Tyr Ala Lys Glu Val Ala Gly Leu Arg Gln
785 790 795 800

Leu Leu Leu Glu Ser Gln Ser Gln Leu Asp Ala Ala Lys Ser Glu Ala
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Gln Lys Gln Ser Asn Glu Leu Ala Leu Val Arg Gln Gln Leu Ser Glu
820 825 830

Met Gln Ser His Val Glu Asp Gly Asp Val Ala Gly Ser Pro Ala Val
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Pro Pro Glu Ala Pro Pro Ala Glu Gln Asp Pro Val Glu Leu Lys Thr

850 855 860

Gln Leu Glu Gln Thr Glu Ala Leu Leu Glu Asp Glu Gln Thr Gln Arg
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Gln Lys Leu Thr Ala Glu Phe Glu Glu Ala Gln Ser Ser Ala Cys Arg
885 890 895

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

Lys Ile Ser Glu Val Glu Gln Gln Lys Gln Thr Ala Leu Asp Gln Val
820 825 830

Lys Ile Leu Glu Lys Thr Ile Glu Lys Ile Asn Ala Glu Met Gln Asp
835 840 845

Thr Asp Gln Leu Lys Gly Gln Val Met Leu Leu Glu Ala Gln Leu Glu
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Lys Gln Leu Glu Ser Val Thr Ile Ser Gln Ile Tyr Ala Glu Glu Met
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Ala Gln Leu Lys Thr Leu Leu Ser Asp Thr Gln Thr Gln Leu Leu Ser
885 890 895

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CLAIMS

1. A recombinant cell having enhanced expression of an RNA-binding protein containing an RNA recognition motif (RRM), or having enhanced expression of both a p180 protein and an RNA-binding protein containing an RRM, and having enhanced intracellular synthetic or secretory capacity of a protein as a product of interest,

wherein the RNA-binding protein containing an RRM is

(1) a protein that consists of the full length of the amino acid sequence of the splicing factor 3B subunit 4 (SF3b4) protein specified by the amino acid sequence shown in SEQ ID NO: 4,

(2) a protein that consists of an amino acid sequence with at least 90 % sequence identity to the amino acid sequence shown in SEQ ID NO: 4, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4, or

(3) a protein that consists of an amino acid sequence encoded by a nucleotide sequence with at least 90 % sequence identity to the nucleotide sequence shown in SEQ ID NO: 3, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4.

2. The recombinant cell according to claim 1, wherein the p180 protein is

(a) a protein specified by the amino acid sequence shown in SEQ ID NO: 2,

(b) a protein that consists of an amino acid sequence with at least 90% sequence identity to the amino acid sequence shown in SEQ ID NO: 2, and which has a capability of promoting polysome formation on an intracellular endoplasmic reticulum membrane, or

(c) a protein that consists of an amino acid sequence encoded by a nucleotide sequence with at least 90% sequence identity to the nucleotide sequence shown in SEQ ID NO: 1, and which has a capability of promoting polysome formation on the intracellular endoplasmic reticulum membrane.

3. The recombinant cell according to claim 1, wherein the p180 protein is derived from an animal except for human.

4. The recombinant cell according to claim 3, wherein the p180 protein is a protein that consists of an amino acid sequence encoded by a nucleotide sequence described in SEQ ID NO: 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 69, 71, 73, 75, 77, 79, 81, 83, 85 or 87, or of a protein specified by an amino acid sequence described in SEQ ID NO: 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 64, 65, 66, 67, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86 or 88.

5. A cell line designated by Accession No. NITE BP-01753 (CHO 3D5), Accession No. NITE BP-1535 (CHO YA7), or Accession No. NITE BP-01811 (CHO 1B2).

6. A method for producing a protein as a product of interest, wherein, in a recombinant cell having enhanced expression of an RNA-binding protein containing an RRM or in a recombinant cell having enhanced expression of both a p180 protein and an RNA-binding protein containing an RRM, a nucleic acid molecule encoding the protein as a product of interest is transformed or production of the protein as a product of interest is increased, whereby the protein as a product of interest is produced,

wherein the RNA-binding protein containing an RRM is

(1) a protein that consists of the full length of the amino acid sequence of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4,

(2) a protein that consists of an amino acid sequence with at least 90 % sequence identity to the amino acid sequence shown in SEQ ID NO: 4, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or

secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4, or

(3) a protein that consists of an amino acid sequence encoded by a nucleotide sequence with at least 90 % sequence identity to the nucleotide sequence shown in SEQ ID NO: 3, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4.

7. The method according to claim 6, wherein the p180 protein is

(a) a protein specified by the amino acid sequence shown in SEQ ID NO: 2,

(b) a protein that consists of an amino acid sequence with at least 90% sequence identity to the amino acid sequence shown in SEQ ID NO: 2, and which has a capability of promoting polysome formation on an intracellular endoplasmic reticulum membrane, or

(c) a protein that consists of an amino acid sequence encoded by a nucleotide sequence with at least 90% sequence identity to the nucleotide sequence shown in SEQ ID NO: 1, and which has a capability of promoting polysome formation on an intracellular endoplasmic reticulum membrane.

8. The method according to claim 6, wherein the p180 protein is derived from an animal except for human.

9. The method according to claim 8, wherein the p180 protein is a protein that consists of an amino acid sequence encoded by a nucleotide sequence described in SEQ ID NO: 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 69, 71, 73, 75, 77, 79, 81, 83, 85 or 87, or of a protein specified by an amino acid sequence described in SEQ ID NO: 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 64, 65, 66, 67, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86 or 88.

10. The method according to any one of claims 6 - 9, wherein the recombinant cell

line is designated by Accession No. NITE BP-01753 (CHO 3D5), Accession No. NITE BP-1535 (CHO YA7), or Accession No. NITE BP-01811 (CHO 1B2).

11. The method according to any one of claims 6 - 10, wherein the protein as a product of interest is a glycoprotein.

12. The method according to claim 11, wherein the protein as a product of interest is a collagen, a fibronectin, or an antibody.

13. A method for increasing an amount of a protein as a product of interest to be expressed in a cell as an expression system, wherein, in an expression unit for expressing the protein as a product of interest, a cis-element to be recognized by an RNA-binding protein, to be bound by an RNA-binding protein, or to be interacted with an RNA-binding protein, is inserted, downstream of a promoter and upstream of the start codon in the nucleotide sequence of DNA encoding the protein as a product of interest, whereby the amount of the protein as a product of interest to be expressed in the cell as an expression system is increased,

wherein the cis-element has a nucleotide sequence containing 9mer to 12mer sequence motifs GAN_1-$(X)_n$-ACN_2 (in the formula, n = 3 to 6, and N_1 and N_2 can be independently nucleotide A, T, C or G),

wherein the RNA-binding protein is

(1) a protein that consists of the full length of the amino acid sequence of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4,

(2) a protein that consists of an amino acid sequence with at least 90 % sequence identity to the amino acid sequence shown in SEQ ID NO: 4, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4, or

(3) a protein that consists of an amino acid sequence encoded by a nucleotide sequence with at least 90 % sequence identity to the nucleotide sequence shown in SEQ

ID NO: 3, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4.

14. The method according to claim 13, wherein the cis-element has a nucleotide sequence containing 9mer to 12mer sequence motifs GAG-$(X)_n$-ACV (in the formula. n = 3 to 6 and V represents A, G or C), and is a sequence that is shown in any one of SEQ ID NOs: 17 to 20.

15. The method according to any one of claims 13 or 14, wherein the nucleotide sequence of the cis-element is a sequence selected from the group consisting of: a sequence derived from the nucleotide sequence of the 5' untranslated region of a type I collagen gene; a sequence derived from the nucleotide sequence of the 5' untranslated region of a fibronectin gene; a sequence derived from the nucleotide sequence of the 5' untranslated region of a matrix metalloproteinase 14 (MMP14) gene; a sequence derived from the nucleotide sequence of the 5' untranslated region of a prolyl 4-hydroxylase A2 (P4HA2) gene; and a sequence derived from the nucleotide sequence of the 5' untranslated region of a prolyl 4-hydroxylase A1 (P4HA1) gene.

16. The method according to any one of claims 13 - 14, wherein the nucleotide sequence of the cis-element is the full length of SEQ ID NO: 5, the full length of SEQ ID NO: 7, or the nucleotides at positions 1 to 102, positions 1 to 78, positions 1 to 60, positions 61 to 126, positions 16 to 57, positions 79 to 126, positions 103 to 126, positions 58 to 78, positions 51 to 78, positions 1 to 27, or positions 70 to 78 of SEQ ID NO: 5.

17. The method according to any one of claims 13 to 16, wherein the cell as an expression system is an intact host cell, a cell having enhanced expression of a p180 protein, a cell having enhanced expression of a SF3b4 protein, or a cell having enhanced expression of both a p180 protein and a SF3b4 protein.

18. An expression unit for expressing a protein as a product of interest, wherein, in the expression unit for expressing the protein as a product of interest, a cis-element to be recognized by an RNA-binding protein, to be bound by an RNA-binding protein, or to be interacted with an RNA-binding protein, is inserted, downstream of a promoter and upstream of the start codon in the nucleotide sequence of DNA encoding the protein as a product of interest, whereby the amount of the protein as a product of interest to be expressed in the cell as an expression system is increased,

wherein the cis-element has a nucleotide sequence containing 9mer to 12mer sequence motifs GAN_1-$(X)_n$-ACN_2 (in the formula, n = 3 to 6, and N_1 and N_2 can be independently nucleotide A, T, C or G),

wherein the RNA-binding protein is

(1) a protein that consists of the full length of the amino acid sequence of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4,

(2) a protein that consists of an amino acid sequence with at least 90 % sequence identity to the amino acid sequence shown in SEQ ID NO: 4, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4, or

(3) a protein that consists of an amino acid sequence encoded by a nucleotide sequence with at least 90 % sequence identity to the nucleotide sequence shown in SEQ ID NO: 3, and which has, when expressed in the cell, an ability to enhance capacity of the cell for synthesis or secretion of the protein as a product of interest, wherein the ability is comparable to that of the SF3b4 protein specified by the amino acid sequence shown in SEQ ID NO: 4.

19. An expression vector having the expression unit according to claim 18.