SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION KOBE UNIVERSITY

<120> Method of modifying genomic sequence comprising specifically converting nucleobase in targeted DNA sequence and molecular complex used therefor

<130> 092301

<150> JP 2014-043348
<151> 2014-03-05

<150> JP 2014-201859
<151> 2014-09-30

<160> 42

<170> PatentIn version 3.5

<210> 1
<211> 624
<212> DNA
<213> Petromyzon marinus

<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

acg ttt aag aaa cag ttt ttc aac aac aaa aaa tcc gtg tcg cat aga        96
Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg
            20                  25                  30

tgc tac gtt ctc ttt gaa tta aaa cga cgg ggt gaa cgt aga gcg tgt       144
Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys
        35                  40                  45

ttt tgg ggc tat gct gtg aat aaa cca cag agc ggg aca gaa cgt ggc       192
Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly
    50                  55                  60

att cac gcc gaa atc ttt agc att aga aaa gtc gaa gaa tac ctg cgc       240
Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg
65                  70                  75                  80

gac aac ccc gga caa ttc acg ata aat tgg tac tca tcc tgg agt cct       288
Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro
                85                  90                  95

tgt gca gat tgc gct gaa aag atc tta gaa tgg tat aac cag gag ctg       336
Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu
            100                 105                 110

cgg ggg aac ggc cac act ttg aaa atc tgg gct tgc aaa ctc tat tac       384
Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr
        115                 120                 125

gag aaa aat gcg agg aat caa att ggg ctg tgg aac ctc aga gat aac       432
Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn
    130                 135                 140

ggg gtt ggg ttg aat gta atg gta agt gaa cac tac caa tgt tgc agg       480
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Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg
145                 150                 155                 160

aaa ata ttc atc caa tcg tcg cac aat caa ttg aat gag aat aga tgg       528
Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp
                165                 170                 175

ctt gag aag act ttg aag cga gct gaa aaa cga cgg agc gag ttg tcc       576
Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Arg Arg Ser Glu Leu Ser
            180                 185                 190

att atg att cag gta aaa ata ctc cac acc act aag agt cct gct gtt       624
Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val
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<213>  Petromyzon marinus

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


Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg
            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


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
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180 185 190

Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val
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<222> (1)..(600)

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atg gac agc ctc ttg atg aac cgg agg aag ttt ctt tac caa ttc aaa        48
Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
1               5                  10                  15

aat gtc cgc tgg gct aag ggt cgg cgt gag acc tac ctg tgc tac gta        96
Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
            20                  25                  30

gtg aag agg cgt gac agt gct aca tcc ttt tca ctg gac ttt ggt tat       144
Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
        35                  40                  45

ctt cgc aat aag aac ggc tgc cac gtg gaa ttg ctc ttc ctc cgc tac       192
Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
    50                  55                  60

atc tcg gac tgg gac cta gac cct ggc cgc tgc tac cgc gtc acc tgg       240
Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
65                  70                  75                  80

ttc acc tcc tgg agc ccc tgc tac gac tgt gcc cga cat gtg gcc gac       288
Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
                85                  90                  95

ttt ctg cga ggg aac ccc tac ctc agt ctg agg atc ttc acc gcg cgc       336
Phe Leu Arg Gly Asn Pro Tyr Leu Ser Leu Arg Ile Phe Thr Ala Arg
            100                 105                 110

ctc tac ttc tgt gag gac cgc aag gct gag ccc gag ggg ctg cgg cgg       384
Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
        115                 120                 125

ctg cac cgc gcc ggg gtg caa ata gcc atc atg acc ttc aaa gat tat       432
Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
    130                 135                 140

ttt tac tgc tgg aat act ttt gta gaa aac cat gaa aga act ttc aaa       480
Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
145                 150                 155                 160

gcc tgg gaa ggg ctg cat gaa aat tca gtt cgt ctc tcc aga cag ctt       528
Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
                165                 170                 175

cgg cgc atc ctt ttg ccc ctg tat gag gtt gat gac tta cga gac gca       576
Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
            180                 185                 190

ttt cgt act ttg gga ctt ctc gac                                      600
Phe Arg Thr Leu Gly Leu Leu Asp
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195 200

<210> 4
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Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
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Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
20 25 30

Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
35 40 45

Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
50 55 60

Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
65 70 75 80

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
85 90 95

Phe Leu Arg Gly Asn Pro Tyr Leu Ser Leu Arg Ile Phe Thr Ala Arg
100 105 110

Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
115 120 125

Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
130 135 140

Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
145 150 155 160

Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
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Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
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Phe Arg Thr Leu Gly Leu Leu Asp
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<223> Streptococcus pyogenes-derived Cas9 CDS optimized for eucaryotic expression.

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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
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
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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

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
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ctg ctg tac gag tac ttc aca gtt tat aac gag ctc acc aag gtc aaa      1584
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

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
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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
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
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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

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> 6
<211> 1372
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
1               5                  10                  15

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

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
```

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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

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

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
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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

Ser Arg Ala Asp
1370

<210> 7
<211> 83
<212> DNA
<213> Streptococcus pyogenes

<400> 7
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ggcaccgagt cggtggtgct ttt 83

<210> 8
<211> 665
<212> DNA
<213> Saccharomyces cerevisiae

<400> 8
tttcaaaaat tcttactttt tttttggatg gacgcaaaga agtttaataa tcatattaca 60

tggcattacc accatataca tatccatata catatccata tctaatctta cttatatgtt 120

gtggaaatgt aaagagcccc attatcttag cctaaaaaaa ccttctcttt ggaactttca 180

gtaatacgct taactgctca ttgctatatt gaagtacgga ttagaagccg ccgagcgggt 240

gacagccctc cgaaggaaga ctctcctccg tgcgtcctcg tcttcaccgg tcgcgttcct 300

gaaacgcaga tgtgcctcgc gccgcactgc tccgaacaat aaagattcta caatactagc 360

ttttatggtt atgaagagga aaaattggca gtaacctggc cccacaaacc ttcaaatgaa 420

cgaatcaaat taacaaccat aggatgataa tgcgattagt tttttagcct tatttctggg 480

gtaattaatc agcgaagcga tgatttttga tctattaaca gatatataaa tgcaaaaact 540

gcataaccac tttaactaat actttcaaca ttttcggttt gtattacttc ttattcaaat 600

gtaataaaag tatcaacaaa aaattgttaa tatacctcta tactttaacg tcaaggagaa 660

aaaac 665

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Nuclear transition signal.

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

<400> 9
ccc aag aag aag agg aag gtg 21
Pro Lys Lys Lys Arg Lys Val
1 5

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 10

Pro Lys Lys Lys Arg Lys Val
1 5

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

<220>
<223> GS linker

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

<400> 11
ggt gga gga ggt tct 15
Gly Gly Gly Gly Ser
1 5

<210> 12
<211> 5
<212> PRT
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<220>
<223> Synthetic Construct

<400> 12

Gly Gly Gly Gly Ser
1 5

<210> 13
<211> 66
<212> DNA
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<220>
<223> Flag tag

<220>
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<222> (1)..(66)

<400> 13
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Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
1 5 10 15

aaa gac gat gac gat aag 66
Lys Asp Asp Asp Asp Lys
20

<210> 14
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
1 5 10 15

Lys Asp Asp Asp Asp Lys
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<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Strep-tag

<220>
<221> CDS

<222> (1)..(24)

<400> 15
tgg agc cac ccg cag ttc gaa aaa 24
Trp Ser His Pro Gln Phe Glu Lys
1 5

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

<220>
<223> Synthetic Construct

<400> 16

Trp Ser His Pro Gln Phe Glu Lys
1 5

<210> 17
<211> 171
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<220>
<221> CDS
<222> (1)..(171)

<400> 17
gca gag tat gtg cgg gcc ctc ttt gac ttt aat ggg aat gat gaa gaa 48
Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu
1 5 10 15

gat ctt ccc ttt aag aaa gga gac atc ctg aga atc cgg gat aag cct 96
Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro
20 25 30

gaa gag cag tgg tgg aat gca gag gac agc gaa gga aag agg ggg atg 144
Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly Met
35 40 45

att cct gtc cct tac gtg gag aag tat 171
Ile Pro Val Pro Tyr Val Glu Lys Tyr
50 55

<210> 18
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu
1 5 10 15

Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro

20 25 30

Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly Met
35 40 45

Ile Pro Val Pro Tyr Val Glu Lys Tyr
50 55

<210> 19
<211> 188
<212> DNA
<213> Saccharomyces cerevisiae

<400> 19
gcgaatttct tatgatttat gatttttatt attaaataag ttataaaaaa aataagtgta 60

tacaaatttt aaagtgactc ttaggtttta aaacgaaaat tcttattctt gagtaactct 120

ttcctgtagg tcaggttgct ttctcaggta tagcatgagg tcgctcttat tgaccacacc 180

tctaccgg 188

<210> 20
<211> 417
<212> DNA
<213> Saccharomyces cerevisiae

<400> 20
ataccaggca tggagcttat ctggtccgtt cgagttttcg acgagtttgg agacattctt 60

tatagatgtc ctttttttt aatgatattc gttaaagaac aaaaagtcaa agcagtttaa 120

cctaacacct gttgttgatg ctacttgaaa caaggcttct aggcgaatac ttaaaaaggt 180

aatttcaata gcggtttata tatctgtttg cttttcaaga tattatgtaa acgcacgatg 240

tttttcgccc aggctttatt ttttttgttg ttgttgtctt ctcgaagaat tttctcgggc 300

agatctttgt cggaatgtaa aaaagcgcgt aattaaactt tctattatgc tgactaaaat 360

ggaagtgatc accaaaggct atttctgatt atataatcta gtcattactc gctcgag 417

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

<220>
<223> SH3-binding ligand

<220>
<221> CDS
<222> (1)..(33)

<400> 21
cct cca cct gct ctg cca cct aag aga agg aga 33
Pro Pro Pro Ala Leu Pro Pro Lys Arg Arg Arg
1 5 10

<210> 22
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

Pro Pro Pro Ala Leu Pro Pro Lys Arg Arg Arg
1 5 10

<210> 23
<211> 269
<212> DNA
<213> Saccharomyces cerevisiae

<400> 23
tctttgaaaa gataatgtat gattatgctt tcactcatat ttatacagaa acttgatgtt 60

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agtgccctct tgggctagcg gtaaaggtgc gcatttttc acaccctaca atgttctgtt 180

caaaagattt tggtcaaacg ctgtagaagt gaaagttggt gcgcatgttt cggcgttcga 240

aacttctccg cagtgaaaga taaatgatc 269

<210> 24
<211> 14
<212> DNA
<213> Saccharomyces cerevisiae

<400> 24
tgtttttat gtct 14

<210> 25
<211> 20
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<400> 25
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<210> 26
<211> 20
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<210> 27
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<210> 28
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<213> Saccharomyces cerevisiae

<400> 28
ttggccaagt cattcaattt 20

<210> 29
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<400> 30
gtcaattacg aagactgaac 20

<210> 31
<211> 19
<212> DNA
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<400> 31
gtcaatagga tccccttttt 19

<210> 32
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<220>
<223> Plasmid carrying dCas9-PmCDA1 fusion protein and chimeric RNA targeting galK gene of E.coli

<220>
<221> misc_feature
<222> (5561)..(5580)
<223> n is a, c, g, or t

<400> 32
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cagggtttc ccagtcacga cgttgtaaaa cgacggccag tgaattcgag ctcggtaccc 180

ggccgcaaac aacagataaa acgaaaggcc cagtctttcg actgagcctt tcgttttatt 240

tgatgcctgt caagtaacag caggactctt agtggtgtgg agtattttta cctgaatcat 300

aatggacaac tcgctccgtc gtttttcagc tcgcttcaaa gtcttctcaa gccatctatt 360

ctcattcaat tgattgtgcg acgattggat gaatattttc ctgcaacatt ggtagtgttc 420

acttaccatt acattcaacc caaccccgtt atctctgagg ttccacagcc caatttgatt 480

cctcgcattt ttctcgtaat agagtttgca agcccagatt ttcaaagtgt ggccgttccc 540

ccgcagctcc tggttatacc attctaagat cttttcagcg caatctgcac aaggactcca 600

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actatattta ggtagtttaa tgattaagtc ttttttaact tccttatatc ctttagcttc    1800
taaaaagtca atcggatttt tttcaaagga acttctttcc ataattgtga tccctagtaa    1860
ctctttaacg gattttaact tcttcgattt ccctttttcc accttagcaa ccactaggac    1920
tgaataagct accgttggac tatcaaaacc accatatttt tttggatccc agtctttttt    1980
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tagagggcgt ttgcgaatct ctccatttgc aagtgtaatt tctgttttga agaagttcat    2220
gatattagag taaaagaaat attttgcggt tgctttgcct atttcttgct cagacttagc    2280
aatcatttta cgaacatcat aaactttata atcaccatag acaaactccg attcaagttt    2340
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taatttagat tttaaggtaa tcactttaac ctctcgaata agtttatcat tttcatcgta    2520
tttagtattc atgcgactat ccaaaatttg tgccacatgc ttagtgattt ggcgagtttc    2580
aaccaattgg cgtttgataa aaccagcttt atcaagttca ctcaaacctc cacgttcagc    2640
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