SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION KOBE UNIVERSITY

<120> Method for improving mutation introduction efficiency in genomic sequence modification technology, and molecular complex for use in same

<130> 092589

<150> JP 2016-085631
<151> 2016-04-21

<160> 60

<170> PatentIn version 3.5

<210> 1
<211> 624
<212> DNA
<213> Artificial Sequence

<220>
<223> PmCDA1 CDS optimized for human cell expression

<220>
<221> CDS
<222> (1)..(624)

<400> 1

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Met Thr Asp Ala Glu Tyr Val Arg Ile His Glu Lys Leu Asp Ile Tyr
1               5                   10                  15

acc ttc aag aag cag ttc ttc aac aac aag aaa tct gtg tca cac cgc         96
Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg
            20                  25                  30

tgc tac gtg ctg ttt gag ttg aag cga agg ggc gaa aga agg gct tgc        144
Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys
        35                  40                  45

ttt tgg ggc tat gcc gtc aac aag ccc caa agt ggc acc gag aga gga        192
Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly
    50                  55                  60

ata cac gct gag ata ttc agt atc cga aag gtg gaa gag tat ctt cgg        240
Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg
65                  70                  75                  80

gat aat cct ggg cag ttt acg atc aac tgg tat tcc agc tgg agt cct        288
Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro
                85                  90                  95

tgc gct gat tgt gcc gag aaa att ctg gaa tgg tat aat cag gaa ctt        336
Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu
            100                 105                 110
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cgg gga aac ggg cac aca ttg aaa atc tgg gcc tgc aag ctg tac tac        384
Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr
        115                 120                 125

gag aag aat gcc cgg aac cag ata gga ctc tgg aat ctg agg gac aat        432
Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn
    130                 135                 140

ggt gta ggc ctg aac gtg atg gtt tcc gag cac tat cag tgt tgt cgg        480
Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg
145                 150                 155                 160

aag att ttc atc caa agc tct cat aac cag ctc aat gaa aac cgc tgg        528
Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp
                165                 170                 175

ttg gag aaa aca ctg aaa cgt gcg gag aag cgg aga tcc gag ctg agc        576
Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Arg Arg Ser Glu Leu Ser
            180                 185                 190

atc atg atc cag gtc aag att ctg cat acc act aag tct cca gcc gtt        624
Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val
        195                 200                 205
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            20                  25                  30

Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys
        35                  40                  45

Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly
    50                  55                  60

Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg
65                  70                  75                  80

Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro
                85                  90                  95
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Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu
            100                 105                 110

Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr
        115                 120                 125

Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn
    130                 135                 140

Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg
145                 150                 155                 160

Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp
                165                 170                 175

Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Arg Arg Ser Glu Leu Ser
            180                 185                 190

Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val
        195                 200                 205
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<210> 3
<211> 4116
<212> DNA
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<223> Streptococcus pyogenes-derived Cas9 CDS optimized for eucaryotic cell expression

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<222> (1)..(4116)

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1               5                   10                  15

ggt tgg gcc gtc att acg gac gag tac aag gtg ccg agc aaa aaa ttc         96
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30

aaa gtt ctg ggc aat acc gat cgc cac agc ata aag aag aac ctc att        144
Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45

ggc gcc ctc ctg ttc gac tcc ggg gag acg gcc gaa gcc acg cgg ctc        192
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Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60

aaa aga aca gca cgg cgc aga tat acc cgc aga aag aat cgg atc tgc        240
Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80

tac ctg cag gag atc ttt agt aat gag atg gct aag gtg gat gac tct        288
Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95

ttc ttc cat agg ctg gag gag tcc ttt ttg gtg gag gag gat aaa aag        336
Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110

cac gag cgc cac cca atc ttt ggc aat atc gtg gac gag gtg gcg tac        384
His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125

cat gaa aag tac cca acc ata tat cat ctg agg aag aag ctt gta gac        432
His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140

agt act gat aag gct gac ttg cgg ttg atc tat ctc gcg ctg gcg cat        480
Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160

atg atc aaa ttt cgg gga cac ttc ctc atc gag ggg gac ctg aac cca        528
Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175

gac aac agc gat gtc gac aaa ctc ttt atc caa ctg gtt cag act tac        576
Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190

aat cag ctt ttc gaa gag aac ccg atc aac gca tcc gga gtt gac gcc        624
Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205

aaa gca atc ctg agc gct agg ctg tcc aaa tcc cgg cgg ctc gaa aac        672
Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220

ctc atc gca cag ctc cct ggg gag aag aag aac ggc ctg ttt ggt aat        720
Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240

ctt atc gcc ctg tca ctc ggg ctg acc ccc aac ttt aaa tct aac ttc        768
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255

gac ctg gcc gaa gat gcc aag ctt caa ctg agc aaa gac acc tac gat        816
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270

gat gat ctc gac aat ctg ctg gcc cag atc ggc gac cag tac gca gac        864
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285
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ctt ttt ttg gcg gca aag aac ctg tca gac gcc att ctg ctg agt gat        912
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300

att ctg cga gtg aac acg gag atc acc aaa gct ccg ctg agc gct agt        960
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320

atg atc aag cgc tat gat gag cac cac caa gac ttg act ttg ctg aag       1008
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
                325                 330                 335

gcc ctt gtc aga cag caa ctg cct gag aag tac aag gaa att ttc ttc       1056
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
            340                 345                 350

gat cag tct aaa aat ggc tac gcc gga tac att gac ggc gga gca agc       1104
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
        355                 360                 365

cag gag gaa ttt tac aaa ttt att aag ccc atc ttg gaa aaa atg gac       1152
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
    370                 375                 380

ggc acc gag gag ctg ctg gta aag ctt aac aga gaa gat ctg ttg cgc       1200
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385                 390                 395                 400

aaa cag cgc act ttc gac aat gga agc atc ccc cac cag att cac ctg       1248
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
                405                 410                 415

ggc gaa ctg cac gct atc ctc agg cgg caa gag gat ttc tac ccc ttt       1296
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
            420                 425                 430

ttg aaa gat aac agg gaa aag att gag aaa atc ctc aca ttt cgg ata       1344
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
        435                 440                 445

ccc tac tat gta ggc ccc ctc gcc cgg gga aat tcc aga ttc gcg tgg       1392
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
    450                 455                 460

atg act cgc aaa tca gaa gag acc atc act ccc tgg aac ttc gag gaa       1440
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465                 470                 475                 480

gtc gtg gat aag ggg gcc tct gcc cag tcc ttc atc gaa agg atg act       1488
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
                485                 490                 495

aac ttt gat aaa aat ctg cct aac gaa aag gtg ctt cct aaa cac tct       1536
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
            500                 505                 510

ctg ctg tac gag tac ttc aca gtt tat aac gag ctc acc aag gtc aaa       1584
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Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
        515                 520                 525

tac gtc aca gaa ggg atg aga aag cca gca ttc ctg tct gga gag cag       1632
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
    530                 535                 540

aag aaa gct atc gtg gac ctc ctc ttc aag acg aac cgg aaa gtt acc       1680
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545                 550                 555                 560

gtg aaa cag ctc aaa gaa gac tat ttc aaa aag att gaa tgt ttc gac       1728
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
                565                 570                 575

tct gtt gaa atc agc gga gtg gag gat cgc ttc aac gca tcc ctg gga       1776
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
            580                 585                 590

acg tat cac gat ctc ctg aaa atc att aaa gac aag gac ttc ctg gac       1824
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
        595                 600                 605

aat gag gag aac gag gac att ctt gag gac att gtc ctc acc ctt acg       1872
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
    610                 615                 620

ttg ttt gaa gat agg gag atg att gaa gaa cgc ttg aaa act tac gct       1920
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625                 630                 635                 640

cat ctc ttc gac gac aaa gtc atg aaa cag ctc aag agg cgc cga tat       1968
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
                645                 650                 655

aca gga tgg ggg cgg ctg tca aga aaa ctg atc aat ggg atc cga gac       2016
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
            660                 665                 670

aag cag agt gga aag aca atc ctg gat ttt ctt aag tcc gat gga ttt       2064
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
        675                 680                 685

gcc aac cgg aac ttc atg cag ttg atc cat gat gac tct ctc acc ttt       2112
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
    690                 695                 700

aag gag gac atc cag aaa gca caa gtt tct ggc cag ggg gac agt ctt       2160
Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705                 710                 715                 720

cac gag cac atc gct aat ctt gca ggt agc cca gct atc aaa aag gga       2208
His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735

ata ctg cag acc gtt aag gtc gtg gat gaa ctc gtc aaa gta atg gga       2256
Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
            740                 745                 750
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agg cat aag ccc gag aat atc gtt atc gag atg gcc cga gag aac caa       2304
Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
        755                 760                 765

act acc cag aag gga cag aag aac agt agg gaa agg atg aag agg att       2352
Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
    770                 775                 780

gaa gag ggt ata aaa gaa ctg ggg tcc caa atc ctt aag gaa cac cca       2400
Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785                 790                 795                 800

gtt gaa aac acc cag ctt cag aat gag aag ctc tac ctg tac tac ctg       2448
Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
                805                 810                 815

cag aac ggc agg gac atg tac gtg gat cag gaa ctg gac atc aat cgg       2496
Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
            820                 825                 830

ctc tcc gac tac gac gtg gat cat atc gtg ccc cag tct ttt ctc aaa       2544
Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
        835                 840                 845

gat gat tct att gat aat aaa gtg ttg aca aga tcc gat aaa aat aga       2592
Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
    850                 855                 860

ggg aag agt gat aac gtc ccc tca gaa gaa gtt gtc aag aaa atg aaa       2640
Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865                 870                 875                 880

aat tat tgg cgg cag ctg ctg aac gcc aaa ctg atc aca caa cgg aag       2688
Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
                885                 890                 895

ttc gat aat ctg act aag gct gaa cga ggt ggc ctg tct gag ttg gat       2736
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
            900                 905                 910

aaa gcc ggc ttc atc aaa agg cag ctt gtt gag aca cgc cag atc acc       2784
Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
        915                 920                 925

aag cac gtg gcc caa att ctc gat tca cgc atg aac acc aag tac gat       2832
Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
    930                 935                 940

gaa aat gac aaa ctg att cga gag gtg aaa gtt att act ctg aag tct       2880
Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960

aag ctg gtc tca gat ttc aga aag gac ttt cag ttt tat aag gtg aga       2928
Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975

gag atc aac aat tac cac cat gcg cat gat gcc tac ctg aat gca gtg       2976
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Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
           980                 985                 990

gta ggc act gca ctt atc aaa aaa  tat ccc aag ctt gaa  tct gaa ttt     3024
Val Gly Thr Ala Leu Ile Lys Lys  Tyr Pro Lys Leu Glu  Ser Glu Phe
        995                1000                1005

gtt tac  gga gac tat aaa gtg  tac gat gtt agg aaa  atg atc gca        3069
Val Tyr  Gly Asp Tyr Lys Val  Tyr Asp Val Arg Lys  Met Ile Ala
    1010                1015                1020

aag tct  gag cag gaa ata ggc  aag gcc acc gct aag  tac ttc ttt        3114
Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
    1025                1030                1035

tac agc  aat att atg aat ttt  ttc aag acc gag att  aca ctg gcc        3159
Tyr Ser  Asn Ile Met Asn Phe  Phe Lys Thr Glu Ile  Thr Leu Ala
    1040                1045                1050

aat gga  gag att cgg aag cga  cca ctt atc gaa aca  aac gga gaa        3204
Asn Gly  Glu Ile Arg Lys Arg  Pro Leu Ile Glu Thr  Asn Gly Glu
    1055                1060                1065

aca gga  gaa atc gtg tgg gac  aag ggt agg gat ttc  gcg aca gtc        3249
Thr Gly  Glu Ile Val Trp Asp  Lys Gly Arg Asp Phe  Ala Thr Val
    1070                1075                1080

cgg aag  gtc ctg tcc atg ccg  cag gtg aac atc gtt  aaa aag acc        3294
Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095

gaa gta  cag acc gga ggc ttc  tcc aag gaa agt atc  ctc ccg aaa        3339
Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110

agg aac  agc gac aag ctg atc  gca cgc aaa aaa gat  tgg gac ccc        3384
Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
    1115                1120                1125

aag aaa  tac ggc gga ttc gat  tct cct aca gtc gct  tac agt gta        3429
Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140

ctg gtt  gtg gcc aaa gtg gag  aaa ggg aag tct aaa  aaa ctc aaa        3474
Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155

agc gtc  aag gaa ctg ctg ggc  atc aca atc atg gag  cga tca agc        3519
Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170

ttc gaa  aaa aac ccc atc gac  ttt ctc gag gcg aaa  gga tat aaa        3564
Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
    1175                1180                1185

gag gtc  aaa aaa gac ctc atc  att aag ctt ccc aag  tac tct ctc        3609
Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
    1190                1195                1200
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ttt gag  ctt gaa aac ggc cgg  aaa cga atg ctc gct  agt gcg ggc        3654
Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                 1210                 1215

gag ctg  cag aaa ggt aac gag  ctg gca ctg ccc tct  aaa tac gtt        3699
Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                 1225                 1230

aat ttc  ttg tat ctg gcc agc  cac tat gaa aag ctc  aaa ggg tct        3744
Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                 1240                 1245

ccc gaa  gat aat gag cag aag  cag ctg ttc gtg gaa  caa cac aaa        3789
Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                 1255                 1260

cac tac  ctt gat gag atc atc  gag caa ata agc gaa  ttc tcc aaa        3834
His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                 1270                 1275

aga gtg  atc ctc gcc gac gct  aac ctc gat aag gtg  ctt tct gct        3879
Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                 1285                 1290

tac aat  aag cac agg gat aag  ccc atc agg gag cag  gca gaa aac        3924
Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                 1300                 1305

att atc  cac ttg ttt act ctg  acc aac ttg ggc gcg  cct gca gcc        3969
Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                 1315                 1320

ttc aag  tac ttc gac acc acc  ata gac aga aag cgg  tac acc tct        4014
Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                 1330                 1335

aca aag  gag gtc ctg gac gcc  aca ctg att cat cag  tca att acg        4059
Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
    1340                 1345                 1350

ggg ctc  tat gaa aca aga atc  gac ctc tct cag ctc  ggt gga gac        4104
Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
    1355                 1360                 1365

agc agg  gct gac                                                   4116
Ser Arg  Ala Asp
    1370
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<210> 4
<211> 1372
<212> PRT
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<223> Synthetic Construct

<400> 4

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Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
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Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
            20                  25                  30

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220
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Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385 390 395 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
405 410 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
420 425 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
435 440 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
450 455 460

```
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465                 470                 475                 480

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

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
            500                 505                 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
        515                 520                 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
    530                 535                 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545                 550                 555                 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
                565                 570                 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
            580                 585                 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
        595                 600                 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
    610                 615                 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625                 630                 635                 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
                645                 650                 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
            660                 665                 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
        675                 680                 685
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Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
    690                 695                 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705                 710                 715                 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
            740                 745                 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
        755                 760                 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
    770                 775                 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785                 790                 795                 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
                805                 810                 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
            820                 825                 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
        835                 840                 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
    850                 855                 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865                 870                 875                 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
                885                 890                 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
            900                 905                 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
        915                 920                 925
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Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
    930                 935                 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
            980                 985                 990

Val Gly Thr Ala Leu Ile Lys Lys  Tyr Pro Lys Leu Glu  Ser Glu Phe
        995                 1000                1005

Val Tyr  Gly Asp Tyr Lys Val  Tyr Asp Val Arg Lys  Met Ile Ala
    1010                1015                1020

Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
    1025                1030                1035

Tyr Ser  Asn Ile Met Asn Phe  Phe Lys Thr Glu Ile  Thr Leu Ala
    1040                1045                1050

Asn Gly  Glu Ile Arg Lys Arg  Pro Leu Ile Glu Thr  Asn Gly Glu
    1055                1060                1065

Thr Gly  Glu Ile Val Trp Asp  Lys Gly Arg Asp Phe  Ala Thr Val
    1070                1075                1080

Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095

Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110

Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
    1115                1120                1125

Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140
```

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Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155

Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170

Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
    1175                1180                1185

Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
    1190                1195                1200

Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                1210                1215

Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                1225                1230

Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                1240                1245

Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                1255                1260

His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                1270                1275

Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                1285                1290

Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                1300                1305

Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                1315                1320

Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                1330                1335

Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
    1340                1345                1350

Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
    1355                1360                1365
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Ser Arg Ala Asp
    1370

<210> 5
<211> 252
<212> DNA
<213> Artificial Sequence

<220>
<223> PBS2-derived Ugi CDS optimized for eucaryotic cell expression

<220>
<221> CDS
<222> (1)..(252)

<400> 5
atg acc aac ctt tcc gac atc ata gag aag gaa aca ggc aaa cag ttg 48
Met Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu
1   5   10   15

gtc atc caa gag tcg ata ctc atg ctt cct gaa gaa gtt gag gag gtc 96
Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val
            20   25   30

att ggg aat aag ccg gaa agt gac att ctc gta cac act gcg tat gat 144
Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp
        35   40   45

gag agc acc gat gag aac gtg atg ctg ctc acg tca gat gcc cca gag 192
Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu
    50   55   60

tac aaa ccc tgg gct ctg gtg att cag gac tct aat gga gag aac aag 240
Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys
65   70   75   80

atc aag atg cta   252
Ile Lys Met Leu

<210> 6
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

Met Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu
1   5   10   15

Val Ile Gln Glu Ser Ile Leu Met Leu Pro Glu Glu Val Glu Glu Val
20 25 30

Ile Gly Asn Lys Pro Glu Ser Asp Ile Leu Val His Thr Ala Tyr Asp
35 40 45

Glu Ser Thr Asp Glu Asn Val Met Leu Leu Thr Ser Asp Ala Pro Glu
50 55 60

Tyr Lys Pro Trp Ala Leu Val Ile Gln Asp Ser Asn Gly Glu Asn Lys
65 70 75 80

Ile Lys Met Leu

<210> 7
<211> 20
<212> DNA
<213> Cricetulus griseus

<400> 7
ccgagatgtc atgaaagaga 20

<210> 8
<211> 20
<212> DNA
<213> Cricetulus griseus

<400> 8
ccatgacgga atcggtcggc 20

<210> 9
<211> 83
<212> DNA
<213> Streptococcus pyogenes

<400> 9
gttttagagc tagaaatagc aagttaaaat aaggctagtc cgttatcaac ttgaaaaagt 60

ggcaccgagt cggtggtgct ttt 83

<210> 10
<211> 229
<212> DNA
<213> Homo sapiens

<400> 10
aattcgaacg ctgacgtcat caacccgctc caaggaatcg cgggcccagt gtcactaggc 60

gggaacaccc agcgcgcgtg cgccctggca ggaagatggc tgtgagggac aggggagtgg 120

cgccctgcaa tatttgcatg tcgctatgtg ttctgggaaa tcaccataaa cgtgaaatgt 180

ctttggattt gggaatctta taagttctgt atgaggacca cagatcccc 229

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Nuclear transition signal

<220>
<221> CDS
<222> (1)..(21)

<400> 11
ccc aag aag aag agg aag gtg 21
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 12
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 13
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 2A peptide

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

<400> 13
gaa ggc agg gga agc ctt ctg act tgt ggg gat gtg gaa gaa aac cct 48
Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

ggt cca 54
Gly Pro

<210> 14
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

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

<220>
<223> GS linker

<220>
<221> CDS
<222> (1)..(15)

<400> 15
ggt gga gga ggt tct 15
Gly Gly Gly Gly Ser
1 5

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

Gly Gly Gly Gly Ser
1 5

<210> 17
<211> 122

<212> DNA
<213> Artificial Sequence

<220>
<223> SV40 poly A signal terminator

<400> 17
aacttgttta ttgcagctta taatggttac aaataaagca atagcatcac aaatttcaca 60

aataaagcat ttttttcact gcattctagt tgtggtttgt ccaaactcat caatgtatct 120

ta 122

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR forward primer

<400> 18
ggctacatag agggatcctg tgtca 25

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

<220>
<223> PCR reverse primer

<400> 19
acagtagctc ttcagtctga taaaa 25

<210> 20
<211> 19
<212> RNA
<213> Francisella novicida

<220>
<221> misc_structure
<222> (1)..(19)
<223> crRNA direct repeat sequence.

<400> 20
aauuucuacu guuguagau 19

<210> 21
<211> 20
<212> DNA
<213> Homo sapiens

<400> 21
gagtccgagc agaagaagaa 20

<210> 22
<211> 20
<212> DNA
<213> Homo sapiens

<400> 22
gagttagagc agaagaagaa 20

<210> 23
<211> 20
<212> DNA
<213> Homo sapiens

<400> 23
gagtctaagc agaagaagaa 20

<210> 24
<211> 20
<212> DNA
<213> Homo sapiens

<400> 24
gaggccgagc agaagaaaga 20

<210> 25
<211> 20
<212> DNA
<213> Homo sapiens

<400> 25
gagtcctagc aggagaagaa 20

<210> 26
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX 1st primer)

<400> 26
gtagtctggc tgtcacaggc catactcttc cacat 35

<210> 27
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer (EMX 1st primer)

<400> 27
gtgggtgacc cacccaagca gcaggctctc cacca 35

<210> 28
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX 2nd primer)

<400> 28
tctttcccta cacgacgctc ttccgatcta cttagctgga gtgtggaggc tatcttggc 59

<210> 29
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX 2nd primer)

<400> 29
gtgactggag ttcagacgtg tgctcttccg atctggctag ggactggcca gagtccagc 59

<210> 30
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off1 1st primer)

<400> 30
ctgcccatat ccaccacaag caagttagtc atcaa 35

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

<220>
<223> PCR primer (EMX-off1 1st primer)

<400> 31
aatcaaaatc tctatgtgtg gggcacaggg 30

<210> 32
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off1 2nd primer)

<400> 32
tctttcccta cacgacgctc ttccgatctc attggctaga attcagactt caag 54

<210> 33
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off1 2nd primer)

<400> 33
gtgactggag ttcagacgtg tgctcttccg atctatgagg gagatgtact ctcaagtga 59

<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off2 1st primer)

<400> 34
catgttccct cacccttggc atctacacac tttct 35

<210> 35
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off2 1st primer)

<400> 35
tagtttaccc tgaggcaata tctgactcca 30

<210> 36
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off2 2nd primer)

<400> 36
tctttcccta cacgacgctc ttccgatctt cattttcaaa tgcctattga gcgg 54

<210> 37
<211> 59

<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off2 2nd primer)

<400> 37
gtgactggag ttcagacgtg tgctcttccg atctaaggct ccttgccttt acatatagg 59

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off3 1st primer)

<400> 38
tcacttttgt caattcatgc caccatcagt 30

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off3 1st primer)

<400> 39
gccacctcca ctctgccagg aataggttca 30

<210> 40
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off3 2nd primer)

<400> 40
tctttcccta cacgacgctc ttccgatcta tggactgtcc tgtgagcccg tggc 54

<210> 41
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off3 2nd primer)

<400> 41
gtgactggag ttcagacgtg tgctcttccg atctctcggt ggcctgcaag tggaaagcc 59

<210> 42
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off4 1st primer)

<400> 42
gggaccactt gaagtgagta aaattatagg 30

<210> 43
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off4 1st primer)

<400> 43
cccagctgtt gctagcttat ggccagtcct 30

<210> 44
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off4 2nd primer)

<400> 44
tctttcccta cacgacgctc ttccgatctc actgcctttc gggctagcct ccaa 54

<210> 45
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer (EMX-off4 2nd primer)

<400> 45
gtgactggag ttcagacgtg tgctcttccg atcttagatg ttaataggtt attggggtg 59

<210> 46
<211> 18
<212> PRT
<213> Cricetulus griseus

<400> 46

Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His
1 5 10 15

Ile Val

<210> 47
<211> 55
<212> DNA
<213> Cricetulus griseus

<400> 47
gactgaaaga cttgcccgag atgtcatgaa agagatggga ggccatcaca ttgtg 55

<210> 48
<211> 29
<212> DNA
<213> Cricetulus griseus

<400> 48
gactgaaaga cttgcccgag atgtcatga 29

<210> 49
<211> 53
<212> DNA
<213> Cricetulus griseus

<400> 49
gactgaaaga cttgcccgag atgtcatgaa agatggaagg ccatcacatt gtg 53

<210> 50
<211> 55
<212> DNA
<213> Cricetulus griseus

<400> 50
gactgaaaga cttgcccgag atgtcatgaa agagatggga ggccatcaca ttgtg 55

<210> 51
<211> 56
<212> DNA
<213> Cricetulus griseus

<400> 51
gactgaaaga cttgcccgag atgtcatgaa agaggatggg aggccatcac attgtg 56

<210> 52
<211> 45
<212> DNA
<213> Cricetulus griseus

<400> 52
gactgaaaga cttgcctgaa agagatggga ggccatcaca ttgtg 45

<210> 53
<211> 42
<212> DNA
<213> Cricetulus griseus

<400> 53
gactgaaaga ctttgaaaga gatgggaggc catcacattg tg 42

<210> 54
<211> 55
<212> DNA
<213> Cricetulus griseus

<400> 54
gactgaaaga cttgtttgag atgtcatgaa agagatggga ggccatcaca ttgtg 55

<210> 55
<211> 55
<212> DNA
<213> Cricetulus griseus

<400> 55
gactgaaaga cttgcttgag atgtcatgaa agagatggga ggccatcaca ttgtg 55

<210> 56
<211> 55
<212> DNA
<213> Cricetulus griseus

<400> 56
gactgaaaga cttgcctgag atgtcatgaa agagatggga ggccatcaca ttgtg 55

<210> 57
<211> 31
<212> DNA
<213> Homo sapiens

<400> 57
ggcctgagtc cgagcagaag aagaagggct c 31

<210> 58
<211> 31
<212> DNA
<213> Homo sapiens

<400> 58
gacaagagtc taagcagaag aagaagagag c 31

<210> 59
<211> 31
<212> DNA

<213> Homo sapiens

<400> 59
atgaggaggc cgagcagaag aaagacggcg a 31

<210> 60
<211> 31
<212> DNA
<213> Homo sapiens

<400> 60
gacctgagtc ctagcaggag aagaagaggc a 31