SEQUENCE LISTING

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

<120> METHOD OF EFFICIENTLY ESTABLISHING INDUCED PLURIPOTENT STEM CELLS

<130> 091667

<150> US 61/305,107
<151> 2010-02-16

<150> US 61/379,949
<151> 2010-09-03

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<170> PatentIn version 3.5

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Met Ala Glu Ala Arg Thr Ser Leu Ser
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gcc cac tgt cgg ggc ccg ctg gcc act ggc ctg cac cca gac ctg gac 642
Ala His Cys Arg Gly Pro Leu Ala Thr Gly Leu His Pro Asp Leu Asp
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ctc ccg ggc cga agc ctc gcc acc cct gcg cct tcc tgc tac ctt ctg 690
Leu Pro Gly Arg Ser Leu Ala Thr Pro Ala Pro Ser Cys Tyr Leu Leu
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ggc agc gaa ccc agc tct ggc ctg ggc ctc cag ccc gag acc cac ctc 738
Gly Ser Glu Pro Ser Ser Gly Leu Gly Leu Gln Pro Glu Thr His Leu
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ccc gag ggc agc ctg aag cgg tgc tgc gtc ttg ggc cta ccc ccc acc 786
Pro Glu Gly Ser Leu Lys Arg Cys Cys Val Leu Gly Leu Pro Pro Thr
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Ser Pro Ala Ser Ser Ser Pro Cys Ala Ser Ser Asp Val Thr Ser Ile
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atc cgc tcc tcc cag acg tct ctg gtc acc tgt gta aat gga ctc cgg 882
Ile Arg Ser Ser Gln Thr Ser Leu Val Thr Cys Val Asn Gly Leu Arg

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agc ccc cct ctg acg gga gat ctg ggg ggc cct tcc aag cgg gcc cgg      930
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                110                 115                 120

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

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

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

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

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

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

aag agc cac atc gac cag cgc aag ggc gag gac ttc acc tgc ttc tgg     1266
Lys Ser His Ile Asp Gln Arg Lys Gly Glu Asp Phe Thr Cys Phe Trp
        220                 225                 230

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

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

ttt gaa ggc tgc agc aag gcc ttc tca cgg ctg gag aac ctc aag atc     1410
Phe Glu Gly Cys Ser Lys Ala Phe Ser Arg Leu Glu Asn Leu Lys Ile
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cac ctg agg agc cac acg ggc gag aag ccg tac ctg tgc cag cac ccg     1458
His Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Leu Cys Gln His Pro
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ggt tgc cag aag gcc ttc agc aac tcc agc gac cgc gcc aag cac cag     1506
Gly Cys Gln Lys Ala Phe Ser Asn Ser Ser Asp Arg Ala Lys His Gln
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cgc acc cac cta gac acg aag ccg tac gcc tgt cag atc cct ggc tgc     1554
Arg Thr His Leu Asp Thr Lys Pro Tyr Ala Cys Gln Ile Pro Gly Cys
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tcc aag cgc tac aca gac ccc agc tcc ctc cgc aag cac gtc aag gcc     1602
Ser Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys His Val Lys Ala
330                 335                 340                 345

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

gac acc gag gcc gac gtc ctg acc gag tgt ctg gtc ctg cag cag ctc     1698
Asp Thr Glu Ala Asp Val Leu Thr Glu Cys Leu Val Leu Gln Gln Leu
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cac acg tcc aca cag ctg gct gcc agc gac ggc aag ggt ggc tgt ggc     1746
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ctg ggc cag gag ctg ctc cca ggt gtg tat cct ggc tcc atc acc ccc     1794
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cat aac gga ctt gca tcg ggc ctc ctg ccc cca gcg cac gac gta cct      1842
His Asn Gly Leu Ala Ser Gly Leu Leu Pro Pro Ala His Asp Val Pro
410                 415                 420                 425

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

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

ctc ctc tca cca ata gtc agc ccc ctg aag ggg ctg ggg cca ccg ccg      1986
Leu Leu Ser Pro Ile Val Ser Pro Leu Lys Gly Leu Gly Pro Pro Pro
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ctg ccc cca tcc tct cag agc cat tct ccg ggg ggc cag ccc ttc ccc      2034
Leu Pro Pro Ser Ser Gln Ser His Ser Pro Gly Gly Gln Pro Phe Pro
    475                 480                 485

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

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

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

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

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

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

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

ccc aat gga gcc ttt gac cac tgc ctg ggc cac atc ccc tcc atc tac      2418
Pro Asn Gly Ala Phe Asp His Cys Leu Gly His Ile Pro Ser Ile Tyr
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aca gac acc tga aggagccccc acatgcgcct gcccatccag cactgcagat          2470
Thr Asp Thr
        620

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Leu Gly Leu Gln Pro Glu Thr His Leu Pro Glu Gly Ser Leu Lys Arg
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Cys Cys Val Leu Gly Leu Pro Pro Thr Ser Pro Ala Ser Ser Ser Pro
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Cys Ala Ser Ser Asp Val Thr Ser Ile Ile Arg Ser Ser Gln Thr Ser
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Leu Val Thr Cys Val Asn Gly Leu Arg Ser Pro Pro Leu Thr Gly Asp
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Leu Gly Gly Pro Ser Lys Arg Ala Arg Pro Gly Pro Ala Ser Thr Asp
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Ser His Glu Gly Ser Leu Gln Leu Glu Ala Cys Arg Lys Ala Ser Phe
130 135 140

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

Gln Glu Glu Leu Val Arg His Ile Glu Lys Ser His Ile Asp Gln Arg
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Lys Gly Glu Asp Phe Thr Cys Phe Trp Ala Gly Cys Val Arg Arg Tyr
225 230 235 240

Lys Pro Phe Asn Ala Arg Tyr Lys Leu Leu Ile His Met Arg Val His
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Ser Gly Glu Lys Pro Asn Lys Cys Met Phe Glu Gly Cys Ser Lys Ala
260 265 270

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

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Glu Lys Pro Tyr Leu Cys Gln His Pro Gly Cys Gln Lys Ala Phe Ser
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Asn Ser Ser Asp Arg Ala Lys His Gln Arg Thr His Leu Asp Thr Lys
305                 310                 315                 320

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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                565                 570                 575

Ser Cys Pro Thr Ala Leu Pro Gln Gln Pro Ser Glu Asp Val Val Ser
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gaggctccgg cgtgagactt gcggctgccg gcggagcgga gtgtgagccg gtgaatgggg      180

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

gcc gag gca ctt tcg gac aag agg cca aag gag gcc cct ggt gct cct      284
Ala Glu Ala Leu Ser Asp Lys Arg Pro Lys Glu Ala Pro Gly Ala Pro
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ggc cag ggc cgc ggg cct gtc agc ctg gga gcg cac atg gcc ttc agg      332
Gly Gln Gly Arg Gly Pro Val Ser Leu Gly Ala His Met Ala Phe Arg
            25                  30                  35

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

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

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

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

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

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

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

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

cta ccg gac tac cag gcc atg gtc agc gcc cac aca ccc ctg ccc acc      764
Leu Pro Asp Tyr Gln Ala Met Val Ser Ala His Thr Pro Leu Pro Thr
                170                 175                 180
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cac tgc cga gcc cca tcg tcc atg ggt ctg ccc tca gac ctg gac ttt        812
His Cys Arg Ala Pro Ser Ser Met Gly Leu Pro Ser Asp Leu Asp Phe
            185                 190                 195

cca gac cga ggc ctc acc aac cct gca cct tcc tgc tac ctt ctg ggc        860
Pro Asp Arg Gly Leu Thr Asn Pro Ala Pro Ser Cys Tyr Leu Leu Gly
        200                 205                 210

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

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

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

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

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

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

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

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

cct cag ttg cca act ggc ccc ggc ctc gga ggc cta ggg ctg ggc ctg       1292
Pro Gln Leu Pro Thr Gly Pro Gly Leu Gly Gly Leu Gly Leu Gly Leu
            345                 350                 355

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

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

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

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

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

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

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

tgc cag aag gcc ttc agc aac tcc agc gac cgt gcc aag cac caa cgc       1676
Cys Gln Lys Ala Phe Ser Asn Ser Ser Asp Arg Ala Lys His Gln Arg
470                 475                 480                 485
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acc cac ctc gac acg aag cca tat gct tgt cag atc cct ggc tgc tcc      1724
Thr His Leu Asp Thr Lys Pro Tyr Ala Cys Gln Ile Pro Gly Cys Ser
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aag cgc tac acg gac ccc agc tcc ctc cgc aag cac gtg aag gcc cac      1772
Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys His Val Lys Ala His
            505                 510                 515

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

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

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

agc cag gag ctc ctc cca ggt gtg tat cct ggc tcc gtc acc cca caa      1964
Ser Gln Glu Leu Leu Pro Gly Val Tyr Pro Gly Ser Val Thr Pro Gln
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aac ggg ctt gct tca ggc atc ctg tcc ccc tcc cac gat gtc cct tcc      2012
Asn Gly Leu Ala Ser Gly Ile Leu Ser Pro Ser His Asp Val Pro Ser
            585                 590                 595

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

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

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

cca cca gcc tcc cag agt cag tct cca ggg gga cag tca ttc tct aca      2204
Pro Pro Ala Ser Gln Ser Gln Ser Pro Gly Gly Gln Ser Phe Ser Thr
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Val Pro Ser Lys Pro Thr Tyr Pro Ser Phe Gln Ser Pro Pro Pro Leu
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ccc agc ccc caa ggc tac caa ggc agt ttc cat tcc atc cag aac tgc      2300
Pro Ser Pro Gln Gly Tyr Gln Gly Ser Phe His Ser Ile Gln Asn Cys
        680                 685                 690

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

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

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

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

gac ctg gta cct agt ggt cct gag gac tgt ggc ttc ttc ccc aat ggg      2540
Asp Leu Val Pro Ser Gly Pro Glu Asp Cys Gly Phe Phe Pro Asn Gly
        760                 765                 770

gcc ttt gac cac tgt ctg agt cac atc ccg tcc atc tac act gac acc      2588
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775 780 785

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35 40 45

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

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

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

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

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

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

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

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

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

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

Cys Tyr Leu Leu Gly Asn Glu Pro Ile Ser Asp Leu Gly Pro Gln Pro

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    210                 215                 220

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ile Pro Gly Cys Ser Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg Lys
            500                 505                 510
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His Val Lys Ala His Ser Ala Lys Glu Gln Gln Val Arg Lys Lys Leu
515 520 525

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

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

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

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

His Asp Val Pro Ser Arg His His Pro Leu Glu Val Pro Thr Gly Ser
595 600 605

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

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

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

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

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

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

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

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

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

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

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

Ile Tyr Thr Asp Thr
785

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<211> 2949
<212> DNA

<213> Homo sapiens

<220>
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<222> (595)..(2034)

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ctcccacccg cccgtggccc gcgcccatgg ccgcgcgcgc tccacacaac tcaccggagt 180

ccgcgccttg cgccgccgac cagttcgcag ctccgcgcca cggcagccag tctcacctgg 240

cggcaccgcc cgcccaccgc cccggccaca gcccctgcgc ccacggcagc actcgaggcg 300

accgcgacag tggtggggga cgctgctgag tggaagagag cgcagcccgg ccaccggacc 360

tacttactcg ccttgctgat tgtctatttt tgcgtttaca acttttctaa gaacttttgt 420

atacaaagga acttttaaa aaagacgctt ccaagttata tttaatccaa agaagaagga 480

tctcggccaa tttggggttt tgggttttgg cttcgtttct tctcttcgtt gactttgggg 540

ttcaggtgcc ccagctgctt cgggctgccg aggaccttct gggcccccac atta atg 597
Met
1

agg cag cca cct ggc gag tct gac atg gct gtc agc gac gcg ctg ctc 645
Arg Gln Pro Pro Gly Glu Ser Asp Met Ala Val Ser Asp Ala Leu Leu
5 10 15

cca tct ttc tcc acg ttc gcg tct ggc ccg gcg gga agg gag aag aca 693
Pro Ser Phe Ser Thr Phe Ala Ser Gly Pro Ala Gly Arg Glu Lys Thr
20 25 30

ctg cgt caa gca ggt gcc ccg aat aac cgc tgg cgg gag gag ctc tcc 741
Leu Arg Gln Ala Gly Ala Pro Asn Asn Arg Trp Arg Glu Glu Leu Ser
35 40 45

cac atg aag cga ctt ccc cca gtg ctt ccc ggc cgc ccc tat gac ctg 789
His Met Lys Arg Leu Pro Pro Val Leu Pro Gly Arg Pro Tyr Asp Leu
50 55 60 65

gcg gcg gcg acc gtg gcc aca gac ctg gag agc ggc gga gcc ggt gcg 837
Ala Ala Ala Thr Val Ala Thr Asp Leu Glu Ser Gly Gly Ala Gly Ala
70 75 80

gct tgc ggc ggt agc aac ctg gcg ccc cta cct cgg aga gag acc gag 885
Ala Cys Gly Gly Ser Asn Leu Ala Pro Leu Pro Arg Arg Glu Thr Glu
85 90 95

gag ttc aac gat ctc ctg gac ctg gac ttt att ctc tcc aat tcg ctg 933
Glu Phe Asn Asp Leu Leu Asp Leu Asp Phe Ile Leu Ser Asn Ser Leu
100 105 110

acc cat cct ccg gag tca gtg gcc gcc acc gtg tcc tcg tca gcg tca 981
Thr His Pro Pro Glu Ser Val Ala Ala Thr Val Ser Ser Ser Ala Ser
115 120 125

gcc tcc tct tcg tcg tcg ccg tcg agc agc ggc cct gcc agc gcg ccc 1029
Ala Ser Ser Ser Ser Ser Pro Ser Ser Ser Gly Pro Ala Ser Ala Pro
130 135 140 145

tcc acc tgc agc ttc acc tat ccg atc cgg gcc ggg aac gac ccg ggc 1077
Ser Thr Cys Ser Phe Thr Tyr Pro Ile Arg Ala Gly Asn Asp Pro Gly
150 155 160

gtg gcg ccg ggc ggc acg ggc gga ggc ctc ctc tat ggc agg gag tcc 1125
Val Ala Pro Gly Gly Thr Gly Gly Gly Leu Leu Tyr Gly Arg Glu Ser
165 170 175

gct ccc cct ccg acg gct ccc ttc aac ctg gcg gac atc aac gac gtg 1173

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Ala Pro Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp Val
        180                 185                 190

agc ccc tcg ggc ggc ttc gtg gcc gag ctc ctg cgg cca gaa ttg gac      1221
Ser Pro Ser Gly Gly Phe Val Ala Glu Leu Leu Arg Pro Glu Leu Asp
    195                 200                 205

ccg gtg tac att ccg ccg cag cag ccg cag ccg cca ggt ggc ggg ctg      1269
Pro Val Tyr Ile Pro Pro Gln Gln Pro Gln Pro Pro Gly Gly Gly Leu
210                 215                 220                 225

atg ggc aag ttc gtg ctg aag gcg tcg ctg agc gcc cct ggc agc gag      1317
Met Gly Lys Phe Val Leu Lys Ala Ser Leu Ser Ala Pro Gly Ser Glu
                230                 235                 240

tac ggc agc ccg tcg gtc atc agc gtc agc aaa ggc agc cct gac ggc      1365
Tyr Gly Ser Pro Ser Val Ile Ser Val Ser Lys Gly Ser Pro Asp Gly
            245                 250                 255

agc cac ccg gtg gtg gtg gcg ccc tac aac ggc ggg ccg ccg cgc acg      1413
Ser His Pro Val Val Val Ala Pro Tyr Asn Gly Gly Pro Pro Arg Thr
        260                 265                 270

tgc ccc aag atc aag cag gag gcg gtc tct tcg tgc acc cac ttg ggc      1461
Cys Pro Lys Ile Lys Gln Glu Ala Val Ser Ser Cys Thr His Leu Gly
    275                 280                 285

gct gga ccc cct ctc agc aat ggc cac cgg ccg gct gca cac gac ttc      1509
Ala Gly Pro Pro Leu Ser Asn Gly His Arg Pro Ala Ala His Asp Phe
290                 295                 300                 305

ccc ctg ggg cgg cag ctc ccc agc agg act acc ccg acc ctg ggt ctt      1557
Pro Leu Gly Arg Gln Leu Pro Ser Arg Thr Thr Pro Thr Leu Gly Leu
                310                 315                 320

gag gaa gtg ctg agc agc agg gac tgt cac cct gcc ctg ccg ctt cct      1605
Glu Glu Val Leu Ser Ser Arg Asp Cys His Pro Ala Leu Pro Leu Pro
            325                 330                 335

ccc ggc ttc cat ccc cac ccg ggg ccc aat tac cca tcc ttc ctg ccc      1653
Pro Gly Phe His Pro His Pro Gly Pro Asn Tyr Pro Ser Phe Leu Pro
        340                 345                 350

gat cag atg cag ccg caa gtc ccg ccg ctc cat tac caa gag ctc atg      1701
Asp Gln Met Gln Pro Gln Val Pro Pro Leu His Tyr Gln Glu Leu Met
    355                 360                 365

cca ccc ggt tcc tgc atg cca gag gag ccc aag cca aag agg gga aga      1749
Pro Pro Gly Ser Cys Met Pro Glu Glu Pro Lys Pro Lys Arg Gly Arg
370                 375                 380                 385

cga tcg tgg ccc cgg aaa agg acc gcc acc cac act tgt gat tac gcg      1797
Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr His Thr Cys Asp Tyr Ala
                390                 395                 400

ggc tgc ggc aaa acc tac aca aag agt tcc cat ctc aag gca cac ctg      1845
Gly Cys Gly Lys Thr Tyr Thr Lys Ser Ser His Leu Lys Ala His Leu
            405                 410                 415

cga acc cac aca ggt gag aaa cct tac cac tgt gac tgg gac ggc tgt      1893
Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Asp Trp Asp Gly Cys
        420                 425                 430

gga tgg aaa ttc gcc cgc tca gat gaa ctg acc agg cac tac cgt aaa      1941
Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg Lys
    435                 440                 445

cac acg ggg cac cgc ccg ttc cag tgc caa aaa tgc gac cga gca ttt      1989
His Thr Gly His Arg Pro Phe Gln Cys Gln Lys Cys Asp Arg Ala Phe
450                 455                 460                 465

tcc agg tcg gac cac ctc gcc tta cac atg aag agg cat ttt taa          2034
Ser Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Phe
                470                 475
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atcccagaca gtggatatga cccacactgc cagaagagaa ttcagtattt tttacttttc 2094

acactgtctt cccgatgagg gaaggagccc agccagaaag cactacaatc atggtcaagt 2154

tcccaactga gtcatcttgt gagtggataa tcaggaaaaa tgaggaatcc aaaagacaaa 2214

aatcaaagaa cagatggggt ctgtgactgg atcttctatc attccaattc taaatccgac 2274

ttgaatattc ctggacttac aaaatgccaa gggggtgact ggaagttgtg gatatcaggg 2334

tataaattat atccgtgagt tgggggaggg aagaccagaa ttcccttgaa ttgtgtattg 2394

atgcaatata agcataaaag atcaccttgt attctcttta ccttctaaaa gccattatta 2454

tgatgttaga agaagaggaa gaaattcagg tacagaaaac atgtttaaat agcctaaatg 2514

atggtgcttg gtgagtcttg gttctaaagg taccaaacaa ggaagccaaa gttttcaaac 2574

tgctgcatac tttgacaagg aaaatctata tttgtcttcc gatcaacatt tatgacctaa 2634

gtcaggtaat atacctggtt tacttcttta gcatttttat gcagacagtc tgttatgcac 2694

tgtggtttca gatgtgcaat aatttgtaca atggtttatt cccaagtatg ccttaagcag 2754

aacaaatgtg tttttctata tagttccttg ccttaataaa tatgtaatat aaatttaagc 2814

aaacgtctat tttgtatatt tgtaaactac aaagtaaaat gaacattttg tggagtttgt 2874

attttgcata ctcaaggtga gaattaagtt ttaaataaac ctataatatt ttatctgaaa 2934

aaaaaaaaaa aaaaa 2949

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<212> PRT
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<400> 6

Met Arg Gln Pro Pro Gly Glu Ser Asp Met Ala Val Ser Asp Ala Leu
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Leu Pro Ser Phe Ser Thr Phe Ala Ser Gly Pro Ala Gly Arg Glu Lys
20 25 30

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

Ser His Met Lys Arg Leu Pro Pro Val Leu Pro Gly Arg Pro Tyr Asp
50 55 60

Leu Ala Ala Ala Thr Val Ala Thr Asp Leu Glu Ser Gly Gly Ala Gly
65 70 75 80

Ala Ala Cys Gly Gly Ser Asn Leu Ala Pro Leu Pro Arg Arg Glu Thr
85 90 95

Glu Glu Phe Asn Asp Leu Leu Asp Leu Asp Phe Ile Leu Ser Asn Ser
100 105 110

Leu Thr His Pro Pro Glu Ser Val Ala Ala Thr Val Ser Ser Ser Ala
115 120 125

Ser Ala Ser Ser Ser Ser Ser Pro Ser Ser Ser Gly Pro Ala Ser Ala
130 135 140

Pro Ser Thr Cys Ser Phe Thr Tyr Pro Ile Arg Ala Gly Asn Asp Pro
145 150 155 160

Gly Val Ala Pro Gly Gly Thr Gly Gly Gly Leu Leu Tyr Gly Arg Glu
165 170 175

Ser Ala Pro Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp
180 185 190

Val Ser Pro Ser Gly Gly Phe Val Ala Glu Leu Leu Arg Pro Glu Leu
195 200 205

Asp Pro Val Tyr Ile Pro Pro Gln Gln Pro Gln Pro Pro Gly Gly Gly
210 215 220

Leu Met Gly Lys Phe Val Leu Lys Ala Ser Leu Ser Ala Pro Gly Ser
225 230 235 240

Glu Tyr Gly Ser Pro Ser Val Ile Ser Val Ser Lys Gly Ser Pro Asp
245 250 255

Gly Ser His Pro Val Val Val Ala Pro Tyr Asn Gly Gly Pro Pro Arg
260 265 270

Thr Cys Pro Lys Ile Lys Gln Glu Ala Val Ser Ser Cys Thr His Leu
275 280 285

Gly Ala Gly Pro Pro Leu Ser Asn Gly His Arg Pro Ala Ala His Asp
290 295 300

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

Leu Glu Glu Val Leu Ser Ser Arg Asp Cys His Pro Ala Leu Pro Leu
325 330 335

Pro Pro Gly Phe His Pro His Pro Gly Pro Asn Tyr Pro Ser Phe Leu
340 345 350

Pro Asp Gln Met Gln Pro Gln Val Pro Pro Leu His Tyr Gln Glu Leu
355 360 365

Met Pro Pro Gly Ser Cys Met Pro Glu Glu Pro Lys Pro Lys Arg Gly
370 375 380

Arg Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr His Thr Cys Asp Tyr
385 390 395 400

Ala Gly Cys Gly Lys Thr Tyr Thr Lys Ser Ser His Leu Lys Ala His
405 410 415

Leu Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys Asp Trp Asp Gly
420 425 430

Cys Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr Arg His Tyr Arg
435 440 445

Lys His Thr Gly His Arg Pro Phe Gln Cys Gln Lys Cys Asp Arg Ala
450 455 460

Phe Ser Arg Ser Asp His Leu Ala Leu His Met Lys Arg His Phe
465 470 475

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<211> 3057
<212> DNA
<213> Mus musculus

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<222> (605)..(2056)

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gcaacccgcc cgtgacccgc gcccatggcc gcgcgcaccc ggcacagtcc ccaggactcc 180

gcaccccgcg ccaccgccca gctcgcagtt ccgcgccacc gcggccattc tcacctggcg 240

gcgccgcccg cccaccgccc ggaccacagc ccccgcgccg ccgacagcca cagtggccgc 300

gacaacggtg ggggacactg ctgagtccaa gagcgtgcag cctggccatc ggacctactt 360

atctgccttg ctgattgtct atttttataa gagtttacaa cttttctaag aatttttgta 420

tacaaaggaa ctttttaaa gacatcgccg gtttatattg aatccaaaga agaaggatct 480

cgggcaatct gggggttttg gtttgaggtt ttgtttctaa agtttttaat cttcgttgac 540

tttggggctc aggtacccct ctctcttctt cggactccgg aggaccttct gggcccccac 600

atta atg agg cag cca cct ggc gag tct gac atg gct gtc agc gac gct 649
Met Arg Gln Pro Pro Gly Glu Ser Asp Met Ala Val Ser Asp Ala
1 5 10 15

ctg ctc ccg tcc ttc tcc acg ttc gcg tcc ggc ccg gcg gga agg gag 697
Leu Leu Pro Ser Phe Ser Thr Phe Ala Ser Gly Pro Ala Gly Arg Glu
20 25 30

aag aca ctg cgt cca gca ggt gcc ccg act aac cgt tgg cgt gag gaa 745
Lys Thr Leu Arg Pro Ala Gly Ala Pro Thr Asn Arg Trp Arg Glu Glu
35 40 45

ctc tct cac atg aag cga ctt ccc cca ctt ccc ggc cgc ccc tac gac 793
Leu Ser His Met Lys Arg Leu Pro Pro Leu Pro Gly Arg Pro Tyr Asp
50 55 60

ctg gcg gcg acg gtg gcc aca gac ctg gag agt ggc gga gct ggt gca 841
Leu Ala Ala Thr Val Ala Thr Asp Leu Glu Ser Gly Gly Ala Gly Ala
65 70 75

gct tgc agc agt aac aac ccg gcc ctc cta gcc cgg agg gag acc gag 889
Ala Cys Ser Ser Asn Asn Pro Ala Leu Leu Ala Arg Arg Glu Thr Glu
80 85 90 95

gag ttc aac gac ctc ctg gac cta gac ttt atc ctt tcc aac tcg cta 937
Glu Phe Asn Asp Leu Leu Asp Leu Asp Phe Ile Leu Ser Asn Ser Leu
100 105 110

acc cac cag gaa tcg gtg gcc gcc acc gtg acc acc tcg gcg tca gct 985
Thr His Gln Glu Ser Val Ala Ala Thr Val Thr Thr Ser Ala Ser Ala
115 120 125

tca tcc tcg tct tcc ccg gcg agc agc ggc cct gcc agc gcg ccc tcc 1033
Ser Ser Ser Ser Ser Pro Ala Ser Ser Gly Pro Ala Ser Ala Pro Ser

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        130                 135                 140

acc tgc agc ttc agc tat ccg atc cgg gcc ggg ggt gac ccg ggc gtg      1081
Thr Cys Ser Phe Ser Tyr Pro Ile Arg Ala Gly Gly Asp Pro Gly Val
    145                 150                 155

gct gcc agc aac aca ggt gga ggg ctc ctc tac agc cga gaa tct gcg      1129
Ala Ala Ser Asn Thr Gly Gly Gly Leu Leu Tyr Ser Arg Glu Ser Ala
160                 165                 170                 175

cca cct ccc acg gcc ccc ttc aac ctg gcg gac atc aat gac gtg agc      1177
Pro Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp Val Ser
                180                 185                 190

ccc tcg ggc ggc ttc gtg gct gag ctc ctg cgg ccg gag ttg gac cca      1225
Pro Ser Gly Gly Phe Val Ala Glu Leu Leu Arg Pro Glu Leu Asp Pro
            195                 200                 205

gta tac att ccg cca cag cag cct cag ccg cca ggt ggc ggg ctg atg      1273
Val Tyr Ile Pro Pro Gln Gln Pro Gln Pro Pro Gly Gly Gly Leu Met
        210                 215                 220

ggc aag ttt gtg ctg aag gcg tct ctg acc acc cct ggc agc gag tac      1321
Gly Lys Phe Val Leu Lys Ala Ser Leu Thr Thr Pro Gly Ser Glu Tyr
    225                 230                 235

agc agc cct tcg gtc atc agt gtt agc aaa gga agc cca gac ggc agc      1369
Ser Ser Pro Ser Val Ile Ser Val Ser Lys Gly Ser Pro Asp Gly Ser
240                 245                 250                 255

cac ccc gtg gta gtg gcg ccc tac agc ggt ggc ccg ccg cgc atg tgc      1417
His Pro Val Val Val Ala Pro Tyr Ser Gly Gly Pro Pro Arg Met Cys
                260                 265                 270

ccc aag att aag caa gag gcg gtc ccg tcc tgc acg gtc agc cgg tcc      1465
Pro Lys Ile Lys Gln Glu Ala Val Pro Ser Cys Thr Val Ser Arg Ser
            275                 280                 285

cta gag gcc cat ttg agc gct gga ccc cag ctc agc aac ggc cac cgg      1513
Leu Glu Ala His Leu Ser Ala Gly Pro Gln Leu Ser Asn Gly His Arg
        290                 295                 300

ccc aac aca cac gac ttc ccc ctg ggg cgg cag ctc ccc acc agg act      1561
Pro Asn Thr His Asp Phe Pro Leu Gly Arg Gln Leu Pro Thr Arg Thr
    305                 310                 315

acc cct aca ctg agt ccc gag gaa ctg ctg aac agc agg gac tgt cac      1609
Thr Pro Thr Leu Ser Pro Glu Glu Leu Leu Asn Ser Arg Asp Cys His
320                 325                 330                 335

cct ggc ctg cct ctt ccc cca gga ttc cat ccc cat ccg ggg ccc aac      1657
Pro Gly Leu Pro Leu Pro Pro Gly Phe His Pro His Pro Gly Pro Asn
                340                 345                 350

tac cct cct ttc ctg cca gac cag atg cag tca caa gtc ccc tct ctc      1705
Tyr Pro Pro Phe Leu Pro Asp Gln Met Gln Ser Gln Val Pro Ser Leu
            355                 360                 365

cat tat caa gag ctc atg cca ccg ggt tcc tgc ctg cca gag gag ccc      1753
His Tyr Gln Glu Leu Met Pro Pro Gly Ser Cys Leu Pro Glu Glu Pro
        370                 375                 380

aag cca aag agg gga aga agg tcg tgg ccc cgg aaa aga aca gcc acc      1801
Lys Pro Lys Arg Gly Arg Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr
    385                 390                 395

cac act tgt gac tat gca ggc tgt ggc aaa acc tat acc aag agt tct      1849
His Thr Cys Asp Tyr Ala Gly Cys Gly Lys Thr Tyr Thr Lys Ser Ser
400                 405                 410                 415

cat ctc aag gca cac ctg cga act cac aca ggc gag aaa cct tac cac      1897
His Leu Lys Ala His Leu Arg Thr His Thr Gly Glu Lys Pro Tyr His
                420                 425                 430

tgt gac tgg gac ggc tgt ggg tgg aaa ttc gcc cgc tcc gat gaa ctg      1945
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Cys Asp Trp Asp Gly Cys Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu
            435                 440                 445

acc agg cac tac cgc aaa cac aca ggg cac cgg ccc ttt cag tgc cag      1993
Thr Arg His Tyr Arg Lys His Thr Gly His Arg Pro Phe Gln Cys Gln
        450                 455                 460

aag tgt gac agg gcc ttt tcc agg tcg gac cac ctt gcc tta cac atg      2041
Lys Cys Asp Arg Ala Phe Ser Arg Ser Asp His Leu Ala Leu His Met
    465                 470                 475

aag agg cac ttt taa atcccacgta gtggatgtga cccacactgc caggagagag      2096
Lys Arg His Phe
480

agttcagtat ttttttttct aacctttcac actgtcttcc cacgagggga ggagcccagc    2156

tggcaagcgc tacaatcatg gtcaagttcc cagcaagtca gcttgtgaat ggataatcag    2216

gagaaaggaa gagttcaaga gacaaaacag aaatactaaa aacaaacaaa caaaaaaaca    2276

aacaaaaaaa acaagaaaaa aaaatcacag aacagatggg gtctgatact ggatggatct    2336

tctatcattc caataccaaa tccaacttga acatgcccgg acttacaaaa tgccaagggg    2396

tgactggaag tttgtggata tcagggtata cactaaatca gtgagcttgg ggggagggaa    2456

gaccaggatt cccttgaatt gtgtttcgat gatgcaatac acacgtaaag atcaccttgt    2516

atgctctttg ccttcttaaa aaaaaaaaaa gccattattg tgtcggagga agaggaagcg    2576

attcaggtac agaacatgtt ctaacagcct aaatgatggt gcttggtgag tcgtggttct    2636

aaaggtacca aacgggggag ccaaagttct ccaactgctg catacttttg acaaggaaaa    2696

tctagttttg tcttccgatc tacattgatg acctaagcca ggtaaataag cctggtttat    2756

ttctgtaaca tttttatgca gacagtctgt tatgcactgt ggtttcagat gtgcaataat    2816

ttgtacaatg gtttattccc aagtatgcct ttaagcagaa caaatgtgtt tttctatata    2876

gttccttgcc ttaataaata tgtaatataa atttaagcaa acttctattt tgtatatttg    2936

taaactacaa agtaaaaaaa aatgaacatt ttgtggagtt tgtattttgc atactcaagg    2996

tgagaaataa gttttaaata aacctataat attttatctg aacgacaaaa aaaaaaaaaa    3056

a                                                                    3057
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<210> 8
<211> 483
<212> PRT
<213> Mus musculus

<400> 8

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Met Arg Gln Pro Pro Gly Glu Ser Asp Met Ala Val Ser Asp Ala Leu
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Leu Pro Ser Phe Ser Thr Phe Ala Ser Gly Pro Ala Gly Arg Glu Lys
            20                  25                  30

Thr Leu Arg Pro Ala Gly Ala Pro Thr Asn Arg Trp Arg Glu Glu Leu
        35                  40                  45

Ser His Met Lys Arg Leu Pro Pro Leu Pro Gly Arg Pro Tyr Asp Leu
    50                  55                  60

Ala Ala Thr Val Ala Thr Asp Leu Glu Ser Gly Gly Ala Gly Ala Ala
65                  70                  75                  80
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Cys Ser Ser Asn Asn Pro Ala Leu Leu Ala Arg Arg Glu Thr Glu Glu
85 90 95

Phe Asn Asp Leu Leu Asp Leu Asp Phe Ile Leu Ser Asn Ser Leu Thr
100 105 110

His Gln Glu Ser Val Ala Ala Thr Val Thr Thr Ser Ala Ser Ala Ser
115 120 125

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

Cys Ser Phe Ser Tyr Pro Ile Arg Ala Gly Gly Asp Pro Gly Val Ala
145 150 155 160

Ala Ser Asn Thr Gly Gly Gly Leu Leu Tyr Ser Arg Glu Ser Ala Pro
165 170 175

Pro Pro Thr Ala Pro Phe Asn Leu Ala Asp Ile Asn Asp Val Ser Pro
180 185 190

Ser Gly Gly Phe Val Ala Glu Leu Leu Arg Pro Glu Leu Asp Pro Val
195 200 205

Tyr Ile Pro Pro Gln Gln Pro Gln Pro Pro Gly Gly Gly Leu Met Gly
210 215 220

Lys Phe Val Leu Lys Ala Ser Leu Thr Thr Pro Gly Ser Glu Tyr Ser
225 230 235 240

Ser Pro Ser Val Ile Ser Val Ser Lys Gly Ser Pro Asp Gly Ser His
245 250 255

Pro Val Val Val Ala Pro Tyr Ser Gly Gly Pro Pro Arg Met Cys Pro
260 265 270

Lys Ile Lys Gln Glu Ala Val Pro Ser Cys Thr Val Ser Arg Ser Leu
275 280 285

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

Asn Thr His Asp Phe Pro Leu Gly Arg Gln Leu Pro Thr Arg Thr Thr
305 310 315 320

Pro Thr Leu Ser Pro Glu Glu Leu Leu Asn Ser Arg Asp Cys His Pro
325 330 335

Gly Leu Pro Leu Pro Pro Gly Phe His Pro His Pro Gly Pro Asn Tyr
340 345 350

Pro Pro Phe Leu Pro Asp Gln Met Gln Ser Gln Val Pro Ser Leu His
355 360 365

Tyr Gln Glu Leu Met Pro Pro Gly Ser Cys Leu Pro Glu Glu Pro Lys

370 375 380

Pro Lys Arg Gly Arg Arg Ser Trp Pro Arg Lys Arg Thr Ala Thr His
385 390 395 400

Thr Cys Asp Tyr Ala Gly Cys Gly Lys Thr Tyr Thr Lys Ser Ser His
405 410 415

Leu Lys Ala His Leu Arg Thr His Thr Gly Glu Lys Pro Tyr His Cys
420 425 430

Asp Trp Asp Gly Cys Gly Trp Lys Phe Ala Arg Ser Asp Glu Leu Thr
435 440 445

Arg His Tyr Arg Lys His Thr Gly His Arg Pro Phe Gln Cys Gln Lys
450 455 460

Cys Asp Arg Ala Phe Ser Arg Ser Asp His Leu Ala Leu His Met Lys
465 470 475 480

Arg His Phe

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<211> 81
<212> DNA
<213> Foot-and-mouth disease virus

<400> 9
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gtagaaagca atccaggtcc a 81

<210> 10
<211> 34
<212> DNA
<213> Bacteriophage P1

<400> 10
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<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> mutant loxP (lox71) sequence

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<210> 12
<211> 34
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<220>
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<220>
<223> shRNA

<400> 13
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<210> 14
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<212> DNA
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<220>
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<400> 14
gcccttcaat gcccgctaca a 21

<210> 15
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<223> shRNA

<400> 15
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