SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> CRISPR/CAS SCREENING PLATFORM TO IDENTIFY GENETIC MODIFIERS OF TAU SEEDING OR AGGREGATION

<130> 057766-544635

<150> US 62/820,086
<151> 2019-03-18

<160> 43

<170> PatentIn version 3.5

<210> 1
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 1

Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser Lys
1 5 10 15

Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly Lys
20 25 30

<210> 2
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 2

Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser Lys
1 5 10 15

Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser
20 25 30

<210> 3
<211> 31
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 3

Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys
1 5 10 15

Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
20 25 30

<210> 4
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 4

Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
1 5 10 15

Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
20 25 30

<210> 5
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 5
cagacagccc ccgtgcccat gccagacctg aagaatgtca agtccaagat cggctccact 60

gagaacctga agcaccagcc gggaggcggg aag 93

<210> 6
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 6
gtgcagataa ttaataagaa gctggatctt agcaacgtcc agtccaagtg tggctcaaag 60

gataatatca aacacgtccc gggaggcggc agt 93

<210> 7
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 7
gtgcaaatag tctacaaacc agttgacctg agcaaggtga cctccaagtg tggctcatta 60

ggcaacatcc atcataaacc aggaggtggc cag 93

<210> 8
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 8
gtggaagtaa aatctgagaa gcttgacttc aaggacagag tccagtcgaa gattgggtcc 60

ctggacaata tcacccacgt ccctggcgga ggaaat 96

<210> 9
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 9

Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser
1 5 10 15

Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly Lys
20 25 30

Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser Lys
35 40 45

Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly Ser Val
    50   55   60

Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys Cys
65   70   75   80

Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val Glu
                85   90   95

Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys Ile
            100   105   110

Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys Lys
        115   120   125

Ile Glu Thr His Lys
    130

<210> 10
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 10
ctgcagacag cccccgtgcc catgccagac ctgaagaatg tcaagtccaa gatcggctcc 60

actgagaacc tgaagcacca gccgggaggc gggaaggtgc agataattaa taagaagctg 120

gatcttagca acgtccagtc caagtgtggc tcaaaggata atatcaaaca cgtcccggga 180

ggcggcagtg tgcaaatagt ctacaaacca gttgacctga gcaaggtgac ctccaagtgt 240

ggctcattag gcaacatcca tcataaacca ggaggtggcc aggtggaagt aaaatctgag 300

aagcttgact tcaaggacag agtccagtcg aagattgggt ccctggacaa tatcacccac 360

gtccctggcg gaggaaataa aaagattgaa acccacaag   399

<210> 11
<211> 133
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 11

Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val Lys Ser
1 5 10 15

Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly Gly Lys
20 25 30

Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln Ser Lys
35 40 45

Cys Gly Ser Lys Asp Asn Ile Lys His Val Ser Gly Gly Gly Ser Val
50 55 60

Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser Lys Cys
65 70 75 80

Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln Val Glu
85 90 95

Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser Lys Ile
100 105 110

Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn Lys Lys
115 120 125

Ile Glu Thr His Lys
130

<210> 12
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 12
ctgcagacag cccccgtgcc catgccagac ctgaagaatg tcaagtccaa gatcggctcc 60

actgagaacc tgaagcacca gccgggaggc gggaaggtgc agataattaa taagaagctg 120

gatcttagca acgtccagtc caagtgtggc tcaaaggata atatcaaaca cgtctcggga 180

ggcggcagtg tgcaaatagt ctacaaacca gttgacctga gcaaggtgac ctccaagtgt 240

ggctcattag gcaacatcca tcataaacca ggaggtggcc aggtggaagt aaaatctgag 300

aagcttgact tcaaggacag agtccagtcg aagattgggt ccctggacaa tatcacccac 360

gtccctggcg gaggaaataa aaagattgaa acccacaag 399

<210> 13
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 13

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

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

```
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160


Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165                 170                 175


Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190


Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205


Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210                 215                 220


Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225                 230                 235


<210>  14
<211>  714
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  14
gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctggtcga gctggacggc       60

gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc      120

aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc      180

gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag      240

cacgacttct tcaagtccgc catgcccgaa ggctacgtcc aggagcgcac catcttcttc      300

aaggacgacg gcaactacaa gacccgcgcc gaggtgaagt tcgagggcga caccctggtg      360

aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag      420

ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc      480

atcaaggcca acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac      540

cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac      600

ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg      660
```

ctggagttcg tgaccgccgc cgggatcact ctcggcatgg acgagctgta caag 714

<210> 15
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 15

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

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
225 230 235

<210> 16
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 16
gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctggtcga gctggacggc 60

gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 120

aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gcccaccctc 180

gtgaccacct tcggctacgg cctgcagtgc ttcgcccgct accccgacca catgaagcag 240

cacgacttct tcaagtccgc catgcccgaa ggctacgtcc aggagcgcac catcttcttc 300

aaggacgacg gcaactacaa gacccgcgcc gaggtgaagt tcgagggcga caccctggtg 360

aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 420

ctggagtaca actacaacag ccacaacgtc tatatcatgg ccgacaagca gaagaacggc 480

atcaaggtga acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 540

cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 600

ctgagctacc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 660

ctggagttcg tgaccgccgc cgggatcact ctcggcatgg acgagctg 708

<210> 17
<211> 77
<212> RNA

<213> Artificial Sequence

<220>
<223> Synthetic

<400> 17
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu 60

ggcaccgagu cggugcu 77

<210> 18
<211> 82
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 18
guuggaacca uucaaaacag cauagcaagu uaaaauaagg cuaguccguu aucaacuuga 60

aaaaguggca ccgagucggu gc 82

<210> 19
<211> 76
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 19
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu 60

ggcaccgagu cggugc 76

<210> 20
<211> 86
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 20
guuuaagagc uaugcuggaa acagcauagc aaguuuaaau aaggcuaguc cguuaucaac 60

uugaaaaagu ggcaccgagu cggugc 86

<210> 21
<211> 1392

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1384)
<223> Cas9

<220>
<221> MISC_FEATURE
<222> (1385)..(1392)
<223> FLAG

<400> 21

```
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

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

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

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

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
1370 1375 1380

Lys Asp Tyr Lys Asp Asp Asp Asp Lys
1385 1390

<210> 22
<211> 4176
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<221> misc_feature
<222> (1)..(4152)
<223> Cas9

<220>
<221> misc_feature
<222> (4153)..(4176)
<223> FLAG

<400> 22
atggacaaga agtacagcat cggcctggac atcggcacca actctgtggg ctgggccgtg 60

atcaccgacg agtacaaggt gcccagcaag aaattcaagg tgctgggcaa caccgaccgg 120

cacagcatca agaagaacct gatcggagcc ctgctgttcg acagcggcga aacagccgag 180

gccacccggc tgaagagaac cgccagaaga agatacacca gacggaagaa ccggatctgc 240

tatctgcaag agatcttcag caacgagatg gccaaggtgg acgacagctt cttccacaga 300

ctggaagagt ccttcctggt ggaagaggat aagaagcacg agcggcaccc catcttcggc 360

aacatcgtgg acgaggtggc ctaccacgag aagtacccca ccatctacca cctgagaaag 420

aaactggtgg acagcaccga caaggccgac ctgcggctga tctatctggc cctggcccac 480

atgatcaagt tccggggcca cttcctgatc gagggcgacc tgaaccccga caacagcgac 540

gtggacaagc tgttcatcca gctggtgcag acctacaacc agctgttcga ggaaaacccc 600

atcaacgcca gcggcgtgga cgccaaggcc atcctgtctg ccagactgag caagagcaga 660

cggctggaaa atctgatcgc ccagctgccc ggcgagaaga agaatggcct gttcggaaac 720

ctgattgccc tgagcctggg cctgaccccc aacttcaaga gcaacttcga cctggccgag 780

gatgccaaac tgcagctgag caaggacacc tacgacgacg acctggacaa cctgctggcc 840

cagatcggcg accagtacgc cgacctgttt ctggccgcca agaacctgtc cgacgccatc 900

ctgctgagcg acatcctgag agtgaacacc gagatcacca aggcccccct gagcgcctct 960

atgatcaaga gatacgacga gcaccaccag gacctgaccc tgctgaaagc tctcgtgcgg 1020

cagcagctgc ctgagaagta caaagagatt ttcttcgacc agagcaagaa cggctacgcc 1080

ggctacattg acggcggagc cagccaggaa gagttctaca agttcatcaa gcccatcctg 1140

gaaaagatgg acggcaccga ggaactgctc gtgaagctga acagagagga cctgctgcgg 1200

aagcagcgga ccttcgacaa cggcagcatc ccccaccaga tccacctggg agagctgcac 1260

gccattctgc ggcggcagga agatttttac ccattcctga aggacaaccg ggaaaagatc 1320

gagaagatcc tgaccttccg catcccctac tacgtgggcc ctctggccag gggaaacagc 1380

agattcgcct ggatgaccag aaagagcgag gaaaccatca ccccctggaa cttcgaggaa 1440

gtggtggaca agggcgcttc cgcccagagc ttcatcgagc ggatgaccaa cttcgataag 1500

aacctgccca acgagaaggt gctgcccaag cacagcctgc tgtacgagta cttcaccgtg 1560

tataacgagc tgaccaaagt gaaatacgtg accgagggaa tgagaaagcc cgccttcctg 1620

agcggcgagc agaaaaaggc catcgtggac ctgctgttca agaccaaccg gaaagtgacc 1680

gtgaagcagc tgaaagagga ctacttcaag aaaatcgagt gcttcgactc cgtggaaatc 1740

tccggcgtgg aagatcggtt caacgcctcc ctgggcacat accacgatct gctgaaaatt 1800

atcaaggaca aggacttcct ggacaatgag gaaaacgagg acattctgga agatatcgtg 1860

ctgaccctga cactgtttga ggacagagag atgatcgagg aacggctgaa aacctatgcc 1920

cacctgttcg acgacaaagt gatgaagcag ctgaagcggc ggagatacac cggctggggc 1980

aggctgagcc ggaagctgat caacggcatc cgggacaagc agtccggcaa gacaatcctg 2040

gatttcctga agtccgacgg cttcgccaac agaaacttca tgcagctgat ccacgacgac 2100

agcctgacct ttaaagagga catccagaaa gcccaggtgt ccggccaggg cgatagcctg 2160

cacgagcaca ttgccaatct ggccggcagc cccgccatta agaagggcat cctgcagaca 2220

gtgaaggtgg tggacgagct cgtgaaagtg atgggccggc acaagcccga gaacatcgtg 2280

atcgaaatgg ccagagagaa ccagaccacc cagaagggac agaagaacag ccgcgagaga 2340

atgaagcgga tcgaagaggg catcaaagag ctgggcagcc agatcctgaa agaacacccc 2400

gtggaaaaca cccagctgca gaacgagaag ctgtacctgt actacctgca gaatgggcgg 2460

gatatgtacg tggaccagga actggacatc aaccggctgt ccgactacga tgtggaccat 2520

atcgtgcctc agagctttct gaaggacgac tccatcgaca acaaggtgct gaccagaagc 2580

gacaagaacc ggggcaagag cgacaacgtg ccctccgaag aggtcgtgaa gaagatgaag 2640

aactactggc ggcagctgct gaacgccaag ctgattaccc agagaaagtt cgacaatctg 2700

accaaggccg agagaggcgg cctgagcgaa ctggataagg ccggcttcat caagagacag 2760

ctggtggaaa cccggcagat cacaaagcac gtggcacaga tcctggactc ccggatgaac 2820

actaagtacg acgagaatga caagctgatc cgggaagtga aagtgatcac cctgaagtcc 2880

aagctggtgt ccgatttccg gaaggatttc cagttttaca aagtgcgcga gatcaacaac 2940

taccaccacg cccacgacgc ctacctgaac gccgtcgtgg gaaccgccct gatcaaaaag 3000

taccctaagc tggaaagcga gttcgtgtac ggcgactaca aggtgtacga cgtgcggaag 3060

atgatcgcca agagcgagca ggaaatcggc aaggctaccg ccaagtactt cttctacagc 3120

aacatcatga acttttttcaa gaccgagatt accctggcca acggcgagat ccggaagcgg 3180

cctctgatcg agacaaacgg cgaaaccggg gagatcgtgt gggataaggg ccgggatttt 3240

gccaccgtgc ggaaagtgct gagcatgccc caagtgaata tcgtgaaaaa gaccgaggtg 3300

cagacaggcg gcttcagcaa agagtctatc ctgcccaaga ggaacagcga taagctgatc 3360

gccagaaaga aggactggga ccctaagaag tacggcggct tcgacagccc caccgtggcc 3420

tattctgtgc tggtggtggc caaagtggaa aagggcaagt ccaagaaact gaagagtgtg 3480

aaagagctac tggggatcac catcatggaa agaagcagct tcgagaagaa tcccatcgac 3540

tttctggaag ccaagggcta caaagaagtg aaaaaggacc tgatcatcaa gctgcctaag 3600

tactccctgt tcgagctgga aaacggccgg aagagaatgc tggcctctgc cggcgaactg 3660

cagaagggaa acgaactggc cctgccctcc aaatatgtga acttcctgta cctggccagc 3720

cactatgaga agctgaaggg ctcccccgag gataatgagc agaaacagct gtttgtggaa 3780

cagcacaagc actacctgga cgagatcatc gagcagatca gcgagttctc caagagagtg 3840

atcctggccg acgctaatct ggacaaagtg ctgtccgcct acaacaagca ccgggataag 3900

cccatcagag agcaggccga gaatatcatc cacctgttta ccctgaccaa tctgggagcc 3960

cctgccgcct tcaagtactt tgacaccacc atcgaccgga agaggtacac cagcaccaaa 4020

gaggtgctgg acgccaccct gatccaccag agcatcaccg gcctgtacga gacacggatc 4080

gacctgtctc agctgggagg cgacaagcga cctgccgcca caaagaaggc tggacaggct 4140

aagaagaaga aagattacaa agacgatgac gataag 4176

<210> 23
<211> 16
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 23
guuuuagagc uaugcu 16

<210> 24
<211> 67

<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 24
agcauagcaa guuaaaauaa ggcuaguccg uuaucaacuu gaaaaagugg caccgagucg 60

gugcuuu 67

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (2)..(21)
<223> n = A, T, C, or G

<400> 25
gnnnnnnnnn nnnnnnnnnn ngg 23

<210> 26
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(21)
<223> n = A, T, C, or G

<400> 26
nnnnnnnnnn nnnnnnnnnn ngg 23

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

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (3)..(23)
<223> n = A, T, C, or G

<400> 27
ggnnnnnnnn nnnnnnnnnn nnngg 25

<210> 28
<211> 72
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28
aaacagcaua gcaaguuaaa auaaggcuag uccguuauca acuugaaaaa guggcaccga 60

gucggugcuu uu 72

<210> 29
<211> 82
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 29
guuggaacca uucaaaacag cauagcaagu uaaaauaagg cuaguccguu aucaacuuga 60

aaaaguggca ccgagucggu gc 82

<210> 30
<211> 83
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 30
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu 60

ggcaccgagu cggugcuuuu uuu 83

<210> 31
<211> 80

<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu 60

ggcaccgagu cggugcuuuu 80

<210> 32
<211> 92
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 32
guuuaagagc uaugcuggaa acagcauagc aaguuuaaau aaggcuaguc cguuaucaac 60

uugaaaaagu ggcaccgagu cggugcuuuu uu 92

<210> 33
<211> 34
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 33
ggccaacaug aggaucaccc augucugcag ggcc 34

<210> 34
<211> 137
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 34
guuuuagagc uaggccaaca ugaggaucac ccaugucugc agggccuagc aaguuaaaau 60

aaggcuaguc cguuaucaac uuggccaaca ugaggaucac ccaugucugc agggccaagu 120

ggcaccgagu cggugcu 137

<210> 35

<211> 157
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(20)
<223> n is a, c, g, or u

<400> 35
nnnnnnnnnn nnnnnnnnnn guuuuagagc uaggccaaca ugaggaucac ccaugucugc 60

agggccuagc aaguuaaaau aaggcuaguc cguuaucaac uuggccaaca ugaggaucac 120

ccaugucugc agggccaagu ggcaccgagu cggugcu 157

<210> 36
<211> 1471
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> MISC_FEATURE
<222> (1)..(1384)
<223> dCas9

<220>
<221> MISC_FEATURE
<222> (1405)..(1409)
<223> NLS

<220>
<221> MISC_FEATURE
<222> (1410)..(1471)
<223> VP64

<400> 36

Met Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys
1 5 10 15

Lys Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn Ser Val
20 25 30

```
Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
        35                  40                  45

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
    50                  55                  60

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
65                  70                  75                  80

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
                85                  90                  95

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
            100                 105                 110

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
        115                 120                 125

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
    130                 135                 140

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
145                 150                 155                 160

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
                165                 170                 175

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
            180                 185                 190

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
        195                 200                 205

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

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
225                 230                 235                 240

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
                245                 250                 255
```

```
Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
            260                 265                 270

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
        275                 280                 285

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
    290                 295                 300

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
305                 310                 315                 320

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

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
            340                 345                 350

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
        355                 360                 365

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
    370                 375                 380

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
385                 390                 395                 400

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
                405                 410                 415

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
            420                 425                 430

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
        435                 440                 445

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
    450                 455                 460

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
465                 470                 475                 480
```

```
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
                485                 490                 495

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
            500                 505                 510

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
        515                 520                 525

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
    530                 535                 540

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
545                 550                 555                 560

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
                565                 570                 575

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
            580                 585                 590

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
        595                 600                 605

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
    610                 615                 620

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
625                 630                 635                 640

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

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
            660                 665                 670

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
        675                 680                 685

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
```

```
    690                 695                 700

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
705                 710                 715                 720

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
                725                 730                 735

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
            740                 745                 750

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
        755                 760                 765

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
    770                 775                 780

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
785                 790                 795                 800

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
                805                 810                 815

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
            820                 825                 830

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
        835                 840                 845

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
    850                 855                 860

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

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
                885                 890                 895

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
            900                 905                 910
```

```
Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
        915                 920                 925

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
    930                 935                 940

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
945                 950                 955                 960

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
                965                 970                 975

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
            980                 985                 990

Glu Ile Asn Asn Tyr His His Ala  His Asp Ala Tyr Leu  Asn Ala Val
        995                 1000                1005

Val Gly  Thr Ala Leu Ile Lys  Lys Tyr Pro Lys Leu  Glu Ser Glu
    1010                1015                1020

Phe Val  Tyr Gly Asp Tyr Lys  Val Tyr Asp Val Arg  Lys Met Ile
    1025                1030                1035

Ala Lys  Ser Glu Gln Glu Ile  Gly Lys Ala Thr Ala  Lys Tyr Phe
    1040                1045                1050

Phe Tyr  Ser Asn Ile Met Asn  Phe Phe Lys Thr Glu  Ile Thr Leu
    1055                1060                1065

Ala Asn  Gly Glu Ile Arg Lys  Arg Pro Leu Ile Glu  Thr Asn Gly
    1070                1075                1080

Glu Thr  Gly Glu Ile Val Trp  Asp Lys Gly Arg Asp  Phe Ala Thr
    1085                1090                1095

Val Arg  Lys Val Leu Ser Met  Pro Gln Val Asn Ile  Val Lys Lys
    1100                1105                1110

Thr Glu  Val Gln Thr Gly Gly  Phe Ser Lys Glu Ser  Ile Leu Pro
    1115                1120                1125
```

```
Lys Arg  Asn Ser Asp Lys Leu  Ile Ala Arg Lys Lys  Asp Trp Asp
    1130                1135                1140

Pro Lys  Lys Tyr Gly Gly Phe  Asp Ser Pro Thr Val  Ala Tyr Ser
    1145                1150                1155

Val Leu  Val Val Ala Lys Val  Glu Lys Gly Lys Ser  Lys Lys Leu
    1160                1165                1170

Lys Ser  Val Lys Glu Leu Leu  Gly Ile Thr Ile Met  Glu Arg Ser
    1175                1180                1185

Ser Phe  Glu Lys Asn Pro Ile  Asp Phe Leu Glu Ala  Lys Gly Tyr
    1190                1195                1200

Lys Glu  Val Lys Lys Asp Leu  Ile Ile Lys Leu Pro  Lys Tyr Ser
    1205                1210                1215

Leu Phe  Glu Leu Glu Asn Gly  Arg Lys Arg Met Leu  Ala Ser Ala
    1220                1225                1230

Gly Glu  Leu Gln Lys Gly Asn  Glu Leu Ala Leu Pro  Ser Lys Tyr
    1235                1240                1245

Val Asn  Phe Leu Tyr Leu Ala  Ser His Tyr Glu Lys  Leu Lys Gly
    1250                1255                1260

Ser Pro  Glu Asp Asn Glu Gln  Lys Gln Leu Phe Val  Glu Gln His
    1265                1270                1275

Lys His  Tyr Leu Asp Glu Ile  Ile Glu Gln Ile Ser  Glu Phe Ser
    1280                1285                1290

Lys Arg  Val Ile Leu Ala Asp  Ala Asn Leu Asp Lys  Val Leu Ser
    1295                1300                1305

Ala Tyr  Asn Lys His Arg Asp  Lys Pro Ile Arg Glu  Gln Ala Glu
    1310                1315                1320

Asn Ile  Ile His Leu Phe Thr  Leu Thr Asn Leu Gly  Ala Pro Ala
    1325                1330                1335
```

```
Ala Phe  Lys Tyr Phe Asp Thr  Thr Ile Asp Arg Lys  Arg Tyr Thr
    1340                1345                1350


Ser Thr  Lys Glu Val Leu Asp  Ala Thr Leu Ile His  Gln Ser Ile
    1355                1360                1365


Thr Gly  Leu Tyr Glu Thr Arg  Ile Asp Leu Ser Gln  Leu Gly Gly
    1370                1375                1380


Asp Ser  Ala Gly Gly Gly Gly  Ser Gly Gly Gly Gly  Ser Gly Gly
    1385                1390                1395


Gly Gly  Ser Gly Pro Lys Lys  Lys Arg Lys Val Ala  Ala Ala Gly
    1400                1405                1410


Ser Gly  Arg Ala Asp Ala Leu  Asp Asp Phe Asp Leu  Asp Met Leu
    1415                1420                1425


Gly Ser  Asp Ala Leu Asp Asp  Phe Asp Leu Asp Met  Leu Gly Ser
    1430                1435                1440


Asp Ala  Leu Asp Asp Phe Asp  Leu Asp Met Leu Gly  Ser Asp Ala
    1445                1450                1455


Leu Asp  Asp Phe Asp Leu Asp  Met Leu Ile Asn Cys  Thr
    1460                1465                1470


<210>  37
<211>  473
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic


<220>
<221>  MISC_FEATURE
<222>  (1)..(130)
<223>  MCP

<220>
<221>  MISC_FEATURE
<222>  (151)..(155)
```

<223> NLS

<220>
<221> MISC_FEATURE
<222> (161)..(341)
<223> P65

<220>
<221> MISC_FEATURE
<222> (350)..(473)
<223> HSF1

<400> 37

```
Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1               5                   10                  15


Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
            20                  25                  30


Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
        35                  40                  45


Val Arg Gln Ser Ser Ala Gln Lys Arg Lys Tyr Thr Ile Lys Val Glu
    50                  55                  60


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


Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
                85                  90                  95


Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
            100                 105                 110


Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
        115                 120                 125


Ile Tyr Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140


Gly Gly Ser Gly Pro Lys Lys Lys Arg Lys Val Ala Ala Ala Gly Ser
145                 150                 155                 160


Pro Ser Gly Gln Ile Ser Asn Gln Ala Leu Ala Leu Ala Pro Ser Ser
```

```
                165                 170                 175

Ala Pro Val Leu Ala Gln Thr Met Val Pro Ser Ser Ala Met Val Pro
            180                 185                 190

Leu Ala Gln Pro Pro Ala Pro Ala Pro Val Leu Thr Pro Gly Pro Pro
        195                 200                 205

Gln Ser Leu Ser Ala Pro Val Pro Lys Ser Thr Gln Ala Gly Glu Gly
    210                 215                 220

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

Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Gly Val Phe Thr Asp
                245                 250                 255

Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln Gly
            260                 265                 270

Val Ser Met Ser His Ser Thr Ala Glu Pro Met Leu Met Glu Tyr Pro
        275                 280                 285

Glu Ala Ile Thr Arg Leu Val Thr Gly Ser Gln Arg Pro Pro Asp Pro
    290                 295                 300

Ala Pro Thr Pro Leu Gly Thr Ser Gly Leu Pro Asn Gly Leu Ser Gly
305                 310                 315                 320

Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala Leu Leu
                325                 330                 335

Ser Gln Ile Ser Ser Ser Gly Gln Gly Gly Gly Gly Ser Gly Phe Ser
            340                 345                 350

Val Asp Thr Ser Ala Leu Leu Asp Leu Phe Ser Pro Ser Val Thr Val
        355                 360                 365

Pro Asp Met Ser Leu Pro Asp Leu Asp Ser Ser Leu Ala Ser Ile Gln
    370                 375                 380
```

```
Glu Leu Leu Ser Pro Gln Glu Pro Pro Arg Pro Pro Glu Ala Glu Asn
385                 390                 395                 400

Ser Ser Pro Asp Ser Gly Lys Gln Leu Val His Tyr Thr Ala Gln Pro
                405                 410                 415

Leu Phe Leu Leu Asp Pro Gly Ser Val Asp Thr Gly Ser Asn Asp Leu
            420                 425                 430

Pro Val Leu Phe Glu Leu Gly Glu Gly Ser Tyr Phe Ser Glu Gly Asp
        435                 440                 445

Gly Phe Ala Glu Asp Pro Thr Ile Ser Leu Leu Thr Gly Ser Glu Pro
    450                 455                 460

Pro Lys Ala Lys Asp Pro Thr Val Ser
465                 470


<210>  38
<211>  4413
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic


<220>
<221>  misc_feature
<222>  (1)..(4152)
<223>  dCas9

<220>
<221>  misc_feature
<222>  (4213)..(4227)
<223>  NLS

<220>
<221>  misc_feature
<222>  (4228)..(4413)
<223>  VP64

<400>  38
atgaaaaggc cggcggccac gaaaaaggcc ggccaggcaa aaaagaaaaa ggacaagaag       60

tacagcatcg gcctggccat cggcaccaac tctgtgggct gggccgtgat caccgacgag      120

tacaaggtgc ccagcaagaa attcaaggtg ctgggcaaca ccgaccggca cagcatcaag      180
```

aagaacctga tcggagccct gctgttcgac agcggcgaaa cagccgaggc cacccggctg 240

aagagaaccg ccagaagaag atacaccaga cggaagaacc ggatctgcta tctgcaagag 300

atcttcagca acgagatggc caaggtggac gacagcttct tccacagact ggaagagtcc 360

ttcctggtgg aagaggataa gaagcacgag cggcacccca tcttcggcaa catcgtggac 420

gaggtggcct accacgagaa gtaccccacc atctaccacc tgagaaagaa actggtggac 480

agcaccgaca aggccgacct gcggctgatc tatctggccc tggcccacat gatcaagttc 540

cggggccact tcctgatcga gggcgacctg aaccccgaca acagcgacgt ggacaagctg 600

ttcatccagc tggtgcagac ctacaaccag ctgttcgagg aaaaccccat caacgccagc 660

ggcgtggacg ccaaggccat cctgtctgcc agactgagca agagcagacg gctggaaaat 720

ctgatcgccc agctgcccgg cgagaagaag aatggcctgt tcggcaacct gattgccctg 780

agcctgggcc tgaccccaa cttcaagagc aacttcgacc tggccgagga tgccaaactg 840

cagctgagca aggacaccta cgacgacgac ctggacaacc tgctggccca gatcggcgac 900

cagtacgccg acctgtttct ggccgccaag aacctgtccg acgccatcct gctgagcgac 960

atcctgagag tgaacaccga gatcaccaag gccccctga gcgcctctat gatcaagaga 1020

tacgacgagc accaccagga cctgaccctg ctgaaagctc tcgtgcggca gcagctgcct 1080

gagaagtaca aagagatttt cttcgaccag agcaagaacg gctacgccgg ctacattgac 1140

ggcggagcca gccaggaaga gttctacaag ttcatcaagc ccatcctgga aaagatggac 1200

ggcaccgagg aactgctcgt gaagctgaac agagaggacc tgctgcggaa gcagcggacc 1260

ttcgacaacg gcagcatccc ccaccagatc cacctgggag agctgcacgc cattctgcgg 1320

cggcaggaag atttttaccc attcctgaag gacaaccggg aaaagatcga gaagatcctg 1380

accttccgca tcccctacta cgtgggccct ctggccaggg gaaacagcag attcgcctgg 1440

atgaccagaa agagcgagga aaccatcacc ccctggaact tcgaggaagt ggtggacaag 1500

ggcgcttccg cccagagctt catcgagcgg atgaccaact tcgataagaa cctgcccaac 1560

gagaaggtgc tgcccaagca cagcctgctg tacgagtact tcaccgtgta taacgagctg 1620

accaaagtga aatacgtgac cgagggaatg agaaagcccg ccttcctgag cggcgagcag 1680

aaaaaggcca tcgtggacct gctgttcaag accaaccgga aagtgaccgt gaagcagctg 1740

aaagaggact acttcaagaa aatcgagtgc ttcgactccg tggaaatctc cggcgtggaa 1800

gatcggttca acgcctccct gggcacatac cacgatctgc tgaaaattat caaggacaag 1860

gacttcctgg acaatgagga aaacgaggac attctggaag atatcgtgct gaccctgaca 1920

ctgtttgagg acagagagat gatcgaggaa cggctgaaaa cctatgccca cctgttcgac 1980

gacaaagtga tgaagcagct gaagcggcgg agatacaccg gctggggcag gctgagccgg 2040

aagctgatca acggcatccg ggacaagcag tccggcaaga caatcctgga tttcctgaag 2100

tccgacggct tcgccaacag aaacttcatg cagctgatcc acgacgacag cctgaccttt 2160

aaagaggaca tccagaaagc ccaggtgtcc ggccagggcg atagcctgca cgagcacatt 2220

gccaatctgg ccggcagccc cgccattaag aagggcatcc tgcagacagt gaaggtggtg 2280

gacgagctcg tgaaagtgat gggccggcac aagcccgaga acatcgtgat cgaaatggcc 2340

agagagaacc agaccaccca gaagggacag aagaacagcc gcgagagaat gaagcggatc 2400

gaagagggca tcaaagagct gggcagccag atcctgaaag aacaccccgt ggaaaacacc 2460

cagctgcaga acgagaagct gtacctgtac tacctgcaga atgggcggga tatgtacgtg 2520

gaccaggaac tggacatcaa ccggctgtcc gactacgatg tggaccacat cgtgcctcag 2580

agctttctga aggacgactc catcgacaac aaggtgctga ccagaagcga caaggcccgg 2640

ggcaagagcg acaacgtgcc ctccgaagag gtcgtgaaga agatgaagaa ctactggcgg 2700

cagctgctga acgccaagct gattacccag agaaagttcg acaatctgac caaggccgag 2760

agaggcggcc tgagcgaact ggataaggcc ggcttcatca agagacagct ggtggaaacc 2820

cggcagatca caaagcacgt ggcacagatc ctggactccc ggatgaacac taagtacgac 2880

gagaatgaca agctgatccg ggaagtgaaa gtgatcaccc tgaagtccaa gctggtgtcc 2940

gatttccgga aggatttcca gttttacaaa gtgcgcgaga tcaacaacta ccaccacgcc 3000

cacgacgcct acctgaacgc cgtcgtggga accgccctga tcaaaaagta ccctaagctg 3060

gaaagcgagt tcgtgtacgg cgactacaag gtgtacgacg tgcggaagat gatcgccaag 3120

agcgagcagg aaatcggcaa ggctaccgcc aagtacttct tctacagcaa catcatgaac 3180

tttttcaaga ccgagattac cctggccaac ggcgagatcc ggaagcggcc tctgatcgag 3240

acaaacggcg aaaccgggga gatcgtgtgg gataagggcc gggattttgc caccgtgcgg 3300

aaagtgctga gcatgcccca agtgaatatc gtgaaaaaga ccgaggtgca gacaggcggc 3360

ttcagcaaag agtctatcct gcccaagagg aacagcgata agctgatcgc cagaaagaag 3420

gactgggacc ctaagaagta cggcggcttc gacagcccca ccgtggccta ttctgtgctg 3480

gtggtggcca aagtggaaaa gggcaagtcc aagaaactga agagtgtgaa agagctgctg 3540

gggatcacca tcatggaaag aagcagcttc gagaagaatc ccatcgactt tctggaagcc 3600

aagggctaca aagaagtgaa aaaggacctg atcatcaagc tgcctaagta ctccctgttc 3660

gagctggaaa acggccggaa gagaatgctg gcctctgccg gcgaactgca gaagggaaac 3720

gaactggccc tgccctccaa atatgtgaac ttcctgtacc tggccagcca ctatgagaag 3780

ctgaagggct cccccgagga taatgagcag aaacagctgt ttgtggaaca gcacaagcac 3840

tacctggacg agatcatcga gcagatcagc gagttctcca agagagtgat cctggccgac 3900

gctaatctgg acaaagtgct gtccgcctac aacaagcacc gggataagcc catcagagag 3960

caggccgaga atatcatcca cctgtttacc ctgaccaatc tgggagcccc tgccgccttc 4020

aagtactttg acaccaccat cgaccggaag aggtacacca gcaccaaaga ggtgctggac 4080

gccaccctga tccaccagag catcaccggc ctgtacgaga cacggatcga cctgtctcag 4140

ctgggaggcg acagcgctgg aggaggtgga agcggaggag gaggaagcgg aggaggaggt 4200

agcggaccta agaaaaagag gaaggtggcg gccgctggat ccggacgggc tgacgcattg 4260

gacgattttg atctggatat gctgggaagt gacgccctcg atgattttga ccttgacatg 4320

cttggttcgg atgcccttga tgactttgac ctcgacatgc tcggcagtga cgcccttgat 4380

gatttcgacc tggacatgct gattaactgt aca 4413

<210> 39
<211> 1419
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (1)..(390)
<223> MCP

<220>
<221> misc_feature
<222> (451)..(465)
<223> NLS

<220>
<221> misc_feature
<222> (481)..(1023)

<223> P65

<220>
<221> misc_feature
<222> (1048)..(1419)
<223> HSF1

<400> 39
atggcttcaa actttactca gttcgtgctc gtggacaatg gtgggacagg ggatgtgaca 60

gtggctcctt ctaatttcgc taatggggtg gcagagtgga tcagctccaa ctcacggagc 120

caggcctaca aggtgacatg cagcgtcagg cagtctagtg cccagaagag aaagtatacc 180

atcaaggtgg aggtccccaa agtggctacc cagacagtgg gcggagtcga actgcctgtc 240

gccgcttgga ggtcctacct gaacatggag ctcactatcc caattttcgc taccaattct 300

gactgtgaac tcatcgtgaa ggcaatgcag gggctcctca aagacggtaa tcctatccct 360

tccgccatcg ccgctaactc aggtatctac agcgctggag gaggtggaag cggaggagga 420

ggaagcggag gaggaggtag cggacctaag aaaaagagga aggtggcggc cgctggatcc 480

ccttcagggc agatcagcaa ccaggccctg gctctggccc ctagctccgc tccagtgctg 540

gcccagacta tggtgccctc tagtgctatg gtgcctctgg cccagccacc tgctccagcc 600

cctgtgctga ccccaggacc accccagtca ctgagcgctc cagtgcccaa gtctacacag 660

gccggcgagg ggactctgag tgaagctctg ctgcacctgc agttcgacgc tgatgaggac 720

ctgggagctc tgctggggaa cagcaccgat cccggagtgt tcacagatct ggcctccgtg 780

gacaactctg agtttcagca gctgctgaat cagggcgtgt ccatgtctca tagtacagcc 840

gaaccaatgc tgatggagta ccccgaagcc attacccggc tggtgaccgg cagccagcgg 900

ccccccgacc ccgctccaac tcccctggga accagcggcc tgcctaatgg gctgtccgga 960

gatgaagact tctcaagcat cgctgatatg gactttagtg ccctgctgtc acagatttcc 1020

tctagtgggc agggaggagg tggaagcggc ttcagcgtgg acaccagtgc cctgctggac 1080

ctgttcagcc cctcggtgac cgtgcccgac atgagcctgc ctgaccttga cagcagcctg 1140

gccagtatcc aagagctcct gtctccccag gagcccccca ggcctcccga ggcagagaac 1200

agcagcccgg attcagggaa gcagctggtg cactacacag cgcagccgct gttcctgctg 1260

gaccccggct ccgtggacac cgggagcaac gacctgccgg tgctgtttga gctgggagag 1320

ggctcctact tctccgaagg ggacggcttc gccgaggacc ccaccatctc cctgctgaca 1380

ggctcggagc ctcccaaagc caaggacccc actgtctcc 1419

<210> 40
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 40

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Gln Lys Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60

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

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr
130

<210> 41
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 41
atggcttcaa actttactca gttcgtgctc gtggacaatg gtgggacagg ggatgtgaca 60

gtggctcctt ctaatttcgc taatggggtg gcagagtgga tcagctccaa ctcacggagc 120

caggcctaca aggtgacatg cagcgtcagg cagtctagtg cccagaagag aaagtatacc 180

atcaaggtgg aggtccccaa agtggctacc cagacagtgg gcggagtcga actgcctgtc 240

gccgcttgga ggtcctacct gaacatggag ctcactatcc caattttcgc taccaattct 300

gactgtgaac tcatcgtgaa ggcaatgcag gggctcctca aagacggtaa tcctatccct 360

tccgccatcg ccgctaactc aggtatctac 390

<210> 42
<211> 6673
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 42
gtgcccgtca gtgggcagag cgcacatcgc ccacagtccc cgagaagttg gggggagggg 60

tcggcaattg aaccggtgcc tagagaaggt ggcgcggggt aaactgggaa agtgatgtcg 120

tgtactggct ccgccttttt cccgagggtg ggggagaacc gtatataagt gcagtagtcg 180

ccgtgaacgt tctttttcgc aacgggtttg ccgccagaac acaggtaagt gccgtgtgtg 240

gttcccgcgg gcctggcctc tttacgggtt atggcccttg cgtgccttga attacttcca 300

cctggctgca gtacgtgatt cttgatcccg agcttcgggt tggaagtggg tgggagagtt 360

cgaggccttg cgcttaagga gcccccttcgc ctcgtgcttg agttgaggcc tggcctgggc 420

gctggggccg ccgcgtgcga atctggtggc accttcgcgc ctgtctcgct gctttcgata 480

agtctctagc catttaaaat ttttgatgac ctgctgcgac gctttttttc tggcaagata 540

gtcttgtaaa tgcgggccaa gatctgcaca ctggtatttc ggtttttggg gccgcgggcg 600

gcgacggggc ccgtgcgtcc cagcgcacat gttcggcgag gcggggcctg cgagcgcggc 660

caccgagaat cggacggggg tagtctcaag ctggccggcc tgctctggtg cctggcctcg 720

cgccgccgtg tatcgccccg ccctgggcgg caaggctggc ccggtcggca ccagttgcgt 780

gagcggaaag atggccgctt cccggccctg ctgcagggag ctcaaaatgg aggacgcggc 840

gctcgggaga gcgggcgggt gagtcaccca cacaaaggaa aagggccttt ccgtcctcag 900

ccgtcgcttc atgtgactcc acggagtacc gggcgccgtc caggcacctc gattagttct 960

cgagcttttg gagtacgtcg tctttaggtt ggggggaggg gttttatgcg atggagtttc 1020

cccacactga gtgggtggag actgaagtta ggccagcttg gcacttgatg taattctcct 1080

tggaatttgc ccttttgag tttggatctt ggttcattct caagcctcag acagtggttc 1140

aaagtttttt tcttccattt caggtgtcgt gacgtacggc caccatgaaa aggccggcgg 1200

ccacgaaaaa ggccggccag gcaaaaaaga aaaaggacaa gaagtacagc atcggcctgg 1260

ccatcggcac caactctgtg ggctgggccg tgatcaccga cgagtacaag gtgcccagca 1320

agaaattcaa ggtgctgggc aacaccgacc ggcacagcat caagaagaac ctgatcggag 1380

ccctgctgtt cgacagcggc gaaacagccg aggccacccg gctgaagaga accgccagaa 1440

gaagatacac cagacggaag aaccggatct gctatctgca agagatcttc agcaacgaga 1500

tggccaaggt ggacgacagc ttcttccaca gactggaaga gtccttcctg gtggaagagg 1560

ataagaagca cgagcggcac cccatcttcg gcaacatcgt ggacgaggtg gcctaccacg 1620

agaagtaccc caccatctac cacctgagaa agaaactggt ggacagcacc gacaaggccg 1680

acctgcggct gatctatctg gccctggccc acatgatcaa gttccggggc cacttcctga 1740

tcgagggcga cctgaacccc gacaacagcg acgtggacaa gctgttcatc cagctggtgc 1800

agacctacaa ccagctgttc gaggaaaacc ccatcaacgc cagcggcgtg gacgccaagg 1860

ccatcctgtc tgccagactg agcaagagca gacggctgga aaatctgatc gcccagctgc 1920

ccggcgagaa gaagaatggc ctgttcggca acctgattgc cctgagcctg ggcctgaccc 1980

ccaacttcaa gagcaacttc gacctggccg aggatgccaa actgcagctg agcaaggaca 2040

cctacgacga cgacctggac aacctgctgg cccagatcgg cgaccagtac gccgacctgt 2100

ttctggccgc caagaacctg tccgacgcca tcctgctgag cgacatcctg agagtgaaca 2160

ccgagatcac caaggccccc ctgagcgcct ctatgatcaa gagatacgac gagcaccacc 2220

aggacctgac cctgctgaaa gctctcgtgc ggcagcagct gcctgagaag tacaaagaga 2280

ttttcttcga ccagagcaag aacggctacg ccggctacat tgacggcgga gccagccagg 2340

aagagttcta caagttcatc aagcccatcc tggaaaagat ggacggcacc gaggaactgc 2400

tcgtgaagct gaacagagag gacctgctgc ggaagcagcg gaccttcgac aacggcagca 2460

tcccccacca gatccacctg ggagagctgc acgccattct gcggcggcag gaagattttt 2520

acccattcct gaaggacaac cgggaaaaga tcgagaagat cctgaccttc cgcatcccct 2580

actacgtggg ccctctggcc aggggaaaca gcagattcgc ctggatgacc agaaagagcg 2640

aggaaaccat caccccctgg aacttcgagg aagtggtgga caagggcgct tccgcccaga 2700

gcttcatcga gcggatgacc aacttcgata agaacctgcc caacgagaag gtgctgccca 2760

agcacagcct gctgtacgag tacttcaccg tgtataacga gctgaccaaa gtgaaatacg 2820

tgaccgaggg aatgagaaag cccgccttcc tgagcggcga gcagaaaaag gccatcgtgg 2880

acctgctgtt caagaccaac cggaaagtga ccgtgaagca gctgaaagag gactacttca 2940

agaaaatcga gtgcttcgac tccgtggaaa tctccggcgt ggaagatcgg ttcaacgcct 3000

ccctgggcac ataccacgat ctgctgaaaa ttatcaagga caaggacttc ctggacaatg 3060

aggaaaacga ggacattctg gaagatatcg tgctgaccct gacactgttt gaggacagag 3120

agatgatcga ggaacggctg aaaacctatg cccacctgtt cgacgacaaa gtgatgaagc 3180

agctgaagcg gcggagatac accggctggg gcaggctgag ccggaagctg atcaacggca 3240

tccgggacaa gcagtccggc aagacaatcc tggatttcct gaagtccgac ggcttcgcca 3300

acagaaactt catgcagctg atccacgacg acagcctgac ctttaaagag gacatccaga 3360

aagcccaggt gtccggccag ggcgatagcc tgcacgagca cattgccaat ctggccggca 3420

gccccgccat taagaagggc atcctgcaga cagtgaaggt ggtggacgag ctcgtgaaag 3480

tgatgggccg gcacaagccc gagaacatcg tgatcgaaat ggccagagag aaccagacca 3540

cccagaaggg acagaagaac agccgcgaga gaatgaagcg gatcgaagag ggcatcaaag 3600

agctgggcag ccagatcctg aaagaacacc ccgtggaaaa cacccagctg cagaacgaga 3660

agctgtacct gtactacctg cagaatgggc gggatatgta cgtggaccag gaactggaca 3720

tcaaccggct gtccgactac gatgtggacc acatcgtgcc tcagagcttt ctgaaggacg 3780

actccatcga caacaaggtg ctgaccagaa gcgacaaggc ccggggcaag agcgacaacg 3840

tgccctccga agaggtcgtg aagaagatga agaactactg gcggcagctg ctgaacgcca 3900

agctgattac ccagagaaag ttcgacaatc tgaccaaggc cgagagaggc ggcctgagcg 3960

aactggataa ggccggcttc atcaagagac agctggtgga aacccggcag atcacaaagc 4020

acgtggcaca gatcctggac tcccggatga acactaagta cgacgagaat gacaagctga 4080

tccgggaagt gaaagtgatc accctgaagt ccaagctggt gtccgatttc cggaaggatt 4140

tccagtttta caaagtgcgc gagatcaaca actaccacca cgcccacgac gcctacctga 4200

acgccgtcgt gggaaccgcc ctgatcaaaa agtaccctaa gctggaaagc gagttcgtgt 4260

acggcgacta caaggtgtac gacgtgcgga agatgatcgc caagagcgag caggaaatcg 4320

gcaaggctac cgccaagtac ttcttctaca gcaacatcat gaacttttc aagaccgaga 4380

ttaccctggc caacggcgag atccggaagc ggcctctgat cgagacaaac ggcgaaaccg 4440

gggagatcgt gtgggataag ggccgggatt ttgccaccgt gcggaaagtg ctgagcatgc 4500

cccaagtgaa tatcgtgaaa aagaccgagg tgcagacagg cggcttcagc aaagagtcta 4560

tcctgcccaa gaggaacagc gataagctga tcgccagaaa gaaggactgg gaccctaaga 4620

agtacggcgg cttcgacagc cccaccgtgg cctattctgt gctggtggtg gccaaagtgg 4680

aaaagggcaa gtccaagaaa ctgaagagtg tgaaagagct gctggggatc accatcatgg 4740

aaagaagcag cttcgagaag aatcccatcg actttctgga agccaagggc tacaaagaag 4800

tgaaaaagga cctgatcatc aagctgccta agtactccct gttcgagctg gaaaacggcc 4860

ggaagagaat gctggcctct gccggcgaac tgcagaaggg aaacgaactg gccctgccct 4920

ccaaatatgt gaacttcctg tacctggcca gccactatga gaagctgaag ggctcccccg 4980

aggataatga gcagaaacag ctgtttgtgg aacagcacaa gcactacctg gacgagatca 5040

tcgagcagat cagcgagttc tccaagagag tgatcctggc cgacgctaat ctggacaaag 5100

tgctgtccgc ctacaacaag caccgggata agcccatcag agagcaggcc gagaatatca 5160

tccacctgtt taccctgacc aatctgggag cccctgccgc cttcaagtac tttgacacca 5220

ccatcgaccg gaagaggtac accagcacca aagaggtgct ggacgccacc ctgatccacc 5280

agagcatcac cggcctgtac gagacacgga tcgacctgtc tcagctggga ggcgacagcg 5340

ctggaggagg tggaagcgga ggaggaggaa gcggaggagg aggtagcgga cctaagaaaa 5400

agaggaaggt ggcggccgct ggatccggac gggctgacgc attggacgat tttgatctgg 5460

atatgctggg aagtgacgcc ctcgatgatt ttgaccttga catgcttggt tcggatgccc 5520

ttgatgactt tgacctcgac atgctcggca gtgacgccct tgatgatttc gacctggaca 5580

tgctgattaa ctgtacaggc agtggagagg gcagaggaag tctgctaaca tgcggtgacg 5640

tcgaggagaa tcctggccca atggccaagc ctttgtctca agaagaatcc accctcattg 5700

aaagagcaac ggctacaatc aacagcatcc ccatctctga agactacagc gtcgccagcg 5760

cagctctctc tagcgacggc cgcatcttca ctggtgtcaa tgtatatcat tttactgggg 5820

gaccttgtgc agaactcgtg gtgctgggca ctgctgctgc tgcggcagct ggcaacctga 5880

cttgtatcgt cgcgatcgga aatgagaaca ggggcatctt gagcccctgc ggacggtgcc 5940

gacaggtgct tctcgatctg catcctggga tcaaagccat agtgaaggac agtgatggac 6000

agccgacggc agttgggatt cgtgaattgc tgccctctgg ttatgtgtgg gagggctaag 6060

aattcgatat caagcttatc ggtaatcaac ctctggatta caaaatttgt gaaagattga 6120

ctggtattct taactatgtt gctcctttta cgctatgtgg atacgctgct ttaatgcctt 6180

tgtatcatgc tattgcttcc cgtatggctt tcattttctc ctccttgtat aaatcctggt 6240

tgctgtctct ttatgaggag ttgtggcccg ttgtcaggca acgtggcgtg gtgtgcactg 6300

tgtttgctga cgcaaccccc actggttggg gcattgccac cacctgtcag ctcctttccg 6360

ggactttcgc tttccccctc cctattgcca cggcggaact catcgccgcc tgccttgccc 6420

gctgctggac aggggctcgg ctgttgggca ctgacaattc cgtggtgttg tcggggaaat 6480

catcgtcctt tccttggctg ctcgcctgtg ttgccacctg gattctgcgc gggacgtcct 6540

tctgctacgt cccttcggcc ctcaatccag cggaccttcc ttcccgcggc ctgctgccgg 6600

ctctgcggcc tcttccgcgt cttcgccttc gccctcagac gagtcggatc tccctttggg 6660

ccgcctcccc gca 6673

<210> 43
<211> 4324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 43
gtgcccgtca gtgggcagag cgcacatcgc ccacagtccc cgagaagttg gggggagggg 60

tcggcaattg aaccggtgcc tagagaaggt ggcgcggggt aaactgggaa agtgatgtcg 120

tgtactggct ccgccttttt cccgagggtg ggggagaacc gtatataagt gcagtagtcg 180

ccgtgaacgt tctttttcgc aacgggtttg ccgccagaac acaggtaagt gccgtgtgtg 240

gttcccgcgg gcctggcctc tttacgggtt atggcccttg cgtgccttga attacttcca 300

cctggctgca gtacgtgatt cttgatcccg agcttcgggt tggaagtggg tgggagagtt 360

cgaggccttg cgcttaagga gcccccttcgc ctcgtgcttg agttgaggcc tggcctgggc 420

gctggggccg ccgcgtgcga atctggtggc accttcgcgc ctgtctcgct gctttcgata 480

agtctctagc catttaaaat ttttgatgac ctgctgcgac gctttttttc tggcaagata 540

gtcttgtaaa tgcgggccaa gatctgcaca ctggtatttc ggtttttggg gccgcgggcg 600

gcgacggggc ccgtgcgtcc cagcgcacat gttcggcgag gcggggcctg cgagcgcggc 660

caccgagaat cggacggggg tagtctcaag ctggccggcc tgctctggtg cctggcctcg 720

cgccgccgtg tatcgccccg ccctgggcgg caaggctggc ccggtcggca ccagttgcgt 780

gagcggaaag atggccgctt cccggccctg ctgcagggag ctcaaaatgg aggacgcggc 840

gctcgggaga gcgggcgggt gagtcaccca cacaaaggaa aagggccttt ccgtcctcag 900

ccgtcgcttc atgtgactcc acggagtacc gggcgccgtc caggcacctc gattagttct 960

cgagcttttg gagtacgtcg tctttaggtt ggggggaggg gttttatgcg atggagtttc 1020

cccacactga gtgggtggag actgaagtta ggccagcttg gcacttgatg taattctcct 1080

tggaatttgc ccttttgag tttggatctt ggttcattct caagcctcag acagtggttc 1140

aaagtttttt tcttccattt caggtgtcgt gacgtacggc caccatggct tcaaacttta 1200

ctcagttcgt gctcgtggac aatggtggga caggggatgt gacagtggct ccttctaatt 1260

tcgctaatgg ggtggcagag tggatcagct ccaactcacg gagccaggcc tacaaggtga 1320

catgcagcgt caggcagtct agtgcccaga agagaaagta taccatcaag gtggaggtcc 1380

ccaaagtggc tacccagaca gtgggcggag tcgaactgcc tgtcgccgct tggaggtcct 1440

acctgaacat ggagctcact atcccaattt tcgctaccaa ttctgactgt gaactcatcg 1500

tgaaggcaat gcaggggctc ctcaaagacg gtaatcctat cccttccgcc atcgccgcta 1560

actcaggtat ctacagcgct ggaggaggtg gaagcggagg aggaggaagc ggaggaggag 1620

gtagcggacc taagaaaaag aggaaggtgg cggccgctgg atccccttca gggcagatca 1680

gcaaccaggc cctggctctg gcccctagct ccgctccagt gctggcccag actatggtgc 1740

cctctagtgc tatggtgcct ctggcccagc cacctgctcc agcccctgtg ctgaccccag 1800

gaccacccca gtcactgagc gctccagtgc ccaagtctac acaggccggc gaggggactc 1860

tgagtgaagc tctgctgcac ctgcagttcg acgctgatga ggacctggga gctctgctgg 1920

ggaacagcac cgatcccgga gtgttcacag atctggcctc cgtggacaac tctgagtttc 1980

agcagctgct gaatcagggc gtgtccatgt ctcatagtac agccgaacca atgctgatgg 2040

agtaccccga agccattacc cggctggtga ccggcagcca gcggcccccc gaccccgctc 2100

caactcccct gggaaccagc ggcctgccta atgggctgtc cggagatgaa gacttctcaa 2160

gcatcgctga tatggacttt agtgccctgc tgtcacagat ttcctctagt gggcagggag 2220

gaggtggaag cggcttcagc gtggacacca gtgccctgct ggacctgttc agcccctcgg 2280

tgaccgtgcc cgacatgagc ctgcctgacc ttgacagcag cctggccagt atccaagagc 2340

tcctgtctcc ccaggagccc cccaggcctc ccgaggcaga gaacagcagc ccggattcag 2400

ggaagcagct ggtgcactac acagcgcagc cgctgttcct gctggacccc ggctccgtgg 2460

acaccgggag caacgacctg ccggtgctgt ttgagctggg agagggctcc tacttctccg 2520

aaggggacgg cttcgccgag gaccccacca tctccctgct gacaggctcg gagcctccca 2580

aagccaagga ccccactgtc tcctgtacag gcagtggaga gggcagagga agtctgctaa 2640

catgcggtga cgtcgaggag aatcctggcc caaccatgaa aaagcctgaa ctcaccgcta 2700

cctctgtcga gaagtttctg atcgaaaagt tcgacagcgt ctccgacctg atgcagctct 2760

ccgagggcga agaatctcgg gctttcagct tcgatgtggg agggcgtgga tatgtcctgc 2820

gggtgaatag ctgcgccgat ggtttctaca aagatcgcta tgtttatcgg cactttgcat 2880

ccgccgctct ccctattccc gaagtgcttg acattgggga gttcagcgag agcctgacct 2940

attgcatctc ccgccgtgca cagggtgtca ccttgcaaga cctgcctgaa accgaactgc 3000

ccgctgttct ccagcccgtc gccgaggcca tggatgccat cgctgccgcc gatcttagcc 3060

agaccagcgg gttcggccca ttcggacctc aaggaatcgg tcaatacact acatggcgcg 3120

atttcatctg cgctattgct gatccccatg tgtatcactg gcaaactgtg atggacgaca 3180

ccgtcagtgc ctccgtcgcc caggctctcg atgagctgat gctttgggcc gaggactgcc 3240

ccgaagtccg gcacctcgtg cacgccgatt tcggctccaa caatgtcctg accgacaatg 3300

gccgcataac agccgtcatt gactggagcg aggccatgtt cggggattcc caatacgagg 3360

tcgccaacat cttcttctgg aggccctggt tggcttgtat ggagcagcag acccgctact 3420

tcgagcggag gcatcccgag cttgcaggat ctcctcggct ccgggcttat atgctccgca 3480

ttggtcttga ccaactctat cagagcttgg ttgacggcaa tttcgatgat gcagcttggg 3540

ctcagggtcg ctgcgacgca atcgtccggt ccggagccgg gactgtcggg cgtacacaaa 3600

tcgcccgcag aagcgctgcc gtctggaccg atggctgtgt ggaagtgctc gccgatagtg 3660

gaaacagacg ccccagcact cgtcctaggg caaaggatct gcagtaatga gaattcgata 3720

tcaagcttat cggtaatcaa cctctggatt acaaaatttg tgaaagattg actggtattc 3780

ttaactatgt tgctcctttt acgctatgtg gatacgctgc tttaatgcct ttgtatcatg 3840

ctattgcttc ccgtatggct ttcattttct cctccttgta taaatcctgg ttgctgtctc 3900

tttatgagga gttgtggccc gttgtcaggc aacgtggcgt ggtgtgcact gtgtttgctg 3960

acgcaacccc cactggttgg ggcattgcca ccacctgtca gctcctttcc gggactttcg 4020

ctttcccccc ccctattgcc acggcggaac tcatcgccgc ctgccttgcc cgctgctgga 4080

caggggctcg gctgttgggc actgacaatt ccgtggtgtt gtcggggaaa tcatcgtcct 4140

ttccttggct gctcgcctgt gttgccacct ggattctgcg cgggacgtcc ttctgctacg 4200

tcccttcggc cctcaatcca gcggaccttc cttcccgcgg cctgctgccg gctctgcggc 4260

ctcttccgcg tcttcgcctt cgccctcaga cgagtcggat ctccctttgg gccgcctccc 4320

cgca 4324