SEQUENCE LISTING

<110> Tokushima University

<120> Target sequence-specific alteration technique using nucleotide target recognition

<130> 674277

<150> JP2017-158876
<151> 2017-08-21

<150> JP2017-236518
<151> 2017-12-08

<160> 45

<170> PatentIn version 3.5

<210> 1
<211> 224
<212> PRT
<213> Microcystis aeruginosa

<400> 1

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Met Val His Ile Tyr Ser Cys Gln Leu Glu Leu His Asp Ser Leu Tyr
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Tyr Ala Thr Arg Glu Ile Gly Arg Leu Tyr Glu Ser Glu Pro Val Ile
            20                  25                  30


His Asn Tyr Ala Leu Cys Tyr Ala Leu Gly Leu Val Asn Ser Asp Ser
        35                  40                  45


Tyr Arg Tyr Phe Cys Ser Glu Gln Ile Pro Gln Tyr Gln Glu His Leu
    50                  55                  60


Asn Pro Leu Asn Glu Glu Lys Ile Tyr Val Thr Pro Ala Arg Ala Ile
65                  70                  75                  80


Ala His Thr Ala Val Leu Asn Thr Trp Lys Tyr Ala Asn Asn Asn Tyr
                85                  90                  95
```

```
His Val Glu Met Glu Lys Thr Gln Lys Asn Ile Pro Ser Phe Gly Arg
            100                 105                 110


Ala Lys Glu Ile Ala Pro Glu Ser Ile Phe Glu Cys Phe Ile Ile Ser
        115                 120                 125


His His Pro Leu Gln Leu Pro Lys Trp Ile Arg Leu Gly Lys Trp Met
    130                 135                 140


Ser Lys Ala Glu Val Lys Leu Thr Glu Leu Ser Leu Ser Lys Gln Lys
145                 150                 155                 160


Glu Asp Leu Phe Ile Tyr Pro Tyr Pro Leu Asn Pro Leu Asp Val Met
                165                 170                 175


Phe Thr His Gln Val Ile Gly Tyr Asp Val Ile Asn Met Pro Pro Val
            180                 185                 190


Ser Leu Ile Arg Asn Val Arg Met Arg Gly Glu Tyr Tyr Gln Ile Ser
        195                 200                 205


Asp Arg Pro Asp Leu Lys Ile Pro Ala Arg Leu Ser Tyr His Phe Gly
    210                 215                 220


<210>  2
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<213>  Microcystis aeruginosa

<400>  2

Met Pro Tyr Ser Leu Val Leu Asn Leu Thr Pro Arg Ser Pro Ile Tyr
1               5                   10                  15


Pro Asn Phe Leu Thr Gly Arg His Leu His Ala Leu Phe Leu Thr Leu
            20                  25                  30


Val Ser Ser Val Asp Gln Glu Leu Gly Asn Ile Leu His Thr Ala Glu
        35                  40                  45
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```
Ala Asp Lys Ala Phe Thr Leu Ser Pro Leu Gln Met Gln Ser Gly Gly
    50                  55                  60

Lys Thr Ile Asn Ser Pro Gln Trp Arg His Glu Arg Glu Ile Ala Ser
65                  70                  75                  80

Glu Thr Pro Cys Trp Trp Arg Ile Ser Leu Leu Asp Asp Arg Leu Phe
                85                  90                  95

Gly Lys Leu Thr Ser Leu Trp Leu Asn Leu Asn Pro Lys Gln Pro Trp
            100                 105                 110

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

Gln Ser Val Gln Pro Trp Ala Asn Ser Cys Thr Tyr Gln Tyr Leu Tyr
    130                 135                 140

Glu Asn Ala Ser Glu Thr Asn Arg Glu Phe Asp Phe Leu Phe Ala Thr
145                 150                 155                 160

Pro Val Thr Phe Arg Gln Gly Lys Phe Asp Ser Ala Leu Pro Thr Arg
                165                 170                 175

Glu Leu Val Phe Asn Ser Leu Leu Gly Arg Trp Asn Arg Tyr Ser Gly
            180                 185                 190

Ile Pro Phe Asp Ser Ile Ala Leu Glu Ser Ile Phe Pro Ser Phe Phe
        195                 200                 205

Asp Ile Gln Thr Lys Leu Ala Asp Glu Ala Tyr Lys Asn Gln Ser Ile
    210                 215                 220

Gly Cys Val Gly Glu Ile His Tyr Arg Leu Leu Gly Glu Val Glu Pro
225                 230                 235                 240

Ala Lys Ile Lys Ala Ile Asn Ala Leu Ala Asp Phe Ala Leu Tyr Ala
```

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                245                 250                 255

Gly Val Gly Arg Lys Thr Thr Met Gly Met Gly Met Thr Arg Arg Ile
            260                 265                 270

Ser Lys Asp Lys Arg
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<213> Microcystis aeruginosa

<400> 3

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Tyr Lys Pro Met Gly Lys Tyr Val His Phe Leu Thr Ile Arg Val Thr
            20                  25                  30

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

Val Arg Ala Gly Ile Asp Ser Lys Lys Thr Ile Ser Arg Leu Ser Met
    50                  55                  60

Phe Lys Arg Lys Gln Ser Thr Pro Glu Arg Leu Val Gly Arg Glu Leu
65                  70                  75                  80

Leu Arg Asn Tyr Gly Leu Ile Thr Ala Glu Glu Cys Glu Tyr Asn Val
                85                  90                  95

Lys Phe Ala Met Asn Asn Ala Asp Cys Ile Ile Tyr Gly Phe Ala Ile
            100                 105                 110

Gly Asp Ser Gly Ser Glu Lys Ser Lys Val Val Val Asp Thr Ala Phe
        115                 120                 125
```

```
Ser Ile Thr Pro Phe Asp Glu Ser His Glu Ser Phe Thr Leu Asn Ala
    130                 135                 140

Pro Tyr Glu Asn Gly Thr Met Ala Ser Lys Gly Glu Asn Asn Thr Lys
145                 150                 155                 160

Val Gly Glu Val Thr Ser Arg Ile Asn Gln Gln Asp His Ile Arg Pro
                165                 170                 175

Gln Val Phe Phe Pro Ser Ile Val Thr Leu Lys Asp Pro Thr Glu Ala
            180                 185                 190

Ser Phe Leu Tyr Val Phe Asn Asn Ile Leu Arg Thr Arg His Tyr Gly
        195                 200                 205

Ala Gln Thr Thr Arg Thr Gly Arg Val Arg Asn Glu Leu Ile Gly Val
    210                 215                 220

Ile Phe Ala Asp Gly Glu Ile Val Ser Asn Leu Arg Trp Thr Gln Ala
225                 230                 235                 240

Ile Tyr Asp Arg Leu Pro Asp Glu Val Leu His Ser Ile Asp Pro Leu
                245                 250                 255

Asp Glu Asp Leu Val Met Glu Lys Ala Thr Glu Ala Ile Gln Ala Leu
            260                 265                 270

Met Ala Glu Glu Phe Ile Val His Thr Asp Phe Ile Gly Glu Asn Phe
        275                 280                 285

Gln Pro Leu Leu Thr Glu Val Lys Thr Leu Thr Gly Thr Glu Ala Gly
    290                 295                 300

Ile Leu Ser Val Leu Asp Gln Ala Asn Lys Glu Ser Lys Lys Tyr Phe
305                 310                 315                 320

Glu Gln Tyr Ile Glu Lys Lys Lys Ala Glu Lys Lys
                325                 330
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<210> 4
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<212> PRT
<213> Microcystis aeruginosa

<400> 4

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Met Gly Asn Tyr Gln Val Thr Leu Lys Pro Val Tyr Ser Cys Pro Ala
1               5                  10                  15


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


Trp His Gln Val Glu Thr Trp Lys Ala Leu Asn Asp Pro Asp Ile Asp
        35                  40                  45


Val Ile Phe Asn Thr Ala Met Thr Gly Asp Gly Lys Ser Leu Ala Ala
    50                  55                  60


Tyr Leu Arg Thr Leu Gln Gly Tyr Phe Pro Ile Met Gly Leu Tyr Pro
65                  70                  75                  80


Thr Asn Glu Leu Ala Arg Asp Gln Arg Gly Gln Ile Glu Ala Tyr Ile
                85                  90                  95


Gln Arg Phe Gln Pro Thr Asp Gln Pro Arg Val Asn Leu Leu Thr Gly
            100                 105                 110


Pro Glu Leu Glu Leu Tyr Ala Glu Arg Asp Gly Lys Thr Lys Ala Ile
        115                 120                 125


Ala Leu Glu Thr Arg Ser Lys Gln Ser Glu Ile Leu Leu Thr Asn Pro
    130                 135                 140


Asp Ile Phe His Tyr Leu His Arg Ala Ala Tyr Leu Thr Pro Tyr Asp
145                 150                 155                 160


Asn Pro Asp Gln Leu Trp Asn Arg Ile Asp Lys His Phe Asp Leu Phe
```

```
                165                 170                 175

Leu Phe Asp Glu Phe His Val Phe Gly Thr Pro Gln Val Ala Ser Ile
            180                 185                 190

Ile Asn Thr Met Leu Leu Ile Arg Arg Ala Asn Arg Gly Lys Arg Tyr
        195                 200                 205

Leu Phe Leu Ser Ala Thr Pro Asp Glu Gly Leu Leu Lys Arg Leu Asp
    210                 215                 220

Lys Ala Gly Phe Arg Tyr Arg Ser Ile Asp Pro Val Arg Glu Gly Lys
225                 230                 235                 240

Tyr Arg Phe Pro Asp Thr Pro Glu Glu Ala Asn Ser Leu Ala Gln Gln
                245                 250                 255

Gly Trp Arg Gln Val Thr Ser Glu Ile Glu Leu Ser Phe Ile Pro Leu
            260                 265                 270

Pro Ser Ser Phe Gln Thr Ser Glu Asn Trp Leu Lys Glu Asn Lys Glu
        275                 280                 285

Arg Ile Leu Asp Tyr Phe Lys Arg Tyr Pro Gly Ser Lys Gly Ala Ile
    290                 295                 300

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

Glu Leu Leu Ala Thr Ile Gly Leu Thr Val Gly Glu Asn Thr Gly Leu
                325                 330                 335

Ser Gly Thr Arg Glu Lys Leu Ala Ser Leu Asn Arg Asp Leu Val Ile
            340                 345                 350

Gly Thr Ser Thr Ile Asp Val Gly Val Asp Phe Lys Ile Asn Phe Leu
        355                 360                 365
```

```
Ile Phe Glu Ser Ser Asp Ala Gly Asn Phe Ile Gln Arg Phe Gly Arg
    370                 375                 380

Leu Gly Arg His Ser Gly Tyr Asp Arg Lys Gly Thr Ala Val Lys Phe
385                 390                 395                 400

Thr Asn Phe Thr Ala Ile Ala Leu Val Pro Lys Phe Phe Leu Glu Arg
                405                 410                 415

Leu Phe Glu Lys Lys Asp Ala Pro Leu Gln Val Gly Glu Arg Tyr Asp
            420                 425                 430

Arg Ile Gln Leu Gln Glu Ala Ile Lys Ser Asn Tyr Arg His Ile Asn
        435                 440                 445

Asn Phe Glu Gly Tyr Tyr Gln Arg Trp Gly Ala Val Gln Ser Phe Gln
    450                 455                 460

Leu Trp Trp Asn Leu Gly Ser Pro Lys Ile Lys Ser Gln Tyr Gly Glu
465                 470                 475                 480

Ser Arg Gln Lys Phe Gln Gln Glu Cys Glu Glu Val Phe Asp Thr Ser
                485                 490                 495

Leu Lys Arg Val Ala Gly Arg Val Lys Gly Trp Ala Asp Glu Trp Lys
            500                 505                 510

Glu Leu Ser Gly Lys Asn Gly Asn Pro Ile Phe Glu Asp Ala Ser Ser
        515                 520                 525

Phe Arg Gly Ser Ser Pro Leu Leu Cys Gly Leu Tyr Asp Ser Thr Glu
    530                 535                 540

Pro Glu Glu Cys Asp Arg Phe Lys Thr Tyr Asp Leu Pro Ser Ile Leu
545                 550                 555                 560

Gly Asn Leu Glu Val Glu Val Trp Arg Lys Gly Glu Phe Lys Arg Gln
```

```
                565                 570                 575

Ile Glu Ala Thr Lys Thr Pro Ile Ala Arg Arg Arg Phe Asp Tyr Cys
            580                 585                 590

Leu Ala Phe Leu Asn Leu Lys Gly Tyr Arg Glu Glu Arg Leu Asn Trp
        595                 600                 605

Arg Phe Thr Tyr Asp Gly Asp Leu Gly Glu Ile Ala Ser Ala Trp Lys
    610                 615                 620

Val Gln Val Leu Thr Gly Ile Gly Val Trp Gln Pro Asp Asn Pro Trp
625                 630                 635                 640

Leu Asp Arg Ile Ser Arg Glu Leu Arg Asp Leu Ala Leu Val Ser Phe
                645                 650                 655

Val Phe Ala Tyr Pro Val Ala Ala Val Arg Gln Arg Leu Gln Leu Pro
            660                 665                 670

Met His Phe Gly Ile Tyr Pro Ile Ser Asp Glu Ser Ser Leu His Ser
        675                 680                 685

Pro Leu Ser Pro Tyr Ser Ile Ala Ile Gly Gln Ala Ala Leu Leu Leu
    690                 695                 700

Asp Thr Leu Ala His Arg Phe Lys Gly Lys Gly Gly Glu Val Trp Ile
705                 710                 715                 720

Cys
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<210> 5
<211> 1156
<212> PRT
<213> Microcystis aeruginosa

<400> 5

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Met Pro Lys Lys Gln Lys Lys Leu Glu Glu Thr Gly Gln Leu Asn Leu
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Phe Asp Asn Thr Thr Glu Ile Asp Asp Glu Asp Leu Asp Phe Glu Phe
            20                  25                  30

Glu Asp Ile Asp Leu Glu Ser Leu Val Ser Glu Asp Leu Gly Ile Thr
        35                  40                  45

Glu Ser Val Ser Asp Arg Arg Val Glu Thr Val Arg Gln Leu Leu Thr
    50                  55                  60

Leu Lys Leu Leu Arg Glu Ala Ile Arg Ala Glu Asn Pro Asp Asp Arg
65                  70                  75                  80

Val Met Ala Asp Phe Ala Glu Met Val Leu Pro Asn Leu Leu Arg Leu
                85                  90                  95

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

Arg Gly Arg Glu Leu Arg Asn Lys Pro Lys Ala Lys Arg Asp Asn Ala
        115                 120                 125

Gly Asp Gln Ser Leu Asn Thr His Leu Leu Asn Gly Leu Phe Pro Ala
    130                 135                 140

Asn Leu Ile Glu Lys Arg Leu Gln Lys Leu Asn Thr Thr Val Arg Arg
145                 150                 155                 160

Ile Ile Lys Glu Phe Glu Arg Arg Leu Ala Ile Ala Gly Phe Leu Val
                165                 170                 175

His Asp Phe Glu Lys Phe Ser Tyr Asp Arg Phe Pro Ser Met Ser Glu
            180                 185                 190

Arg Tyr Ile Gln Ile Gln Arg Asp Phe Ile Gln Asp Pro Phe Lys Asn
        195                 200                 205
```

```
Gln Asp Pro Arg Lys Leu Ser Arg Glu Glu His Arg Glu Ile Leu Gln
    210                 215                 220

Val Leu Ile Pro Glu Leu Gly Leu Asp Arg Phe Leu Phe Pro Asp Asn
225                 230                 235                 240

Pro Glu Arg Trp Leu Glu Tyr Leu Asp Asp Leu Leu Tyr Ile Ala Lys
                245                 250                 255

Asn Thr Gln Arg Arg Asn Asp Thr Asp Leu Asn Thr Ser Glu Asp Gly
            260                 265                 270

Leu Asn Val Arg Leu Asn Asp Arg Val Ile Glu Ser Leu Cys Asp Leu
        275                 280                 285

Ala Cys Leu Ala Asp Arg Leu Ala Ser Ile Ile Lys His Pro His Asp
    290                 295                 300

Ala Glu Lys Ala Ser Leu Gln Asp Leu Leu Tyr Ser Leu Ser Asp Gly
305                 310                 315                 320

Glu Leu Lys Phe Thr Tyr His Ser Ile Ala Glu Asn Arg Gly Val Leu
                325                 330                 335

Thr Asn Val Leu Asn Asn Ala Val Met Glu Ala His Gln Glu Leu Asp
            340                 345                 350

Tyr Gln Pro Leu Leu Tyr Leu Pro Thr Gly Val Val Tyr Ile Ala Pro
        355                 360                 365

Lys Asn Ala Pro Glu Val Ser Leu Glu Thr Leu Pro Asn Arg Val Val
    370                 375                 380

Asp Thr Ile Lys Ser Leu Cys Ser Gly Glu Leu Gln Arg Lys Gln Thr
385                 390                 395                 400
```

```
Gly Phe Gly Arg Asp Gly Lys Gly Met Lys Tyr Ala Asp Tyr Tyr Ser
                405                 410                 415

Gln Phe Phe Asp Asp Ala Gly Leu Met Arg Ala Ala Leu Asn Ala Thr
            420                 425                 430

Leu Arg Ile Leu Gly Asp Asn Lys Ala Ser Val Ala Arg Ser Arg Gly
        435                 440                 445

Glu Asn Leu Ile Lys Phe Gln Gln Gln Gly Val Leu Pro Thr Asp Tyr
    450                 455                 460

Asp Phe His Cys Glu Asp Asp Ile Arg Ile Asp Arg Leu Ala Glu Phe
465                 470                 475                 480

Gly Asp Val Val Thr Arg Lys Ile Trp Gly Asp Arg Leu Glu Lys Ile
                485                 490                 495

Glu Gln Ala Arg Lys Leu Gln Lys Asn Leu Pro Ala Pro Pro Asp Leu
            500                 505                 510

Asp Leu Ile Ser Glu Ile Ala His Tyr Trp Asn Leu Glu Asn Tyr Leu
        515                 520                 525

Pro Gln Ile Arg Ala Ile Lys Arg Ile Asn Glu Ser Leu Lys Glu Leu
    530                 535                 540

Lys Leu Lys Gly Asn Thr Gly Gly Val Pro Tyr Glu Trp Tyr Tyr Leu
545                 550                 555                 560

Ala Ala Gln Tyr Leu Lys Gln His Pro Gly Ile Glu Asp Ile Arg Pro
                565                 570                 575

Val Ala Glu Asp Leu Ile Ala Phe Leu Ala Ala Lys Ile Ala Ala Ile
            580                 585                 590

Val Ala Gly Tyr Asn Leu Pro Asp Gly Trp Glu Asp Leu Arg Glu Trp
        595                 600                 605
```

```
Val Asn Gln Val Val Gln Leu Pro Gly Arg Glu Leu Ala His Ser Ile
    610                 615                 620

Glu Thr Phe Gln Lys Glu Leu Asn His Tyr Asn Ala Ala Lys Lys Gln
625                 630                 635                 640

Gly Arg Gly Arg Gln Leu Leu Cys Ser Ile Ser His Ser Pro Tyr Ser
                645                 650                 655

Val Ser Glu Gln Met Glu Ser Ala Val Leu Phe Thr Pro Gln Val Tyr
            660                 665                 670

Thr Asn Lys Gln Met Leu Ala Gly Ser Asn Ala Lys Arg Asn Ile Ser
        675                 680                 685

Ser Ile Ala Gly Thr Glu Met Met Leu Arg Gln Ile Leu Met Asn Gln
    690                 695                 700

Thr Gln Ala Val Gly Lys Arg Phe Glu Asp Gly Lys Tyr Arg Tyr Leu
705                 710                 715                 720

Tyr Phe Tyr Pro Thr Tyr Tyr Phe Thr Pro Glu Thr Asn Ser Phe Leu
                725                 730                 735

Gln Lys Ala Tyr Ala Asn Ile Ala Gln Thr Arg Phe Asp Ser Ser Ile
            740                 745                 750

Lys Leu His Phe Val Asp Lys Asn Leu Val Ala Asn Phe Asp Arg Thr
        755                 760                 765

Arg Tyr Gln Ser Val Asp Ser Phe Leu Ile Asp Glu Lys Leu Arg Gln
    770                 775                 780

Lys Lys Glu Thr Ile Asn Glu Glu Glu Asp Gly Lys Lys Asp Arg Thr
785                 790                 795                 800
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```
Phe Lys Leu Ser Tyr Pro Glu Asp Lys Pro Leu Thr Phe Tyr Phe Met
                805                 810                 815

Ala Leu Pro Pro Gly Arg Asn Pro Thr Asp Thr Glu Ser Trp Val Met
            820                 825                 830

Pro Ala Trp Leu Gly Leu Ala Phe Pro Met Ile Leu Asp Val Lys Thr
        835                 840                 845

Val Val Ser Glu Ser Pro Ile Pro Pro Tyr Arg Asp Gly Ala Glu Phe
    850                 855                 860

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

Thr Arg Cys Asp Arg Phe Arg Leu Asp Arg Val Leu Asn Pro Trp Gln
                885                 890                 895

Asp Asn Asp Gly Lys Lys Tyr Ser Ala Pro Leu Asn Thr Leu Thr Ala
            900                 905                 910

Ala Tyr Ser Ile His Leu Asp Val Asn Ser Lys Gln Gly Lys Thr Gly
        915                 920                 925

Tyr Asp Pro Asn Trp Gly Lys Leu Thr Glu Leu Ala Ile Asn Leu Glu
    930                 935                 940

Thr Ser Pro Leu Tyr Val Phe His Tyr Phe Lys Gln Trp Lys Arg Gly
945                 950                 955                 960

Lys Asp Ala Asp Ile Pro Ser Ala Asn Arg Ile Ala Leu Tyr Leu Tyr
                965                 970                 975

Asp Phe Tyr Pro Cys Phe Asp Pro Tyr Val Gln Ala Asn Arg Thr Asn
            980                 985                 990

Leu Thr Ile Asp Met Thr Ala Glu  Ser Pro Leu Asn His  Pro Lys Asn
        995                 1000                1005
```

```
Leu Thr  Glu Leu Tyr Arg Gln  Phe Tyr Arg Ala Lys  Ser Ser Lys
    1010                1015                1020

Gly Lys  Pro Ile Lys Ala Asn  Ala Ile Leu Lys Pro  Ile Asp Glu
    1025                1030                1035

Ala Ala  Asp Ile Ile Leu Lys  Ala Asp Lys Ala Ile  Ser Asp Asp
    1040                1045                1050

Leu Thr  Ser Leu Val Ala Ala  Arg Leu Phe Lys Leu  Met Asp Arg
    1055                1060                1065

Val Arg  Ser Gln Thr Ala Glu  Gly Arg Tyr Val Ile  Lys Glu Arg
    1070                1075                1080

Asp Gln  Glu Arg Glu Lys Ile  Leu Asp Phe Ala Lys  Tyr Phe Val
    1085                1090                1095

Lys Asn  Val Phe Glu Glu Ser  Phe Glu Ser Asp Arg  Ala Arg Leu
    1100                1105                1110

Ala Gly  Arg Gln Leu Asn Ile  Ile Arg Asp Thr Cys  Glu Phe Leu
    1115                1120                1125

Tyr Arg  Leu Glu Met Asp Lys  Glu Arg Arg Gln Arg  Gln Val Gln
    1130                1135                1140

Pro Leu  Asp Thr Ser Asn Ser  Ser Ser Glu Glu Glu  Glu
    1145                1150                1155
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<220>
<223> TiDcrRNA

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<221> misc_feature
<222> (38)..(72)
<223> n is a, c, g, or u

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guuccaauua aucuuaagcc cuauuaggga uugaaacnnn nnnnnnnnnn nnnnnnnnnn 60

nnnnnnnnnn nnguuccaau uaaucuuaag cccuauuagg gauugaaac 109

<210> 7
<211> 675
<212> DNA
<213> Artificial

<220>
<223> Cas5d nucleotide sequence for expression in Escherichia coli

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gaaattggcc gcctgtatga aagcgaaccg gtgattcata actatgcgct gtgctatgcg 120

ctgggcctgg tgaacagcga tagctatcgc tatttctgca gcgaacagat tccgcagtat 180

caggaacatc tgaacccgct gaacgaagaa aaaatttatg tgaccccggc gcgcgcgatt 240

gcgcataccg cggtgctgaa cacctggaaa tatgcgaaca acaactatca tgtggaaatg 300

gaaaaaaccc agaaaaacat tccgagcttc ggccgcgcga aagaaattgc gccggaaagc 360

attttcgaat gcttcattat tagccatcat ccgctgcagc tgccgaaatg gattcgcctg 420

ggcaaatgga tgagcaaagc ggaagtgaaa ctgaccgaac tgagcctgag caaacagaaa 480

gaagatctgt tcatttatcc gtatccgctg aacccgctgg atgtgatgtt cacccatcag 540

gtgattggct atgatgtgat taacatgccg ccggtgagcc tgattcgcaa cgtgcgcatg 600

cgcggcgaat attatcagat tagcgatcgc ccggatctga aaattccggc acgtctgagc 660

tatcatttcg gctaa 675

<210> 8
<211> 834
<212> DNA
<213> Artificial

<220>
<223> Cas6d nucleotide sequence for expression in Escherichia coli

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accggccgcc atctgcatgc gctgttcctg accctggtga gcagcgtgga tcaggaactg 120

ggcaacattc tgcataccgc ggaagcggat aaagcgttca ccctgagccc gctgcagatg 180

cagagcggcg gcaaaaccat taacagcccg cagtggcgcc atgaacgcga aattgcgagc 240

gaaaccccgt gctggtggcg cattagcctg ctggatgatc gcctgttcgg caaactgacc 300

agcctgtggc tgaacctgaa cccgaaacag ccgtggcatc tgggcagcgc ggatctggtg 360

attaccagcg tgctggcgac cccgcagagc gtgcagccgt gggcgaacag ctgcacctat 420

cagtatctgt atgaaaacgc gagcgaaacc aaccgcgaat tcgatttcct gttcgcgacc 480

ccggtgacct tccgccaggg caaattcgat agcgcgctgc cgacccgcga actggtgttc 540

aacagcctgc tgggccgctg gaaccgctat agcggcattc cgttcgatag cattgcgctg 600

gaaagcattt tcccgagctt cttcgatatt cagaccaaac tggcggatga agcgtataaa 660

aaccagagca ttggctgcgt gggcgaaatt cattatcgcc tgctgggcga agtggaaccg 720

gcgaaaatta aagcgattaa cgcgctggcg gatttcgcgc tgtatgcggg cgtgggccgc 780

aaaaccacca tgggcatggg catgacccgc cgcattagca aagataaacg ctaa 834

<210> 9
<211> 1002
<212> DNA
<213> Artificial

<220>
<223> Cas7d nucleotide sequence for expression in Escherichia coli

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atgggcaaat atgtgcattt cctgaccatt cgcgtgaccg aaagctatcc gctgttccag 120

accgatggcg aactgaacaa agcgcgcgtg cgcgcgggca ttgacagcaa gaaaaccatt 180

agccgcctga gcatgttcaa acgcaaacag agcaccccgg aacgcctggt gggccgcgaa 240

ctgctgcgca actatggcct gattaccgcg gaagaatgcg aatataacgt gaaattcgcg 300

atgaacaacg cggattgcat tatttatggc ttcgcgattg gcgatagcgg cagcgaaaaa 360

agcaaagtgg tggtggatac cgcgttcagc attaccccgt tcgatgaaag ccatgagagc 420

ttcaccctga acgcgccgta tgaaaacggc acgatggcga gcaaaggcga aaacaacacc 480

aaagtgggcg aagtgaccag ccgcattaac cagcaggatc atattcgccc gcaggtgttc 540

ttcccgagca ttgtgaccct gaaagatccg accgaagcga gcttcctgta tgtgttcaac 600

aacattctgc gcacccgcca ttatggcgcg cagaccaccc gcaccggccg cgtgcgcaac 660

gaactgattg gcgtgatttt cgcggatggc gaaattgtga gcaacctgcg ctggacccag 720

gcgatttatg atcgcctgcc ggatgaagtg ctgcatagca ttgatccgct ggatgaagat 780

ctggtgatgg aaaaagcgac cgaagcgatt caggcgctga tggcggaaga atttattgtg 840

cataccgatt tcattggcga aaacttccag ccgctgctga ccgaagtgaa aaccctgacc 900

ggcaccgaag cgggcattct gagcgtgctg gatcaggcga acaaagaaag caaaaaatat 960

ttcgaacagt atattgaaaa gaaaaaggcg gaaaagaaat aa 1002

<210> 10
<211> 2166
<212> DNA
<213> Artificial

<220>
<223> Cas3d nucleotide sequence for expression in Escherichia coli

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gacggaatca aggtgccaca gggatggaga ctttcttggc accaggtgga gacttggaag 120

gctcttaacg acccagacat cgacgtgatc ttcaacactg ctatgactgg agacggaaag 180

tctcttgctg cttatcttag aactcttcag ggatatttcc caatcatggg actttatcca 240

actaacgagc ttgctagaga tcagagagga cagatcgagg cttatatcca gagattccag 300

ccaactgacc agccaagagt gaaccttctt actggaccag agcttgagct ttatgctgag 360

agagacggaa agactaaggc tatcgctctt gagactagat ctaagcagtc tgagatcctt 420

cttactaacc cagacatctt ccactatctt cacagagctg cttatcttac tccatatgac 480

aacccagacc agctttggaa cagaatcgac aagcacttcg acctttttcct tttcgacgag 540

ttccacgtgt tcggaactcc acaggtggct tctatcatca acactatgct tcttatcaga 600

agagctaaca gaggaaagag atatcttttc ctttctgcta ctccagacga gggacttctt 660

aagagacttg acaaggctgg attcagatat agatctatcg acccagtgag agagggaaag 720

tatagattcc cagacactcc agaggaggct aactctcttg ctcagcaggg atggagacag 780

gtgacttctg agatcgagct ttctttcatc ccacttccat cttctttcca gacttctgag 840

aactggctta aggagaacaa ggagagaatc cttgactatt tcaagagata tccaggatct 900

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tgctag 2166

<210> 11
<211> 3471
<212> DNA
<213> Artificial

<220>
<223> Cas10d nucleotide sequence for expression in Escherichia coli

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actgagatcg acgacgagga ccttgacttc gagttcgagg acatcgacct tgagtctctt 120

gtgtctgagg accttggaat cactgagtct gtgtctgaca gaagagtgga gactgtgaga 180

cagcttctta ctcttaagct tcttagagag gctatcagag ctgagaaccc agacgacaga 240

gtgatggctg acttcgctga gatggtgctt ccaaaccttc ttagacttgc tatcggagtg 300

actgctaagg gaggaaactt catcgaggct gtggacagag gaagagagct tagaaacaag 360

ccaaaggcta agagagacaa cgctggagat cagtctctta acactcacct tcttaacgga 420

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atcatcaagg agttcgagag aagacttgct atcgctggat tccttgtgca cgacttcgag 540

aagttctctt atgacagatt cccatctatg tctgagagat atatccagat ccagagagac 600

ttcatccagg acccattcaa gaaccaggac ccaagaaagc tttcaagaga ggagcacaga 660

gagatccttc aggtgcttat cccagagctt ggacttgaca gattcctttt cccagacaac 720

ccagagagat ggcttgagta tcttgacgac cttctttata tcgctaagaa cactcagaga 780

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gagcttaagt tcacttatca ctctatcgct gagaacagag gagtgcttac taacgtgctt 1020

aacaacgctg tgatggaggc tcaccaggag cttgactatc agccacttct ttatcttcca 1080

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gcttctgtgg ctagatctag aggagagaac cttatcaagt tccagcagca gggagtgctt 1380

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aagcttcaga agaaccttcc agctccacca gaccttgacc ttatctctga gatcgctcac 1560

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atcagagaca cttgcgagtt cctttataga cttgagatgg acaaggagag aagacagaga 3420

caggtgcagc cacttgacac ttctaactct tcttctgagg aggaggagta a 3471

<210> 12
<211> 35
<212> DNA
<213> Artificial

<220>
<223> J23108 synthesis promoter

<400> 12
ctgacagcta gctcagtcct aggtataatg ctagc 35

<210> 13
<211> 36
<212> DNA
<213> Artificial

<220>
<223> Ribosomal binding sequence

<400> 13
aataattttg tttaacttta agaaggagat atacat 36

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Terminator sequence STOP767

<400> 14
agatcctgta aaacgacggc cagt 24

<210> 15
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Terminator sequence STOP768(1)

<400> 15
cgccagggtt ttcccagtc 19

<210> 16
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Terminator sequence TOP768(2)

<400> 16
cgccagggtt ttcccagtc 19

<210> 17
<211> 47

<212> DNA
<213> Artificial

<220>
<223> T7 terminator sequence

<400> 17
tagcataacc ccttggggcc tctaaacggg tcttgagggg ttttttg 47

<210> 18
<211> 37
<212> DNA
<213> Artificial

<220>
<223> CRISPR repeat sequence

<400> 18
gttccaatta atcttaagcc ctattaggga ttgaaac 37

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

<220>
<223> T7 promoter sequence

<400> 19
taatacgact cactatagg 19

<210> 20
<211> 109
<212> DNA
<213> Artificial

<220>
<223> crRNA expression cassette

<400> 20
gttccaatta atcttaagcc ctattaggga ttgaaacggt aataatacga ctcactatag 60

ggagaaagga tcgttccaat taatcttaag ccctattagg gattgaaac 109

<210> 21
<211> 581

<212> DNA
<213> Artificial

<220>
<223> Synthesis cccdB gene expression cassette

<400> 21
aggctttaat acgactcact atagggagaa aggatccata aaggaggtaa ataatgaagc 60

agcgtattac agtgacagtt gacagcgaca gctatcagtt gctcaaggca tatatgatgt 120

caatatctcc ggtctggtaa gcacaaccat gcagaatgaa gcccgtcgtc tgcgtgccga 180

acgctggaaa gcggaaaatc aggaagggat ggctgaggtc gcccggttta ttgaaatgaa 240

cggctctttt gctgacgaga acagggactg gtgaaatgca gtttaaggtt tacacctata 300

aaagagagag ccgttatcgt ctgtttgtgg atgtacagag tgatattatt gacacgcccg 360

ggcgacggat ggtgatcccc ctggccagtg cacgtctgct gtcagataaa gtctcccgtg 420

aactttaccc ggtggtgcat atcggggatg aaagctggcg catgatgacc accgatatgg 480

ccagtgtgcc ggtctccgtt atcggggaag aagtggctga tctcagccac cgcgaaaatg 540

acatcaaaaa cgccattaac ctgatgttct ggggaatata a 581

<210> 22
<211> 18
<212> PRT
<213> Artificial

<220>
<223> Nuclear localizing signal (NLS) amino acid sequence

<400> 22

Asp Pro Lys Lys Lys Arg Lys Val Asp Pro Lys Lys Lys Arg Lys Val
1 5 10 15

Ser Gly

<210> 23
<211> 54
<212> DNA
<213> Artificial

<220>
<223> NLS nucleotide sequence

<400> 23
gacccaaaga agaagcggaa ggtagaccct aagaagaagc gcaaggtttc tgga 54

<210> 24
<211> 20
<212> PRT
<213> Artificial

<220>
<223> Self-cleaving peptide 2A amino acid sequence

<400> 24

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

Asn Pro Gly Pro
            20

<210> 25
<211> 60
<212> DNA
<213> Artificial

<220>
<223> Self-cleaving peptide 2A(1) coding sequence

<400> 25
ggctctgagg gcagaggcag cctgctgacc tgcggcgacg tggaggaaaa ccctggccct 60

<210> 26
<211> 60
<212> DNA
<213> Artificial

<220>
<223> Self-cleaving peptide 2A(2) coding sequence

<400> 26
gggtctgagg gacgcggctc cctgctcacc tgtggagatg tggaagagaa cccaggcccc 60

<210> 27
<211> 60
<212> DNA
<213> Artificial

<220>
<223> Self-cleaving peptide 2A(3) coding sequence

<400> 27
ggttctgaag gcagaggctc tctgctgaca tgtggggatg tggaggaaaa tcctggccct 60

<210> 28
<211> 60
<212> DNA
<213> Artificial

<220>
<223> Self-cleaving peptide 2A(4) coding sequence

<400> 28
ggatccgagg gcagaggaag tctgctaaca tgcggtgacg ttgaggagaa tcccgggcca 60

<210> 29
<211> 820
<212> DNA
<213> Artificial

<220>
<223> 2 x cauliflower mosaic virus 35S gene promoter + omega sequence

<400> 29
gccaacatgg tggagcacga cactctcgtc tactccaaga atatcaaaga tacagtctca 60

gaagaccaaa gggctattga gacttttcaa caaagggtaa tatcgggaaa cctcctcgga 120

ttccattgcc cagctatctg tcacttcatc aaaaggacag tagaaaagga aggtggcacc 180

tacaaatgcc atcattgcga taaaggaaag gctatcgttc aagatgcctc tgccgacagt 240

ggtcccaaag atggaccccc acccacgagg agcatcgtgg aaaaagaaga cgttccaacc 300

acgtcttcaa agcaagtgga ttgatgtgaa catggtggag cacgacactc tcgtctactc 360

caagaatatc aaagatacag tctcagaaga ccaaagggct attgagactt ttcaacaaag 420

ggtaatatcg ggaaacctcc tcggattcca ttgcccagct atctgtcact tcatcaaaag 480

gacagtagaa aaggaaggtg gcacctacaa atgccatcat tgcgataaag gaaaggctat 540

cgttcaagat gcctctgccg acagtggtcc caaagatgga cccccaccca cgaggagcat 600

cgtggaaaaa gaagacgttc caaccacgtc ttcaaagcaa gtggattgat gtgatatctc 660

cactgacgta agggatgacg cacaatccca ctatccttcg caagaccctt cctctatata 720

aggaagttca tttcatttgg agaggccggt ctagagtatt tttacaacaa ttaccaacaa 780

caacaaacaa caaacaacat tacaattact atttacaatt 820

<210> 30
<211> 447
<212> DNA
<213> Artificial

<220>
<223> Arabidopsis shock protein 18.2kDa gene terminator

<400> 30
atatgaagat gaagatgaaa tatttggtgt gtcaaataaa aagcttgtgt gcttaagttt 60

gtgtttttt cttggcttgt tgtgttatga atttgtggct ttttctaata ttaaatgaat 120

gtaagatctc attataatga ataaacaaat gtttctataa tccattgtga atgttttgtt 180

ggatctcttc tgcagcatat aactactgta tgtgctatgg tatggactat ggaatatgat 240

taaagataag atgggctcat agagtaaaac gaggcgaggg acctataaac ctcccttcat 300

catgctattt catgatctat tttataaaat aaagatgtag aaaaaagtaa gcgtaataac 360

cgcaaaacaa atgatttaaa acatggcaca taatgaggag attaagttcg gtttacgttt 420

attttagtac taattgtaac gtgagac 447

<210> 31
<211> 97
<212> DNA
<213> Artificial

<220>
<223> crRNA expression cassette

<400> 31
gttccaatta atcttaagcc ctattaggga ttgaaacgga gaccctcaat tgtcggtctc 60

gttccaatta atcttaagcc ctattaggga ttgaaac 97

<210> 32
<211> 448
<212> DNA
<213> Artificial

<220>
<223> Arabidopsis U6 snRNA-26 gene promoter sequence

<400> 32
aagcttcgtt gaacaacgga aactcgactt gccttccgca caatacatca tttcttctta 60

gctttttttc ttcttcttcg ttcatacagt tttttttgt ttatcagctt acattttctt 120

gaaccgtagc tttcgttttc ttctttttaa ctttccattc ggagtttttg tatcttgttt 180

catagtttgt cccaggatta gaatgattag gcatcgaacc ttcaagaatt tgattgaata 240

aaacatcttc attcttaaga tatgaagata atcttcaaaa ggcccctggg aatctgaaag 300

aagagaagca ggcccattta tatgggaaag aacaatagta tttcttatat aggcccattt 360

aagttgaaaa caatcttcaa aagtcccaca tcgcttagat aagaaaacga agctgagttt 420

atatacagct agagtcgaag tagtgatt 448

<210> 33
<211> 723
<212> DNA
<213> Artificial

<220>
<223> 2xNLS + Cas5d

<400> 33
gacccaaaga agaagcggaa ggtagaccct aagaagaagc gcaaggtttc tggagtgcac 60

atctattctt gccagcttga gcttcacgac tctctttatt atgctactag agagatcgga 120

agactttatg agtctgagcc agtgatccac aactatgctc tttgctatgc tcttggactt 180

gtgaactctg actcttatag atatttctgc tctgagcaga tcccacagta tcaggagcac 240

cttaacccac ttaacgagga gaagatctat gtgactccag ctagagctat cgctcacact 300

gctgtgctta acacttggaa gtatgctaac aacaactatc acgtggagat ggagaagact 360

cagaagaaca tcccatcttt cggaagagct aaggagatcg ctccagagtc tatcttcgag 420

tgcttcatca tctctcacca cccacttcag cttccaaagt ggatcagact tggaaagtgg 480

atgtctaagg ctgaggtgaa gcttactgag ctttctcttt ctaagcagaa ggaggacctt 540

ttcatctatc catatccact taacccactt gacgtgatgt tcactcacca ggttatcgga 600

tatgacgtga tcaacatgcc accagtgtct cttatcagaa acgtgagaat gagaggagag 660

tattatcaga tctctgacag accagacctt aagatcccag ctagactttc ttatcacttc 720

gga 723

<210> 34
<211> 882
<212> DNA
<213> Artificial

<220>
<223> 2xNLS + Cas6d

<400> 34
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tctcttgtgc ttaaccttac tccaagatct ccaatctatc caaacttcct tactggaaga 120

caccttcacg ctcttttcct tactcttgtg tcttctgtgg accaggagct tggaaacatc 180

cttcacactg ctgaggctga caaggctttc actctttctc cacttcagat gcagtctgga 240

ggaaagacta tcaactctcc acagtggaga cacgagagag agatcgcttc tgagactcca 300

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atcggatgcg tgggagagat ccactataga cttcttggag aggtggagcc agctaagatc 780

aaggctatca acgctcttgc tgacttcgct ctttatgctg gagtgggaag aaagactact 840

atgggaatgg gaatgactag aagaatctct aaggacaaga ga 882

<210> 35
<211> 1053
<212> DNA
<213> Artificial

<220>
<223> 2xNLS + Cas7d

<400> 35
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tatgtgcact tccttactat cagagtgact gagtcttatc cacttttcca gactgacgga 180

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aactatggac ttatcactgc tgaggagtgc gagtataacg tgaagttcgc tatgaacaac 360

gctgactgca tcatctatgg attcgctatc ggagactctg gatctgagaa gtctaaggtg 420

gtggtggaca ctgctttctc tatcactcca ttcgacgagt ctcacgagtc tttcactctt 480

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atcgtgactc ttaaggaccc aactgaggct tctttccttt atgtgttcaa caacatcctt 660

agaactagac actatggtgc tcagactact agaactggaa gagtgagaaa cgagcttatc 720

ggagtgatct tcgctgacgg agagatcgtg tctaacctta gatggactca ggctatctat 780

gacagacttc cagacgaggt gcttcactct atcgacccac ttgacgagga ccttgtgatg 840

gagaaggcta ctgaggctat ccaggctctt atggctgagg agttcatcgt gcacactgac 900

ttcatcggag agaacttcca gccacttctt actgaggtga agactcttac tggaactgag 960

gctggaatcc tttctgtgct tgaccaggct aacaaggagt ctaagaagta tttcgagcag 1020

tatatcgaga agaagaaggc tgagaagaag taa 1053

<210> 36
<211> 2217
<212> DNA
<213> Artificial

<220>
<223> 2xNLS + Cas3d

<400> 36
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aactatcagg tgactcttaa gccagtgtat tcttgcccag ctgacgagat cccagacgga 120

atcaaggtgc cacagggatg gagactttct tggcaccagg tggagacttg gaaggctctt 180

aacgacccag acatcgacgt gatcttcaac actgctatga ctggagacgg aaagtctctt 240

gctgcttatc ttagaactct tcagggatat ttcccaatca tgggacttta tccaactaac 300

gagcttgcta gagatcagag aggacagatc gaggcttata tccagagatt ccagccaact 360

gaccagccaa gagtgaacct tcttactgga ccagagcttg agctttatgc tgagagagac 420

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aacccagaca tcttccacta tcttcacaga gctgcttatc ttactccata tgacaaccca 540

gaccagcttt ggaacagaat cgacaagcac ttcgaccttt tccttttcga cgagttccac 600

gtgttcggaa ctccacaggt ggcttctatc atcaacacta tgcttcttat cagaagagct 660

aacagaggaa agagatatct tttcctttct gctactccag acgagggact tcttaagaga 720

cttgacaagg ctggattcag atatagatct atcgacccag tgagagaggg aaagtataga 780

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cttaaggaga acaaggagag aatccttgac tatttcaaga gatatccagg atctaaggga 960

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<210> 40
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<213> Solanum lycopersicum

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<210> 41
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<223> Cytomegalovirus enhancer + universal chicken beta-actin gene hybrid promoter

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gcaaggggga ggattgggaa gagaatagca ggcatgctgg gga 223

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<211> 249
<212> DNA
<213> Artificial

<220>
<223> Human U6 snRNA gene promoter

<400> 43
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aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat ggactatcat 180

atgcttaccg taacttgaaa gtatttcgat ttcttggctt tatatatctt gtggaaagga 240

cgaaacacc 249

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<212> DNA
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<210> 45
<211> 35
<212> DNA
<213> Homo sapiens

<400> 45
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