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(19) AUSTRALIAN PATENT OFFICE

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Base editing of ANGPTL3 and methods of using same for treatment of disease

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C12N 15/11 (2006.01) ***C12N 15/00*** (2006.01)
A61K 48/00 (2006.01) ***C12N 15/82*** (2006.01)
C07H 21/04 (2006.01)

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A61K 48/00 (2006.01) *C07H 21/04* (2006.01)
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63/007,797	09 April 2020 (09.04.2020)	US
63/045,032	26 June 2020 (26.06.2020)	US
63/045,033	26 June 2020 (26.06.2020)	US
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(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH,

(54) Title: BASE EDITING OF ANGPTL3 AND METHODS OF USING SAME FOR TREATMENT OF DISEASE

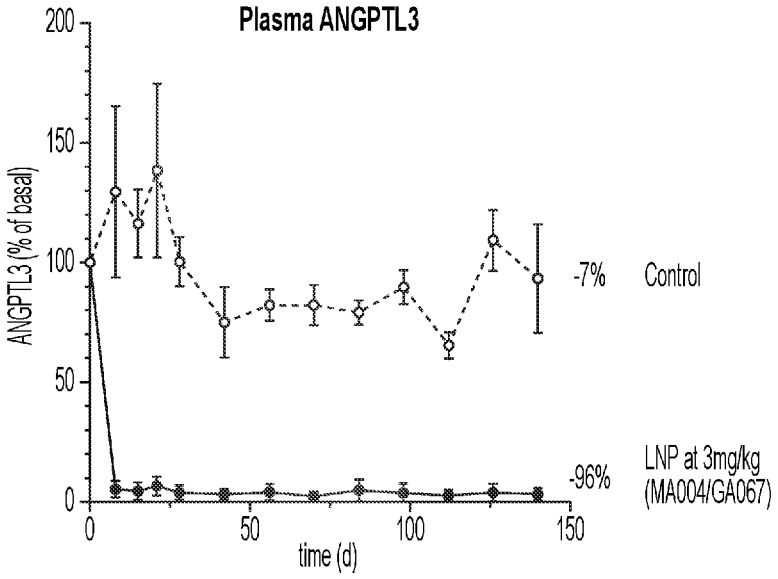


FIG. 49A

(57) Abstract: Provided herein are compositions for gene modification or editing and methods of using same to treat or prevent certain conditions. Specific compositions and methods capable of safely and effectively editing gene targets expressed in the liver to durably lower LDL-C thereby treating a leading cause of cardiovascular disease are disclosed.

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[Continued on next page]

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Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

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SEQUENCE LISTING

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Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His
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Glu Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile
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Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys
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```

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Ile Val  Pro Gln Ser Phe Leu  Lys Asp Asp Ser Ile  Asp Asn Lys
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Pro Ser  Glu Glu Val Val Lys  Lys Met Lys Asn Tyr  Trp Arg Gln
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Thr Lys  Ala Glu Arg Gly Gly  Leu Ser Glu Leu Asp  Lys Ala Gly
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Asn Asp  Lys Leu Ile Arg Glu  Val Lys Val Ile Thr  Leu Lys Ser
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Lys Leu  Val Ser Asp Phe Arg  Lys Asp Phe Gln Phe  Tyr Lys Val
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taaagtcact gtctatttaa gattaaacat acaatcacat aaccttaaag aataccgttt 12480

acatttctca atcaaaattc ttataatact atttgtttta aattttgtga tgtgggaatc 12540

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ctggtaattg tacagttctt aaatgttgta gtattaattt caaaactaaa aatcgtcagc 12780

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gaaaggagct ctttatggtt cacacgactg tctcctgtcc taactacttt gcttaaagtg 13980

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cacagaagcc tggaacccgg aagacatctc tggcttttca ctcaactttg taaactacct 14880

cttttgtatc ataagccacc aagttcaata caatcttctc ttgaaacgtc tcttaatctt 14940

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<210> 8
<211> 460
<212> PRT
<213> Homo sapiens

<400> 8
Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser
1 5 10 15

Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu
20 25 30

Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn
35 40 45

Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr
50 55 60

Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln
65 70 75 80

Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu
85 90 95

Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu
100 105 110

Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu
115 120 125

Glu Glu Lys Ile Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln
130 135 140

Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu
145 150 155 160

Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys
165 170 175

Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln
180 185 190

His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile
195 200 205

Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg
210 215 220

```
Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp
225                 230                 235                 240

Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr
                245                 250                 255

Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val
            260                 265                 270

Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg
        275                 280                 285

Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr
    290                 295                 300

Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile
305                 310                 315                 320

Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu
                325                 330                 335

Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly
            340                 345                 350

Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
        355                 360                 365

Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
    370                 375                 380

Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
385                 390                 395                 400

Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
                405                 410                 415

Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
            420                 425                 430

Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
        435                 440                 445

Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
    450                 455                 460


<210> 9
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide
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<400> 9
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 10
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 10
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaacaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 11
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 11
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 12
<211> 101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 12
ccgcaccuug gcgcagcggu uuuagagcua gaaauagcaa guuaaaauaa ggcuaguccg 60

uuaucaacuu gaaaaagugg caccgagucg gugcuuuuuu u 101

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 13
cccgcacctt ggcgcagcgg 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
aagatacctg aataactctc 20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
aagatacctg aataaccctc 20

<210> 16
<211> 84
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Bacillus phage PBS2 sequence

<400> 16
Met Thr Asn Leu Ser Asp Ile Ile Glu Lys Glu Thr Gly Lys Gln Leu
1 5 10 15

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

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

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

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

Ile Lys Met Leu

<210> 17
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 17
Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser
1 5 10 15

<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 18
Ser Gly Gly Ser
1

<210> 19
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 19
Ser Gly Gly Ser Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
1 5 10 15

Thr Pro Glu Ser Ser Gly Gly Ser
20

<210> 20
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 20
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Ser Glu Thr Pro Gly Thr
1 5 10 15

Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly Gly Ser Ser Gly Gly Ser
20 25 30

<210> 21
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 21
Gly Gly Ser Gly Gly Ser Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
1 5 10 15

Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
20 25 30

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly

35 40 45

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
50 55 60

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
65 70 75 80

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
85 90 95

Thr Ser Gly Gly Ser Gly Gly Ser
100

<210> 22
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 22
Gly Gly Gly Gly Ser
1 5

<210> 23
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 23
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Ser Glu Thr Pro Gly Thr
1 5 10 15

Ser Glu Ser Ala Thr Pro Glu Ser
20

<210> 24
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 24
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Ser Glu Thr Pro Gly Thr
1 5 10 15

Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly Gly Ser Ser Gly Gly Ser
20 25 30

Ser Gly Gly Ser Ser Gly Gly Ser
        35   40

<210> 25
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 25
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Ser Glu Thr Pro Gly Thr
1   5   10   15

Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly Gly Ser Ser Gly Gly Ser
            20   25   30

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Ser Glu Thr Pro Gly Thr
        35   40   45

Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly Gly Ser Ser Gly Gly Ser
    50   55   60

<210> 26
<211> 92
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 26
Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser
1   5   10   15

Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser
            20   25   30

Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu
        35   40   45

Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser
    50   55   60

Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr
65   70   75   80

Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser
                85   90

<210> 27
<211> 7
<212> PRT
<213> Macaca mulatta polyomavirus 1

<400> 27
Pro Lys Lys Lys Arg Lys Val
1   5

<210> 28
<211> 30
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      NLS sequence

<400> 28
Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
1   5   10   15

Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys
            20   25   30

<210> 29
<211> 36
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      Zn -coordinating motif sequence

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (4)..(29)
<223> Any amino acid

<220>
<221> SITE
<222> (4)..(29)
<223> This sequence may encompass 23-26 residues

<220>
<221> MOD_RES
<222> (32)..(35)
<223> Any amino acid

<220>
<221> SITE
<222> (32)..(35)
<223> This sequence may encompass 2-4 residues

<400> 29
His Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Xaa
            20   25   30

Xaa Xaa Xaa Cys
        35

<210> 30
<211> 160
<212> PRT
<213> Staphylococcus aureus

<400> 30
Met Gly Ser His Met Thr Asn Asp Ile Tyr Phe Met Thr Leu Ala Ile
1   5   10   15

Glu Glu Ala Lys Lys Ala Ala Gln Leu Gly Glu Val Pro Ile Gly Ala
            20   25   30

Ile Ile Thr Lys Asp Asp Glu Val Ile Ala Arg Ala His Asn Leu Arg
        35   40   45

Glu Thr Leu Gln Gln Pro Thr Ala His Ala Glu His Ile Ala Ile Glu
    50   55   60

Arg Ala Ala Lys Val Leu Gly Ser Trp Arg Leu Glu Gly Cys Thr Leu
65   70   75   80

Tyr Val Thr Leu Glu Pro Cys Val Met Cys Ala Gly Thr Ile Val Met
                85   90   95

Ser Arg Ile Pro Arg Val Val Tyr Gly Ala Asp Asp Pro Lys Gly Gly
            100   105   110

Cys Ser Gly Ser Leu Met Asn Leu Leu Gln Gln Ser Asn Phe Asn His
        115   120   125

Arg Ala Ile Val Asp Lys Gly Val Leu Lys Glu Ala Cys Ser Thr Leu
    130   135   140

Leu Thr Thr Phe Phe Lys Asn Leu Arg Ala Asn Lys Lys Ser Thr Asn
145   150   155   160

<210> 31
<211> 161
<212> PRT
<213> Bacillus subtilis

<400> 31
Met Thr Gln Asp Glu Leu Tyr Met Lys Glu Ala Ile Lys Glu Ala Lys
1   5   10   15

Lys Ala Glu Glu Lys Gly Glu Val Pro Ile Gly Ala Val Leu Val Ile
            20   25   30

Asn Gly Glu Ile Ile Ala Arg Ala His Asn Leu Arg Glu Thr Glu Gln
        35   40   45

Arg Ser Ile Ala His Ala Glu Met Leu Val Ile Asp Glu Ala Cys Lys
    50   55   60

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Ala Leu Gly Thr Trp Arg Leu Glu Gly Ala Thr Leu Tyr Val Thr Leu
65                  70                  75                  80

Glu Pro Cys Pro Met Cys Ala Gly Ala Val Val Leu Ser Arg Val Glu
                85                  90                  95

Lys Val Val Phe Gly Ala Phe Asp Pro Lys Gly Gly Cys Ser Gly Thr
            100                 105                 110

Leu Met Asn Leu Leu Gln Glu Glu Arg Phe Asn His Gln Ala Glu Val
        115                 120                 125

Val Ser Gly Val Leu Glu Glu Glu Cys Gly Gly Met Leu Ser Ala Phe
    130                 135                 140

Phe Arg Glu Leu Arg Lys Lys Lys Lys Ala Ala Arg Lys Asn Leu Ser
145                 150                 155                 160

Glu
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<210> 32
<211> 183
<212> PRT
<213> Salmonella typhimurium

<400> 32

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Met Pro Pro Ala Phe Ile Thr Gly Val Thr Ser Leu Ser Asp Val Glu
1               5                   10                  15

Leu Asp His Glu Tyr Trp Met Arg His Ala Leu Thr Leu Ala Lys Arg
            20                  25                  30

Ala Trp Asp Glu Arg Glu Val Pro Val Gly Ala Val Leu Val His Asn
        35                  40                  45

His Arg Val Ile Gly Glu Gly Trp Asn Arg Pro Ile Gly Arg His Asp
    50                  55                  60

Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg Gln Gly Gly Leu Val
65                  70                  75                  80

Leu Gln Asn Tyr Arg Leu Leu Asp Thr Thr Leu Tyr Val Thr Leu Glu
                85                  90                  95

Pro Cys Val Met Cys Ala Gly Ala Met Val His Ser Arg Ile Gly Arg
            100                 105                 110

Val Val Phe Gly Ala Arg Asp Ala Lys Thr Gly Ala Ala Gly Ser Leu
        115                 120                 125

Ile Asp Val Leu His His Pro Gly Met Asn His Arg Val Glu Ile Ile
    130                 135                 140
```

```
Glu Gly Val Leu Arg Asp Glu Cys Ala Thr Leu Leu Ser Asp Phe Phe
145                 150                 155                 160


Arg Met Arg Arg Gln Glu Ile Lys Ala Leu Lys Lys Ala Asp Arg Ala
                165                 170                 175


Glu Gly Ala Gly Pro Ala Val
            180


<210> 33
<211> 164
<212> PRT
<213> Shewanella putrefaciens

<400> 33
Met Asp Glu Tyr Trp Met Gln Val Ala Met Gln Met Ala Glu Lys Ala
1               5                   10                  15


Glu Ala Ala Gly Glu Val Pro Val Gly Ala Val Leu Val Lys Asp Gly
            20                  25                  30


Gln Gln Ile Ala Thr Gly Tyr Asn Leu Ser Ile Ser Gln His Asp Pro
        35                  40                  45


Thr Ala His Ala Glu Ile Leu Cys Leu Arg Ser Ala Gly Lys Lys Leu
    50                  55                  60


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


Cys Ala Met Cys Ala Gly Ala Met Val His Ser Arg Ile Ala Arg Val
                85                  90                  95


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


Asn Leu Leu Gln His Pro Ala Phe Asn His Gln Val Glu Val Thr Ser
        115                 120                 125


Gly Val Leu Ala Glu Ala Cys Ser Ala Gln Leu Ser Arg Phe Phe Lys
    130                 135                 140


Arg Arg Arg Asp Glu Lys Lys Ala Leu Lys Leu Ala Gln Arg Ala Gln
145                 150                 155                 160


Gln Gly Ile Glu



<210> 34
<211> 173
<212> PRT
<213> Haemophilus influenzae
```

<400> 34
Met Asp Ala Ala Lys Val Arg Ser Glu Phe Asp Glu Lys Met Met Arg
1   5   10   15

Tyr Ala Leu Glu Leu Ala Asp Lys Ala Glu Ala Leu Gly Glu Ile Pro
            20   25   30

Val Gly Ala Val Leu Val Asp Asp Ala Arg Asn Ile Ile Gly Glu Gly
        35   40   45

Trp Asn Leu Ser Ile Val Gln Ser Asp Pro Thr Ala His Ala Glu Ile
    50   55   60

Ile Ala Leu Arg Asn Gly Ala Lys Asn Ile Gln Asn Tyr Arg Leu Leu
65   70   75   80

Asn Ser Thr Leu Tyr Val Thr Leu Glu Pro Cys Thr Met Cys Ala Gly
                85   90   95

Ala Ile Leu His Ser Arg Ile Lys Arg Leu Val Phe Gly Ala Ser Asp
            100   105   110

Tyr Lys Thr Gly Ala Ile Gly Ser Arg Phe His Phe Phe Asp Asp Tyr
        115   120   125

Lys Met Asn His Thr Leu Glu Ile Thr Ser Gly Val Leu Ala Glu Glu
    130   135   140

Cys Ser Gln Lys Leu Ser Thr Phe Phe Gln Lys Arg Arg Glu Glu Lys
145   150   155   160

Lys Ile Glu Lys Ala Leu Leu Lys Ser Leu Ser Asp Lys
                165   170

<210> 35
<211> 161
<212> PRT
<213> Caulobacter crescentus

<400> 35
Met Arg Thr Asp Glu Ser Glu Asp Gln Asp His Arg Met Met Arg Leu
1   5   10   15

Ala Leu Asp Ala Ala Arg Ala Ala Ala Glu Ala Gly Glu Thr Pro Val
            20   25   30

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

Gly Asn Gly Pro Ile Ala Ala His Asp Pro Thr Ala His Ala Glu Ile
    50   55   60

Ala Ala Met Arg Ala Ala Ala Ala Lys Leu Gly Asn Tyr Arg Leu Thr
65   70   75   80

```
Asp Leu Thr Leu Val Val Thr Leu Glu Pro Cys Ala Met Cys Ala Gly
                85                  90                  95

Ala Ile Ser His Ala Arg Ile Gly Arg Val Val Phe Gly Ala Asp Asp
            100                 105                 110

Pro Lys Gly Gly Ala Val Val His Gly Pro Lys Phe Phe Ala Gln Pro
        115                 120                 125

Thr Cys His Trp Arg Pro Glu Val Thr Gly Gly Val Leu Ala Asp Glu
    130                 135                 140

Ser Ala Asp Leu Leu Arg Gly Phe Phe Arg Ala Arg Arg Lys Ala Lys
145                 150                 155                 160

Ile
```

<210> 36
<211> 179
<212> PRT
<213> Geobacter sulfurreducens

<400> 36

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Met Ser Ser Leu Lys Lys Thr Pro Ile Arg Asp Asp Ala Tyr Trp Met
1               5                   10                  15

Gly Lys Ala Ile Arg Glu Ala Ala Lys Ala Ala Ala Arg Asp Glu Val
            20                  25                  30

Pro Ile Gly Ala Val Ile Val Arg Asp Gly Ala Val Ile Gly Arg Gly
        35                  40                  45

His Asn Leu Arg Glu Gly Ser Asn Asp Pro Ser Ala His Ala Glu Met
    50                  55                  60

Ile Ala Ile Arg Gln Ala Ala Arg Arg Ser Ala Asn Trp Arg Leu Thr
65                  70                  75                  80

Gly Ala Thr Leu Tyr Val Thr Leu Glu Pro Cys Leu Met Cys Met Gly
                85                  90                  95

Ala Ile Ile Leu Ala Arg Leu Glu Arg Val Val Phe Gly Cys Tyr Asp
            100                 105                 110

Pro Lys Gly Gly Ala Ala Gly Ser Leu Tyr Asp Leu Ser Ala Asp Pro
        115                 120                 125

Arg Leu Asn His Gln Val Arg Leu Ser Pro Gly Val Cys Gln Glu Glu
    130                 135                 140

Cys Gly Thr Met Leu Ser Asp Phe Phe Arg Asp Leu Arg Arg Arg Lys
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145 150 155 160

Lys Ala Lys Ala Thr Pro Ala Leu Phe Ile Asp Glu Arg Lys Val Pro
165 170 175

Pro Glu Pro

<210> 37
<211> 4107
<212> DNA
<213> Streptococcus pyogenes

<400> 37
atggataaga aatactcaat aggcttagat atcggcacaa atagcgtcgg atgggcggtg 60

atcactgatg aatataaggt tccgtctaaa aagttcaagg ttctgggaaa tacagaccgc 120

cacagtatca aaaaaaatct tataggggct cttttatttg acagtggaga gacagcggaa 180

gcgactcgtc tcaaacggac agctcgtaga aggtatacac gtcggaagaa tcgtatttgt 240

tatctacagg agatttttc aaatgagatg gcgaaagtag atgatagttt ctttcatcga 300

cttgaagagt ctttttggt ggaagaagac aagaagcatg aacgtcatcc tatttttgga 360

aatatagtag atgaagttgc ttatcatgag aaatatccaa ctatctatca tctgcgaaaa 420

aaattggtag attctactga taaagcggat ttgcgcttaa tctatttggc cttagcgcat 480

atgattaagt ttcgtggtca ttttttgatt gagggagatt taaatcctga taatagtgat 540

gtggacaaac tatttatcca gttggtacaa acctacaatc aattatttga agaaaaccct 600

attaacgcaa gtggagtaga tgctaaagcg attctttctg cacgattgag taaatcaaga 660

cgattagaaa atctcattgc tcagctcccc ggtgagaaga aaaatggctt atttgggaat 720

ctcattgctt tgtcattggg tttgacccct aattttaaat caaattttga tttggcagaa 780

gatgctaaat tacagctttc aaaagatact tacgatgatg atttagataa tttattggcg 840

caaattggag atcaatatgc tgatttgttt ttggcagcta agaatttatc agatgctatt 900

ttactttcag atatcctaag agtaaatact gaaataacta aggctcccct atcagcttca 960

atgattaaac gctacgatga acatcatcaa gacttgactc ttttaaaagc tttagttcga 1020

caacaacttc cagaaaagta taaagaaatc ttttttgatc aatcaaaaaa cggatatgca 1080

ggttatattg atgggggagc tagccaagaa gaattttata aatttatcaa accaatttta 1140

gaaaaaatgg atggtactga ggaattattg gtgaaactaa atcgtgaaga tttgctgcgc 1200

aagcaacgga cctttgacaa cggctctatt ccccatcaaa ttcacttggg tgagctgcat 1260

gctattttga gaagacaaga agacttttat ccatttttaa aagacaatcg tgagaagatt 1320

gaaaaaatct tgacttttcg aattccttat tatgttggtc cattggcgcg tggcaatagt 1380

cgttttgcat ggatgactcg gaagtctgaa gaaacaatta ccccatggaa ttttgaagaa 1440

gttgtcgata aaggtgcttc agctcaatca tttattgaac gcatgacaaa ctttgataaa 1500

aatcttccaa atgaaaaagt actaccaaaa catagtttgc tttatgagta ttttacggtt 1560

tataacgaat tgacaaaggt caaatatgtt actgaaggaa tgcgaaaacc agcatttctt 1620

tcaggtgaac agaagaaagc cattgttgat ttactcttca aaacaaatcg aaaagtaacc 1680

gttaagcaat taaaagaaga ttatttcaaa aaaatagaat gttttgatag tgttgaaatt 1740

tcaggagttg aagatagatt taatgcttca ttaggtacct accatgattt gctaaaaatt 1800

attaaagata aagatttttt ggataatgaa gaaaatgaag atatcttaga ggatattgtt 1860

ttaacattga ccttatttga agatagggag atgattgagg aaagacttaa aacatatgct 1920

cacctctttg atgataaggt gatgaaacag cttaaacgtc gccgttatac tggttgggga 1980

cgtttgtctc gaaaattgat taatggtatt agggataagc aatctggcaa aacaatatta 2040

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agtttgacat ttaaagaaga cattcaaaaa gcacaagtgt ctggacaagg cgatagttta 2160

catgaacata ttgcaaattt agctggtagc cctgctatta aaaaaggtat tttacagact 2220

gtaaaagttg ttgatgaatt ggtcaaagta atggggcggc ataagccaga aaatatcgtt 2280

attgaaatgg cacgtgaaaa tcagacaact caaaagggcc agaaaaattc gcgagagcgt 2340

atgaaacgaa tcgaagaagg tatcaaagaa ttaggaagtc agattcttaa agagcatcct 2400

gttgaaaata ctcaattgca aaatgaaaag ctctatctct attatctcca aaatggaaga 2460

gacatgtatg tggaccaaga attagatatt aatcgtttaa gtgattatga tgtcgatcac 2520

attgttccac aaagtttcct taaagacgat tcaatagaca ataaggtctt aacgcgttct 2580

gataaaaatc gtggtaaatc ggataacgtt ccaagtgaag aagtagtcaa aaagatgaaa 2640

aactattgga gacaacttct aaacgccaag ttaatcactc aacgtaagtt tgataattta 2700

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actaaatacg atgaaaatga taaacttatt cgagaggtta aagtgattac cttaaaatct 2880

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taccatcatg cccatgatgc gtatctaaat gccgtcgttg gaactgcttt gattaagaaa 3000

tatccaaaac ttgaatcgga gtttgtctat ggtgattata aagtttatga tgttcgtaaa 3060

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cctctaatcg aaactaatgg ggaaactgga gaaattgtct gggataaagg gcgagatttt 3240

gccacagtgc gcaaagtatt gtccatgccc caagtcaata ttgtcaagaa aacagaagta 3300

cagacaggcg gattctccaa ggagtcaatt ttaccaaaaa gaaattcgga caagcttatt 3360

gctcgtaaaa aagactggga tccaaaaaaa tatggtggtt ttgatagtcc aacggtagct 3420

tattcagtcc tagtggttgc taaggtggaa aaagggaaat cgaagaagtt aaaatccgtt 3480

aaagagttac tagggatcac aattatggaa agaagttcct ttgaaaaaaa tccgattgac 3540

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tatagtcttt ttgagttaga aaacggtcgt aaacggatgc tggctagtgc cggagaatta 3660

caaaaaggaa atgagctggc tctgccaagc aaatatgtga atttttttata tttagctagt 3720

cattatgaaa agttgaaggg tagtccagaa gataacgaac aaaaacaatt gtttgtggag 3780

cagcataagc attatttaga tgagattatt gagcaaatca gtgaattttc taagcgtgtt 3840

attttagcag atgccaattt agataaagtt cttagtgcat ataacaaaca tagagacaaa 3900

ccaatacgtg aacaagcaga aaatattatt catttattta cgttgacgaa tcttggagct 3960

cccgctgctt ttaaatattt tgatacaaca attgatcgta aacgatatac gtctacaaaa 4020

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<210> 38
<211> 1368
<212> PRT
<213> Streptococcus pyogenes

<400> 38
Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
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Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
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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
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```
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
```

<210> 39
<211> 1368
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39

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Met Asp Lys Lys Tyr Ser Ile Gly Leu Ala 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 Ala 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


<210> 40
<211> 1367
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 40
Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn Ser Val Gly
1               5                  10                  15


Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe Lys
            20                  25                  30


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


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


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

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

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

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

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

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

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

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

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

Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
    210                 215                 220

Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
225                 230                 235                 240

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

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

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

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

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

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

Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe Asp
            340                 345                 350
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Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser Gln
        355                 360                 365

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala His
```

625 630 635 640

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

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

Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
675 680 685

Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
690 695 700

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

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

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

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

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

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

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

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

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

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

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

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

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

```
Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925

His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
    930                 935                 940

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Lys  Glu Leu Leu Gly Ile  Thr Ile Met Glu Arg  Ser Ser Phe
    1160                1165                1170
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Glu Lys  Asn Pro Ile Asp Phe  Leu Glu Ala Lys Gly  Tyr Lys Glu
    1175                1180                1185


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


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


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


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


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


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


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


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


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


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


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


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


<210> 41
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide


<220>
<221> SITE
<222> (1)..(120)
<223> This sequence may encompass 1-30 "Ser Gly Gly Ser"
      repeating units
```

<400> 41
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
1   5   10   15

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
            20   25   30

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
        35   40   45

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
    50   55   60

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
65   70   75   80

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
                85   90   95

Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Gly Ser
            100   105   110

Ser Gly Gly Ser Ser Gly Gly Ser
        115   120

<210> 42
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<221> SITE
<222> (1)..(120)
<223> This sequence may encompass 1-30 "Gly Gly Gly Ser"
      repeating units

<400> 42
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1   5   10   15

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
            20   25   30

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
        35   40   45

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
    50   55   60

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
65   70   75   80

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
85 90 95

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
100 105 110

Gly Gly Gly Ser Gly Gly Gly Ser
115 120

<210> 43
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<220>
<221> SITE
<222> (1)..(150)
<223> This sequence may encompass 1-30 "Gly Gly Gly Gly Ser" repeating units

<400> 43
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
35 40 45

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
50 55 60

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
65 70 75 80

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
85 90 95

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
100 105 110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
130 135 140

Ser Gly Gly Gly Gly Ser
145 150

<210> 44
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> SITE
<222> (1)..(30)
<223> This sequence may encompass 1-30 residues

<400> 44
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
20 25 30

<210> 45
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<220>
<221> SITE
<222> (1)..(150)
<223> This sequence may encompass 1-30 "Glu Ala Ala Ala Lys"
repeating units

<400> 45
Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
1 5 10 15

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala
20 25 30

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala
35 40 45

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
50 55 60

Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
65 70 75 80

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
85 90 95

Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala
100 105 110

Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala
        115   120   125

Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala
    130   135   140

Lys Glu Ala Ala Ala Lys
145   150

<210> 46
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<221> SITE
<222> (1)..(90)
<223> This sequence may encompass 1-30 "Gly Gly Ser"
      repeating units

<400> 46
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1   5   10   15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
            20   25   30

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
        35   40   45

Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
    50   55   60

Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
65   70   75   80

Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser
                85   90

<210> 47
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (11)..(11)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (15)..(15)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (17)..(17)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (19)..(19)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (21)..(21)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (23)..(23)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (25)..(25)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (27)..(27)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (29)..(29)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (31)..(31)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (33)..(33)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (35)..(35)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (37)..(37)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (39)..(39)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (41)..(41)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (43)..(43)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (45)..(45)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (47)..(47)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (49)..(49)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (51)..(51)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (53)..(53)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (55)..(55)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (57)..(57)

<223> Any amino acid

<220>
<221> MOD_RES
<222> (59)..(59)
<223> Any amino acid

<220>
<221> SITE
<222> (1)..(60)
<223> This sequence may encompass 1-30 "Xaa Pro"
repeating units

<400> 47
Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
1 5 10 15

Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
20 25 30

Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
35 40 45

Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
50 55 60

<210> 48
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 48
Glu Ala Ala Ala Lys
1 5

<210> 49
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 49
Ser Gly Gly Ser
1

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 50
gccaatggcc tccttcagtt 20

<210> 51
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(21)
<223> This sequence may encompass 1, 3 or 7 "Gly Gly Ser"
repeating units

<400> 51
Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly
1 5 10 15

Gly Ser Gly Gly Ser
20

<210> 52
<211> 1052
<212> PRT
<213> Staphylococcus aureus

<400> 52
Lys Arg Asn Tyr Ile Leu Gly Leu Asp Ile Gly Ile Thr Ser Val Gly
1 5 10 15

Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly Val
20 25 30

Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg Ser
35 40 45

Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile Gln
50 55 60

Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His Ser
65 70 75 80

Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu Ser
85 90 95

Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu Ala
100 105 110

Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr Gly
115 120 125

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

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Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu Glu Arg Leu Lys Lys Asp
145                 150                 155                 160

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

Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln Leu
            180                 185                 190

Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg Arg
        195                 200                 205

Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys Asp
    210                 215                 220

Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe Pro
225                 230                 235                 240

Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr Asn
                245                 250                 255

Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn Glu
            260                 265                 270

Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe Lys
        275                 280                 285

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

Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys Pro
305                 310                 315                 320

Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr Ala
                325                 330                 335

Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala Lys
            340                 345                 350

Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu Thr
        355                 360                 365

Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser Asn
    370                 375                 380

Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile Asn
385                 390                 395                 400

Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala Ile
                405                 410                 415

Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln Gln
```

```
            420                 425                 430

Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro Val
        435                 440                 445

Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile Ile
    450                 455                 460

Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg Glu
465                 470                 475                 480

Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys Arg
                485                 490                 495

Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr Gly
            500                 505                 510

Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp Met
        515                 520                 525

Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu Asp
    530                 535                 540

Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro Arg
545                 550                 555                 560

Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys Gln
                565                 570                 575

Glu Glu Asn Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu Ser
            580                 585                 590

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

Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu Tyr
    610                 615                 620

Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp Phe
625                 630                 635                 640

Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu Met
                645                 650                 655

Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys Val
            660                 665                 670

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

Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp Ala
    690                 695                 700
```

```
Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys Leu
705                 710                 715                 720

Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys Gln
                725                 730                 735

Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu Ile
            740                 745                 750

Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp Tyr
        755                 760                 765

Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile Asn
    770                 775                 780

Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu Ile
785                 790                 795                 800

Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu Lys
                805                 810                 815

Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His Asp
            820                 825                 830

Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly Asp
        835                 840                 845

Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr Leu
    850                 855                 860

Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile Lys
865                 870                 875                 880

Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp Tyr
                885                 890                 895

Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr Arg
            900                 905                 910

Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val Lys
        915                 920                 925

Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser Lys
    930                 935                 940

Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala Glu
945                 950                 955                 960

Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly Glu
                965                 970                 975
```

```
Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile Glu
            980                 985                 990


Val Asn Met Ile Asp Ile Thr Tyr  Arg Glu Tyr Leu Glu  Asn Met Asn
        995                 1000                1005


Asp Lys  Arg Pro Pro Arg Ile  Ile Lys Thr Ile Ala  Ser Lys Thr
    1010                1015                1020


Gln Ser  Ile Lys Lys Tyr Ser  Thr Asp Ile Leu Gly  Asn Leu Tyr
    1025                1030                1035


Glu Val  Lys Ser Lys Lys His  Pro Gln Ile Ile Lys  Lys Gly
    1040                1045                1050


<210> 53
<211> 1300
<212> PRT
<213> Francisella sp.

<400> 53
Met Ser Ile Tyr Gln Glu Phe Val Asn Lys Tyr Ser Leu Ser Lys Thr
1               5                   10                  15


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


Ala Arg Gly Leu Ile Leu Asp Asp Glu Lys Arg Ala Lys Asp Tyr Lys
        35                  40                  45


Lys Ala Lys Gln Ile Ile Asp Lys Tyr His Gln Phe Phe Ile Glu Glu
    50                  55                  60


Ile Leu Ser Ser Val Cys Ile Ser Glu Asp Leu Leu Gln Asn Tyr Ser
65                  70                  75                  80


Asp Val Tyr Phe Lys Leu Lys Lys Ser Asp Asp Asp Asn Leu Gln Lys
                85                  90                  95


Asp Phe Lys Ser Ala Lys Asp Thr Ile Lys Lys Gln Ile Ser Glu Tyr
            100                 105                 110


Ile Lys Asp Ser Glu Lys Phe Lys Asn Leu Phe Asn Gln Asn Leu Ile
        115                 120                 125


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


Ser Lys Asp Asn Gly Ile Glu Leu Phe Lys Ala Asn Ser Asp Ile Thr
145                 150                 155                 160


Asp Ile Asp Glu Ala Leu Glu Ile Ile Lys Ser Phe Lys Gly Trp Thr
                165                 170                 175
```

```
Thr Tyr Phe Lys Gly Phe His Glu Asn Arg Lys Asn Val Tyr Ser Ser
            180                 185                 190

Asn Asp Ile Pro Thr Ser Ile Ile Tyr Arg Ile Val Asp Asp Asn Leu
        195                 200                 205

Pro Lys Phe Leu Glu Asn Lys Ala Lys Tyr Glu Ser Leu Lys Asp Lys
    210                 215                 220

Ala Pro Glu Ala Ile Asn Tyr Glu Gln Ile Lys Lys Asp Leu Ala Glu
225                 230                 235                 240

Glu Leu Thr Phe Asp Ile Asp Tyr Lys Thr Ser Glu Val Asn Gln Arg
                245                 250                 255

Val Phe Ser Leu Asp Glu Val Phe Glu Ile Ala Asn Phe Asn Asn Tyr
            260                 265                 270

Leu Asn Gln Ser Gly Ile Thr Lys Phe Asn Thr Ile Ile Gly Gly Lys
        275                 280                 285

Phe Val Asn Gly Glu Asn Thr Lys Arg Lys Gly Ile Asn Glu Tyr Ile
    290                 295                 300

Asn Leu Tyr Ser Gln Gln Ile Asn Asp Lys Thr Leu Lys Lys Tyr Lys
305                 310                 315                 320

Met Ser Val Leu Phe Lys Gln Ile Leu Ser Asp Thr Glu Ser Lys Ser
                325                 330                 335

Phe Val Ile Asp Lys Leu Glu Asp Asp Ser Asp Val Val Thr Thr Met
            340                 345                 350

Gln Ser Phe Tyr Glu Gln Ile Ala Ala Phe Lys Thr Val Glu Glu Lys
        355                 360                 365

Ser Ile Lys Glu Thr Leu Ser Leu Leu Phe Asp Asp Leu Lys Ala Gln
    370                 375                 380

Lys Leu Asp Leu Ser Lys Ile Tyr Phe Lys Asn Asp Lys Ser Leu Thr
385                 390                 395                 400

Asp Leu Ser Gln Gln Val Phe Asp Asp Tyr Ser Val Ile Gly Thr Ala
                405                 410                 415

Val Leu Glu Tyr Ile Thr Gln Gln Ile Ala Pro Lys Asn Leu Asp Asn
            420                 425                 430

Pro Ser Lys Lys Glu Gln Glu Leu Ile Ala Lys Lys Thr Glu Lys Ala
        435                 440                 445
```

```
Lys Tyr Leu Ser Leu Glu Thr Ile Lys Leu Ala Leu Glu Glu Phe Asn
    450                 455                 460

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

Asn Phe Ala Ala Ile Pro Met Ile Phe Asp Glu Ile Ala Gln Asn Lys
                485                 490                 495

Asp Asn Leu Ala Gln Ile Ser Ile Lys Tyr Gln Asn Gln Gly Lys Lys
            500                 505                 510

Asp Leu Leu Gln Ala Ser Ala Glu Asp Asp Val Lys Ala Ile Lys Asp
        515                 520                 525

Leu Leu Asp Gln Thr Asn Asn Leu Leu His Lys Leu Lys Ile Phe His
    530                 535                 540

Ile Ser Gln Ser Glu Asp Lys Ala Asn Ile Leu Asp Lys Asp Glu His
545                 550                 555                 560

Phe Tyr Leu Val Phe Glu Glu Cys Tyr Phe Glu Leu Ala Asn Ile Val
                565                 570                 575

Pro Leu Tyr Asn Lys Ile Arg Asn Tyr Ile Thr Gln Lys Pro Tyr Ser
            580                 585                 590

Asp Glu Lys Phe Lys Leu Asn Phe Glu Asn Ser Thr Leu Ala Asn Gly
        595                 600                 605

Trp Asp Lys Asn Lys Glu Pro Asp Asn Thr Ala Ile Leu Phe Ile Lys
    610                 615                 620

Asp Asp Lys Tyr Tyr Leu Gly Val Met Asn Lys Lys Asn Asn Lys Ile
625                 630                 635                 640

Phe Asp Asp Lys Ala Ile Lys Glu Asn Lys Gly Glu Gly Tyr Lys Lys
                645                 650                 655

Ile Val Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro Lys Val
            660                 665                 670

Phe Phe Ser Ala Lys Ser Ile Lys Phe Tyr Asn Pro Ser Glu Asp Ile
        675                 680                 685

Leu Arg Ile Arg Asn His Ser Thr His Thr Lys Asn Gly Ser Pro Gln
    690                 695                 700

Lys Gly Tyr Glu Lys Phe Glu Phe Asn Ile Glu Asp Cys Arg Lys Phe
705                 710                 715                 720
```

```
Ile Asp Phe Tyr Lys Gln Ser Ile Ser Lys His Pro Glu Trp Lys Asp
                725                 730                 735

Phe Gly Phe Arg Phe Ser Asp Thr Gln Arg Tyr Asn Ser Ile Asp Glu
            740                 745                 750

Phe Tyr Arg Glu Val Glu Asn Gln Gly Tyr Lys Leu Thr Phe Glu Asn
        755                 760                 765

Ile Ser Glu Ser Tyr Ile Asp Ser Val Val Asn Gln Gly Lys Leu Tyr
    770                 775                 780

Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Ala Tyr Ser Lys Gly Arg
785                 790                 795                 800

Pro Asn Leu His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu Arg Asn
                805                 810                 815

Leu Gln Asp Val Val Tyr Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr
            820                 825                 830

Arg Lys Gln Ser Ile Pro Lys Lys Ile Thr His Pro Ala Lys Glu Ala
        835                 840                 845

Ile Ala Asn Lys Asn Lys Asp Asn Pro Lys Lys Glu Ser Val Phe Glu
    850                 855                 860

Tyr Asp Leu Ile Lys Asp Lys Arg Phe Thr Glu Asp Lys Phe Phe Phe
865                 870                 875                 880

His Cys Pro Ile Thr Ile Asn Phe Lys Ser Ser Gly Ala Asn Lys Phe
                885                 890                 895

Asn Asp Glu Ile Asn Leu Leu Leu Lys Glu Lys Ala Asn Asp Val His
            900                 905                 910

Ile Leu Ser Ile Asp Arg Gly Glu Arg His Leu Ala Tyr Tyr Thr Leu
        915                 920                 925

Val Asp Gly Lys Gly Asn Ile Ile Lys Gln Asp Thr Phe Asn Ile Ile
    930                 935                 940

Gly Asn Asp Arg Met Lys Thr Asn Tyr His Asp Lys Leu Ala Ala Ile
945                 950                 955                 960

Glu Lys Asp Arg Asp Ser Ala Arg Lys Asp Trp Lys Lys Ile Asn Asn
                965                 970                 975

Ile Lys Glu Met Lys Glu Gly Tyr Leu Ser Gln Val Val His Glu Ile
            980                 985                 990

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

995 1000 1005

Asn Phe Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Lys Gln Val
1010 1015 1020

Tyr Gln Lys Leu Glu Lys Met Leu Ile Glu Lys Leu Asn Tyr Leu
1025 1030 1035

Val Phe Lys Asp Asn Glu Phe Asp Lys Thr Gly Gly Val Leu Arg
1040 1045 1050

Ala Tyr Gln Leu Thr Ala Pro Phe Glu Thr Phe Lys Lys Met Gly
1055 1060 1065

Lys Gln Thr Gly Ile Ile Tyr Tyr Val Pro Ala Gly Phe Thr Ser
1070 1075 1080

Lys Ile Cys Pro Val Thr Gly Phe Val Asn Gln Leu Tyr Pro Lys
1085 1090 1095

Tyr Glu Ser Val Ser Lys Ser Gln Glu Phe Phe Ser Lys Phe Asp
1100 1105 1110

Lys Ile Cys Tyr Asn Leu Asp Lys Gly Tyr Phe Glu Phe Ser Phe
1115 1120 1125

Asp Tyr Lys Asn Phe Gly Asp Lys Ala Ala Lys Gly Lys Trp Thr
1130 1135 1140

Ile Ala Ser Phe Gly Ser Arg Leu Ile Asn Phe Arg Asn Ser Asp
1145 1150 1155

Lys Asn His Asn Trp Asp Thr Arg Glu Val Tyr Pro Thr Lys Glu
1160 1165 1170

Leu Glu Lys Leu Leu Lys Asp Tyr Ser Ile Glu Tyr Gly His Gly
1175 1180 1185

Glu Cys Ile Lys Ala Ala Ile Cys Gly Glu Ser Asp Lys Lys Phe
1190 1195 1200

Phe Ala Lys Leu Thr Ser Val Leu Asn Thr Ile Leu Gln Met Arg
1205 1210 1215

Asn Ser Lys Thr Gly Thr Glu Leu Asp Tyr Leu Ile Ser Pro Val
1220 1225 1230

Ala Asp Val Asn Gly Asn Phe Phe Asp Ser Arg Gln Ala Pro Lys
1235 1240 1245

Asn Met Pro Gln Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Gly
1250 1255 1260

```
Leu Lys  Gly Leu Met Leu Leu  Gly Arg Ile Lys Asn  Asn Gln Glu
    1265                1270                1275


Gly Lys  Lys Leu Asn Leu Val  Ile Lys Asn Glu Glu  Tyr Phe Glu
    1280                1285                1290


Phe Val  Gln Asn Arg Asn Asn
    1295                1300


<210> 54
<211> 1140
<212> PRT
<213> Bacillus sp.

<400> 54
Met Ala Pro Lys Lys Lys Arg Lys Val Gly Ile His Gly Val Pro Ala
1               5                   10                  15


Ala Ala Thr Arg Ser Phe Ile Leu Lys Ile Glu Pro Asn Glu Glu Val
            20                  25                  30


Lys Lys Gly Leu Trp Lys Thr His Glu Val Leu Asn His Gly Ile Ala
        35                  40                  45


Tyr Tyr Met Asn Ile Leu Lys Leu Ile Arg Gln Glu Ala Ile Tyr Glu
    50                  55                  60


His His Glu Gln Asp Pro Lys Asn Pro Lys Lys Val Ser Lys Ala Glu
65                  70                  75                  80


Ile Gln Ala Glu Leu Trp Asp Phe Val Leu Lys Met Gln Lys Cys Asn
                85                  90                  95


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


Glu Leu Tyr Glu Glu Leu Val Pro Ser Ser Val Glu Lys Lys Gly Glu
        115                 120                 125


Ala Asn Gln Leu Ser Asn Lys Phe Leu Tyr Pro Leu Val Asp Pro Asn
    130                 135                 140


Ser Gln Ser Gly Lys Gly Thr Ala Ser Ser Gly Arg Lys Pro Arg Trp
145                 150                 155                 160


Tyr Asn Leu Lys Ile Ala Gly Asp Pro Ser Trp Glu Glu Glu Lys Lys
                165                 170                 175


Lys Trp Glu Glu Asp Lys Lys Lys Asp Pro Leu Ala Lys Ile Leu Gly
            180                 185                 190


Lys Leu Ala Glu Tyr Gly Leu Ile Pro Leu Phe Ile Pro Tyr Thr Asp
```

```
        195                 200                 205

Ser Asn Glu Pro Ile Val Lys Glu Ile Lys Trp Met Glu Lys Ser Arg
    210                 215                 220

Asn Gln Ser Val Arg Arg Leu Asp Lys Asp Met Phe Ile Gln Ala Leu
225                 230                 235                 240

Glu Arg Phe Leu Ser Trp Glu Ser Trp Asn Leu Lys Val Lys Glu Glu
                245                 250                 255

Tyr Glu Lys Val Glu Lys Glu Tyr Lys Thr Leu Glu Glu Arg Ile Lys
            260                 265                 270

Glu Asp Ile Gln Ala Leu Lys Ala Leu Glu Gln Tyr Glu Lys Glu Arg
        275                 280                 285

Gln Glu Gln Leu Leu Arg Asp Thr Leu Asn Thr Asn Glu Tyr Arg Leu
    290                 295                 300

Ser Lys Arg Gly Leu Arg Gly Trp Arg Glu Ile Ile Gln Lys Trp Leu
305                 310                 315                 320

Lys Met Asp Glu Asn Glu Pro Ser Glu Lys Tyr Leu Glu Val Phe Lys
                325                 330                 335

Asp Tyr Gln Arg Lys His Pro Arg Glu Ala Gly Asp Tyr Ser Val Tyr
            340                 345                 350

Glu Phe Leu Ser Lys Lys Glu Asn His Phe Ile Trp Arg Asn His Pro
        355                 360                 365

Glu Tyr Pro Tyr Leu Tyr Ala Thr Phe Cys Glu Ile Asp Lys Lys Lys
    370                 375                 380

Lys Asp Ala Lys Gln Gln Ala Thr Phe Thr Leu Ala Asp Pro Ile Asn
385                 390                 395                 400

His Pro Leu Trp Val Arg Phe Glu Glu Arg Ser Gly Ser Asn Leu Asn
                405                 410                 415

Lys Tyr Arg Ile Leu Thr Glu Gln Leu His Thr Glu Lys Leu Lys Lys
            420                 425                 430

Lys Leu Thr Val Gln Leu Asp Arg Leu Ile Tyr Pro Thr Glu Ser Gly
        435                 440                 445

Gly Trp Glu Glu Lys Gly Lys Val Asp Ile Val Leu Leu Pro Ser Arg
    450                 455                 460

Gln Phe Tyr Asn Gln Ile Phe Leu Asp Ile Glu Glu Lys Gly Lys His
465                 470                 475                 480
```

```
Ala Phe Thr Tyr Lys Asp Glu Ser Ile Lys Phe Pro Leu Lys Gly Thr
                485                 490                 495

Leu Gly Gly Ala Arg Val Gln Phe Asp Arg Asp His Leu Arg Arg Tyr
            500                 505                 510

Pro His Lys Val Glu Ser Gly Asn Val Gly Arg Ile Tyr Phe Asn Met
        515                 520                 525

Thr Val Asn Ile Glu Pro Thr Glu Ser Pro Val Ser Lys Ser Leu Lys
    530                 535                 540

Ile His Arg Asp Asp Phe Pro Lys Val Val Asn Phe Lys Pro Lys Glu
545                 550                 555                 560

Leu Thr Glu Trp Ile Lys Asp Ser Lys Gly Lys Lys Leu Lys Ser Gly
                565                 570                 575

Ile Glu Ser Leu Glu Ile Gly Leu Arg Val Met Ser Ile Asp Leu Gly
            580                 585                 590

Gln Arg Gln Ala Ala Ala Ala Ser Ile Phe Glu Val Val Asp Gln Lys
        595                 600                 605

Pro Asp Ile Glu Gly Lys Leu Phe Phe Pro Ile Lys Gly Thr Glu Leu
    610                 615                 620

Tyr Ala Val His Arg Ala Ser Phe Asn Ile Lys Leu Pro Gly Glu Thr
625                 630                 635                 640

Leu Val Lys Ser Arg Glu Val Leu Arg Lys Ala Arg Glu Asp Asn Leu
                645                 650                 655

Lys Leu Met Asn Gln Lys Leu Asn Phe Leu Arg Asn Val Leu His Phe
            660                 665                 670

Gln Gln Phe Glu Asp Ile Thr Glu Arg Glu Lys Arg Val Thr Lys Trp
        675                 680                 685

Ile Ser Arg Gln Glu Asn Ser Asp Val Pro Leu Val Tyr Gln Asp Glu
    690                 695                 700

Leu Ile Gln Ile Arg Glu Leu Met Tyr Lys Pro Tyr Lys Asp Trp Val
705                 710                 715                 720

Ala Phe Leu Lys Gln Leu His Lys Arg Leu Glu Val Glu Ile Gly Lys
                725                 730                 735

Glu Val Lys His Trp Arg Lys Ser Leu Ser Asp Gly Arg Lys Gly Leu
            740                 745                 750
```

```
Tyr Gly Ile Ser Leu Lys Asn Ile Asp Glu Ile Asp Arg Thr Arg Lys
        755                 760                 765

Phe Leu Leu Arg Trp Ser Leu Arg Pro Thr Glu Pro Gly Glu Val Arg
    770                 775                 780

Arg Leu Glu Pro Gly Gln Arg Phe Ala Ile Asp Gln Leu Asn His Leu
785                 790                 795                 800

Asn Ala Leu Lys Glu Asp Arg Leu Lys Lys Met Ala Asn Thr Ile Ile
                805                 810                 815

Met His Ala Leu Gly Tyr Cys Tyr Asp Val Arg Lys Lys Lys Trp Gln
            820                 825                 830

Ala Lys Asn Pro Ala Cys Gln Ile Ile Leu Phe Glu Asp Leu Ser Asn
        835                 840                 845

Tyr Asn Pro Tyr Glu Glu Arg Ser Arg Phe Glu Asn Ser Lys Leu Met
    850                 855                 860

Lys Trp Ser Arg Arg Glu Ile Pro Arg Gln Val Ala Leu Gln Gly Glu
865                 870                 875                 880

Ile Tyr Gly Leu Gln Val Gly Glu Val Gly Ala Gln Phe Ser Ser Arg
                885                 890                 895

Phe His Ala Lys Thr Gly Ser Pro Gly Ile Arg Cys Ser Val Val Thr
            900                 905                 910

Lys Glu Lys Leu Gln Asp Asn Arg Phe Phe Lys Asn Leu Gln Arg Glu
        915                 920                 925

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

Tyr Pro Asp Lys Gly Gly Glu Lys Phe Ile Ser Leu Ser Lys Asp Arg
945                 950                 955                 960

Lys Cys Val Thr Thr His Ala Asp Ile Asn Ala Ala Gln Asn Leu Gln
                965                 970                 975

Lys Arg Phe Trp Thr Arg Thr His Gly Phe Tyr Lys Val Tyr Cys Lys
            980                 985                 990

Ala Tyr Gln Val Asp Gly Gln Thr  Val Tyr Ile Pro Glu  Ser Lys Asp
        995                 1000                1005

Gln Lys  Gln Lys Ile Ile Glu  Glu Phe Gly Glu Gly  Tyr Phe Ile
    1010                1015                1020
```

Leu Lys Asp Gly Val Tyr Glu Trp Val Asn Ala Gly Lys Leu Lys
1025 1030 1035

Ile Lys Lys Gly Ser Ser Lys Gln Ser Ser Ser Glu Leu Val Asp
1040 1045 1050

Ser Asp Ile Leu Lys Asp Ser Phe Asp Leu Ala Ser Glu Leu Lys
1055 1060 1065

Gly Glu Lys Leu Met Leu Tyr Arg Asp Pro Ser Gly Asn Val Phe
1070 1075 1080

Pro Ser Asp Lys Trp Met Ala Ala Gly Val Phe Phe Gly Lys Leu
1085 1090 1095

Glu Arg Ile Leu Ile Ser Lys Leu Thr Asn Gln Tyr Ser Ile Ser
1100 1105 1110

Thr Ile Glu Asp Asp Ser Ser Lys Gln Ser Met Lys Arg Pro Ala
1115 1120 1125

Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
1130 1135 1140

<210> 55
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 55
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 56
<211> 20
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 56
cagguuccau gggaugcucu 20

<210> 57
<211> 80
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 57
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu 60

ggcaccgagu cggugcuuuu 80

<210> 58
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 58
cccgcacctt ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 59
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 59
aagauaccug aauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 60
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 60
aagauaccug aauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 61
<211> 80
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 61
guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc cguuaucaac uugaaaaagu 60

ggcaccgagu cggugcuuuu 80

<210> 62
<211> 3166
<212> DNA
<213> Homo sapiens

<400> 62
ctgctcagtt catccctaga ggcagctgct ccaggtaatg ccctctgggg aggggaaaga 60

ggaggggagg aggatgaaga ggggcaagag gagctccctg cccagcccag ccagcaagcc 120

tggagaagca cttgctagag ctaaggaagc ctcggagctg gacgggtgcc ccccacccct 180

catcataacc tgaagaacat ggaggcccgg gaggggtgtc acttgcccaa agctacacag 240

ggggtggggc tggaagtggc tccaagtgca ggttcccccc tcattcttca ggcttagggc 300

tggaggaagc cttagacagc ccagtcctac cccagacagg gaaactgagg cctggagagg 360

gccagaaatc acccaaagac acacagcatg ttggctggac tggacggaga tcagtccaga 420

ccgcaggtgc cttgatgttc agtctggtgg gttttctgct ccatcccacc cacctccctt 480

tgggcctcga tccctcgccc ctcaccagtc ccccttctga gagcccgtat tagcagggag 540

ccggccccta ctccttctgg cagacccagc taaggttcta ccttaggggc cacgccacct 600

ccccagggag gggtccagag gcatggggac ctggggtgcc cctcacagga cacttccttg 660

caggaacaga ggtgccatgc agccccgggt actccttgtt gttgccctcc tggcgctcct 720

ggcctctgcc cgtaagcact tggtgggact gggctggggg cagggtggag gcaacttggg 780

gatcccagtc ccaatgggtg gtcaagcagg agcccagggc tcgtccagag gccgatccac 840

cccactcagc cctgctcttt cctcaggagc ttcagaggcc gaggatgcct cccttctcag 900

cttcatgcag ggttacatga agcacgccac caagaccgcc aaggatgcac tgagcagcgt 960

gcaggagtcc caggtggccc agcaggccag gtacacccgc tggcctccct ccccatcccc 1020

cctgccagct gcctccattc ccacccgccc ctgccctggt gagatcccaa caatggaatg 1080

gaggtgctcc agcctcccct gggcctgtgc ctcttcagcc tcctctttcc tcacagggcc 1140

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ctttctcccc ggagcagtcc tagggcgtgc cgttttagcc ctcatttcca ttttcctttc 1260

ctttcccttt ctttctcttt ctatttcttt ctttctttct ttctttcttt ctttctttct 1320

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ccattctcct gcctcagcct cccaagtagc tgggattaca ggcacgcgcc accacaccca 1620

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agccttttttg gcaccaggga ccagttttgt ggtggacaat ttttccatgg gccagcgggg 1860

atggttttgg gatgaagctg ttccacctca gatcatcagg cattagattc tcataaggag 1920

ccctccacct agatccctgg catgtgcagt tcacaatagg gttcacactc ctatgagaat 1980

gtaaggccac ttgatctgac aggaggcgga gctcaggcgg tattgctcac tcacccacca 2040

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ttgggggttg gggacccctg ggctaggggt ttgccttggg aggccccacc tgacccaatt 2160

caagcccgtg agtgcttctg ctttgttcta agacctgggg ccagtgtgag cagaagtgtg 2220

tccttcctct cccatcctgc ccctgcccat cagtactctc ctctccccta ctcccttctc 2280

cacctcaccc tgactggcat tagctggcat agcagaggtg ttcataaaca ttcttagtcc 2340

ccagaaccgg ctttggggta ggtgttattt tctcactttg cagatgagaa aattgaggct 2400

cagagcgatt aggtgacctg ccccagatca cacaactaat caatcctcca atgactttcc 2460

aaatgagagg ctgcctccct ctgtcctacc ctgctcagag ccaccaggtt gtgcaactcc 2520

aggcggtgct gtttgcacag aaaacaatga cagccttgac ctttcacatc tccccaccct 2580

gtcactttgt gcctcaggcc caggggcata aacatctgag gtgacctgga gatggcaggg 2640

tttgacttgt gctggggttc ctgcaaggat atctcttctc ccagggtggc agctgtgggg 2700

gattcctgcc tgaggtctca gggctgtcgt ccagtgaagt tgagagggtg gtgtggtcct 2760

gactggtgtc gtccagtggg gacatgggtg tgggtcccat ggttgcctac agaggagttc 2820

tcatgccctg ctctgttgct tcccctgact gatttagggg ctgggtgacc gatggcttca 2880

gttccctgaa agactactgg agcaccgtta aggacaagtt ctctgagttc tgggatttgg 2940

accctgaggt cagaccaact tcagccgtgg ctgcctgaga cctcaatacc ccaagtccac 3000

ctgcctatcc atcctgcgag ctccttgggt cctgcaatct ccagggctgc ccctgtaggt 3060

tgcttaaaag ggacagtatt ctcagtgctc tcctacccca cctcatgcct ggccccctc 3120

caggcatgct ggcctcccaa taaagctgga caagaagctg ctatga 3166

<210> 63
<211> 99
<212> PRT
<213> Homo sapiens

<400> 63
Met Gln Pro Arg Val Leu Leu Val Val Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ser Ala Arg Ala Ser Glu Ala Glu Asp Ala Ser Leu Leu Ser Phe Met
20 25 30

Gln Gly Tyr Met Lys His Ala Thr Lys Thr Ala Lys Asp Ala Leu Ser
35 40 45

Ser Val Gln Glu Ser Gln Val Ala Gln Gln Ala Arg Gly Trp Val Thr
50 55 60

Asp Gly Phe Ser Ser Leu Lys Asp Tyr Trp Ser Thr Val Lys Asp Lys
65 70 75 80

```
Phe Ser Glu Phe Trp Asp Leu Asp Pro Glu Val Arg Pro Thr Ser Ala
                85                  90                  95

Val Ala Ala
```

<210> 64
<211> 4548
<212> PRT
<213> Homo sapiens

<400> 64

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Met Glu His Lys Glu Val Val Leu Leu Leu Leu Leu Phe Leu Lys Ser
1               5                   10                  15

Ala Ala Pro Glu Gln Ser His Val Val Gln Asp Cys Tyr His Gly Asp
            20                  25                  30

Gly Gln Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr
        35                  40                  45

Cys Gln Ala Trp Ser Ser Met Thr Pro His Gln His Asn Arg Thr Thr
    50                  55                  60

Glu Asn Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro
65                  70                  75                  80

Asp Ala Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg
                85                  90                  95

Trp Glu Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala
            100                 105                 110

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

Glu Gln Ala Pro Thr Glu Gln Arg Pro Gly Val Gln Glu Cys Tyr His
    130                 135                 140

Gly Asn Gly Gln Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly
145                 150                 155                 160

Arg Thr Cys Gln Ala Trp Ser Ser Met Thr Pro His Ser His Ser Arg
                165                 170                 175

Thr Pro Glu Tyr Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg
            180                 185                 190

Asn Pro Asp Ala Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly
        195                 200                 205

Val Arg Trp Glu Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly
```

```
    210                 215                 220

Thr Ala Val Ala Pro Pro Thr Val Thr Pro Val Pro Ser Leu Glu Ala
225                 230                 235                 240

Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro Gly Val Gln Glu Cys
                245                 250                 255

Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val
            260                 265                 270

Thr Gly Arg Thr Cys Gln Ala Trp Ser Ser Met Thr Pro His Ser His
        275                 280                 285

Ser Arg Thr Pro Glu Tyr Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr
    290                 295                 300

Cys Arg Asn Pro Asp Ala Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp
305                 310                 315                 320

Pro Gly Val Arg Trp Glu Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala
                325                 330                 335

Glu Gly Thr Ala Val Ala Pro Pro Thr Val Thr Pro Val Pro Ser Leu
            340                 345                 350

Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro Gly Val Gln
        355                 360                 365

Glu Cys Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Tyr Ser Thr
    370                 375                 380

Thr Val Thr Gly Arg Thr Cys Gln Ala Trp Ser Ser Met Thr Pro His
385                 390                 395                 400

Ser His Ser Arg Thr Pro Glu Tyr Tyr Pro Asn Ala Gly Leu Ile Met
                405                 410                 415

Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala Ala Pro Tyr Cys Tyr Thr
            420                 425                 430

Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys Asn Leu Thr Gln Cys Ser
        435                 440                 445

Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Val Thr Pro Val Pro
    450                 455                 460

Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro Gly
465                 470                 475                 480

Val Gln Glu Cys Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly Thr Tyr
                485                 490                 495
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Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ala Trp Ser Ser Met Thr
            500                 505                 510

Pro His Ser His Ser Arg Thr Pro Glu Tyr Tyr Pro Asn Ala Gly Leu
        515                 520                 525

Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala Ala Pro Tyr Cys
    530                 535                 540

Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys Asn Leu Thr Gln
545                 550                 555                 560

Cys Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Val Thr Pro
                565                 570                 575

Val Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg
            580                 585                 590

Pro Gly Val Gln Glu Cys Tyr His Gly Asn Gly Gln Ser Tyr Arg Gly
        595                 600                 605

Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ala Trp Ser Ser
    610                 615                 620

Met Thr Pro His Ser His Ser Arg Thr Pro Glu Tyr Tyr Pro Asn Ala
625                 630                 635                 640

Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala Ala Pro
                645                 650                 655

Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys Asn Leu
            660                 665                 670

Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Val
        675                 680                 685

Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu
    690                 695                 700

Gln Arg Pro Gly Val Gln Glu Cys Tyr His Gly Asn Gly Gln Ser Tyr
705                 710                 715                 720

Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ala Trp
                725                 730                 735

Ser Ser Met Thr Pro His Ser His Ser Arg Thr Pro Glu Tyr Tyr Pro
            740                 745                 750

Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala
        755                 760                 765
```

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Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys
    770                 775                 780

Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro
785                 790                 795                 800

Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro
                805                 810                 815

Thr Glu Gln Arg Pro Gly Val Gln Glu Cys Tyr His Gly Asn Gly Gln
            820                 825                 830

Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln
        835                 840                 845

Ala Trp Ser Ser Met Thr Pro His Ser His Ser Arg Thr Pro Glu Tyr
    850                 855                 860

Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala
865                 870                 875                 880

Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu
                885                 890                 895

Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala
            900                 905                 910

Pro Pro Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln
        915                 920                 925

Ala Pro Thr Glu Gln Arg Pro Gly Val Gln Glu Cys Tyr His Gly Asn
    930                 935                 940

Gly Gln Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr
945                 950                 955                 960

Cys Gln Ala Trp Ser Ser Met Thr Pro His Ser His Ser Arg Thr Pro
                965                 970                 975

Glu Tyr Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro
            980                 985                 990

Asp Ala Val Ala Ala Pro Tyr Cys  Tyr Thr Arg Asp Pro  Gly Val Arg
        995                 1000                1005

Trp Glu  Tyr Cys Asn Leu Thr  Gln Cys Ser Asp Ala  Glu Gly Thr
    1010                1015                1020

Ala Val  Ala Pro Pro Thr Val  Thr Pro Val Pro Ser  Leu Glu Ala
    1025                1030                1035
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Pro Ser  Glu Gln Ala Pro Thr  Glu Gln Arg Pro Gly  Val Gln Glu
    1040                 1045                 1050

Cys Tyr  His Gly Asn Gly Gln  Ser Tyr Arg Gly Thr  Tyr Ser Thr
    1055                 1060                 1065

Thr Val  Thr Gly Arg Thr Cys  Gln Ala Trp Ser Ser  Met Thr Pro
    1070                 1075                 1080

His Ser  His Ser Arg Thr Pro  Glu Tyr Tyr Pro Asn  Ala Gly Leu
    1085                 1090                 1095

Ile Met  Asn Tyr Cys Arg Asn  Pro Asp Ala Val Ala  Ala Pro Tyr
    1100                 1105                 1110

Cys Tyr  Thr Arg Asp Pro Gly  Val Arg Trp Glu Tyr  Cys Asn Leu
    1115                 1120                 1125

Thr Gln  Cys Ser Asp Ala Glu  Gly Thr Ala Val Ala  Pro Pro Thr
    1130                 1135                 1140

Val Thr  Pro Val Pro Ser Leu  Glu Ala Pro Ser Glu  Gln Ala Pro
    1145                 1150                 1155

Thr Glu  Gln Arg Pro Gly Val  Gln Glu Cys Tyr His  Gly Asn Gly
    1160                 1165                 1170

Gln Ser  Tyr Arg Gly Thr Tyr  Ser Thr Thr Val Thr  Gly Arg Thr
    1175                 1180                 1185

Cys Gln  Ala Trp Ser Ser Met  Thr Pro His Ser His  Ser Arg Thr
    1190                 1195                 1200

Pro Glu  Tyr Tyr Pro Asn Ala  Gly Leu Ile Met Asn  Tyr Cys Arg
    1205                 1210                 1215

Asn Pro  Asp Ala Val Ala Ala  Pro Tyr Cys Tyr Thr  Arg Asp Pro
    1220                 1225                 1230

Gly Val  Arg Trp Glu Tyr Cys  Asn Leu Thr Gln Cys  Ser Asp Ala
    1235                 1240                 1245

Glu Gly  Thr Ala Val Ala Pro  Pro Thr Val Thr Pro  Val Pro Ser
    1250                 1255                 1260

Leu Glu  Ala Pro Ser Glu Gln  Ala Pro Thr Glu Gln  Arg Pro Gly
    1265                 1270                 1275

Val Gln  Glu Cys Tyr His Gly  Asn Gly Gln Ser Tyr  Arg Gly Thr
    1280                 1285                 1290

Tyr Ser  Thr Thr Val Thr Gly  Arg Thr Cys Gln Ala  Trp Ser Ser
```

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    1295                1300                1305

Met Thr  Pro His Ser His Ser  Arg Thr Pro Glu Tyr  Tyr Pro Asn
    1310                1315                1320

Ala Gly  Leu Ile Met Asn Tyr  Cys Arg Asn Pro Asp  Ala Val Ala
    1325                1330                1335

Ala Pro  Tyr Cys Tyr Thr Arg  Asp Pro Gly Val Arg  Trp Glu Tyr
    1340                1345                1350

Cys Asn  Leu Thr Gln Cys Ser  Asp Ala Glu Gly Thr  Ala Val Ala
    1355                1360                1365

Pro Pro  Thr Val Thr Pro Val  Pro Ser Leu Glu Ala  Pro Ser Glu
    1370                1375                1380

Gln Ala  Pro Thr Glu Gln Arg  Pro Gly Val Gln Glu  Cys Tyr His
    1385                1390                1395

Gly Asn  Gly Gln Ser Tyr Arg  Gly Thr Tyr Ser Thr  Thr Val Thr
    1400                1405                1410

Gly Arg  Thr Cys Gln Ala Trp  Ser Ser Met Thr Pro  His Ser His
    1415                1420                1425

Ser Arg  Thr Pro Glu Tyr Tyr  Pro Asn Ala Gly Leu  Ile Met Asn
    1430                1435                1440

Tyr Cys  Arg Asn Pro Asp Ala  Val Ala Ala Pro Tyr  Cys Tyr Thr
    1445                1450                1455

Arg Asp  Pro Gly Val Arg Trp  Glu Tyr Cys Asn Leu  Thr Gln Cys
    1460                1465                1470

Ser Asp  Ala Glu Gly Thr Ala  Val Ala Pro Pro Thr  Val Thr Pro
    1475                1480                1485

Val Pro  Ser Leu Glu Ala Pro  Ser Glu Gln Ala Pro  Thr Glu Gln
    1490                1495                1500

Arg Pro  Gly Val Gln Glu Cys  Tyr His Gly Asn Gly  Gln Ser Tyr
    1505                1510                1515

Arg Gly  Thr Tyr Ser Thr Thr  Val Thr Gly Arg Thr  Cys Gln Ala
    1520                1525                1530

Trp Ser  Ser Met Thr Pro His  Ser His Ser Arg Thr  Pro Glu Tyr
    1535                1540                1545

Tyr Pro  Asn Ala Gly Leu Ile  Met Asn Tyr Cys Arg  Asn Pro Asp
    1550                1555                1560
```

```
Ala Val  Ala Ala Pro Tyr Cys  Tyr Thr Arg Asp Pro  Gly Val Arg
    1565                1570                1575

Trp Glu  Tyr Cys Asn Leu Thr  Gln Cys Ser Asp Ala  Glu Gly Thr
    1580                1585                1590

Ala Val  Ala Pro Pro Thr Val  Thr Pro Val Pro Ser  Leu Glu Ala
    1595                1600                1605

Pro Ser  Glu Gln Ala Pro Thr  Glu Gln Arg Pro Gly  Val Gln Glu
    1610                1615                1620

Cys Tyr  His Gly Asn Gly Gln  Ser Tyr Arg Gly Thr  Tyr Ser Thr
    1625                1630                1635

Thr Val  Thr Gly Arg Thr Cys  Gln Ala Trp Ser Ser  Met Thr Pro
    1640                1645                1650

His Ser  His Ser Arg Thr Pro  Glu Tyr Tyr Pro Asn  Ala Gly Leu
    1655                1660                1665

Ile Met  Asn Tyr Cys Arg Asn  Pro Asp Ala Val Ala  Ala Pro Tyr
    1670                1675                1680

Cys Tyr  Thr Arg Asp Pro Gly  Val Arg Trp Glu Tyr  Cys Asn Leu
    1685                1690                1695

Thr Gln  Cys Ser Asp Ala Glu  Gly Thr Ala Val Ala  Pro Pro Thr
    1700                1705                1710

Val Thr  Pro Val Pro Ser Leu  Glu Ala Pro Ser Glu  Gln Ala Pro
    1715                1720                1725

Thr Glu  Gln Arg Pro Gly Val  Gln Glu Cys Tyr His  Gly Asn Gly
    1730                1735                1740

Gln Ser  Tyr Arg Gly Thr Tyr  Ser Thr Thr Val Thr  Gly Arg Thr
    1745                1750                1755

Cys Gln  Ala Trp Ser Ser Met  Thr Pro His Ser His  Ser Arg Thr
    1760                1765                1770

Pro Glu  Tyr Tyr Pro Asn Ala  Gly Leu Ile Met Asn  Tyr Cys Arg
    1775                1780                1785

Asn Pro  Asp Ala Val Ala Ala  Pro Tyr Cys Tyr Thr  Arg Asp Pro
    1790                1795                1800

Gly Val  Arg Trp Glu Tyr Cys  Asn Leu Thr Gln Cys  Ser Asp Ala
    1805                1810                1815
```

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Glu Gly  Thr Ala Val Ala Pro  Pro Thr Val Thr Pro  Val Pro Ser
    1820                 1825                 1830

Leu Glu  Ala Pro Ser Glu Gln  Ala Pro Thr Glu Gln  Arg Pro Gly
    1835                 1840                 1845

Val Gln  Glu Cys Tyr His Gly  Asn Gly Gln Ser Tyr  Arg Gly Thr
    1850                 1855                 1860

Tyr Ser  Thr Thr Val Thr Gly  Arg Thr Cys Gln Ala  Trp Ser Ser
    1865                 1870                 1875

Met Thr  Pro His Ser His Ser  Arg Thr Pro Glu Tyr  Tyr Pro Asn
    1880                 1885                 1890

Ala Gly  Leu Ile Met Asn Tyr  Cys Arg Asn Pro Asp  Ala Val Ala
    1895                 1900                 1905

Ala Pro  Tyr Cys Tyr Thr Arg  Asp Pro Gly Val Arg  Trp Glu Tyr
    1910                 1915                 1920

Cys Asn  Leu Thr Gln Cys Ser  Asp Ala Glu Gly Thr  Ala Val Ala
    1925                 1930                 1935

Pro Pro  Thr Val Thr Pro Val  Pro Ser Leu Glu Ala  Pro Ser Glu
    1940                 1945                 1950

Gln Ala  Pro Thr Glu Gln Arg  Pro Gly Val Gln Glu  Cys Tyr His
    1955                 1960                 1965

Gly Asn  Gly Gln Ser Tyr Arg  Gly Thr Tyr Ser Thr  Thr Val Thr
    1970                 1975                 1980

Gly Arg  Thr Cys Gln Ala Trp  Ser Ser Met Thr Pro  His Ser His
    1985                 1990                 1995

Ser Arg  Thr Pro Glu Tyr Tyr  Pro Asn Ala Gly Leu  Ile Met Asn
    2000                 2005                 2010

Tyr Cys  Arg Asn Pro Asp Ala  Val Ala Ala Pro Tyr  Cys Tyr Thr
    2015                 2020                 2025

Arg Asp  Pro Gly Val Arg Trp  Glu Tyr Cys Asn Leu  Thr Gln Cys
    2030                 2035                 2040

Ser Asp  Ala Glu Gly Thr Ala  Val Ala Pro Pro Thr  Val Thr Pro
    2045                 2050                 2055

Val Pro  Ser Leu Glu Ala Pro  Ser Glu Gln Ala Pro  Thr Glu Gln
    2060                 2065                 2070
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Arg Pro  Gly Val Gln Glu Cys  Tyr His Gly Asn Gly  Gln Ser Tyr
    2075                 2080                 2085

Arg Gly  Thr Tyr Ser Thr Thr  Val Thr Gly Arg Thr  Cys Gln Ala
    2090                 2095                 2100

Trp Ser  Ser Met Thr Pro His  Ser His Ser Arg Thr  Pro Glu Tyr
    2105                 2110                 2115

Tyr Pro  Asn Ala Gly Leu Ile  Met Asn Tyr Cys Arg  Asn Pro Asp
    2120                 2125                 2130

Ala Val  Ala Ala Pro Tyr Cys  Tyr Thr Arg Asp Pro  Gly Val Arg
    2135                 2140                 2145

Trp Glu  Tyr Cys Asn Leu Thr  Gln Cys Ser Asp Ala  Glu Gly Thr
    2150                 2155                 2160

Ala Val  Ala Pro Pro Thr Val  Thr Pro Val Pro Ser  Leu Glu Ala
    2165                 2170                 2175

Pro Ser  Glu Gln Ala Pro Thr  Glu Gln Arg Pro Gly  Val Gln Glu
    2180                 2185                 2190

Cys Tyr  His Gly Asn Gly Gln  Ser Tyr Arg Gly Thr  Tyr Ser Thr
    2195                 2200                 2205

Thr Val  Thr Gly Arg Thr Cys  Gln Ala Trp Ser Ser  Met Thr Pro
    2210                 2215                 2220

His Ser  His Ser Arg Thr Pro  Glu Tyr Tyr Pro Asn  Ala Gly Leu
    2225                 2230                 2235

Ile Met  Asn Tyr Cys Arg Asn  Pro Asp Ala Val Ala  Ala Pro Tyr
    2240                 2245                 2250

Cys Tyr  Thr Arg Asp Pro Gly  Val Arg Trp Glu Tyr  Cys Asn Leu
    2255                 2260                 2265

Thr Gln  Cys Ser Asp Ala Glu  Gly Thr Ala Val Ala  Pro Pro Thr
    2270                 2275                 2280

Val Thr  Pro Val Pro Ser Leu  Glu Ala Pro Ser Glu  Gln Ala Pro
    2285                 2290                 2295

Thr Glu  Gln Arg Pro Gly Val  Gln Glu Cys Tyr His  Gly Asn Gly
    2300                 2305                 2310

Gln Ser  Tyr Arg Gly Thr Tyr  Ser Thr Thr Val Thr  Gly Arg Thr
    2315                 2320                 2325

Cys Gln  Ala Trp Ser Ser Met  Thr Pro His Ser His  Ser Arg Thr
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    2330                2335                2340

Pro Glu  Tyr Tyr Pro Asn Ala  Gly Leu Ile Met Asn  Tyr Cys Arg
    2345                2350                2355

Asn Pro  Asp Ala Val Ala Ala  Pro Tyr Cys Tyr Thr  Arg Asp Pro
    2360                2365                2370

Gly Val  Arg Trp Glu Tyr Cys  Asn Leu Thr Gln Cys  Ser Asp Ala
    2375                2380                2385

Glu Gly  Thr Ala Val Ala Pro  Pro Thr Val Thr Pro  Val Pro Ser
    2390                2395                2400

Leu Glu  Ala Pro Ser Glu Gln  Ala Pro Thr Glu Gln  Arg Pro Gly
    2405                2410                2415

Val Gln  Glu Cys Tyr His Gly  Asn Gly Gln Ser Tyr  Arg Gly Thr
    2420                2425                2430

Tyr Ser  Thr Thr Val Thr Gly  Arg Thr Cys Gln Ala  Trp Ser Ser
    2435                2440                2445

Met Thr  Pro His Ser His Ser  Arg Thr Pro Glu Tyr  Tyr Pro Asn
    2450                2455                2460

Ala Gly  Leu Ile Met Asn Tyr  Cys Arg Asn Pro Asp  Ala Val Ala
    2465                2470                2475

Ala Pro  Tyr Cys Tyr Thr Arg  Asp Pro Gly Val Arg  Trp Glu Tyr
    2480                2485                2490

Cys Asn  Leu Thr Gln Cys Ser  Asp Ala Glu Gly Thr  Ala Val Ala
    2495                2500                2505

Pro Pro  Thr Val Thr Pro Val  Pro Ser Leu Glu Ala  Pro Ser Glu
    2510                2515                2520

Gln Ala  Pro Thr Glu Gln Arg  Pro Gly Val Gln Glu  Cys Tyr His
    2525                2530                2535

Gly Asn  Gly Gln Ser Tyr Arg  Gly Thr Tyr Ser Thr  Thr Val Thr
    2540                2545                2550

Gly Arg  Thr Cys Gln Ala Trp  Ser Ser Met Thr Pro  His Ser His
    2555                2560                2565

Ser Arg  Thr Pro Glu Tyr Tyr  Pro Asn Ala Gly Leu  Ile Met Asn
    2570                2575                2580

Tyr Cys  Arg Asn Pro Asp Ala  Val Ala Ala Pro Tyr  Cys Tyr Thr
    2585                2590                2595
```

```
Arg Asp  Pro Gly Val Arg Trp  Glu Tyr Cys Asn Leu  Thr Gln Cys
    2600                 2605                 2610

Ser Asp  Ala Glu Gly Thr Ala  Val Ala Pro Pro Thr  Val Thr Pro
    2615                 2620                 2625

Val Pro  Ser Leu Glu Ala Pro  Ser Glu Gln Ala Pro  Thr Glu Gln
    2630                 2635                 2640

Arg Pro  Gly Val Gln Glu Cys  Tyr His Gly Asn Gly  Gln Ser Tyr
    2645                 2650                 2655

Arg Gly  Thr Tyr Ser Thr Thr  Val Thr Gly Arg Thr  Cys Gln Ala
    2660                 2665                 2670

Trp Ser  Ser Met Thr Pro His  Ser His Ser Arg Thr  Pro Glu Tyr
    2675                 2680                 2685

Tyr Pro  Asn Ala Gly Leu Ile  Met Asn Tyr Cys Arg  Asn Pro Asp
    2690                 2695                 2700

Ala Val  Ala Ala Pro Tyr Cys  Tyr Thr Arg Asp Pro  Gly Val Arg
    2705                 2710                 2715

Trp Glu  Tyr Cys Asn Leu Thr  Gln Cys Ser Asp Ala  Glu Gly Thr
    2720                 2725                 2730

Ala Val  Ala Pro Pro Thr Val  Thr Pro Val Pro Ser  Leu Glu Ala
    2735                 2740                 2745

Pro Ser  Glu Gln Ala Pro Thr  Glu Gln Arg Pro Gly  Val Gln Glu
    2750                 2755                 2760

Cys Tyr  His Gly Asn Gly Gln  Ser Tyr Arg Gly Thr  Tyr Ser Thr
    2765                 2770                 2775

Thr Val  Thr Gly Arg Thr Cys  Gln Ala Trp Ser Ser  Met Thr Pro
    2780                 2785                 2790

His Ser  His Ser Arg Thr Pro  Glu Tyr Tyr Pro Asn  Ala Gly Leu
    2795                 2800                 2805

Ile Met  Asn Tyr Cys Arg Asn  Pro Asp Ala Val Ala  Ala Pro Tyr
    2810                 2815                 2820

Cys Tyr  Thr Arg Asp Pro Gly  Val Arg Trp Glu Tyr  Cys Asn Leu
    2825                 2830                 2835

Thr Gln  Cys Ser Asp Ala Glu  Gly Thr Ala Val Ala  Pro Pro Thr
    2840                 2845                 2850
```

```
Val Thr  Pro Val Pro Ser Leu  Glu Ala Pro Ser Glu  Gln Ala Pro
    2855                 2860                 2865

Thr Glu  Gln Arg Pro Gly Val  Gln Glu Cys Tyr His  Gly Asn Gly
    2870                 2875                 2880

Gln Ser  Tyr Arg Gly Thr Tyr  Ser Thr Thr Val Thr  Gly Arg Thr
    2885                 2890                 2895

Cys Gln  Ala Trp Ser Ser Met  Thr Pro His Ser His  Ser Arg Thr
    2900                 2905                 2910

Pro Glu  Tyr Tyr Pro Asn Ala  Gly Leu Ile Met Asn  Tyr Cys Arg
    2915                 2920                 2925

Asn Pro  Asp Ala Val Ala Ala  Pro Tyr Cys Tyr Thr  Arg Asp Pro
    2930                 2935                 2940

Gly Val  Arg Trp Glu Tyr Cys  Asn Leu Thr Gln Cys  Ser Asp Ala
    2945                 2950                 2955

Glu Gly  Thr Ala Val Ala Pro  Pro Thr Val Thr Pro  Val Pro Ser
    2960                 2965                 2970

Leu Glu  Ala Pro Ser Glu Gln  Ala Pro Thr Glu Gln  Arg Pro Gly
    2975                 2980                 2985

Val Gln  Glu Cys Tyr His Gly  Asn Gly Gln Ser Tyr  Arg Gly Thr
    2990                 2995                 3000

Tyr Ser  Thr Thr Val Thr Gly  Arg Thr Cys Gln Ala  Trp Ser Ser
    3005                 3010                 3015

Met Thr  Pro His Ser His Ser  Arg Thr Pro Glu Tyr  Tyr Pro Asn
    3020                 3025                 3030

Ala Gly  Leu Ile Met Asn Tyr  Cys Arg Asn Pro Asp  Ala Val Ala
    3035                 3040                 3045

Ala Pro  Tyr Cys Tyr Thr Arg  Asp Pro Gly Val Arg  Trp Glu Tyr
    3050                 3055                 3060

Cys Asn  Leu Thr Gln Cys Ser  Asp Ala Glu Gly Thr  Ala Val Ala
    3065                 3070                 3075

Pro Pro  Thr Val Thr Pro Val  Pro Ser Leu Glu Ala  Pro Ser Glu
    3080                 3085                 3090

Gln Ala  Pro Thr Glu Gln Arg  Pro Gly Val Gln Glu  Cys Tyr His
    3095                 3100                 3105
```

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Gly Asn  Gly Gln Ser Tyr Arg  Gly Thr Tyr Ser Thr  Thr Val Thr
    3110                 3115                 3120

Gly Arg  Thr Cys Gln Ala Trp  Ser Ser Met Thr Pro  His Ser His
    3125                 3130                 3135

Ser Arg  Thr Pro Glu Tyr Tyr  Pro Asn Ala Gly Leu  Ile Met Asn
    3140                 3145                 3150

Tyr Cys  Arg Asn Pro Asp Ala  Val Ala Ala Pro Tyr  Cys Tyr Thr
    3155                 3160                 3165

Arg Asp  Pro Gly Val Arg Trp  Glu Tyr Cys Asn Leu  Thr Gln Cys
    3170                 3175                 3180

Ser Asp  Ala Glu Gly Thr Ala  Val Ala Pro Pro Thr  Val Thr Pro
    3185                 3190                 3195

Val Pro  Ser Leu Glu Ala Pro  Ser Glu Gln Ala Pro  Thr Glu Gln
    3200                 3205                 3210

Arg Pro  Gly Val Gln Glu Cys  Tyr His Gly Asn Gly  Gln Ser Tyr
    3215                 3220                 3225

Arg Gly  Thr Tyr Ser Thr Thr  Val Thr Gly Arg Thr  Cys Gln Ala
    3230                 3235                 3240

Trp Ser  Ser Met Thr Pro His  Ser His Ser Arg Thr  Pro Glu Tyr
    3245                 3250                 3255

Tyr Pro  Asn Ala Gly Leu Ile  Met Asn Tyr Cys Arg  Asn Pro Asp
    3260                 3265                 3270

Ala Val  Ala Ala Pro Tyr Cys  Tyr Thr Arg Asp Pro  Gly Val Arg
    3275                 3280                 3285

Trp Glu  Tyr Cys Asn Leu Thr  Gln Cys Ser Asp Ala  Glu Gly Thr
    3290                 3295                 3300

Ala Val  Ala Pro Pro Thr Val  Thr Pro Val Pro Ser  Leu Glu Ala
    3305                 3310                 3315

Pro Ser  Glu Gln Ala Pro Thr  Glu Gln Arg Pro Gly  Val Gln Glu
    3320                 3325                 3330

Cys Tyr  His Gly Asn Gly Gln  Ser Tyr Arg Gly Thr  Tyr Ser Thr
    3335                 3340                 3345

Thr Val  Thr Gly Arg Thr Cys  Gln Ala Trp Ser Ser  Met Thr Pro
    3350                 3355                 3360

His Ser  His Ser Arg Thr Pro  Glu Tyr Tyr Pro Asn  Ala Gly Leu
```

```
    3365                3370                3375

Ile Met  Asn Tyr Cys Arg Asn  Pro Asp Pro Val Ala  Ala Pro Tyr
    3380                3385                3390

Cys Tyr  Thr Arg Asp Pro Ser  Val Arg Trp Glu Tyr  Cys Asn Leu
    3395                3400                3405

Thr Gln  Cys Ser Asp Ala Glu  Gly Thr Ala Val Ala  Pro Pro Thr
    3410                3415                3420

Ile Thr  Pro Ile Pro Ser Leu  Glu Ala Pro Ser Glu  Gln Ala Pro
    3425                3430                3435

Thr Glu  Gln Arg Pro Gly Val  Gln Glu Cys Tyr His  Gly Asn Gly
    3440                3445                3450

Gln Ser  Tyr Gln Gly Thr Tyr  Phe Ile Thr Val Thr  Gly Arg Thr
    3455                3460                3465

Cys Gln  Ala Trp Ser Ser Met  Thr Pro His Ser His  Ser Arg Thr
    3470                3475                3480

Pro Ala  Tyr Tyr Pro Asn Ala  Gly Leu Ile Lys Asn  Tyr Cys Arg
    3485                3490                3495

Asn Pro  Asp Pro Val Ala Ala  Pro Trp Cys Tyr Thr  Thr Asp Pro
    3500                3505                3510

Ser Val  Arg Trp Glu Tyr Cys  Asn Leu Thr Arg Cys  Ser Asp Ala
    3515                3520                3525

Glu Trp  Thr Ala Phe Val Pro  Pro Asn Val Ile Leu  Ala Pro Ser
    3530                3535                3540

Leu Glu  Ala Phe Phe Glu Gln  Ala Leu Thr Glu Glu  Thr Pro Gly
    3545                3550                3555

Val Gln  Asp Cys Tyr Tyr His  Tyr Gly Gln Ser Tyr  Arg Gly Thr
    3560                3565                3570

Tyr Ser  Thr Thr Val Thr Gly  Arg Thr Cys Gln Ala  Trp Ser Ser
    3575                3580                3585

Met Thr  Pro His Gln His Ser  Arg Thr Pro Glu Asn  Tyr Pro Asn
    3590                3595                3600

Ala Gly  Leu Thr Arg Asn Tyr  Cys Arg Asn Pro Asp  Ala Glu Ile
    3605                3610                3615

Arg Pro  Trp Cys Tyr Thr Met  Asp Pro Ser Val Arg  Trp Glu Tyr
    3620                3625                3630
```

```
Cys Asn  Leu Thr Gln Cys Leu  Val Thr Glu Ser Ser  Val Leu Ala
    3635                 3640                 3645

Thr Leu  Thr Val Val Pro Asp  Pro Ser Thr Glu Ala  Ser Ser Glu
    3650                 3655                 3660

Glu Ala  Pro Thr Glu Gln Ser  Pro Gly Val Gln Asp  Cys Tyr His
    3665                 3670                 3675

Gly Asp  Gly Gln Ser Tyr Arg  Gly Ser Phe Ser Thr  Thr Val Thr
    3680                 3685                 3690

Gly Arg  Thr Cys Gln Ser Trp  Ser Ser Met Thr Pro  His Trp His
    3695                 3700                 3705

Gln Arg  Thr Thr Glu Tyr Tyr  Pro Asn Gly Gly Leu  Thr Arg Asn
    3710                 3715                 3720

Tyr Cys  Arg Asn Pro Asp Ala  Glu Ile Ser Pro Trp  Cys Tyr Thr
    3725                 3730                 3735

Met Asp  Pro Asn Val Arg Trp  Glu Tyr Cys Asn Leu  Thr Gln Cys
    3740                 3745                 3750

Pro Val  Thr Glu Ser Ser Val  Leu Ala Thr Ser Thr  Ala Val Ser
    3755                 3760                 3765

Glu Gln  Ala Pro Thr Glu Gln  Ser Pro Thr Val Gln  Asp Cys Tyr
    3770                 3775                 3780

His Gly  Asp Gly Gln Ser Tyr  Arg Gly Ser Phe Ser  Thr Thr Val
    3785                 3790                 3795

Thr Gly  Arg Thr Cys Gln Ser  Trp Ser Ser Met Thr  Pro His Trp
    3800                 3805                 3810

His Gln  Arg Thr Thr Glu Tyr  Tyr Pro Asn Gly Gly  Leu Thr Arg
    3815                 3820                 3825

Asn Tyr  Cys Arg Asn Pro Asp  Ala Glu Ile Arg Pro  Trp Cys Tyr
    3830                 3835                 3840

Thr Met  Asp Pro Ser Val Arg  Trp Glu Tyr Cys Asn  Leu Thr Gln
    3845                 3850                 3855

Cys Pro  Val Met Glu Ser Thr  Leu Leu Thr Thr Pro  Thr Val Val
    3860                 3865                 3870

Pro Val  Pro Ser Thr Glu Leu  Pro Ser Glu Glu Ala  Pro Thr Glu
    3875                 3880                 3885
```

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Asn Ser  Thr Gly Val Gln Asp  Cys Tyr Arg Gly Asp  Gly Gln Ser
    3890                 3895                 3900

Tyr Arg  Gly Thr Leu Ser Thr  Thr Ile Thr Gly Arg  Thr Cys Gln
    3905                 3910                 3915

Ser Trp  Ser Ser Met Thr Pro  His Trp His Arg Arg  Ile Pro Leu
    3920                 3925                 3930

Tyr Tyr  Pro Asn Ala Gly Leu  Thr Arg Asn Tyr Cys  Arg Asn Pro
    3935                 3940                 3945

Asp Ala  Glu Ile Arg Pro Trp  Cys Tyr Thr Met Asp  Pro Ser Val
    3950                 3955                 3960

Arg Trp  Glu Tyr Cys Asn Leu  Thr Arg Cys Pro Val  Thr Glu Ser
    3965                 3970                 3975

Ser Val  Leu Thr Thr Pro Thr  Val Ala Pro Val Pro  Ser Thr Glu
    3980                 3985                 3990

Ala Pro  Ser Glu Gln Ala Pro  Pro Glu Lys Ser Pro  Val Val Gln
    3995                 4000                 4005

Asp Cys  Tyr His Gly Asp Gly  Arg Ser Tyr Arg Gly  Ile Ser Ser
    4010                 4015                 4020

Thr Thr  Val Thr Gly Arg Thr  Cys Gln Ser Trp Ser  Ser Met Ile
    4025                 4030                 4035

Pro His  Trp His Gln Arg Thr  Pro Glu Asn Tyr Pro  Asn Ala Gly
    4040                 4045                 4050

Leu Thr  Glu Asn Tyr Cys Arg  Asn Pro Asp Ser Gly  Lys Gln Pro
    4055                 4060                 4065

Trp Cys  Tyr Thr Thr Asp Pro  Cys Val Arg Trp Glu  Tyr Cys Asn
    4070                 4075                 4080

Leu Thr  Gln Cys Ser Glu Thr  Glu Ser Gly Val Leu  Glu Thr Pro
    4085                 4090                 4095

Thr Val  Val Pro Val Pro Ser  Met Glu Ala His Ser  Glu Ala Ala
    4100                 4105                 4110

Pro Thr  Glu Gln Thr Pro Val  Val Arg Gln Cys Tyr  His Gly Asn
    4115                 4120                 4125

Gly Gln  Ser Tyr Arg Gly Thr  Phe Ser Thr Thr Val  Thr Gly Arg
    4130                 4135                 4140
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Thr Cys  Gln Ser Trp Ser Ser  Met Thr Pro His Arg  His Gln Arg
    4145                 4150                 4155

Thr Pro  Glu Asn Tyr Pro Asn  Asp Gly Leu Thr Met  Asn Tyr Cys
    4160                 4165                 4170

Arg Asn  Pro Asp Ala Asp Thr  Gly Pro Trp Cys Phe  Thr Met Asp
    4175                 4180                 4185

Pro Ser  Ile Arg Trp Glu Tyr  Cys Asn Leu Thr Arg  Cys Ser Asp
    4190                 4195                 4200

Thr Glu  Gly Thr Val Val Ala  Pro Pro Thr Val Ile  Gln Val Pro
    4205                 4210                 4215

Ser Leu  Gly Pro Pro Ser Glu  Gln Asp Cys Met Phe  Gly Asn Gly
    4220                 4225                 4230

Lys Gly  Tyr Arg Gly Lys Lys  Ala Thr Thr Val Thr  Gly Thr Pro
    4235                 4240                 4245

Cys Gln  Glu Trp Ala Ala Gln  Glu Pro His Arg His  Ser Thr Phe
    4250                 4255                 4260

Ile Pro  Gly Thr Asn Lys Trp  Ala Gly Leu Glu Lys  Asn Tyr Cys
    4265                 4270                 4275

Arg Asn  Pro Asp Gly Asp Ile  Asn Gly Pro Trp Cys  Tyr Thr Met
    4280                 4285                 4290

Asn Pro  Arg Lys Leu Phe Asp  Tyr Cys Asp Ile Pro  Leu Cys Ala
    4295                 4300                 4305

Ser Ser  Ser Phe Asp Cys Gly  Lys Pro Gln Val Glu  Pro Lys Lys
    4310                 4315                 4320

Cys Pro  Gly Ser Ile Val Gly  Gly Cys Val Ala His  Pro His Ser
    4325                 4330                 4335

Trp Pro  Trp Gln Val Ser Leu  Arg Thr Arg Phe Gly  Lys His Phe
    4340                 4345                 4350

Cys Gly  Gly Thr Leu Ile Ser  Pro Glu Trp Val Leu  Thr Ala Ala
    4355                 4360                 4365

His Cys  Leu Lys Lys Ser Ser  Arg Pro Ser Ser Tyr  Lys Val Ile
    4370                 4375                 4380

Leu Gly  Ala His Gln Glu Val  Asn Leu Glu Ser His  Val Gln Glu
    4385                 4390                 4395

Ile Glu  Val Ser Arg Leu Phe  Leu Glu Pro Thr Gln  Ala Asp Ile
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    4400                4405                4410

Ala Leu  Leu Lys Leu Ser Arg  Pro Ala Val Ile Thr  Asp Lys Val
    4415                4420                4425

Met Pro  Ala Cys Leu Pro Ser  Pro Asp Tyr Met Val  Thr Ala Arg
    4430                4435                4440

Thr Glu  Cys Tyr Ile Thr Gly  Trp Gly Glu Thr Gln  Gly Thr Phe
    4445                4450                4455

Gly Thr  Gly Leu Leu Lys Glu  Ala Gln Leu Leu Val  Ile Glu Asn
    4460                4465                4470

Glu Val  Cys Asn His Tyr Lys  Tyr Ile Cys Ala Glu  His Leu Ala
    4475                4480                4485

Arg Gly  Thr Asp Ser Cys Gln  Gly Asp Ser Gly Gly  Pro Leu Val
    4490                4495                4500

Cys Phe  Glu Lys Asp Lys Tyr  Ile Leu Gln Gly Val  Thr Ser Trp
    4505                4510                4515

Gly Leu  Gly Cys Ala Arg Pro  Asn Lys Pro Gly Val  Tyr Ala Arg
    4520                4525                4530

Val Ser  Arg Phe Val Thr Trp  Ile Glu Gly Met Met  Arg Asn Asn
    4535                4540                4545


<210> 65
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 65
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc       60

cguuaacaac uugaaaaagu ggcaccgagu cggugcuuuu                           100


<210> 66
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 66
ggtgctagcc ttgcgttccg                                                  20


<210> 67
<211> 20
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 67
gcttacctgt ctgtggaagc 20

<210> 68
<211> 20
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 68
tgcttacctg tctgtggaag 20

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 69
cccatacctt ggagcaacgg 20

<210> 70
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 70
ccagccaagc gcacctaatt tcc 23

<210> 71
<211> 98
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 71
ggaaauuagg ugcgcuuggc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuu 98

<210> 72
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 72
ggcgcauaaa gaugagacgc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu gucaccgagu cggugcuucg 100

<210> 73
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 73
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 74
<211> 118
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 74
ggcgcauaaa gaugagacgc guuuuagagc uaugcuguuu ugaaaaaaac agcauagcaa 60

guuaaaauaa ggcuaguccg uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 118

<210> 75
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 75
gctgcgccaa ggcgcgggtg tagggatgg 29

<210> 76
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (11)..(11)
<223> a, c, t, g, unknown or other

<220>
<221> modified_base
<222> (13)..(13)
<223> a, c, t, g, unknown or other

<400> 76
ggttattcag ncntcttttt ctgatac 27

<210> 77
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 77
acacccgcac cttggcgcag cggtggaagg tgg 33

<210> 78
<211> 33
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 78
acacccgcac cttggcgcag gggggagggg ggg 33

<210> 79
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 79
acacccgcgc cttggcgcag cggtggaagg tgg 33

<210> 80
<211> 23
<212> DNA
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oligonucleotide

<400> 80
cccgcacctt ggcgcagcgg tgg 23

<210> 81
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 81
caggttccat gggatgctct 20

<210> 82
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 82
ggtggctcac cagctccagc 20

<210> 83
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 83
ttggaaagac ggaggcagcc 20

<210> 84
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 84
gaaagacgga ggcagcctgg 20

<210> 85
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 85
tcccaggcct ggagtttatt 20

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

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 86
agcacctacc tcgggagctg 20

<210> 87
<211> 20
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 87
ctttccaggt catcacagtt 20

<210> 88
<211> 20
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 88
cctttccagg tcatcacagt 20

<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 89
tttccaggtc atcacagttg 20

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 90
cttacctgcc ccatgggtgc 20

<210> 91
<211> 20
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 91
taaggcccaa gggggcaagc 20

<210> 92
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
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oligonucleotide

<400> 92
cctcttcacc tgctcctgag 20

<210> 93
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 93
gcctcttcac ctgctcctga 20

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 94
ttcacctgct cctgaggggc 20

<210> 95
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 95
tcacctgctc ctgaggggcc 20

<210> 96
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 96
cccaggctgc agctcccact 20

<210> 97
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 97
ccccaggctg cagctcccac 20

<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 98
gcaggtgacc gtggcctgcg 20

<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 99
ctcctttagg aggctggtgg 20

<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 100
ttttcaggag aattttggtt 20

<210> 101
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 101
cttttcagga gaattttggt 20

<210> 102
<211> 20
<212> DNA
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oligonucleotide

<400> 102
taatttggcc cttcgtctta 20

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 103
agactttgtc cataagacga 20

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 104
gactttgtcc ataagacgaa 20

<210> 105
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 105
agccaatggc ctccttcagt 20

<210> 106
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 106
tcccaactga aggaggccat 20

<210> 107
<211> 20
<212> DNA
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oligonucleotide

<400> 107
ggcctccttc agttgggaca 20

<210> 108
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<212> DNA
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<220>
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oligonucleotide

<400> 108
gaccatgtcc caactgaagg 20

<210> 109
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oligonucleotide

<400> 109
gccaatggcc tccttcagtt 20

<210> 110
<211> 20
<212> DNA
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<400> 110
attgtcttga tcaattctgg 20

<210> 111
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oligonucleotide

<400> 111
attctggagg aaataactag 20

<210> 112
<211> 20
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oligonucleotide

<400> 112
tctgggtgtt ctggagtttc 20

<210> 113
<211> 20
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 113
aacatagcaa atcttgattt 20

<210> 114
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oligonucleotide

<400> 114
gtagaatttt ttcttctagg 20

<210> 115
<211> 20
<212> DNA
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<223> Description of Artificial Sequence: Synthetic
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<400> 115
actacaagtc aaaaatgaag 20

<210> 116
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 116
tatattggtc ttccacggtc 20

<210> 117
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 117
caaagacctt ctccagaccg 20

<210> 118
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oligonucleotide

<400> 118

ggtcttccac ggtctggaga 20

<210> 119
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 119
ttgtttatat tggtcttcca 20

<210> 120
<211> 20
<212> DNA
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oligonucleotide

<400> 120
cttttatttg actatgctgt 20

<210> 121
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 121
aaagtctgga tatagagagt 20

<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 122
gttggtttaa ttgtttatat 20

<210> 123
<211> 20
<212> DNA
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oligonucleotide

<400> 123
tgatggtaag acactttggt 20

<210> 124

<211> 20
<212> DNA
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oligonucleotide

<400> 124
ggagtagttc ttggtgctct 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 125
aacatgatgg taagacactt 20

<210> 126
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 126
tgaagaaagg gagtagttct 20

<210> 127
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 127
agttcttggt gctcttggct 20

<210> 128
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 128
atgatggtaa gacactttgg 20

<210> 129
<211> 20
<212> DNA
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 129
gaagatagag aaatttctgt 20

<210> 130
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 130
ggaagataga gaaatttctg 20

<210> 131
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<220>
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oligonucleotide

<400> 131
tatttcattc aactgaagaa 20

<210> 132
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 132
atttcattca actgaagaaa 20

<210> 133
<211> 20
<212> DNA
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oligonucleotide

<400> 133
gtctactgtg atgttatatc 20

<210> 134
<211> 20
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<400> 134
taaatggtgg tacattcagc 20

<210> 135
<211> 20
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oligonucleotide

<400> 135
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<210> 136
<211> 20
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oligonucleotide

<400> 136
tgtaccacca tttataacag 20

<210> 137
<211> 20
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oligonucleotide

<400> 137
ttcacctctg ttataaatgg 20

<210> 138
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oligonucleotide

<400> 138
aacagaggtg aacatacaag 20

<210> 139
<211> 20
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oligonucleotide

<400> 139
ttgagagttg ctgggtctga 20

<210> 140
<211> 20
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oligonucleotide

<400> 140
tgaaaaactt gagagttgct 20

<210> 141
<211> 20
<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 141
ttaattcaac atcgaataga 20

<210> 142
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 142
tttgggaggc ttgatggtaa 20

<210> 143
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 143
cattatattc aggtagtcca 20

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 144
ttgggaggct tgatggtaag 20

<210> 145
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 145
ttttgggagg cttgatggta 20

<210> 146
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 146
acaaaacttc aatgaaacgt 20

<210> 147
<211> 20
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oligonucleotide

<400> 147
tatggttttg ggaggcttga 20

<210> 148
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<400> 148
actacaaata tggttttggg 20

<210> 149
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oligonucleotide

<400> 149
gagaactaca aatatggttt 20

<210> 150
<211> 20
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oligonucleotide

<400> 150
aggacacttc aactgtccag 20

<210> 151
<211> 20
<212> DNA
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oligonucleotide

<400> 151
gccgtcctcc tcggaacgca 20

<210> 152
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<400> 152
gctagccttg cgttccgagg 20

<210> 153
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oligonucleotide

<400> 153
gcgttccgag gaggacggcc 20

<210> 154
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<220>
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oligonucleotide

<400> 154
gccttgcgtt ccgaggagga 20

<210> 155
<211> 20
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 155
ggacgaggac ggcgactacg 20

<210> 156
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 156
ggacggcgac tacgaggagc 20

<210> 157
<211> 20
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<400> 157
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<210> 158
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oligonucleotide

<400> 158
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<210> 159
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oligonucleotide

<400> 159
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<210> 160
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oligonucleotide

<400> 160
cgcccgtgcg caggaggacg 20

<210> 161
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oligonucleotide

<400> 161
tcagctccag gcggtcctgg 20

<210> 162
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oligonucleotide

<400> 162
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<210> 163
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oligonucleotide

<400> 163
cgtgcgcagg aggacgagga 20

<210> 164
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oligonucleotide

<400> 164
ccaggaccgc ctggagctga 20

<210> 165
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oligonucleotide

<400> 165
tcttggtgag gtatccccgg 20

<210> 166
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<220>
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oligonucleotide

<400> 166
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<210> 167
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oligonucleotide

<400> 167
cttggtgagg tatccccggc 20

<210> 168
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oligonucleotide

<400> 168
ggatcttggt gaggtatccc 20

<210> 169
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oligonucleotide

<400> 169
gaagatgagt ggcgacctgc 20

<210> 170
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oligonucleotide

<400> 170
agcaccacca cgtaggtgcc 20

<210> 171
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oligonucleotide

<400> 171
ggtcgccact catcttcacc 20

<210> 172
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oligonucleotide

<400> 172
ctccttcagc accaccacgt 20

<210> 173
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oligonucleotide

<400> 173
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<210> 174
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oligonucleotide

<400> 174
gcgcactgcc cgccgcctgc 20

<210> 175
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oligonucleotide

<400> 175
ggcttcctgg tgaagatgag 20

<210> 176
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oligonucleotide

<400> 176
cacctacgtg gtggtgctga 20

<210> 177
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oligonucleotide

<400> 177
ctacgtggtg gtgctgaagg 20

<210> 178
<211> 20
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oligonucleotide

<400> 178
atggaagaca tgcaggatct 20

<210> 179
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 179
agacatgcag gatcttggtg 20

<210> 180
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<220>
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oligonucleotide

<400> 180
ctcatcttca ccaggaagcc 20

<210> 181
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<220>
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oligonucleotide

<400> 181
ctcctcgatg tagtcgacat 20

<210> 182
<211> 20
<212> DNA
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<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 182
tattcatccg cccggtaccg 20

<210> 183
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<220>
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oligonucleotide

<400> 183
tcctcgatgt agtcgacatg 20

<210> 184
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oligonucleotide

<400> 184
cctcctcgat gtagtcgaca 20

<210> 185
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 185
gccccatgtc gactacatcg 20

<210> 186
<211> 20
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oligonucleotide

<400> 186
ccatgtcgac tacatcgagg 20

<210> 187
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 187

ggggctggta ttcatccgcc 20

<210> 188
<211> 20
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<220>
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oligonucleotide

<400> 188
gtcgacatgg ggcaacttca 20

<210> 189
<211> 20
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<220>
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oligonucleotide

<400> 189
accaccggga aatcgagggc 20

<210> 190
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 190
gagtgaccac cgggaaatcg 20

<210> 191
<211> 20
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<220>
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oligonucleotide

<400> 191
agtgaccacc gggaaatcga 20

<210> 192
<211> 20
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<220>
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oligonucleotide

<400> 192
ccaccgggaa atcgagggca 20

<210> 193

<211> 20
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<220>
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oligonucleotide

<400> 193
gaagcgggtc ccgtcctcct 20

<210> 194
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 194
ctaggagata cacctccacc 20

<210> 195
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 195
cagcatacag agtgaccacc 20

<210> 196
<211> 20
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<220>
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oligonucleotide

<400> 196
aagcgggtcc cgtcctcctc 20

<210> 197
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 197
tgaccctgcc ctcgatttcc 20

<210> 198
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 198
cactctgtat gctggtgtct 20

<210> 199
<211> 20
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<220>
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oligonucleotide

<400> 199
ccctgccctc gatttcccgg 20

<210> 200
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 200
ccggtggtca ctctgtatgc 20

<210> 201
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 201
ggaaatcgag ggcagggtca 20

<210> 202
<211> 20
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<220>
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oligonucleotide

<400> 202
ccagcataca gagtgaccac 20

<210> 203
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<220>
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oligonucleotide

<400> 203
cttggcagtt gagcacgcgc 20

<210> 204
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 204
ctgcgcgtgc tcaactgcca 20

<210> 205
<211> 20
<212> DNA
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<220>
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<400> 205
tgcgcgtgct caactgccaa 20

<210> 206
<211> 20
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<220>
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<400> 206
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<210> 207
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<220>
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oligonucleotide

<400> 207
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<210> 208
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<220>
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oligonucleotide

<400> 208
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<210> 209
<211> 20
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<220>
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oligonucleotide

<400> 209
cagcggccgg gatgccggcg 20

<210> 210
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 210
ccgggatgcc ggcgtggcca 20

<210> 211
<211> 20
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<220>
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oligonucleotide

<400> 211
gtggtcagcg gccgggatgc 20

<210> 212
<211> 20
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<220>
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oligonucleotide

<400> 212
cgctgaccac ccctgccagg 20

<210> 213
<211> 20
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<220>
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oligonucleotide

<400> 213
ggcaggggtg gtcagcggcc 20

<210> 214
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<212> DNA
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<220>
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oligonucleotide

<400> 214
gtgctcaact gccaagggaa 20

<210> 215
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 215
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<210> 216
<211> 20
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<400> 216
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<210> 217
<211> 20
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oligonucleotide

<400> 217
gctgaccacc cctgccaggt 20

<210> 218
<211> 20
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<220>
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oligonucleotide

<400> 218
ggccgctgac cacccctgcc 20

<210> 219
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<220>
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<400> 219
ggcatcgtcc cggaagttgc 20

<210> 220
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<220>
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<400> 220
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<210> 221
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<220>
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oligonucleotide

<400> 221
gtcccggaag ttgccggcag 20

<210> 222
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<400> 222
cggctgtacc cacccgccag 20

<210> 223
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oligonucleotide

<400> 223
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<210> 224
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<220>
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<400> 224
agtagaggca ggcatcgtcc 20

<210> 225
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<220>
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<210> 226
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<220>
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<400> 226
gtttattcgg aaaagccagc 20

<210> 227
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<220>
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oligonucleotide

<400> 227
gcggctgtac ccacccgcca 20

<210> 228
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<400> 228
caccgctgcc ggcaacttcc 20

<210> 229
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<220>
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<400> 229
agccctcgcc aggcgctggc 20

<210> 230
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<220>
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<400> 230
caacgccgcc tgccagcgcc 20

<210> 231
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<220>
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oligonucleotide

<400> 231
gcacgacccc agccctcgcc 20

<210> 232
<211> 20
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<220>
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<400> 232
ccgcctgcca gcgcctggcg 20

<210> 233
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<220>
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oligonucleotide

<400> 233
tgccagcgcc tggcgagggc 20

<210> 234
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<220>
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oligonucleotide

<400> 234
tgctgctgcc cctggcgggt 20

<210> 235
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<220>
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oligonucleotide

<400> 235
tcaccgctgc cggcaacttc 20

<210> 236
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<220>
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oligonucleotide

<400> 236
ggcgagggct ggggtcgtgc 20

<210> 237
<211> 20
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<220>
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oligonucleotide

<400> 237
ttccgaataa actccaggcc 20

<210> 238
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<220>
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oligonucleotide

<400> 238
gtgctgctgc ccctggcggg 20

<210> 239
<211> 20
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 239
gccagcgcct ggcgagggct 20

<210> 240
<211> 20
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 240
cctcgccagg cgctggcagg 20

<210> 241
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 241
gagatacctg agtaactttc 20

<210> 242
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 242
acgtgggaga actacaaata 20

<210> 243
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 243
cgatgttgaa ttaatgtcca 20

<210> 244
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 244
cacaaaactt caatgaaacg 20

<210> 245
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 245
tacgaattga gttggaagac 20

<210> 246
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 246
ctatggagta tatcttctct 20

<210> 247
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 247
ccgcaccttg gcgcagcgg 19

<210> 248
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 248
agatacctga ataaccctc 19

<210> 249
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 249
gatacctgaa taaccctc 18

<210> 250
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 250
atacctgaat aaccctc 17

<210> 251
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 251
ggctgatgag gccgcacatg 20

<210> 252
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 252
cgcctgccag cgcctggcga 20

<210> 253
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 253
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 254
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 254
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 255
<211> 101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 255
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu u 101

<210> 256
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 256
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 257
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 257
aagauaccug aauaacucuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 258
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 258
gguggcucac cagcuccagc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 259
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 259
gcuuaccugu cuguggaagc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 260
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 260
ugcuuaccug ucuguggaag guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 261
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 261
uuggaaagac ggaggcagcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 262
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 262
gaaagacgga ggcagccugg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 263
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 263
ucccaggccu ggaguuuauu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 264
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 264
agcaccuacc ucgggagctg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 265
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 265
cuuuccaggu caucacaguu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<213> Artificial Sequence

<220>
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polynucleotide

<400> 266
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 267
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polynucleotide

<400> 267
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 268
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<220>
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polynucleotide

<400> 268
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 269
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<220>
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<400> 269
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 270
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<220>
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polynucleotide

<400> 270
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 271
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polynucleotide

<400> 271
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 272
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polynucleotide

<400> 272
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 273
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 274
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<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 274
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 275
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 275
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 276
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<220>
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polynucleotide

<400> 276
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 277
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<220>
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polynucleotide

<400> 277
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 278
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<212> RNA
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<220>
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polynucleotide

<400> 278
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 279
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 280
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 281
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 282
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 283
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 284
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 285
<211> 100
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 285
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 286
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 287
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 287
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 288
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
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polynucleotide

<400> 288
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 289
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 289
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 290
<211> 100
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<220>
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polynucleotide

<400> 290
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 291
<211> 100
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<220>
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polynucleotide

<400> 291
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 292
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 292
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 293
<211> 100
<212> RNA
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 294
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<212> RNA
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<220>
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polynucleotide

<400> 294
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 295
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<220>
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polynucleotide

<400> 295
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 296
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<220>
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polynucleotide

<400> 296
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 297
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<212> RNA
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<220>

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polynucleotide

<400> 297
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 298
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polynucleotide

<400> 298
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 299
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<212> RNA
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<220>
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polynucleotide

<400> 299
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 300
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 300
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 301
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 301
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 302
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<220>
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polynucleotide

<400> 302
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 303
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polynucleotide

<400> 303
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 304
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polynucleotide

<400> 304
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 305
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polynucleotide

<400> 305
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 306
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<220>
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polynucleotide

<400> 306
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 307
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polynucleotide

<400> 307
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 308
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 309
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 310
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 311
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<213> Artificial Sequence

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 312
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polynucleotide

<400> 312
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 313
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 314
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 315
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 316
<211> 100
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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polynucleotide

<400> 317
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 318
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polynucleotide

<400> 318
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 319
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 320
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 321
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 322
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 323
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 324
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 325
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 326
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 327
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 328
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<210> 330
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 333
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 334
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<213> Artificial Sequence

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<400> 334
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 335
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 336
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<400> 336
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 337
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<400> 337
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 338
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 338
cgcccgugcg caggaggacg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 339
<211> 100
<212> RNA
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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 339
ucagcuccag gcgguccugg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 340
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 340
cuuggcgcag cgguggaagg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 341
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 341
cgugcgcagg aggacgagga guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 342
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 342
ccaggaccgc cuggagcuga guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 343
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 343
ucuuggugag guaucccccgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 344
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 344
cagugcgcuc ugacugcgag guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 345
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 345
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 346
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 346
ggaucuuggu gagguauccc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 347
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<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 347
gaagaugagu ggcgaccugc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 348
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 348
agcaccacca cguaggugcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 349
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 349
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 350
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 350
cuccuucagc accaccacgu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 351
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 351
gaguggcgac cugcuggagc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 352
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 352
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 353
<211> 100
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 353
ggcuuccugg ugaagaugag guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 354
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 354
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 355
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 355
cuacguggug gugcugaagg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 356
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 356
auggaagaca ugcaggaucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 357
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 357
agacaugcag gaucuuggug guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 358
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 358
cucaucuuca ccaggaagcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 359
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 359
cuccucgaug uagucgacau guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 360
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 360
uauucauccg cccgguaccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 361
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 361
uccucgaugu agucgacaug guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 362
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 362
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 363
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 363
gccccauguc gacuacaucg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 364
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 364
ccaugucgac uacaucgagg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 365
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 365
ggggcuggua uucauccgcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 366
<211> 100
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 366
gucgacaugg ggcaacuuca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 367
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 367
accaccggga aaucgagggc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 368
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 368
gagugaccac cgggaaaucg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 369
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 369
agugaccacc gggaaaucga guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 370
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 370
ccaccgggaa aucgagggca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 371
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 371
gaagcggguc ccguccuccu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 372
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 372
cuaggagaua caccuccacc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 373
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 373
cagcauacag agugaccacc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 374
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 374
aagcgggucc cguccuccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 375
<211> 100
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<220>
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polynucleotide

<400> 375
ugacccugcc cucgauuucc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 376
<211> 100
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<220>
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polynucleotide

<400> 376
cacucuguau gcuggugucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 377
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 377
cccugcccuc gauuucccgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 378
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 378
ccggugguca cucuguaugc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 379
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 379
ggaaaucgag ggcaggguca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 380
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
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polynucleotide

<400> 380
ccagcauaca gagugaccac guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 381
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 381
cuuggcaguu gagcacgcgc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 382
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 382
cugcgcgugc ucaacugcca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 383
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 383
ugcgcgugcu caacugccaa guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 384
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 384
cgggaugccg gcguggccaa guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 385
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 385
cgugcucaac ugccaaggga guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 386
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 386
ccuuggccac gccggcaucc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 387
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 387
cagcggccgg gaugccggcg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 388
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 388
ccgggaugcc ggcguggcca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 389
<211> 100
<212> RNA
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<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 389
guggucagcg gccgggaugc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 390
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<212> RNA
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polynucleotide

<400> 390
cgcugaccac cccugccagg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 391
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<212> RNA
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polynucleotide

<400> 391
ggcaggggug gucagcggcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 392
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 392
gugcucaacu gccaagggaa guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 393
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 393
ucauggcacc caccuggcag guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 394
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 394
uggcaggggu ggucagcggc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 395
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 395
gcugaccacc ccugccaggu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 396
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 396
ggccgcugac cacccugcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 397
<211> 100
<212> RNA
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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 397
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 398
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 398
ggcuuuuccg aauaaacucc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 399
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 399
gucccggaag uugccggcag guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 400
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 401
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 401
gucgugcugg ucaccgcugc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 402
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 402
aguagaggca ggcaucgucc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 403
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
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polynucleotide

<400> 403
uccgaauaaa cuccaggccu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 404
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 404
guuuauucgg aaaagccagc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 405
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 405
gcggcuguac ccacccgcca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 406
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 406
caccgcugcc ggcaacuucc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 407
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 407
agcccucgcc aggcgcuggc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 408
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 408
caacgccgcc ugccagcgcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 409
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 409
gcacgacccc agcccucgcc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 410
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 410
ccgccugcca gcgccuggcg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 411
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 411
ugccagcgcc uggcgagggc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 412
<211> 100
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 412
ugcugcugcc ccuggcgggu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 413
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 413
ucaccgcugc cggcaacuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 414
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 414
ggcgagggcu ggggucgugc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 415
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 415
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 416
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<220>
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polynucleotide

<400> 416
gugcugcugc cccuggcggg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 417
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 417
gccagcgccu ggcgagggcu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 418
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<212> RNA
<213> Artificial Sequence

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polynucleotide

<400> 418
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 419
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 419
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 420
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 420
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 421
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 421
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 422
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 422
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 423
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 424
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<212> RNA
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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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cgauguugaa uuaaugucca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 425
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 425
cacaaaacuu caaugaaacg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 426
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
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polynucleotide

<400> 426
uacgaauuga guuggaagac guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 427
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 427
cuauggagua uaucuucucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 428
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 428
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaacaac gggaaaccgu ggcaccgagu cggugcuuuu 100

<210> 429
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 429
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 430
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 430
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 431
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 431
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 432
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<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<220>
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oligonucleotide

<400> 432
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 433
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<212> DNA
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<220>
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oligonucleotide

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oligonucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 434

<211> 100
<212> DNA
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<220>
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oligonucleotide

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oligonucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 435
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<212> DNA
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<220>
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oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 436
<211> 102
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 436
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guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuuu uu 102

<210> 437
<211> 99
<212> RNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 437
ccgcaccuug gcgcagcggg uuuuagagcu agaaauagca aguuaaaaua aggcuagucc 60

guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuu 99

<210> 438
<211> 103

<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 438
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 439
<211> 100
<212> RNA
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<220>
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polynucleotide

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<222> (3)..(3)
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<400> 439
aanauaccug aauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 440
<211> 100
<212> RNA
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<220>
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polynucleotide

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<223> Inosine

<220>
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<223> Inosine

<400> 440
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<212> RNA
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polynucleotide

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<222> (10)..(10)
<223> Inosine

<400> 441
aagauaccun aauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 442
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 442
agauaccuga auaacccucg uuuuagagcu agaaauagca aguuaaaaua aggcuagucc 60

guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuu 99

<210> 443
<211> 98
<212> RNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 443
gauaccugaa uaacccucgu uuuagagcua gaaauagcaa guuaaaauaa ggcuaguccg 60

uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 98

<210> 444
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<212> RNA
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<220>
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oligonucleotide

<400> 444
auaccugaau aacccucguu uuagagcuag aaauagcaag uuaaaauaag gcuaguccgu 60

uaucaacuug aaaaaguggc accgagucgg ugcuuuu 97

<210> 445
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 445
aagauaccug aauaacucuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 446
<211> 100
<212> RNA
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<220>
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polynucleotide

<400> 446
ggcugaugag gccgcacaug guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 447
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<212> RNA
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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 447
ucagcuccag gcgguccugg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 448
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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 448
ucagcuccag gcgguccugg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 449
<211> 103
<212> RNA
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<220>
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polynucleotide

<400> 449
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 450
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<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 450
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 451
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<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 451
ucagcuccag gcgguccugg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 452
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<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 452
cgccugccag cgccuggcga guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 453
<211> 22
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 453
ctagcacctg ccccagcggt gg 22

<210> 454
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 454
tccctaccct ggcacagcag ggg 23

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 455
cccacactca gacgcagcga ggg 23

<210> 456
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 456
cccgcactgg agcagcaggg a 21

<210> 457
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 457
cttgcacctt ggtagcagct gggg 24

<210> 458
<211> 23
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 458
ctggcaccat ggcccagcag tgg 23

<210> 459
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 459
actgcatctt agtgcagagg tgg 23

<210> 460
<211> 23
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 460
tccacacctt ggcgcactgg aag 23

<210> 461
<211> 23
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<220>
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oligonucleotide

<400> 461
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<210> 462
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<220>
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oligonucleotide

<400> 462
accgcaccat tgcacagcct agg 23

<210> 463
<211> 24
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 463
gccgcaccat gggcacagcg ggga 24

<210> 464
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 464
cccatacctg gcacagcggt gg 22

<210> 465
<211> 22
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<220>
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oligonucleotide

<400> 465
caagcacctg gctcagaggt gg 22

<210> 466
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 466
accgcacctg gcacagtgga ag 22

<210> 467
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 467
ccccaccctt ggcacagagc agg 23

<210> 468
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<220>
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oligonucleotide

<400> 468
ccagcaccta gcgcagagct gg 22

<210> 469
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 469
cccgcaccta cctcagcagg gg 22

<210> 470
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<220>
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oligonucleotide

<400> 470
cccgcacccc accgcagcgg ggg 23

<210> 471
<211> 23
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<213> Artificial Sequence

<220>
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oligonucleotide

<400> 471
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<210> 472
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<220>
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oligonucleotide

<400> 472
cccgcaccac agtgcaccgg ggg 23

<210> 473
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<220>
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oligonucleotide

<400> 473
cctccacaat ggcgcagggg cgg 23

<210> 474
<211> 22
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<220>
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oligonucleotide

<400> 474
ccagcacctg gcacagaaga gg 22

<210> 475
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 475
accgcaccaa ggtgcatagg agg 23

<210> 476
<211> 22
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 476
ccagcacttg ccccagcaga gg 22

<210> 477
<211> 23
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<220>
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oligonucleotide

<400> 477
ctcccaccct ggcccagcgg ggg 23

<210> 478
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<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide

<400> 478
acagcacctt ggcccagagg cga 23

<210> 479
<211> 23
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<220>
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oligonucleotide

<400> 479
acggcacctt gggctagcgg ggg 23

<210> 480
<211> 23
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<220>
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oligonucleotide

<400> 480
cccgcaccca gctgcagccg agg 23

<210> 481
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oligonucleotide

<400> 481
ccagcacctg gtgcagagta gg 22

<210> 482
<211> 23
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<220>
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oligonucleotide

<400> 482
cccacacctg ggcccagtgg agg 23

<210> 483
<211> 22
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<220>
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oligonucleotide

<400> 483
ccagcacctg gtgcagctta gg 22

<210> 484
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<220>
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oligonucleotide

<400> 484
tccacacaat ggcacagcag agg 23

<210> 485
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<220>
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oligonucleotide

<400> 485
cccgcacctg gctcagaggg tc 22

<210> 486
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oligonucleotide

<400> 486
cgggcaccat ggcagcagcg gagg 24

<210> 487
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<212> DNA
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oligonucleotide

<400> 487
cccacaccat ggcccagtga gag 23

<210> 488
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oligonucleotide

<400> 488
ccagcacctg gcacagtgaa gg 22

<210> 489
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<220>
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oligonucleotide

<400> 489
cccacacatg gccacagcag tgg 23

<210> 490
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<220>
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oligonucleotide

<400> 490
ctggcacctt agcacagagg agg 23

<210> 491
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<220>
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oligonucleotide

<400> 491
cccgcaccag agcgcagggg gag 23

<210> 492
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<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 492
gccacacctg gcccagcagg gg 22

<210> 493
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<210> 632
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<210> 636
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<210> 638
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oligonucleotide

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<210> 639
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<210> 640
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<210> 641

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<210> 642
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<210> 643
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<210> 644
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<210> 647
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<210> 648
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<210> 649
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<210> 652
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<210> 653
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<210> 655
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<400> 655
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<210> 657
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<210> 660
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<210> 662
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<210> 663
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<210> 664
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<400> 683
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<210> 685
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<210> 687
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oligonucleotide

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<400> 688
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<210> 689
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<210> 690
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<400> 691
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<210> 692
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<400> 692
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<210> 693
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<210> 694
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<400> 695
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<210> 696
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<400> 696
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<210> 697
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<400> 697
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<210> 698
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<400> 698
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<210> 699
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<400> 699
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<210> 700
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<400> 700
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<210> 701
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<400> 701
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<210> 702
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<210> 703
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oligonucleotide

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<210> 704
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<220>
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oligonucleotide

<400> 704

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<210> 705
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oligonucleotide

<400> 705
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<210> 706
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<400> 706
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<210> 707
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<400> 707
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oligonucleotide

<400> 708
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oligonucleotide

<400> 709
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<210> 710

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oligonucleotide

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oligonucleotide

<400> 711
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oligonucleotide

<400> 712
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<210> 713
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<400> 713
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<210> 714
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oligonucleotide

<400> 714
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<210> 715
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oligonucleotide

<400> 715
tagataccta taagcctctg g 21

<210> 716
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oligonucleotide

<400> 716
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<210> 717
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oligonucleotide

<400> 717
aagatacctt aaaacccttc agc 23

<210> 718
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oligonucleotide

<400> 718
aatttacctg aatagtcatt agg 23

<210> 719
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<210> 794
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<210> 795
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<210> 798
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<210> 801
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<400> 802
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<400> 803
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<210> 804
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<400> 804
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<400> 805
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<210> 809
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<400> 811
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<400> 812
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oligonucleotide

<400> 814
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<210> 815
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<400> 815
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<210> 816
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oligonucleotide

<400> 816
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<210> 817
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<210> 818
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<400> 818
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<210> 819
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<400> 820
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oligonucleotide

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<400> 823
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oligonucleotide

<400> 824
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<210> 827
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<210> 897
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<210> 898
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<210> 905
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<210> 906
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<210> 907
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<210> 909
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<400> 909
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<210> 910
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<400> 914
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<210> 923
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<210> 924
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oligonucleotide

<400> 924
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<210> 926
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<400> 926
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<210> 927
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oligonucleotide

<400> 928
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<400> 929
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oligonucleotide

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oligonucleotide

<400> 932
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<210> 933
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oligonucleotide

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<210> 934
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<210> 1004
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<210> 1017
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<210> 1019
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<210> 1020
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<210> 1037
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<210> 1039
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<210> 1040
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<400> 1047
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<210> 1094
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<210> 1114
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<210> 1125
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<210> 1128
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<210> 1130
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<210> 1131
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<210> 1133
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<210> 1134
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<210> 1137
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<210> 1138
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<210> 1139
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<210> 1144
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<210> 1145
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<210> 1146
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oligonucleotide

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<210> 1148
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<210> 1149
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oligonucleotide

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<210> 1150
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<210> 1151
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<210> 1152
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<210> 1153
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oligonucleotide

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<210> 1154
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<210> 1155
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<210> 1156
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<210> 1157
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<210> 1158
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oligonucleotide

<400> 1158
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<210> 1159
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oligonucleotide

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<210> 1160
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oligonucleotide

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<210> 1161
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<400> 1161
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<210> 1162
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<210> 1163
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<210> 1164
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<210> 1209
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<210> 1214
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<210> 1219
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<210> 1232
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<210> 1245
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<210> 1246
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<400> 1252
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<210> 1253
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<210> 1254
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<210> 1255
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<400> 1255
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<210> 1256
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<210> 1259
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<210> 1260
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<210> 1261
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<210> 1262

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oligonucleotide

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<210> 1263
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oligonucleotide

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<210> 1265
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oligonucleotide

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<210> 1266
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<210> 1267
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<210> 1270
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oligonucleotide

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oligonucleotide

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<210> 1272
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oligonucleotide

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<210> 1273
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oligonucleotide

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<210> 1274
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<400> 1274
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<210> 1275
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oligonucleotide

<400> 1275
aagatataca tactaaccct ctgg 24

<210> 1276
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<210> 1277
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<400> 1307
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<210> 1308
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<400> 1308
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<210> 1310
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<210> 1311
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<210> 1313
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oligonucleotide

<400> 1313
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<210> 1314
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oligonucleotide

<400> 1314
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<210> 1315
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<212> DNA
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oligonucleotide

<400> 1315
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<210> 1316
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oligonucleotide

<400> 1316
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<210> 1317
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<210> 1318
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<400> 1318
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<210> 1319
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<210> 1320
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<210> 1321
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<210> 1322
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oligonucleotide

<400> 1322
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<210> 1323
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<400> 1323
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<210> 1324
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<220>
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oligonucleotide

<400> 1324
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<210> 1325
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<212> DNA
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oligonucleotide

<400> 1325

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<210> 1326
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<400> 1326
actatactga ctaaccctct ag 22

<210> 1327
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<400> 1327
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<210> 1328
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<400> 1328
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<210> 1329
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<210> 1330
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<400> 1330
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<210> 1331

<211> 22
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<210> 1332
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<210> 1333
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<400> 1333
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<210> 1334
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<400> 1334
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<210> 1335
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oligonucleotide

<400> 1335
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<210> 1336
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<400> 1336
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<210> 1337
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oligonucleotide

<400> 1337
aagatatctg aaaatccctg cgc 23

<210> 1338
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<400> 1338
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<210> 1339
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<400> 1339
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<210> 1340
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<400> 1340
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<400> 1341
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<210> 1342
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<400> 1342
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<210> 1343
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<400> 1343
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<210> 1344
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<400> 1344
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<210> 1345
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oligonucleotide

<400> 1345
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<210> 1346
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<220>
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<400> 1346
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<210> 1347
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<400> 1347
catataccaa aataacccat ggg 23

<210> 1348
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1348
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<210> 1349
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<220>
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oligonucleotide

<400> 1349
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<210> 1350
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oligonucleotide

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<400> 1351
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<210> 1352
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<220>
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<400> 1352
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<210> 1353
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<220>
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oligonucleotide

<400> 1353
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<210> 1354
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oligonucleotide

<400> 1354
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<210> 1355
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oligonucleotide

<400> 1355
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<210> 1356
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<400> 1356
aagaaagctg gaaaacactc cag 23

<210> 1357
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oligonucleotide

<400> 1357
aagatgcctg agtctccccc gtg 23

<210> 1358
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oligonucleotide

<400> 1358
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<210> 1359
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oligonucleotide

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<210> 1360
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<220>
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oligonucleotide

<400> 1360
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<210> 1361
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<400> 1361
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<210> 1362
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<220>
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oligonucleotide

<400> 1362
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<210> 1363
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<220>
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oligonucleotide

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<210> 1364
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oligonucleotide

<400> 1364
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<210> 1365
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oligonucleotide

<400> 1365
aagatacttg acaactctct ga 22

<210> 1366
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oligonucleotide

<400> 1366
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<210> 1367
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oligonucleotide

<400> 1367
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<210> 1368
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oligonucleotide

<400> 1368
aatataccta aataacttac agc 23

<210> 1369
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oligonucleotide

<400> 1369
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<210> 1370
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oligonucleotide

<400> 1370
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<210> 1371
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oligonucleotide

<400> 1371
aagataccta aatatatatc tga 23

<210> 1372
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<220>
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oligonucleotide

<400> 1372
aggatgactg aaaaatcccc agg 23

<210> 1373
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<220>
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oligonucleotide

<400> 1373
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<210> 1374
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<220>
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oligonucleotide

<400> 1374
aagataccaa aatgtaactc agg 23

<210> 1375
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oligonucleotide

<400> 1375
aagataactt aaaaactcta agg 23

<210> 1376
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<220>
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oligonucleotide

<400> 1376
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<210> 1377
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<220>
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oligonucleotide

<400> 1377
aagatgcctg aactagtcct tggg 24

<210> 1378
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1378
aaaataactg aaaaccctca ac 22

<210> 1379
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<220>
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oligonucleotide

<400> 1379
aacatacatc cacaaccatc agg 23

<210> 1380
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<220>
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oligonucleotide

<400> 1380
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<210> 1381
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<220>
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oligonucleotide

<400> 1381
catatacttg aataaccaac tgg 23

<210> 1382
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<220>
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oligonucleotide

<400> 1382
aagatcttaa taatcatctg g 21

<210> 1383
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oligonucleotide

<400> 1383
aagaaacccg agtccctctg g 21

<210> 1384
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<212> DNA
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oligonucleotide

<400> 1384
aagatatctc atatcactca gg 22

<210> 1385
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oligonucleotide

<400> 1385
acaatacctt gaataaccca caag 24

<210> 1386
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oligonucleotide

<400> 1386
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<210> 1387
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oligonucleotide

<400> 1387
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<210> 1388
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oligonucleotide

<400> 1388
gaataacctg aataaccccc aga 23

<210> 1389
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<210> 1415
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<210> 1419
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<210> 1420
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<210> 1422
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<210> 1423
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<210> 1424
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<210> 1425
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<210> 1426
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<210> 1427
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<210> 1429
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<400> 1430
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<210> 1431
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<210> 1432
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<210> 1433
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<210> 1435
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<210> 1436
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<210> 1437
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<210> 1438
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<210> 1439
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<210> 1454
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<210> 1455
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<210> 1458
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<210> 1459
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<210> 1460
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<210> 1461
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oligonucleotide

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<210> 1462
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oligonucleotide

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<210> 1463
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oligonucleotide

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<210> 1464
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oligonucleotide

<400> 1464
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<210> 1465
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oligonucleotide

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<210> 1466
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oligonucleotide

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oligonucleotide

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<210> 1468
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oligonucleotide

<400> 1468
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<210> 1469

<211> 23
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oligonucleotide

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<210> 1472
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<210> 1473
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oligonucleotide

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<210> 1474
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oligonucleotide

<400> 1474
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<210> 1476
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oligonucleotide

<400> 1476
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<210> 1477
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oligonucleotide

<400> 1477
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<210> 1478
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oligonucleotide

<400> 1478
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<210> 1479
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oligonucleotide

<400> 1479
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<210> 1480
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oligonucleotide

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<210> 1481
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oligonucleotide

<400> 1481
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<210> 1482
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oligonucleotide

<400> 1482
aagatacctg gataagcaac tgc 23

<210> 1483
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oligonucleotide

<400> 1483
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<210> 1484
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oligonucleotide

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<210> 1485
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oligonucleotide

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<210> 1486
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oligonucleotide

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<400> 1487
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<210> 1488
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oligonucleotide

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<210> 1489
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oligonucleotide

<400> 1489
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<210> 1490
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<210> 1491
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<210> 1492
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oligonucleotide

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<210> 1493
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oligonucleotide

<400> 1493
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<210> 1494
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oligonucleotide

<400> 1494
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oligonucleotide

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<210> 1496
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<400> 1497
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<210> 1498
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<400> 1498
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<210> 1499
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<210> 1501
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oligonucleotide

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<210> 1524
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<210> 1525
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<210> 1529
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<210> 1531
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<210> 1532
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<400> 1532

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<210> 1533
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<400> 1533
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<210> 1534
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<400> 1534
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<210> 1535
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<210> 1536
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<210> 1537
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<210> 1538

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<210> 1539
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<210> 1540
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<210> 1544
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<210> 1546
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<210> 1547
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<210> 1548
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<210> 1549
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<210> 1555
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<210> 1556
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<210> 1559
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<210> 1560
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<210> 1561
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oligonucleotide

<400> 1561
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<210> 1562
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<210> 1563
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<400> 1563
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<210> 1564
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<210> 1565
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oligonucleotide

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<210> 1566
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oligonucleotide

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<210> 1567
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oligonucleotide

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<210> 1568
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<400> 1568
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<210> 1569
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<210> 1570
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<210> 1571
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<210> 1572
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oligonucleotide

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<210> 1573
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<210> 1574
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<210> 1575
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oligonucleotide

<400> 1575
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<210> 1576
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<210> 1577
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oligonucleotide

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<400> 1578
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<210> 1579
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oligonucleotide

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<210> 1580
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oligonucleotide

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oligonucleotide

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<210> 1582
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oligonucleotide

<400> 1582
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<210> 1583
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oligonucleotide

<400> 1583
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<210> 1584
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oligonucleotide

<400> 1584
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<210> 1585
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oligonucleotide

<400> 1585
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<210> 1586
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oligonucleotide

<400> 1586
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<400> 1587
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<210> 1588
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oligonucleotide

<400> 1588
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<210> 1589
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oligonucleotide

<400> 1589
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<210> 1590
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oligonucleotide

<400> 1590
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<210> 1591
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oligonucleotide

<400> 1591
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<210> 1592
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oligonucleotide

<400> 1592
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<210> 1593
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oligonucleotide

<400> 1593
aagatcccag aataactact gg 22

<210> 1594
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oligonucleotide

<400> 1594
ccaatggcct ccttcagtt 19

<210> 1595
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oligonucleotide

<400> 1595
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<210> 1596
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oligonucleotide

<400> 1596
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<210> 1597
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oligonucleotide

<400> 1597
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<210> 1598
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oligonucleotide

<400> 1598
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<210> 1599
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oligonucleotide

<400> 1599
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<210> 1600
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<400> 1600
taagaccatg tcccaactga 20

<210> 1601
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oligonucleotide

<400> 1601

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<210> 1602
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oligonucleotide

<400> 1602
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<210> 1603
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oligonucleotide

<400> 1603
tttgttttcc gggattgcat 20

<210> 1604
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oligonucleotide

<400> 1604
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<210> 1605
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oligonucleotide

<400> 1605
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<210> 1606
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oligonucleotide

<400> 1606
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<210> 1607

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<400> 1607
atacctgaat aactctc 17

<210> 1608
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oligonucleotide

<400> 1608
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<210> 1609
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oligonucleotide

<400> 1609
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<210> 1610
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oligonucleotide

<400> 1610
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<210> 1611
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<400> 1611
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<210> 1612
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oligonucleotide

<400> 1612
aagatttggt gttttctact 20

<210> 1613
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1613
aaggagtacc cggggctgca 20

<210> 1614
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1614
cagaggccag gagcgccagg 20

<210> 1615
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1615
agaggccagg agcgccagga 20

<210> 1616
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1616
ctcggcctct gaagctcctg 20

<210> 1617
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1617
cagctccagg cggtcctgg 19

<210> 1618
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1618
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1619
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1619
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1620
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1620
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1621
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1621
ggugcuagcc uugcguuccg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1622
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (1)..(1)
<223> Inosine

<400> 1622
nccaauggcc uccuucaguu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1623
<211> 99
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1623
ccaauggccu ccuucaguug uuuuagagcu agaaauagca aguuaaaaua aggcuagucc 60

guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuu 99

<210> 1624
<211> 98
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1624
caauggccuc cuucaguugu uuuagagcua gaaauagcaa guuaaaauaa ggcuaguccg 60

uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 98

<210> 1625
<211> 98
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1625
caauggccuc cuucaguugu uuuagagcua gaaauagcaa guuaaaauaa ggcuaguccg 60

uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 98

<210> 1626
<211> 97
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1626
aauggccucc uucaguuguu uuagagcuag aaauagcaag uuaaaauaag gcuaguccgu 60

uaucaacuug aaaaaguggc accgagucgg ugcuuuu 97

<210> 1627
<211> 97
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1627
aauggccucc uucaguuguu uuagagcuag aaauagcaag uuaaaauaag gcuaguccgu 60

uaucaacuug aaaaaguggc accgagucgg ugcuuuu 97

<210> 1628
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (18)..(18)
<223> Inosine

<400> 1628
gccaauggcc uccuucanuu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1629
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (1)..(1)
<223> Inosine

<220>
<221> modified_base
<222> (18)..(18)
<223> Inosine

<400> 1629
nccaauggcc uccuucanuu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1630
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (7)..(8)
<223> Inosine

<220>
<221> modified_base
<222> (18)..(18)
<223> Inosine

<400> 1630
gccaaunncc uccuucanuu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1631
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1631
accaauggcc uccuucaguu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1632
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (1)..(1)
<223> Inosine

<220>
<221> modified_base
<222> (7)..(7)
<223> Inosine

<400> 1632
nccaaungcc uccuucaguu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1633
<211> 100

<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (7)..(7)
<223> Inosine

<400> 1633
gccaaungcc uccuucaguu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1634
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1634
gcgaauggcc uccugcagcu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1635
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1635
agcccuucaa cacaagguca guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1636
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1636
uaagaccaug ucccaacuga guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1637
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1637
caaugucccc aaugcaaucc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1638
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1638
uuguuuuccg ggauugcauu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1639
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1639
uuuguuuucc gggauugcau guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1640
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1640
aaucccggaa aacaaagauu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1641
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1641
uguuuuccgg gauugcauug guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1642
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1642
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1643
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1643
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1644
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1644
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1645
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1645
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1646
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1646
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1647
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1647
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1648
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 1648
cccgcaccuu ggcgcagcgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1649
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

<400> 1649
cccgcaccuu ggcgcagcgg guuuuagagu uuuagagcua gaaauagcaa guuaaaauaa 60

ggcuaguccg uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 108

<210> 1650
<211> 99
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1650
agauaccuga auaacccucg uuuuagagcu agaaauagca aguuaaaaua aggcuagucc 60

guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuu 99

<210> 1651
<211> 98
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1651
gauaccugaa uaacccucgu uuuagagcua gaaauagcaa guuaaaauaa ggcuaguccg 60

uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 98

<210> 1652
<211> 98
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1652
gauaccugaa uaacucucgu uuuagagcua gaaauagcaa guuaaaauaa ggcuaguccg 60

uuaucaacuu gaaaaagugg caccgagucg gugcuuuu 98

<210> 1653
<211> 97
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1653
auaccugaau aacucucguu uuagagcuag aaauagcaag uuaaaauaag gcuaguccgu 60

uaucaacuug aaaaaguggc accgagucgg ugcuuuu 97

<210> 1654
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (6)..(6)
<223> Nebularine

<400> 1654
aagaunccug aauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1655
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (6)..(6)
<223> Nebularine

<220>
<221> modified_base
<222> (11)..(11)
<223> Nebularine

<400> 1655
aagaunccug nauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1656
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (6)..(6)
<223> Nebularine

<220>
<221> modified_base
<222> (15)..(15)
<223> Nebularine

<400> 1656
aagaunccug aauancccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1657
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (6)..(6)
<223> Nebularine

<220>
<221> modified_base
<222> (11)..(11)
<223> Nebularine

<220>
<221> modified_base
<222> (14)..(14)
<223> Nebularine

<400> 1657
aagaunccug naunacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1658
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (4)..(4)
<223> Nebularine

<220>
<221> modified_base
<222> (6)..(6)
<223> Nebularine

<400> 1658
aagnunccug aauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1659
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (4)..(4)
<223> Nebularine

<220>
<221> modified_base
<222> (6)..(6)
<223> Nebularine

<220>
<221> modified_base
<222> (15)..(15)
<223> Nebularine

<400> 1659

aagnunccug aauancccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1660
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (4)..(4)
<223> Nebularine

<220>
<221> modified_base
<222> (14)..(14)
<223> Nebularine

<400> 1660
aagnuaccug aaunacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1661
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (11)..(11)
<223> Nebularine

<400> 1661
aagauaccug nauaacccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1662
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<220>
<221> modified_base
<222> (11)..(11)
<223> Nebularine

<220>
<221> modified_base

<222> (15)..(15)
<223> Nebularine

<400> 1662
aagauaccug nauancccuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1663
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1663
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1664
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1664
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1665
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1665
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1666
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1666
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1667
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1667
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1668
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1668
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1669
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1669
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1670
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1670
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1671
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1671
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1672
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1672
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1673
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1673
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1674
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1674
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1675
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1675
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1676
<211> 100
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1676
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1677
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1677
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1678
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1678
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1679
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1679
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1680
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1680
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1681
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1681
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1682
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1682
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1683
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1683
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1684
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1684
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1685
<211> 100
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1685
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1686
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1686
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1687
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1687
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1688
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1688
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1689
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1689
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1690
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1690
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1691
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1691
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1692
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1692
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1693
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1693
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1694
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1694
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1695
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1695
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1696
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1696
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1697
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1697
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1698
<211> 100
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1698
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 1699
<211> 103
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1699
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1700
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1700
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1701
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1701
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1702
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1702
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1703
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1703
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1704
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1704
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1705
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1705
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1706
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1706
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1707
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1707
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1708
<211> 103
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1708
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1709
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1709
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1710
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1710
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1711
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1711
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1712
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1712
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1713
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1713
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1714
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1714
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1715
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1715
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1716
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1716
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1717
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1717
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1718
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1718
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1719
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1719
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1720
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1720
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1721
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1721
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1722
<211> 103
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1722
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1723
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1723
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1724
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1724
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1725
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1725
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1726
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1726
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1727
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1727
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1728
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1728
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1729
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1729
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1730
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1730
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1731
<211> 103
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1731
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1732
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1732
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1733
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1733
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1734
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1734
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1735
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1735
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1736
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1736
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1737
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1737
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1738
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1738
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1739
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1739
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1740
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1740
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1741
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1741
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1742
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1742
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1743
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1743
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1744
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1744
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1745
<211> 103
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1745
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1746
<211> 102
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1746
gaauaccuga guaacuuucg uuuuagagcu agaaauagca aguuaaaaua aggcuagucc 60

guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuuu uu 102

<210> 1747
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1747
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1748
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1748
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1749
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1749
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1750
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1750
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1751
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1751
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1752
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1752
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1753
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1753
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1754
<211> 103
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1754
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1755
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1755
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1756
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1756
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1757
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1757
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1758
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1758
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1759
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1759
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1760
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1760
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1761
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1761
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1762
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1762
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1763
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1763
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1764
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1764
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1765
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1765
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1766
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1766
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1767
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1767
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1768
<211> 103
<212> RNA

<213> Artificial Sequence

<220>
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polynucleotide

<400> 1768
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1769
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1769
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1770
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1770
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1771
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1771
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1772
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1772
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1773
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1773
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1774
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1774
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1775
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1775
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1776
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1776
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1777
<211> 103
<212> RNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1777
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1778
<211> 103
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<220>
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polynucleotide

<400> 1778
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1779
<211> 103
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<220>
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polynucleotide

<400> 1779
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1780
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<213> Artificial Sequence

<220>
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polynucleotide

<400> 1780
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1781
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1781
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1782
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<212> RNA
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<220>
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polynucleotide

<400> 1782
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1783
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1783
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1784
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1784
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1785
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1785
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1786
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1786
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1787
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1787
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1788
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1788
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1789
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1789
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1790
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1790
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1791
<211> 103
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1791
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1792
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1792
cccauaccuu ggagcaacgg guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1793
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 1793
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1794
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<400> 1794
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 103

<210> 1795
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

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<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1795
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1796
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<222> (101)..(103)
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<400> 1796
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1797
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<400> 1797
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1798
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<223> a, c, u, g, unknown or other

<400> 1798
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1799
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

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<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1799
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1800
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1800
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1801
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
<221> modified_base
<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1801
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1802
<211> 103
<212> RNA

<213> Artificial Sequence

<220>
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polynucleotide

<220>
<221> modified_base
<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1802
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1803
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1803
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1804
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<223> a, c, u, g, unknown or other

<400> 1804
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1805
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1806
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<220>
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polynucleotide

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<400> 1806
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1807
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<220>
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polynucleotide

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<400> 1807
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1808
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<400> 1808
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1809
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
<221> modified_base
<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1809
gagauaccug aguaacuuuc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1810
<211> 103
<212> RNA
<213> Artificial Sequence

<220>
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polynucleotide

<220>
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<223> a, c, u, g, unknown or other

<400> 1810
cagguuccau gggaugcucu guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1811
<211> 103
<212> RNA
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<220>
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polynucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1821
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

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<210> 1825
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1826
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1827
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1828
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<400> 1828
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1829
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<210> 1830
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<210> 1831
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<210> 1832
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1833
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<400> 1833
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1834
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<210> 1835
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1836
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<210> 1837
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1838
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<223> a, c, u, g, unknown or other

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1839
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1841
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<223> a, c, u, g, unknown or other

<400> 1841
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1842
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1843
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1844
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<400> 1844
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guuaucaacu ugaaaaagug gcaccgaguc ggugcuuuun nn 102

<210> 1845
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1846
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<400> 1846
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1847
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<400> 1847
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1848
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<400> 1848
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1849
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<400> 1849
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1850
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<223> a, c, u, g, unknown or other

<400> 1850
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1851
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polynucleotide

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<223> a, c, u, g, unknown or other

<400> 1851
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1852
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<223> a, c, u, g, unknown or other

<400> 1852
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1853
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<400> 1853
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1854
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<400> 1854
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1855
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polynucleotide

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<223> a, c, u, g, unknown or other

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1856
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polynucleotide

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<223> a, c, u, g, unknown or other

<400> 1856
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1857
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<212> RNA
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polynucleotide

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<400> 1857
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1858
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<212> RNA
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<220>
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polynucleotide

<220>
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<223> a, c, u, g, unknown or other

<400> 1858
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1859
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<223> a, c, u, g, unknown or other

<400> 1859
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1860
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<220>
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polynucleotide

<220>
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<223> a, c, u, g, unknown or other

<400> 1860
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1861
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<220>

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<220>
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<222> (101)..(103)
<223> a, c, u, g, unknown or other

<400> 1861
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1862
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<400> 1862
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 1863
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<210> 1865
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<210> 1866
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<220>
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oligonucleotide

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<223> Nebularine

<400> 2102
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<220>
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<223> Nebularine

<400> 2103
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<223> Nebularine

<400> 2104
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<400> 2105
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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oligonucleotide

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cguunucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<400> 2107
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cguunucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<212> DNA
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oligonucleotide

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<223> Nebularine

<400> 2108
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cguunucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<223> Nubularine

<400> 2109
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cguuaucaac uugaaaaagu ggcaccgagu cggugcunnn 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcunnn 100

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<220>
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<222> (99)..(100)
<223> Nubularine

<400> 2111
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuunn 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuunn 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuun 100

<210> 2114
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuun 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcunnn 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcunnn 100

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<220>
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oligonucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuunn 100

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<220>
<223> Description of Combined DNA/RNA Molecule: Synthetic
oligonucleotide

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<400> 2118
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuunn 100

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<400> 2119
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuun 100

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oligonucleotide

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuun 100

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oligonucleotide

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<400> 2121
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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu nnn 103

<210> 2122

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> 2126
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<400> 2126

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

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<220>
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<220>
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uacgugaccu ucgagcccug cgugaugugc gccggcgcca ugauccacag ccggaucggc 300

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ugcgccgccc ugcugugccg guucuuccgg augccccggc ggguguucaa cgcccagaag 480

aaggcccaga gcagcaccga caggaaauaa gagagaaaag aagaguaaga agaaauauaa 540

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ucggccuggc caucggcacc aacagcgugg gcugggccgu gaucaccgac gaguacaagg 720

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accccaagaa guacggcggc uucgacagcc ccaccguggc cuacagcgug cugguggugg 4080

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acgagaucau cgagcagauc agcgaguuca gcaagcgggu gauccuggcc gacgccaacc 4500

uggacaaggu gcugagcgcc uacaacaagc accgggacaa gcccauccgg gagcaggccg 4560

agaacaucau ccaccuguuc acccugacca accugggcgc ccccgccgcc uucaaguacu 4620

ucgacaccac caucgaccgg aagcgguaca ccagcaccaa ggaggugcug gacgccaccc 4680

ugauccacca gagcaucacc ggccuguacg agacacggau cgaccugagc cagcugggcg 4740

gcgacgaggg cgccgacaag cggaccgccg acggcagcga guucgagagc cccaagaaga 4800

agcggaaggu gugagcggcc gcuuaauuaa gcugccuucu gcggggcuug ccuucuggcc 4860

augcccuucu ucucucccuu gcaccuguac cucuuggucu uugaauaaag ccugaguagg 4920

aagucuaga 4929

<210> 2137
<211> 1588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2137
Met Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His Ala Leu
1 5 10 15

Thr Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val Gly Ala
20 25 30

Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Ala
35 40 45

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Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg
    50                  55                  60

Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu
65                  70                  75                  80

Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His
                85                  90                  95

Ser Arg Ile Gly Arg Val Val Phe Gly Val Arg Asn Ala Lys Thr Gly
            100                 105                 110

Ala Ala Gly Ser Leu Met Asp Val Leu His His Pro Gly Met Asn His
        115                 120                 125

Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu
    130                 135                 140

Leu Cys Arg Phe Phe Arg Met Pro Arg Arg Val Phe Asn Ala Gln Lys
145                 150                 155                 160

Lys Ala Gln Ser Ser Thr Asp Ser Gly Gly Ser Ser Gly Gly Ser Ser
                165                 170                 175

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser
            180                 185                 190

Gly Gly Ser Ser Gly Gly Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala
        195                 200                 205

Ile Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys
    210                 215                 220

Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser
225                 230                 235                 240

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

Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg
            260                 265                 270

Arg Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met
        275                 280                 285

Ala Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu
    290                 295                 300

Val Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile
305                 310                 315                 320
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Val Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu
                325                 330                 335

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

Tyr Leu Ala Leu Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile
        355                 360                 365

Glu Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile
    370                 375                 380

Gln Leu Val Gln Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn
385                 390                 395                 400

Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys
                405                 410                 415

Ser Arg Arg Leu Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys
            420                 425                 430

Asn Gly Leu Phe Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro
        435                 440                 445

Asn Phe Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu
    450                 455                 460

Ser Lys Asp Thr Tyr Asp Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile
465                 470                 475                 480

Gly Asp Gln Tyr Ala Asp Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp
                485                 490                 495

Ala Ile Leu Leu Ser Asp Ile Leu Arg Val Asn Thr Glu Ile Thr Lys
            500                 505                 510

Ala Pro Leu Ser Ala Ser Met Ile Lys Arg Tyr Asp Glu His His Gln
        515                 520                 525

Asp Leu Thr Leu Leu Lys Ala Leu Val Arg Gln Gln Leu Pro Glu Lys
    530                 535                 540

Tyr Lys Glu Ile Phe Phe Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr
545                 550                 555                 560

Ile Asp Gly Gly Ala Ser Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro
                565                 570                 575

Ile Leu Glu Lys Met Asp Gly Thr Glu Glu Leu Leu Val Lys Leu Asn
            580                 585                 590
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Arg Glu Asp Leu Leu Arg Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile
        595                 600                 605

Pro His Gln Ile His Leu Gly Glu Leu His Ala Ile Leu Arg Arg Gln
    610                 615                 620

Glu Asp Phe Tyr Pro Phe Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys
625                 630                 635                 640

Ile Leu Thr Phe Arg Ile Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly
                645                 650                 655

Asn Ser Arg Phe Ala Trp Met Thr Arg Lys Ser Glu Glu Thr Ile Thr
            660                 665                 670

Pro Trp Asn Phe Glu Glu Val Val Asp Lys Gly Ala Ser Ala Gln Ser
        675                 680                 685

Phe Ile Glu Arg Met Thr Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys
    690                 695                 700

Val Leu Pro Lys His Ser Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn
705                 710                 715                 720

Glu Leu Thr Lys Val Lys Tyr Val Thr Glu Gly Met Arg Lys Pro Ala
                725                 730                 735

Phe Leu Ser Gly Glu Gln Lys Lys Ala Ile Val Asp Leu Leu Phe Lys
            740                 745                 750

Thr Asn Arg Lys Val Thr Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys
        755                 760                 765

Lys Ile Glu Cys Phe Asp Ser Val Glu Ile Ser Gly Val Glu Asp Arg
    770                 775                 780

Phe Asn Ala Ser Leu Gly Thr Tyr His Asp Leu Leu Lys Ile Ile Lys
785                 790                 795                 800

Asp Lys Asp Phe Leu Asp Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp
                805                 810                 815

Ile Val Leu Thr Leu Thr Leu Phe Glu Asp Arg Glu Met Ile Glu Glu
            820                 825                 830

Arg Leu Lys Thr Tyr Ala His Leu Phe Asp Asp Lys Val Met Lys Gln
        835                 840                 845

Leu Lys Arg Arg Arg Tyr Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu
    850                 855                 860

Ile Asn Gly Ile Arg Asp Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe
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865                 870                 875                 880

Leu Lys Ser Asp Gly Phe Ala Asn Arg Asn Phe Met Gln Leu Ile His
                885                 890                 895

Asp Asp Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val Ser
            900                 905                 910

Gly Gln Gly Asp Ser Leu His Glu His Ile Ala Asn Leu Ala Gly Ser
        915                 920                 925

Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp Glu
    930                 935                 940

Leu Val Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile Glu
945                 950                 955                 960

Met Ala Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg
                965                 970                 975

Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln
            980                 985                 990

Ile Leu Lys Glu His Pro Val Glu  Asn Thr Gln Leu Gln  Asn Glu Lys
        995                 1000                1005

Leu Tyr  Leu Tyr Tyr Leu Gln  Asn Gly Arg Asp Met  Tyr Val Asp
    1010                1015                1020

Gln Glu  Leu Asp Ile Asn Arg  Leu Ser Asp Tyr Asp  Val Asp His
    1025                1030                1035

Ile Val  Pro Gln Ser Phe Leu  Lys Asp Asp Ser Ile  Asp Asn Lys
    1040                1045                1050

Val Leu  Thr Arg Ser Asp Lys  Asn Arg Gly Lys Ser  Asp Asn Val
    1055                1060                1065

Pro Ser  Glu Glu Val Val Lys  Lys Met Lys Asn Tyr  Trp Arg Gln
    1070                1075                1080

Leu Leu  Asn Ala Lys Leu Ile  Thr Gln Arg Lys Phe  Asp Asn Leu
    1085                1090                1095

Thr Lys  Ala Glu Arg Gly Gly  Leu Ser Glu Leu Asp  Lys Ala Gly
    1100                1105                1110

Phe Ile  Lys Arg Gln Leu Val  Glu Thr Arg Gln Ile  Thr Lys His
    1115                1120                1125

Val Ala  Gln Ile Leu Asp Ser  Arg Met Asn Thr Lys  Tyr Asp Glu
    1130                1135                1140
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Asn Asp  Lys Leu Ile Arg Glu  Val Lys Val Ile Thr  Leu Lys Ser
    1145                1150                1155

Lys Leu  Val Ser Asp Phe Arg  Lys Asp Phe Gln Phe  Tyr Lys Val
    1160                1165                1170

Arg Glu  Ile Asn Asn Tyr His  His Ala His Asp Ala  Tyr Leu Asn
    1175                1180                1185

Ala Val  Val Gly Thr Ala Leu  Ile Lys Lys Tyr Pro  Lys Leu Glu
    1190                1195                1200

Ser Glu  Phe Val Tyr Gly Asp  Tyr Lys Val Tyr Asp  Val Arg Lys
    1205                1210                1215

Met Ile  Ala Lys Ser Glu Gln  Glu Ile Gly Lys Ala  Thr Ala Lys
    1220                1225                1230

Tyr Phe  Phe Tyr Ser Asn Ile  Met Asn Phe Phe Lys  Thr Glu Ile
    1235                1240                1245

Thr Leu  Ala Asn Gly Glu Ile  Arg Lys Arg Pro Leu  Ile Glu Thr
    1250                1255                1260

Asn Gly  Glu Thr Gly Glu Ile  Val Trp Asp Lys Gly  Arg Asp Phe
    1265                1270                1275

Ala Thr  Val Arg Lys Val Leu  Ser Met Pro Gln Val  Asn Ile Val
    1280                1285                1290

Lys Lys  Thr Glu Val Gln Thr  Gly Gly Phe Ser Lys  Glu Ser Ile
    1295                1300                1305

Leu Pro  Lys Arg Asn Ser Asp  Lys Leu Ile Ala Arg  Lys Lys Asp
    1310                1315                1320

Trp Asp  Pro Lys Lys Tyr Gly  Gly Phe Asp Ser Pro  Thr Val Ala
    1325                1330                1335

Tyr Ser  Val Leu Val Val Ala  Lys Val Glu Lys Gly  Lys Ser Lys
    1340                1345                1350

Lys Leu  Lys Ser Val Lys Glu  Leu Leu Gly Ile Thr  Ile Met Glu
    1355                1360                1365

Arg Ser  Ser Phe Glu Lys Asn  Pro Ile Asp Phe Leu  Glu Ala Lys
    1370                1375                1380

Gly Tyr  Lys Glu Val Lys Lys  Asp Leu Ile Ile Lys  Leu Pro Lys
    1385                1390                1395
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Tyr Ser  Leu Phe Glu Leu Glu  Asn Gly Arg Lys Arg  Met Leu Ala
    1400                1405                1410

Ser Ala  Gly Glu Leu Gln Lys  Gly Asn Glu Leu Ala  Leu Pro Ser
    1415                1420                1425

Lys Tyr  Val Asn Phe Leu Tyr  Leu Ala Ser His Tyr  Glu Lys Leu
    1430                1435                1440

Lys Gly  Ser Pro Glu Asp Asn  Glu Gln Lys Gln Leu  Phe Val Glu
    1445                1450                1455

Gln His  Lys His Tyr Leu Asp  Glu Ile Ile Glu Gln  Ile Ser Glu
    1460                1465                1470

Phe Ser  Lys Arg Val Ile Leu  Ala Asp Ala Asn Leu  Asp Lys Val
    1475                1480                1485

Leu Ser  Ala Tyr Asn Lys His  Arg Asp Lys Pro Ile  Arg Glu Gln
    1490                1495                1500

Ala Glu  Asn Ile Ile His Leu  Phe Thr Leu Thr Asn  Leu Gly Ala
    1505                1510                1515

Pro Ala  Ala Phe Lys Tyr Phe  Asp Thr Thr Ile Asp  Arg Lys Arg
    1520                1525                1530

Tyr Thr  Ser Thr Lys Glu Val  Leu Asp Ala Thr Leu  Ile His Gln
    1535                1540                1545

Ser Ile  Thr Gly Leu Tyr Glu  Thr Arg Ile Asp Leu  Ser Gln Leu
    1550                1555                1560

Gly Gly  Asp Glu Gly Ala Asp  Lys Arg Thr Ala Asp  Gly Ser Glu
    1565                1570                1575

Phe Glu  Ser Pro Lys Lys Lys  Arg Lys Val
    1580                1585
```

<210> 2138
<211> 47
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2138
aggaaauaag agagaaaaga agaguaagaa gaaauauaag agccacc 47

<210> 2139
<211> 501
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2139
augagcgagg uggaguucag ccacgaguac uggaugcggc acgcccugac ccuggccaag 60

cgggcccggg acgagcggga ggugcccgug ggcgccgugc uggugcugaa caaccgggug 120

aucggcgagg gcuggaaccg ggccaucggc cugcacgacc ccaccgccca cgccgagauc 180

auggcccugc ggcagggcgg ccuggugaug cagaacuacc ggcugaucga cgccacccug 240

uacgugaccu ucgagcccug cgugaugugc gccggcgcca ugauccacag ccggaucggc 300

cggguggugu ucggcgugcg gaacgccaag accggcgccg ccggcagccu gauggacgug 360

cugcaccacc ccggcaugaa ccaccgggug gagaucaccg agggcauccu ggccgacgag 420

ugcgccgccc ugcugugccg guucuuccgg augccccggc ggguguucaa cgcccagaag 480

aaggcccaga gcagcaccga c 501

<210> 2140
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2140
Met Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His Ala Leu
1 5 10 15

Thr Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val Gly Ala
20 25 30

Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Ala
35 40 45

Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg
50 55 60

Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu
65 70 75 80

Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His
85 90 95

Ser Arg Ile Gly Arg Val Val Phe Gly Val Arg Asn Ala Lys Thr Gly
100 105 110

Ala Ala Gly Ser Leu Met Asp Val Leu His His Pro Gly Met Asn His
115 120 125

Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu

130 135 140

Leu Cys Arg Phe Phe Arg Met Pro Arg Arg Val Phe Asn Ala Gln Lys
145 150 155 160

Lys Ala Gln Ser Ser Thr Asp
165

<210> 2141
<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2141
agcggcggca gcagcggcgg cagcagcggc agcgagacac ccggcaccag cgagagcgcc 60

acccccgaga gcagcggcgg cagcagcggc ggcagc 96

<210> 2142
<211> 4101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 2142
gacaagaagu acagcaucgg ccuggccauc ggcaccaaca gcgugggcug ggccgugauc 60

accgacgagu acaaggugcc cagcaagaag uucaaggugc ugggcaacac cgaccggcac 120

agcaucaaga agaaccugau cggcgcccug cuguucgaca gcggcgagac agccgaggcc 180

acccggcuga agcggaccgc ccggcggcgg uacacccggc ggaagaaccg gaucugcuac 240

cugcaggaga ucuucagcaa cgagauggcc aagguggacg acagcuucuu ccaccggcug 300

gaggagagcu uccuggugga ggaggacaag aagcacgagc ggcaccccau cuucggcaac 360

aucguggacg agguggccua ccacgagaag uaccccacca ucuaccaccu gcggaagaag 420

cugguggaca gcaccgacaa ggccgaccug cggcugaucu accuggcccu ggcccacaug 480

aucaaguucc ggggccacuu ccugaucgag ggcgaccuga accccgacaa cagcgacgug 540

gacaagcugu ucauccagcu ggugcagacc uacaaccagc uguucgagga gaaccccauc 600

aacgccagcg gcguggacgc caaggccauc cugagcgccc ggcugagcaa gagccggcgg 660

cuggagaacc ugaucgccca gcugcccggc gagaagaaga acggccuguu cggcaaccug 720

aucgcccuga gccuggccu gacccccaac uucaagagca acuucgaccu ggccgaggac 780

gccaagcugc agcugagcaa ggacaccuac gacgacgacc uggacaaccu gcuggcccag 840

aucggcgacc aguacgccga ccuguuccug gccgccaaga accugagcga cgccauccug 900

cugagcgaca uccugcgggu gaacaccgag aucaccaagg ccccccugag cgccagcaug 960

aucaagcggu acgacgagca ccaccaggac cugacccugc ugaaggcccu ggugcggcag 1020

cagcugcccg agaaguacaa ggagaucuuc uucgaccaga gcaagaacgg cuacgccggc 1080

uacaucgacg gcggcgccag ccaggaggag uucuacaagu ucaucaagcc cauccuggag 1140

aagauggacg gcaccgagga gcugcuggug aagcugaacc gggaggaccu gcugcggaag 1200

cagcggaccu ucgacaacgg cagcaucccc caccagaucc accugggcga gcugcacgcc 1260

auccugcggc ggcaggagga cuucuacccc uuccugaagg acaaccggga gaagaucgag 1320

aagauccuga ccuuccggau ccccuacuac gugggccccc uggcccgggg caacagccgg 1380

uucgccugga ugacccgcaa gagcgaggag acaaucaccc ccuggaacuu cgaggaggug 1440

guggacaagg gcgccagcgc ccagagcuuc aucgagcgga ugaccaacuu cgacaagaac 1500

cugcccaacg agaaggugcu gcccaagcac agccugcugu acgaguacuu caccguguac 1560

aacgagcuga ccaaggugaa guacgugacc gagggcaugc ggaagcccgc cuuccugagc 1620

ggcgagcaga agaaggccau cguggaccug cuguucaaga ccaaccggaa ggugaccgug 1680

aagcagcuga aggaggacua cuucaagaag aucgagugcu ucgacagcgu ggagaucagc 1740

ggcguggagg accgguucaa cgccagccug ggcaccuacc acgaccugcu gaagaucauc 1800

aaggacaagg acuuccugga caacgaggag aacgaggaca uccuggagga caucgugcug 1860

acccugaccc uguucgagga ccgggagaug aucgaggagc ggcugaagac cuacgcccac 1920

cuguucgacg acaaggugau gaagcagcug aagcggcggc gguacaccgg cuggggccgg 1980

cugagccgga agcugaucaa cggcauccgg gacaagcaga gcggcaagac cauccuggac 2040

uuccucaaga gcgacggcuu cgccaaccgg aacuucaugc agcugaucca cgacgacagc 2100

cugaccuuca aggaggacau ccagaaggcc caggugagcg gccagggcga cagccugcac 2160

gagcacaucg ccaaccuggc cggcagcccc gccaucaaga agggcauccu gcagaccgug 2220

aagguggugg acgagcuggu gaaggugaug ggccggcaca agcccgagaa caucgugauc 2280

gagauggccc gggagaacca gaccacccag aagggccaga agaacagccg ggagcggaug 2340

aagcggaucg aggagggcau caaggagcug ggcagccaga uccugaagga gcaccccgug 2400

gagaacaccc agcugcagaa cgagaagcug uaccuguacu accugcagaa cggccgggac 2460

auguacgugg accaggagcu ggacaucaac cggcugagcg acuacgacgu ggaccacauc 2520

gugccccaga gcuuccugaa ggacgacagc aucgacaaca aggugcugac ccggagcgac 2580

aagaaccggg gcaagagcga caacgugccc agcgaggagg uggugaagaa gaugaagaac 2640

uacuggcggc agcugcugaa cgccaagcug aucacccagc ggaaguucga caaccugacc 2700

aaggccgagc ggggcggccu gagcgagcug gacaaggccg gcuucaucaa gcggcagcug 2760

guggagacac ggcagaucac caagcacgug gcccagaucc uggacagccg gaugaacacc 2820

aaguacgacg agaacgacaa gcugauccgg gaggugaagg ugaucacccu caagagcaag 2880

cuggugagcg acuuccggaa ggacuuccag uucuacaagg ugcgggagau caacaacuac 2940

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cccaagcugg agagcgaguu cguguacggc gacuacaagg uguacgacgu gcggaagaug 3060

aucgccaaga gcgagcagga gaucggcaag gccaccgcca aguacuucuu cuacagcaac 3120

aucaugaacu ucuucaagac cgagaucacc cuggccaacg gcgagauccg gaagcggccc 3180

cugaucgaga caaacggcga gacaggcgag aucguguggg acaagggccg ggacuucgcc 3240

accgugcgga aggugcugag caugccccag gugaacaucg ugaagaagac cgaggugcag 3300

accggcggcu ucagcaagga gagcauccug cccaagcgga acagcgacaa gcugaucgcc 3360

cggaagaagg acugggaccc caagaaguac ggcggcuucg acagccccac cguggccuac 3420

agcgugcugg ugguggccaa gguggagaag ggcaagagca agaagcucaa gagcgugaag 3480

gagcugcugg gcaucaccau cauggagcgg agcagcuucg agaagaaccc caucgacuuc 3540

cuggaggcca agggcuacaa ggaggugaag aaggaccuga ucaucaagcu gcccaaguac 3600

agccuguucg agcuggagaa cggccggaag cggaugcugg ccagcgccgg cgagcugcag 3660

aagggcaacg agcuggcccu gcccagcaag uacgugaacu uccuguaccu ggccagccac 3720

uacgagaagc ugaagggcag ccccgaggac aacgagcaga agcagcuguu cguggagcag 3780

cacaagcacu accuggacga gaucaucgag cagaucagcg aguucagcaa gcgggugauc 3840

cuggccgacg ccaaccugga caaggugcug agcgccuaca acaagcaccg ggacaagccc 3900

auccgggagc aggccgagaa caucauccac cuguucaccc ugaccaaccu gggcgccccc 3960

gccgccuuca aguacuucga caccaccauc gaccggaagc gguacaccag caccaaggag 4020

gugcuggacg ccacccugau ccaccagagc aucaccggcc uguacgagac acggaucgac 4080

cugagccagc ugggcggcga c 4101

<210> 2143
<211> 12
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2143
gagggcgccg ac 12

<210> 2144
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2144
Glu Gly Ala Asp
1

<210> 2145
<211> 57
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2145
aagcggaccg ccgacggcag cgaguucgag agccccaaga agaagcggaa gguguga 57

<210> 2146
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2146
Lys Arg Thr Ala Asp Gly Ser Glu Phe Glu Ser Pro Lys Lys Lys Arg
1 5 10 15

Lys Val

<210> 2147
<211> 115
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2147
gcggccgcuu aauuaagcug ccuucugcgg ggcuugccuu cuggccaugc ccuucuucuc 60

ucccuugcac cuguaccucu uggucuuuga auaaagccug aguaggaagu cuaga 115

<210> 2148
<211> 4929
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2148
aggaaauaag agagaaaaga agaguaagaa gaaauauaag agccaccaug agcgaggugg 60

aguucagcca cgaguacugg augcggcacg cccugacccu ggccaagcgg gcccgggacg 120

agcgggaggu gcccgugggc gccgugcugg ugcugaacaa ccgggugauc ggcgagggcu 180

ggaaccgggc caucggccug cacgacccca ccgcccacgc cgagaucaug gcccugcggc 240

agggcggccu ggugaugcag aacuaccggc ugaucgacgc cacccuguac gugaccuucg 300

agcccugcgu gaugugcgcc ggcgccauga uccacagccg gaucggccgg gugguguucg 360

gcgugcggaa cgccaagacc ggcgccgccg gcagccugau ggacgugcug caccaccccg 420

gcaugaacca ccggguggag aucaccgagg gcauccuggc cgacgagugc gccgcccugc 480

ugugccgguu cuuccggaug ccccggcggg uguucaacgc ccagaagaag gcccagagca 540

gcaccgacag cggcggcagc agcggcggca gcagcggcag cgagacaccc ggcaccagcg 600

agagcgccac ccccgagagc agcggcggca gcagcggcgg cagcgacaag aaguacagca 660

ucggccuggc caucggcacc aacagcgugg gcugggccgu gaucaccgac gaguacaagg 720

ugcccagcaa gaaguucaag gugcugggca acaccgaccg gcacagcauc aagaagaacc 780

ugaucggcgc ccugcuguuc gacagcggcg agacagccga ggccacccgg cugaagcgga 840

ccgcccggcg gcgguacacc cggcggaaga accggaucug cuaccugcag gagaucuuca 900

gcaacgagau ggccaaggug gacgacagcu ucuuccaccg gcuggaggag agcuuccugg 960

uggaggagga caagaagcac gagcggcacc ccaucuucgg caacaucgug gacgaggugg 1020

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gccugacccc caacuucaag agcaacuucg accuggccga ggacgccaag cugcagcuga 1440

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ugaaguacgu gaccgagggc augcggaagc ccgccuuccu gagcggcgag cagaagaagg 2280

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<210> 2149
<211> 1588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2149
Met Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His Ala Leu
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Thr Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val Gly Ala
20 25 30

Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Ala
35 40 45

Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg
50 55 60

Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu
65 70 75 80

Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His
85 90 95

Ser Arg Ile Gly Arg Val Val Phe Gly Val Arg Asn Ala Lys Thr Gly
100 105 110

Ala Ala Gly Ser Leu Met Asp Val Leu His His Pro Gly Met Asn His
115 120 125

Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu
130 135 140

Leu Cys Arg Phe Phe Arg Met Pro Arg Arg Val Phe Asn Ala Gln Lys
145 150 155 160

Lys Ala Gln Ser Ser Thr Asp Ser Gly Gly Ser Ser Gly Gly Ser Ser
165 170 175

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser
180 185 190

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Gly Gly Ser Ser Gly Gly Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala
        195                 200                 205

Ile Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys
    210                 215                 220

Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser
225                 230                 235                 240

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

Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg
            260                 265                 270

Arg Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met
        275                 280                 285

Ala Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu
    290                 295                 300

Val Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile
305                 310                 315                 320

Val Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu
                325                 330                 335

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

Tyr Leu Ala Leu Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile
        355                 360                 365

Glu Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile
    370                 375                 380

Gln Leu Val Gln Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn
385                 390                 395                 400

Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys
                405                 410                 415

Ser Arg Arg Leu Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys
            420                 425                 430

Asn Gly Leu Phe Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro
        435                 440                 445

Asn Phe Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu
    450                 455                 460

Ser Lys Asp Thr Tyr Asp Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile
```

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465                 470                 475                 480

Gly Asp Gln Tyr Ala Asp Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp
                485                 490                 495

Ala Ile Leu Leu Ser Asp Ile Leu Arg Val Asn Thr Glu Ile Thr Lys
            500                 505                 510

Ala Pro Leu Ser Ala Ser Met Ile Lys Arg Tyr Asp Glu His His Gln
        515                 520                 525

Asp Leu Thr Leu Leu Lys Ala Leu Val Arg Gln Gln Leu Pro Glu Lys
    530                 535                 540

Tyr Lys Glu Ile Phe Phe Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr
545                 550                 555                 560

Ile Asp Gly Gly Ala Ser Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro
                565                 570                 575

Ile Leu Glu Lys Met Asp Gly Thr Glu Glu Leu Leu Val Lys Leu Asn
            580                 585                 590

Arg Glu Asp Leu Leu Arg Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile
        595                 600                 605

Pro His Gln Ile His Leu Gly Glu Leu His Ala Ile Leu Arg Arg Gln
    610                 615                 620

Glu Asp Phe Tyr Pro Phe Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys
625                 630                 635                 640

Ile Leu Thr Phe Arg Ile Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly
                645                 650                 655

Asn Ser Arg Phe Ala Trp Met Thr Arg Lys Ser Glu Glu Thr Ile Thr
            660                 665                 670

Pro Trp Asn Phe Glu Glu Val Val Asp Lys Gly Ala Ser Ala Gln Ser
        675                 680                 685

Phe Ile Glu Arg Met Thr Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys
    690                 695                 700

Val Leu Pro Lys His Ser Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn
705                 710                 715                 720

Glu Leu Thr Lys Val Lys Tyr Val Thr Glu Gly Met Arg Lys Pro Ala
                725                 730                 735

Phe Leu Ser Gly Glu Gln Lys Lys Ala Ile Val Asp Leu Leu Phe Lys
            740                 745                 750
```

```
Thr Asn Arg Lys Val Thr Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys
        755                 760                 765

Lys Ile Glu Cys Phe Asp Ser Val Glu Ile Ser Gly Val Glu Asp Arg
    770                 775                 780

Phe Asn Ala Ser Leu Gly Thr Tyr His Asp Leu Leu Lys Ile Ile Lys
785                 790                 795                 800

Asp Lys Asp Phe Leu Asp Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp
                805                 810                 815

Ile Val Leu Thr Leu Thr Leu Phe Glu Asp Arg Glu Met Ile Glu Glu
            820                 825                 830

Arg Leu Lys Thr Tyr Ala His Leu Phe Asp Asp Lys Val Met Lys Gln
        835                 840                 845

Leu Lys Arg Arg Arg Tyr Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu
    850                 855                 860

Ile Asn Gly Ile Arg Asp Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe
865                 870                 875                 880

Leu Lys Ser Asp Gly Phe Ala Asn Arg Asn Phe Met Gln Leu Ile His
                885                 890                 895

Asp Asp Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val Ser
            900                 905                 910

Gly Gln Gly Asp Ser Leu His Glu His Ile Ala Asn Leu Ala Gly Ser
        915                 920                 925

Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp Glu
    930                 935                 940

Leu Val Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile Glu
945                 950                 955                 960

Met Ala Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg
                965                 970                 975

Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln
            980                 985                 990

Ile Leu Lys Glu His Pro Val Glu  Asn Thr Gln Leu Gln  Asn Glu Lys
        995                 1000                1005

Leu Tyr  Leu Tyr Tyr Leu Gln  Asn Gly Arg Asp Met  Tyr Val Asp
    1010                1015                1020
```

```
Gln Glu  Leu Asp Ile Asn Arg  Leu Ser Asp Tyr Asp  Val Asp His
    1025                 1030                 1035

Ile Val  Pro Gln Ser Phe Leu  Lys Asp Asp Ser Ile  Asp Asn Lys
    1040                 1045                 1050

Val Leu  Thr Arg Ser Asp Lys  Asn Arg Gly Lys Ser  Asp Asn Val
    1055                 1060                 1065

Pro Ser  Glu Glu Val Val Lys  Lys Met Lys Asn Tyr  Trp Arg Gln
    1070                 1075                 1080

Leu Leu  Asn Ala Lys Leu Ile  Thr Gln Arg Lys Phe  Asp Asn Leu
    1085                 1090                 1095

Thr Lys  Ala Glu Arg Gly Gly  Leu Ser Glu Leu Asp  Lys Ala Gly
    1100                 1105                 1110

Phe Ile  Lys Arg Gln Leu Val  Glu Thr Arg Gln Ile  Thr Lys His
    1115                 1120                 1125

Val Ala  Gln Ile Leu Asp Ser  Arg Met Asn Thr Lys  Tyr Asp Glu
    1130                 1135                 1140

Asn Asp  Lys Leu Ile Arg Glu  Val Lys Val Ile Thr  Leu Lys Ser
    1145                 1150                 1155

Lys Leu  Val Ser Asp Phe Arg  Lys Asp Phe Gln Phe  Tyr Lys Val
    1160                 1165                 1170

Arg Glu  Ile Asn Asn Tyr His  His Ala His Asp Ala  Tyr Leu Asn
    1175                 1180                 1185

Ala Val  Val Gly Thr Ala Leu  Ile Lys Lys Tyr Pro  Lys Leu Glu
    1190                 1195                 1200

Ser Glu  Phe Val Tyr Gly Asp  Tyr Lys Val Tyr Asp  Val Arg Lys
    1205                 1210                 1215

Met Ile  Ala Lys Ser Glu Gln  Glu Ile Gly Lys Ala  Thr Ala Lys
    1220                 1225                 1230

Tyr Phe  Phe Tyr Ser Asn Ile  Met Asn Phe Phe Lys  Thr Glu Ile
    1235                 1240                 1245

Thr Leu  Ala Asn Gly Glu Ile  Arg Lys Arg Pro Leu  Ile Glu Thr
    1250                 1255                 1260

Asn Gly  Glu Thr Gly Glu Ile  Val Trp Asp Lys Gly  Arg Asp Phe
    1265                 1270                 1275
```

```
Ala Thr  Val Arg Lys Val Leu  Ser Met Pro Gln Val  Asn Ile Val
    1280                 1285                 1290

Lys Lys  Thr Glu Val Gln Thr  Gly Gly Phe Ser Lys  Glu Ser Ile
    1295                 1300                 1305

Leu Pro  Lys Arg Asn Ser Asp  Lys Leu Ile Ala Arg  Lys Lys Asp
    1310                 1315                 1320

Trp Asp  Pro Lys Lys Tyr Gly  Gly Phe Glu Ser Pro  Thr Val Ala
    1325                 1330                 1335

Tyr Ser  Val Leu Val Val Ala  Lys Val Glu Lys Gly  Lys Ser Lys
    1340                 1345                 1350

Lys Leu  Lys Ser Val Lys Glu  Leu Leu Gly Ile Thr  Ile Met Glu
    1355                 1360                 1365

Arg Ser  Ser Phe Glu Lys Asn  Pro Ile Asp Phe Leu  Glu Ala Lys
    1370                 1375                 1380

Gly Tyr  Lys Glu Val Lys Lys  Asp Leu Ile Ile Lys  Leu Pro Lys
    1385                 1390                 1395

Tyr Ser  Leu Phe Glu Leu Glu  Asn Gly Arg Lys Arg  Met Leu Ala
    1400                 1405                 1410

Ser Ala  Gly Glu Leu Gln Lys  Gly Asn Glu Leu Ala  Leu Pro Ser
    1415                 1420                 1425

Lys Tyr  Val Asn Phe Leu Tyr  Leu Ala Ser His Tyr  Glu Lys Leu
    1430                 1435                 1440

Lys Gly  Ser Pro Glu Asp Asn  Glu Gln Lys Gln Leu  Phe Val Glu
    1445                 1450                 1455

Gln His  Lys His Tyr Leu Asp  Glu Ile Ile Glu Gln  Ile Ser Glu
    1460                 1465                 1470

Phe Ser  Lys Arg Val Ile Leu  Ala Asp Ala Asn Leu  Asp Lys Val
    1475                 1480                 1485

Leu Ser  Ala Tyr Asn Lys His  Arg Asp Lys Pro Ile  Arg Glu Gln
    1490                 1495                 1500

Ala Glu  Asn Ile Ile His Leu  Phe Thr Leu Thr Asn  Leu Gly Ala
    1505                 1510                 1515

Pro Ala  Ala Phe Lys Tyr Phe  Asp Thr Thr Ile Asp  Arg Lys Arg
    1520                 1525                 1530

Tyr Thr  Ser Thr Lys Glu Val  Leu Asp Ala Thr Leu  Ile His Gln
```

```
    1535                1540                1545

Ser Ile  Thr Gly Leu Tyr Glu  Thr Arg Ile Asp Leu  Ser Gln Leu
    1550                1555                1560

Gly Gly  Asp Glu Gly Ala Asp  Lys Arg Thr Ala Asp  Gly Ser Glu
    1565                1570                1575

Phe Glu  Ser Pro Lys Lys Lys  Arg Lys Val
    1580                1585
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<210> 2150
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

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Ser Glu Ser Ala Thr Pro Glu Ser Ser Gly Gly Ser Ser Gly Gly Ser
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<210> 2151
<211> 4101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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acccggcuga agcggaccgc ccggcggcgg uacacccggc ggaagaaccg gaucugcuac      240

cugcaggaga ucuucagcaa cgagauggcc aagguggacg acagcuucuu ccaccggcug      300

gaggagagcu uccuggugga ggaggacaag aagcacgagc ggcaccccau cuucggcaac      360

aucguggacg agguggccua ccacgagaag uaccccacca ucuaccaccu gcggaagaag      420

cugguggaca gcaccgacaa ggccgaccug cggcugaucu accuggcccu ggcccacaug      480

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gacaagcugu ucauccagcu ggugcagacc uacaaccagc uguucgagga gaaccccauc      600

aacgccagcg gcguggacgc caaggccauc cugagcgccc ggcugagcaa gagccggcgg      660

cuggagaacc ugaucgccca gcugcccggc gagaagaaga acggccuguu cggcaaccug      720

aucgcccuga gccugggccu gaccccaac uucaagagca acuucgaccu ggccgaggac      780
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gccaagcugc agcugagcaa ggacaccuac gacgacgacc uggacaaccu gcuggcccag 840

aucggcgacc aguacgccga ccuguuccug gccgccaaga accugagcga cgccauccug 900

cugagcgaca uccugcgggu gaacaccgag aucaccaagg ccccccugag cgccagcaug 960

aucaagcggu acgacgagca ccaccaggac cugacccugc ugaaggcccu ggugcggcag 1020

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aagauggacg gcaccgagga gcugcuggug aagcugaacc gggaggaccu gcugcggaag 1200

cagcggaccu ucgacaacgg cagcaucccc caccagaucc accugggcga gcugcacgcc 1260

auccugcggc ggcaggagga cuucuacccc uuccugaagg acaaccggga gaagaucgag 1320

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agccuguucg agcuggagaa cggccggaag cggaugcugg ccagcgccgg cgagcugcag 3660

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uacgagaagc ugaagggcag ccccgaggac aacgagcaga agcagcuguu cguggagcag 3780

cacaagcacu accuggacga gaucaucgag cagaucagcg aguucagcaa gcgggugauc 3840

cuggccgacg ccaaccugga caaggugcug agcgccuaca acaagcaccg ggacaagccc 3900

auccgggagc aggccgagaa caucauccac cuguucaccc ugaccaaccu gggcgccccc 3960

gccgccuuca aguacuucga caccaccauc gaccggaagc gguacaccag caccaaggag 4020

gugcuggacg ccacccugau ccaccagagc aucaccggcc uguacgagac acggaucgac 4080

cugagccagc ugggcggcga c 4101

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<211> 1367
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2152
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Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe Lys
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
    210                 215                 220

Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
225                 230                 235                 240

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

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

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

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

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

Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys Ala
                325                 330                 335
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Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe Asp
            340                 345                 350

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr Leu
```

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    610                 615                 620

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

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

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

Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
        675                 680                 685

Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
    690                 695                 700

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925

His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
    930                 935                 940

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

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

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

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

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

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

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

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

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

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

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

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

Lys Tyr  Gly Gly Phe Glu Ser  Pro Thr Val Ala Tyr  Ser Val Leu
    1130                1135                1140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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<211> 4929
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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agcgggaggu gcccgugggc gccgugcugg ugcugaacaa ccgggugauc ggcgagggcu 180

ggaaccgggc caucggccug cacgacccca ccgcccacgc cgagaucaug gcccugcggc 240

agggcggccu ggugaugcag aacuaccggc ugaucgacgc cacccuguac gugaccuucg 300

agcccugcgu gaugugcgcc ggcgccauga uccacagccg gaucggccgg gugguguucg 360

gcgugcggaa cgccaagacc ggcgccgccg gcagccugau ggacgugcug caccaccccg 420

gcaugaacca ccggguggag aucaccgagg gcauccuggc cgacgagugc gccgcccugc 480

ugugccgguu cuuccggaug ccccggcggg uguucaacgc ccagaagaag gcccagagca 540

gcaccgacag cggcggcagc agcggcggca gcagcggcag cgagacaccc ggcaccagcg 600

agagcgccac ccccgagagc agcggcggca gcagcggcgg cagcgacaag aaguacagca 660

ucggccuggc caucggcacc aacagcgugg gcugggccgu gaucaccgac gaguacaagg 720

ugcccagcaa gaaguucaag gugcugggca acaccgaccg gcacagcauc aagaagaacc 780

ugaucggcgc ccugcuguuc gacagcggcg agacagccga ggccacccgg cugaagcgga 840

ccgcccggcg gcgguacacc cggcggaaga accggaucug cuaccugcag gagaucuuca 900

gcaacgagau ggccaaggug gacgacagcu ucuuccaccg gcuggaggag agcuuccugg 960

uggaggagga caagaagcac gagcggcacc ccaucuucgg caacaucgug gacgaggugg 1020

ccuaccacga gaaguacccc accaucuacc accugcggaa gaagcuggug gacagcaccg 1080

acaaggccga ccugcggcug aucuaccugg cccuggccca caugaucaag uuccggggcc 1140

acuuccugau cgagggcgac cugaaccccg acaacagcga cguggacaag cuguucaucc 1200

agcuggugca gaccuacaac cagcuguucg aggagaaccc caucaacgcc agcggcgugg 1260

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cccagcugcc cggcgagaag aagaacggcc uguucggcaa ccugaucgcc cugagccugg 1380

gccugacccc caacuucaag agcaacuucg accuggccga ggacgccaag cugcagcuga 1440

gcaaggacac cuacgacgac gaccuggaca accugcuggc ccagaucggc gaccaguacg 1500

ccgaccuguu ccuggccgcc aagaaccuga gcgacgccau ccugcugagc gacauccugc 1560

gggugaacac cgagaucacc aaggcccccc ugagcgccag caugaucaag cgguacgacg 1620

agcaccacca ggaccugacc cugcugaagg cccuggugcg gcagcagcug cccgagaagu 1680

acaaggagau cuucuucgac cagagcaaga acggcuacgc cggcuacauc gacggcggcg 1740

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aggagcugcu ggugaagcug aaccgggagg accugcugcg gaagcagcgg accuucgaca 1860

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gcgcccagag cuucaucgag cggaugacca acuucgacaa gaaccugccc aacgagaagg 2160

ugcugcccaa gcacagccug cuguacgagu acuucaccgu guacaacgag cugaccaagg 2220

ugaaguacgu gaccgagggc augcggaagc ccgccuuccu gagcggcgag cagaagaagg 2280

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ugaugaagca gcugaagcgg cggcgguaca ccggcugggg ccggcugagc cggaagcuga 2640

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accccaagaa guacggcggc uucgagagcc ccaccguggc cuacagcgug cugguggugg 4080

ccaaggugga gaagggcaag agcaagaagc ucaagagcgu gaaggagcug cugggcauca 4140

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agaacggccg gaagcggaug cuggccagcg ccggcgagcu gcagaagggc aacgagcugg 4320

cccugcccag caaguacgug aacuuccugu accuggccag ccacuacgag aagcugaagg 4380

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agaacaucau ccaccuguuc acccugacca accugggcgc ccccgccgcc uucaaguacu 4620

ucgacaccac caucgaccgg aagcgguaca ccagcaccaa ggaggugcug gacgccaccc 4680

ugauccacca gagcaucacc ggccuguacg agacacggau cgaccugagc cagcugggcg 4740

gcgacgaggg cgccgacaag cggaccgccg acggcagcga guucgagagc cccaagaaga 4800

agcggaaggu gugagcggcc gcuuaauuaa gcugccuucu gcggggcuug ccuucuggcc 4860

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aagucuaga 4929

<210> 2154
<211> 1588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2154
Met Ser Glu Val Glu Phe Ser His Glu Tyr Trp Met Arg His Ala Leu
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Thr Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val Gly Ala
20 25 30

Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Ala
35 40 45

Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg
50 55 60

Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu
65 70 75 80

Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His
85 90 95

Ser Arg Ile Gly Arg Val Val Phe Gly Val Arg Asn Ala Lys Thr Gly
100 105 110

Ala Ala Gly Ser Leu Met Asp Val Leu His His Pro Gly Met Asn His
115 120 125

```
Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu
    130                 135                 140

Leu Cys Arg Phe Phe Arg Met Pro Arg Arg Val Phe Asn Ala Gln Lys
145                 150                 155                 160

Lys Ala Gln Ser Ser Thr Asp Ser Gly Gly Ser Ser Gly Gly Ser Ser
                165                 170                 175

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser
            180                 185                 190

Gly Gly Ser Ser Gly Gly Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala
        195                 200                 205

Ile Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys
    210                 215                 220

Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser
225                 230                 235                 240

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

Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg
            260                 265                 270

Arg Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met
        275                 280                 285

Ala Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu
    290                 295                 300

Val Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile
305                 310                 315                 320

Val Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu
                325                 330                 335

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

Tyr Leu Ala Leu Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile
        355                 360                 365

Glu Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile
    370                 375                 380

Gln Leu Val Gln Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn
385                 390                 395                 400

Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys
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```
                405                 410                 415

Ser Arg Arg Leu Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys
            420                 425                 430

Asn Gly Leu Phe Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro
        435                 440                 445

Asn Phe Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu
    450                 455                 460

Ser Lys Asp Thr Tyr Asp Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile
465                 470                 475                 480

Gly Asp Gln Tyr Ala Asp Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp
                485                 490                 495

Ala Ile Leu Leu Ser Asp Ile Leu Arg Val Asn Thr Glu Ile Thr Lys
            500                 505                 510

Ala Pro Leu Ser Ala Ser Met Ile Lys Arg Tyr Asp Glu His His Gln
        515                 520                 525

Asp Leu Thr Leu Leu Lys Ala Leu Val Arg Gln Gln Leu Pro Glu Lys
    530                 535                 540

Tyr Lys Glu Ile Phe Phe Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr
545                 550                 555                 560

Ile Asp Gly Gly Ala Ser Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro
                565                 570                 575

Ile Leu Glu Lys Met Asp Gly Thr Glu Glu Leu Leu Val Lys Leu Asn
            580                 585                 590

Arg Glu Asp Leu Leu Arg Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile
        595                 600                 605

Pro His Gln Ile His Leu Gly Glu Leu His Ala Ile Leu Arg Arg Gln
    610                 615                 620

Glu Asp Phe Tyr Pro Phe Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys
625                 630                 635                 640

Ile Leu Thr Phe Arg Ile Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly
                645                 650                 655

Asn Ser Arg Phe Ala Trp Met Thr Arg Lys Ser Glu Glu Thr Ile Thr
            660                 665                 670

Pro Trp Asn Phe Glu Glu Val Val Asp Lys Gly Ala Ser Ala Gln Ser
        675                 680                 685
```

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Phe Ile Glu Arg Met Thr Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys
    690                 695                 700

Val Leu Pro Lys His Ser Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn
705                 710                 715                 720

Glu Leu Thr Lys Val Lys Tyr Val Thr Glu Gly Met Arg Lys Pro Ala
                725                 730                 735

Phe Leu Ser Gly Glu Gln Lys Lys Ala Ile Val Asp Leu Leu Phe Lys
            740                 745                 750

Thr Asn Arg Lys Val Thr Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys
        755                 760                 765

Lys Ile Glu Cys Phe Asp Ser Val Glu Ile Ser Gly Val Glu Asp Arg
    770                 775                 780

Phe Asn Ala Ser Leu Gly Thr Tyr His Asp Leu Leu Lys Ile Ile Lys
785                 790                 795                 800

Asp Lys Asp Phe Leu Asp Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp
                805                 810                 815

Ile Val Leu Thr Leu Thr Leu Phe Glu Asp Arg Glu Met Ile Glu Glu
            820                 825                 830

Arg Leu Lys Thr Tyr Ala His Leu Phe Asp Asp Lys Val Met Lys Gln
        835                 840                 845

Leu Lys Arg Arg Arg Tyr Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu
    850                 855                 860

Ile Asn Gly Ile Arg Asp Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe
865                 870                 875                 880

Leu Lys Ser Asp Gly Phe Ala Asn Ala Asn Phe Met Gln Leu Ile His
                885                 890                 895

Asp Asp Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val Ser
            900                 905                 910

Gly Gln Gly Asp Ser Leu His Glu His Ile Ala Asn Leu Ala Gly Ser
        915                 920                 925

Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp Glu
    930                 935                 940

Leu Val Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile Glu
945                 950                 955                 960
```

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Met Ala Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg
               965                 970                 975

Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln
           980                 985                 990

Ile Leu Lys Glu His Pro Val Glu  Asn Thr Gln Leu Gln  Asn Glu Lys
       995                1000                1005

Leu Tyr  Leu Tyr Tyr Leu Gln  Asn Gly Arg Asp Met  Tyr Val Asp
    1010                1015                1020

Gln Glu  Leu Asp Ile Asn Arg  Leu Ser Asp Tyr Asp  Val Asp His
    1025                1030                1035

Ile Val  Pro Gln Ser Phe Leu  Lys Asp Asp Ser Ile  Asp Asn Lys
    1040                1045                1050

Val Leu  Thr Arg Ser Asp Lys  Asn Arg Gly Lys Ser  Asp Asn Val
    1055                1060                1065

Pro Ser  Glu Glu Val Val Lys  Lys Met Lys Asn Tyr  Trp Arg Gln
    1070                1075                1080

Leu Leu  Asn Ala Lys Leu Ile  Thr Gln Arg Lys Phe  Asp Asn Leu
    1085                1090                1095

Thr Lys  Ala Glu Arg Gly Gly  Leu Ser Glu Leu Asp  Lys Ala Gly
    1100                1105                1110

Phe Ile  Lys Arg Gln Leu Val  Glu Thr Arg Gln Ile  Thr Lys His
    1115                1120                1125

Val Ala  Gln Ile Leu Asp Ser  Arg Met Asn Thr Lys  Tyr Asp Glu
    1130                1135                1140

Asn Asp  Lys Leu Ile Arg Glu  Val Lys Val Ile Thr  Leu Lys Ser
    1145                1150                1155

Lys Leu  Val Ser Asp Phe Arg  Lys Asp Phe Gln Phe  Tyr Lys Val
    1160                1165                1170

Arg Glu  Ile Asn Asn Tyr His  His Ala His Asp Ala  Tyr Leu Asn
    1175                1180                1185

Ala Val  Val Gly Thr Ala Leu  Ile Lys Lys Tyr Pro  Lys Leu Glu
    1190                1195                1200

Ser Glu  Phe Val Tyr Gly Asp  Tyr Lys Val Tyr Asp  Val Arg Lys
    1205                1210                1215
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Met Ile  Ala Lys Ser Glu Gln  Glu Ile Gly Lys Ala  Thr Ala Lys
    1220                 1225                 1230

Tyr Phe  Phe Tyr Ser Asn Ile  Met Asn Phe Phe Lys  Thr Glu Ile
    1235                 1240                 1245

Thr Leu  Ala Asn Gly Glu Ile  Arg Lys Arg Pro Leu  Ile Glu Thr
    1250                 1255                 1260

Asn Gly  Glu Thr Gly Glu Ile  Val Trp Asp Lys Gly  Arg Asp Phe
    1265                 1270                 1275

Ala Thr  Val Arg Lys Val Leu  Ser Met Pro Gln Val  Asn Ile Val
    1280                 1285                 1290

Lys Lys  Thr Glu Val Gln Thr  Gly Gly Phe Ser Lys  Glu Ser Ile
    1295                 1300                 1305

Leu Pro  Lys Arg Asn Ser Asp  Lys Leu Ile Ala Arg  Lys Lys Asp
    1310                 1315                 1320

Trp Asp  Pro Lys Lys Tyr Gly  Gly Phe Glu Ser Pro  Thr Val Ala
    1325                 1330                 1335

Tyr Ser  Val Leu Val Val Ala  Lys Val Glu Lys Gly  Lys Ser Lys
    1340                 1345                 1350

Lys Leu  Lys Ser Val Lys Glu  Leu Leu Gly Ile Thr  Ile Met Glu
    1355                 1360                 1365

Arg Ser  Ser Phe Glu Lys Asn  Pro Ile Asp Phe Leu  Glu Ala Lys
    1370                 1375                 1380

Gly Tyr  Lys Glu Val Lys Lys  Asp Leu Ile Ile Lys  Leu Pro Lys
    1385                 1390                 1395

Tyr Ser  Leu Phe Glu Leu Glu  Asn Gly Arg Lys Arg  Met Leu Ala
    1400                 1405                 1410

Ser Ala  Gly Glu Leu Gln Lys  Gly Asn Glu Leu Ala  Leu Pro Ser
    1415                 1420                 1425

Lys Tyr  Val Asn Phe Leu Tyr  Leu Ala Ser His Tyr  Glu Lys Leu
    1430                 1435                 1440

Lys Gly  Ser Pro Glu Asp Asn  Glu Gln Lys Gln Leu  Phe Val Glu
    1445                 1450                 1455

Gln His  Lys His Tyr Leu Asp  Glu Ile Ile Glu Gln  Ile Ser Glu
    1460                 1465                 1470

Phe Ser  Lys Arg Val Ile Leu  Ala Asp Ala Asn Leu  Asp Lys Val
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1475 1480 1485

Leu Ser Ala Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln
1490 1495 1500

Ala Glu Asn Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala
1505 1510 1515

Pro Ala Ala Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg
1520 1525 1530

Tyr Thr Ser Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln
1535 1540 1545

Ser Ile Thr Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu
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Gly Gly Asp Glu Gly Ala Asp Lys Arg Thr Ala Asp Gly Ser Glu
1565 1570 1575

Phe Glu Ser Pro Lys Lys Lys Arg Lys Val
1580 1585

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<211> 4101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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agcaucaaga agaaccugau cggcgcccug cuguucgaca gcggcgagac agccgaggcc 180

acccggcuga agcggaccgc ccggcggcgg uacacccggc ggaagaaccg gaucugcuac 240

cugcaggaga ucuucagcaa cgagauggcc aagguggacg acagcuucuu ccaccggcug 300

gaggagagcu uccuggugga ggaggacaag aagcacgagc ggcaccccau cuucggcaac 360

aucguggacg agguggccua ccacgagaag uaccccacca ucuaccaccu gcggaagaag 420

cugguggaca gcaccgacaa ggccgaccug cggcugaucu accuggcccu ggcccacaug 480

aucaaguucc ggggccacuu ccugaucgag ggcgaccuga accccgacaa cagcgacgug 540

gacaagcugu ucauccagcu ggugcagacc uacaaccagc uguucgagga gaaccccauc 600

aacgccagcg gcguggacgc caaggccauc cugagcgccc ggcugagcaa gagccggcgg 660

cuggagaacc ugaucgccca gcugcccggc gagaagaaga acggccuguu cggcaaccug 720

aucgcccuga gccuggggccu gacccccaac uucaagagca acuucgaccu ggccgaggac 780

gccaagcugc agcugagcaa ggacaccuac gacgacgacc uggacaaccu gcuggcccag 840

aucggcgacc aguacgccga ccuguuccug gccgccaaga accugagcga cgccauccug 900

cugagcgaca uccugcgggu gaacaccgag aucaccaagg ccccccugag cgccagcaug 960

aucaagcggu acgacgagca ccaccaggac cugacccugc ugaaggcccu ggugcggcag 1020

cagcugcccg agaaguacaa ggagaucuuc uucgaccaga gcaagaacgg cuacgccggc 1080

uacaucgacg gcggcgccag ccaggaggag uucuacaagu ucaucaagcc cauccuggag 1140

aagauggacg gcaccgagga gcugcuggug aagcugaacc gggaggaccu gcugcggaag 1200

cagcggaccu ucgacaacgg cagcaucccc caccagaucc accugggcga gcugcacgcc 1260

auccugcggc ggcaggagga cuucuacccc uuccugaagg acaaccggga gaagaucgag 1320

aagauccuga ccuuccggau ccccuacuac gugggccccc uggcccgggg caacagccgg 1380

uucgccugga ugacccgcaa gagcgaggag acaaucaccc ccuggaacuu cgaggaggug 1440

guggacaagg gcgccagcgc ccagagcuuc aucgagcgga ugaccaacuu cgacaagaac 1500

cugcccaacg agaaggugcu gcccaagcac agccugcugu acgaguacuu caccguguac 1560

aacgagcuga ccaaggugaa guacgugacc gagggcaugc ggaagcccgc cuuccugagc 1620

ggcgagcaga agaaggccau cguggaccug cuguucaaga ccaaccggaa ggugaccgug 1680

aagcagcuga aggaggacua cuucaagaag aucgagugcu ucgacagcgu ggagaucagc 1740

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aaggacaagg acuuccugga caacgaggag aacgaggaca uccuggagga caucgugcug 1860

acccugaccc uguucgagga ccgggagaug aucgaggagc ggcugaagac cuacgcccac 1920

cuguucgacg acaaggugau gaagcagcug aagcggcggc gguacaccgg cuggggccgg 1980

cugagccgga agcugaucaa cggcauccgg gacaagcaga gcggcaagac cauccuggac 2040

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cugaccuuca aggaggacau ccagaaggcc caggugagcg gccagggcga cagccugcac 2160

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aagguggugg acgagcuggu gaaggugaug ggccggcaca agcccgagaa caucgugauc 2280

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gagaacaccc agcugcagaa cgagaagcug uaccuguacu accugcagaa cggccgggac 2460

auguacgugg accaggagcu ggacaucaac cggcugagcg acuacgacgu ggaccacauc 2520

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aagaaccggg gcaagagcga caacgugccc agcgaggagg uggugaagaa gaugaagaac 2640

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aaggccgagc ggggcggccu gagcgagcug gacaaggccg gcuucaucaa gcggcagcug 2760

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cccaagcugg agagcgaguu cguguacggc gacuacaagg uguacgacgu gcggaagaug 3060

aucgccaaga gcgagcagga gaucggcaag gccaccgcca aguacuucuu cuacagcaac 3120

aucaugaacu ucuucaagac cgagaucacc cuggccaacg gcgagauccg gaagcggccc 3180

cugaucgaga caaacggcga gacaggcgag aucguguggg acaaggggccg ggacuucgcc 3240

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gagcugcugg gcaucaccau cauggagcgg agcagcuucg agaagaaccc caucgacuuc 3540

cuggaggcca agggcuacaa ggaggugaag aaggaccuga ucaucaagcu gcccaaguac 3600

agccuguucg agcuggagaa cggccggaag cggaugcugg ccagcgccgg cgagcugcag 3660

aagggcaacg agcuggcccu gcccagcaag uacgugaacu uccuguaccu ggccagccac 3720

uacgagaagc ugaagggcag ccccgaggac aacgagcaga agcagcuguu cguggagcag 3780

cacaagcacu accuggacga gaucaucgag cagaucagcg aguucagcaa gcgggugauc 3840

cuggccgacg ccaaccugga caaggugcug agcgccuaca acaagcaccg ggacaagccc 3900

auccgggagc aggccgagaa caucauccac cuguucaccc ugaccaaccu gggcgccccc 3960

gccgccuuca aguacuucga caccaccauc gaccggaagc gguacaccag caccaaggag 4020

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cugagccagc ugggcggcga c 4101

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<211> 1367
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

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

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

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

Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys Tyr

65 70 75 80

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

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

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

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

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

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

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

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

Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
210 215 220

Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
225 230 235 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr Leu
    610                 615                 620
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Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala His
625                 630                 635                 640

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

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

Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
        675                 680                 685

Asn Ala Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
    690                 695                 700

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

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

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

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

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

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

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

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

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

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

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

Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys Phe
                885                 890                 895
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Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp Lys
            900                 905                 910

Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925

His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
    930                 935                 940

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

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

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

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

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

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

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

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

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

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

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

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

Lys Tyr  Gly Gly Phe Glu Ser  Pro Thr Val Ala Tyr  Ser Val Leu
    1130                1135                1140

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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agcgggaggu gcccgugggc gccgugcugg ugcugaacaa ccgggugauc ggcgagggcu 180

ggaaccgggc caucggccug cacgacccca ccgcccacgc cgagaucaug gcccugcggc 240

agggcggccu ggugaugcag aacuaccggc ugaucgacgc cacccuguac gugaccuucg 300

agcccugcgu gaugugcgcc ggcgccauga uccacagccg gaucggccgg gugguguucg 360

gcgugcggaa cgccaagacc ggcgccgccg gcagccugau ggacgugcug caccaccccg 420

gcaugaacca ccggguggag aucaccgagg gcauccuggc cgacgagugc gccgcccugc 480

ugugccgguu cuuccggaug ccccggcggg uguucaacgc ccagaagaag gcccagagca 540

gcaccgacag cggcggcagc agcggcggca gcagcggcag cgagacaccc ggcaccagcg 600

agagcgccac ccccgagagc agcggcggca gcagcggcgg cagcgacaag aaguacagca 660

ucggccuggc caucggcacc aacagcgugg gcugggccgu gaucaccgac gaguacaagg 720

ugcccagcaa gaaguucaag gugcugggca acaccgaccg gcacagcauc aagaagaacc 780

ugaucggcgc ccugcuguuc gacagcggcg agacagccga ggccacccgg cugaagcgga 840

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gcaacgagau ggccaaggug gacgacagcu ucuuccaccg gcuggaggag agcuuccugg 960

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ccuaccacga gaaguacccc accaucuacc accugcggaa gaagcuggug gacagcaccg 1080

acaaggccga ccugcggcug aucuaccugg cccuggccca caugaucaag uuccggggcc 1140

acuuccugau cgagggcgac cugaaccccg acaacagcga cguggacaag cuguucaucc 1200

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gcaagagcga ggagacaauc acccccugga acuucgagga ggugguggac aagggcgcca 2100

gcgcccagag cuucaucgag cggaugacca acuucgacaa gaaccugccc aacgagaagg 2160

ugcugcccaa gcacagccug cuguacgagu acuucaccgu guacaacgag cugaccaagg 2220

ugaaguacgu gaccgagggc augcggaagc ccgccuuccu gagcggcgag cagaagaagg 2280

ccaucgugga ccugcuguuc aagaccaacc ggaaggugac cgugaagcag cugaaggagg 2340

acuacuucaa gaagaucgag ugcuucgaca gcguggagau cagcggcgug gaggaccggu 2400

ucaacgccag ccugggcacc uaccacgacc ugcugaagau caucaaggac aaggacuucc 2460

uggacaacga ggagaacgag gacauccugg aggacaucgu gcugacccug acccuguucg 2520

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ucaacggcau ccgggacaag cagagcggca agaccauccu ggacuuccuc aagagcgacg 2700

gcuucgccaa cgccaacuuc augcagcuga uccacgacga cagccugacc uucaaggagg 2760

acauccagaa ggcccaggug agcggccagg gcgacagccu gcacgagcac aucgccaacc 2820

uggccggcag ccccgccauc aagaagggca uccugcagac cgugaaggug guggacgagc 2880

uggugaaggu gaugggccgg cacaagcccg agaacaucgu gaucgagaug gcccgggaga 2940

accagaccac ccagaagggc cagaagaaca gccgggagcg gaugaagcgg aucgaggagg 3000

gcaucaagga gcugggcagc cagauccuga aggagcaccc cguggagaac acccagcugc 3060

agaacgagaa gcuguaccug uacuaccugc agaacggccg ggacauguac guggaccagg 3120

agcuggacau caaccggcug agcgacuacg acguggacca caucgugccc cagagcuucc 3180

ugaaggacga cagcaucgac aacaaggugc ugacccggag cgacaagaac cggggcaaga 3240

gcgacaacgu gcccagcgag gaggugguga agaagaugaa gaacuacugg cggcagcugc 3300

ugaacgccaa gcugaucacc cagcggaagu ucgacaaccu gaccaaggcc gagcggggcg 3360

gccugagcga gcuggacaag gccggcuuca ucaagcggca gcugguggag acacggcaga 3420

ucaccaagca cguggcccag auccuggaca gccggaugaa caccaaguac gacgagaacg 3480

acaagcugau ccgggaggug aaggugauca cccucaagag caagcuggug agcgacuucc 3540

ggaaggacuu ccaguucuac aaggugcggg agaucaacaa cuaccaccac gcccacgacg 3600

ccuaccugaa cgccguggug ggcaccgccc ugaucaagaa guaccccaag cuggagagcg 3660

aguucgugua cggcgacuac aagguguacg acgugcggaa gaugaucgcc aagagcgagc 3720

aggagaucgg caaggccacc gccaaguacu ucuucuacag caacaucaug aacuucuuca 3780

agaccgagau cacccuggcc aacggcgaga uccggaagcg gccccugauc gagacaaacg 3840

gcgagacagg cgagaucgug ugggacaagg gccgggacuu cgccaccgug cggaaggugc 3900

ugagcaugcc ccaggugaac aucgugaaga agaccgaggu gcagaccggc ggcuucagca 3960

aggagagcau ccugcccaag cggaacagcg acaagcugau cgcccggaag aaggacuggg 4020

accccaagaa guacggcggc uucgacagcc ccaccguggc cuacagcgug cugguggugg 4080

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gcagccccga ggacaacgag cagaagcagc uguucgugga gcagcacaag cacuaccugg 4440

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uggacaaggu gcugagcgcc uacaacaagc accgggacaa gcccauccgg gagcaggccg 4560

agaacaucau ccaccuguuc acccugacca accugggcgc ccccgccgcc uucaaguacu 4620

ucgacaccac caucgaccgg aagcgguaca ccagcaccaa ggaggugcug gacgccaccc 4680

ugauccacca gagcaucacc ggccuguacg agacacggau cgaccugagc cagcugggcg 4740

gcgacgaggg cgccgacaag cggaccgccg acggcagcga guucgagagc cccaagaaga 4800

agcggaaggu gugagcggcc gcuuaauuaa gcugccuucu gcggggcuug ccuucuggcc 4860

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aagucuaga 4929

<210> 2158
<211> 1588
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2158
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Thr Leu Ala Lys Arg Ala Arg Asp Glu Arg Glu Val Pro Val Gly Ala
20 25 30

Val Leu Val Leu Asn Asn Arg Val Ile Gly Glu Gly Trp Asn Arg Ala
35 40 45

Ile Gly Leu His Asp Pro Thr Ala His Ala Glu Ile Met Ala Leu Arg
50 55 60

Gln Gly Gly Leu Val Met Gln Asn Tyr Arg Leu Ile Asp Ala Thr Leu
65 70 75 80

Tyr Val Thr Phe Glu Pro Cys Val Met Cys Ala Gly Ala Met Ile His
85 90 95

Ser Arg Ile Gly Arg Val Val Phe Gly Val Arg Asn Ala Lys Thr Gly
100 105 110

Ala Ala Gly Ser Leu Met Asp Val Leu His His Pro Gly Met Asn His
115 120 125

Arg Val Glu Ile Thr Glu Gly Ile Leu Ala Asp Glu Cys Ala Ala Leu
130 135 140

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Leu Cys Arg Phe Phe Arg Met Pro Arg Arg Val Phe Asn Ala Gln Lys
145                 150                 155                 160

Lys Ala Gln Ser Ser Thr Asp Ser Gly Gly Ser Ser Gly Gly Ser Ser
                165                 170                 175

Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Ser
            180                 185                 190

Gly Gly Ser Ser Gly Gly Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala
        195                 200                 205

Ile Gly Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys
    210                 215                 220

Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His Ser
225                 230                 235                 240

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

Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg
            260                 265                 270

Arg Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met
        275                 280                 285

Ala Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe Leu
    290                 295                 300

Val Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn Ile
305                 310                 315                 320

Val Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His Leu
                325                 330                 335

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

Tyr Leu Ala Leu Ala His Met Ile Lys Phe Arg Gly His Phe Leu Ile
        355                 360                 365

Glu Gly Asp Leu Asn Pro Asp Asn Ser Asp Val Asp Lys Leu Phe Ile
    370                 375                 380

Gln Leu Val Gln Thr Tyr Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn
385                 390                 395                 400

Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys
                405                 410                 415
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Ser Arg Arg Leu Glu Asn Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys
            420                 425                 430

Asn Gly Leu Phe Gly Asn Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro
        435                 440                 445

Asn Phe Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu
    450                 455                 460

Ser Lys Asp Thr Tyr Asp Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile
465                 470                 475                 480

Gly Asp Gln Tyr Ala Asp Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp
                485                 490                 495

Ala Ile Leu Leu Ser Asp Ile Leu Arg Val Asn Thr Glu Ile Thr Lys
            500                 505                 510

Ala Pro Leu Ser Ala Ser Met Ile Lys Arg Tyr Asp Glu His His Gln
        515                 520                 525

Asp Leu Thr Leu Leu Lys Ala Leu Val Arg Gln Gln Leu Pro Glu Lys
    530                 535                 540

Tyr Lys Glu Ile Phe Phe Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr
545                 550                 555                 560

Ile Asp Gly Gly Ala Ser Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro
                565                 570                 575

Ile Leu Glu Lys Met Asp Gly Thr Glu Glu Leu Leu Val Lys Leu Asn
            580                 585                 590

Arg Glu Asp Leu Leu Arg Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile
        595                 600                 605

Pro His Gln Ile His Leu Gly Glu Leu His Ala Ile Leu Arg Arg Gln
    610                 615                 620

Glu Asp Phe Tyr Pro Phe Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys
625                 630                 635                 640

Ile Leu Thr Phe Arg Ile Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly
                645                 650                 655

Asn Ser Arg Phe Ala Trp Met Thr Arg Lys Ser Glu Glu Thr Ile Thr
            660                 665                 670

Pro Trp Asn Phe Glu Glu Val Val Asp Lys Gly Ala Ser Ala Gln Ser
        675                 680                 685
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Phe Ile Glu Arg Met Thr Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys
    690                 695                 700

Val Leu Pro Lys His Ser Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn
705                 710                 715                 720

Glu Leu Thr Lys Val Lys Tyr Val Thr Glu Gly Met Arg Lys Pro Ala
                725                 730                 735

Phe Leu Ser Gly Glu Gln Lys Lys Ala Ile Val Asp Leu Leu Phe Lys
            740                 745                 750

Thr Asn Arg Lys Val Thr Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys
        755                 760                 765

Lys Ile Glu Cys Phe Asp Ser Val Glu Ile Ser Gly Val Glu Asp Arg
    770                 775                 780

Phe Asn Ala Ser Leu Gly Thr Tyr His Asp Leu Leu Lys Ile Ile Lys
785                 790                 795                 800

Asp Lys Asp Phe Leu Asp Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp
                805                 810                 815

Ile Val Leu Thr Leu Thr Leu Phe Glu Asp Arg Glu Met Ile Glu Glu
            820                 825                 830

Arg Leu Lys Thr Tyr Ala His Leu Phe Asp Asp Lys Val Met Lys Gln
        835                 840                 845

Leu Lys Arg Arg Arg Tyr Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu
    850                 855                 860

Ile Asn Gly Ile Arg Asp Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe
865                 870                 875                 880

Leu Lys Ser Asp Gly Phe Ala Asn Ala Asn Phe Met Gln Leu Ile His
                885                 890                 895

Asp Asp Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val Ser
            900                 905                 910

Gly Gln Gly Asp Ser Leu His Glu His Ile Ala Asn Leu Ala Gly Ser
        915                 920                 925

Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp Glu
    930                 935                 940

Leu Val Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile Glu
945                 950                 955                 960

Met Ala Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg
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              965                 970                 975

Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln
            980                 985                 990

Ile Leu Lys Glu His Pro Val Glu  Asn Thr Gln Leu Gln  Asn Glu Lys
        995                 1000                1005

Leu Tyr  Leu Tyr Tyr Leu Gln  Asn Gly Arg Asp Met  Tyr Val Asp
    1010                1015                1020

Gln Glu  Leu Asp Ile Asn Arg  Leu Ser Asp Tyr Asp  Val Asp His
    1025                1030                1035

Ile Val  Pro Gln Ser Phe Leu  Lys Asp Asp Ser Ile  Asp Asn Lys
    1040                1045                1050

Val Leu  Thr Arg Ser Asp Lys  Asn Arg Gly Lys Ser  Asp Asn Val
    1055                1060                1065

Pro Ser  Glu Glu Val Val Lys  Lys Met Lys Asn Tyr  Trp Arg Gln
    1070                1075                1080

Leu Leu  Asn Ala Lys Leu Ile  Thr Gln Arg Lys Phe  Asp Asn Leu
    1085                1090                1095

Thr Lys  Ala Glu Arg Gly Gly  Leu Ser Glu Leu Asp  Lys Ala Gly
    1100                1105                1110

Phe Ile  Lys Arg Gln Leu Val  Glu Thr Arg Gln Ile  Thr Lys His
    1115                1120                1125

Val Ala  Gln Ile Leu Asp Ser  Arg Met Asn Thr Lys  Tyr Asp Glu
    1130                1135                1140

Asn Asp  Lys Leu Ile Arg Glu  Val Lys Val Ile Thr  Leu Lys Ser
    1145                1150                1155

Lys Leu  Val Ser Asp Phe Arg  Lys Asp Phe Gln Phe  Tyr Lys Val
    1160                1165                1170

Arg Glu  Ile Asn Asn Tyr His  His Ala His Asp Ala  Tyr Leu Asn
    1175                1180                1185

Ala Val  Val Gly Thr Ala Leu  Ile Lys Lys Tyr Pro  Lys Leu Glu
    1190                1195                1200

Ser Glu  Phe Val Tyr Gly Asp  Tyr Lys Val Tyr Asp  Val Arg Lys
    1205                1210                1215

Met Ile  Ala Lys Ser Glu Gln  Glu Ile Gly Lys Ala  Thr Ala Lys
    1220                1225                1230
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Tyr Phe  Phe Tyr Ser Asn Ile  Met Asn Phe Phe Lys  Thr Glu Ile
    1235                 1240                 1245

Thr Leu  Ala Asn Gly Glu Ile  Arg Lys Arg Pro Leu  Ile Glu Thr
    1250                 1255                 1260

Asn Gly  Glu Thr Gly Glu Ile  Val Trp Asp Lys Gly  Arg Asp Phe
    1265                 1270                 1275

Ala Thr  Val Arg Lys Val Leu  Ser Met Pro Gln Val  Asn Ile Val
    1280                 1285                 1290

Lys Lys  Thr Glu Val Gln Thr  Gly Gly Phe Ser Lys  Glu Ser Ile
    1295                 1300                 1305

Leu Pro  Lys Arg Asn Ser Asp  Lys Leu Ile Ala Arg  Lys Lys Asp
    1310                 1315                 1320

Trp Asp  Pro Lys Lys Tyr Gly  Gly Phe Asp Ser Pro  Thr Val Ala
    1325                 1330                 1335

Tyr Ser  Val Leu Val Val Ala  Lys Val Glu Lys Gly  Lys Ser Lys
    1340                 1345                 1350

Lys Leu  Lys Ser Val Lys Glu  Leu Leu Gly Ile Thr  Ile Met Glu
    1355                 1360                 1365

Arg Ser  Ser Phe Glu Lys Asn  Pro Ile Asp Phe Leu  Glu Ala Lys
    1370                 1375                 1380

Gly Tyr  Lys Glu Val Lys Lys  Asp Leu Ile Ile Lys  Leu Pro Lys
    1385                 1390                 1395

Tyr Ser  Leu Phe Glu Leu Glu  Asn Gly Arg Lys Arg  Met Leu Ala
    1400                 1405                 1410

Ser Ala  Gly Glu Leu Gln Lys  Gly Asn Glu Leu Ala  Leu Pro Ser
    1415                 1420                 1425

Lys Tyr  Val Asn Phe Leu Tyr  Leu Ala Ser His Tyr  Glu Lys Leu
    1430                 1435                 1440

Lys Gly  Ser Pro Glu Asp Asn  Glu Gln Lys Gln Leu  Phe Val Glu
    1445                 1450                 1455

Gln His  Lys His Tyr Leu Asp  Glu Ile Ile Glu Gln  Ile Ser Glu
    1460                 1465                 1470

Phe Ser  Lys Arg Val Ile Leu  Ala Asp Ala Asn Leu  Asp Lys Val
    1475                 1480                 1485
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Leu Ser Ala Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln
    1490   1495   1500

Ala Glu Asn Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala
    1505   1510   1515

Pro Ala Ala Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg
    1520   1525   1530

Tyr Thr Ser Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln
    1535   1540   1545

Ser Ile Thr Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu
    1550   1555   1560

Gly Gly Asp Glu Gly Ala Asp Lys Arg Thr Ala Asp Gly Ser Glu
    1565   1570   1575

Phe Glu Ser Pro Lys Lys Lys Arg Lys Val
    1580   1585

<210> 2159
<211> 4101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 2159
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accgacgagu acaaggugcc cagcaagaag uucaaggugc ugggcaacac cgaccggcac   120

agcaucaaga agaaccugau cggcgcccug cuguucgaca gcggcgagac agccgaggcc   180

acccggcuga agcggaccgc ccggcggcgg uacacccggc ggaagaaccg gaucugcuac   240

cugcaggaga ucuucagcaa cgagauggcc aagguggacg acagcuucuu ccaccggcug   300

gaggagagcu uccuggugga ggaggacaag aagcacgagc ggcaccccau cuucggcaac   360

aucguggacg agguggccua ccacgagaag uaccccacca ucuaccaccu gcggaagaag   420

cugguggaca gcaccgacaa ggccgaccug cggcugaucu accuggcccu ggcccacaug   480

aucaaguucc ggggccacuu ccugaucgag ggcgaccuga accccgacaa cagcgacgug   540

gacaagcugu ucauccagcu ggugcagacc uacaaccagc uguucgagga gaaccccauc   600

aacgccagcg gcguggacgc caaggccauc cugagcgccc ggcugagcaa gagccggcgg   660

cuggagaacc ugaucgccca gcugcccggc gagaagaaga acggccuguu cggcaaccug   720

aucgcccuga gccugggccu gaccccaac uucaagagca acuucgaccu ggccgaggac   780

gccaagcugc agcugagcaa ggacaccuac gacgacgacc uggacaaccu gcuggcccag   840

aucggcgacc aguacgccga ccuguuccug gccgccaaga accugagcga cgccauccug   900

cugagcgaca uccugcgggu gaacaccgag aucaccaagg ccccccugag cgccagcaug 960

aucaagcggu acgacgagca ccaccaggac cugacccugc ugaaggcccu ggugcggcag 1020

cagcugcccg agaaguacaa ggagaucuuc uucgaccaga gcaagaacgg cuacgccggc 1080

uacaucgacg gcggcgccag ccaggaggag uucuacaagu ucaucaagcc cauccuggag 1140

aagauggacg gcaccgagga gcugcuggug aagcugaacc gggaggaccu gcugcggaag 1200

cagcggaccu ucgacaacgg cagcaucccc caccagaucc accugggcga gcugcacgcc 1260

auccugcggc ggcaggagga cuucuacccc uuccugaagg acaaccggga gaagaucgag 1320

aagauccuga ccuuccggau ccccuacuac gugggccccc uggcccgggg caacagccgg 1380

uucgccugga ugacccgcaa gagcgaggag acaaucaccc ccuggaacuu cgaggaggug 1440

guggacaagg gcgccagcgc ccagagcuuc aucgagcgga ugaccaacuu cgacaagaac 1500

cugcccaacg agaaggugcu gcccaagcac agccugcugu acgaguacuu caccguguac 1560

aacgagcuga ccaaggugaa guacgugacc gagggcaugc ggaagcccgc cuuccugagc 1620

ggcgagcaga agaaggccau cguggaccug cuguucaaga ccaaccggaa ggugaccgug 1680

aagcagcuga aggaggacua cuucaagaag aucgagugcu ucgacagcgu ggagaucagc 1740

ggcguggagg accgguucaa cgccagccug ggcaccuacc acgaccugcu gaagaucauc 1800

aaggacaagg acuuccugga caacgaggag aacgaggaca uccuggagga caucgugcug 1860

acccugaccc uguucgagga ccgggagaug aucgaggagc ggcugaagac cuacgcccac 1920

cuguucgacg acaaggugau gaagcagcug aagcggcggc gguacaccgg cuggggccgg 1980

cugagccgga agcugaucaa cggcauccgg gacaagcaga gcggcaagac cauccuggac 2040

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cugaccuuca aggaggacau ccagaaggcc caggugagcg gccagggcga cagccugcac 2160

gagcacaucg ccaaccuggc cggcagcccc gccaucaaga agggcauccu gcagaccgug 2220

aagguggugg acgagcuggu gaaggugaug ggccggcaca agcccgagaa caucgugauc 2280

gagauggccc gggagaacca gaccacccag aagggccaga agaacagccg ggagcggaug 2340

aagcggaucg aggagggcau caaggagcug ggcagccaga uccugaagga gcaccccgug 2400

gagaacaccc agcugcagaa cgagaagcug uaccuguacu accugcagaa cggccgggac 2460

auguacgugg accaggagcu ggacaucaac cggcugagcg acuacgacgu ggaccacauc 2520

gugccccaga gcuuccugaa ggacgacagc aucgacaaca aggugcugac ccggagcgac 2580

aagaaccggg gcaagagcga caacgugccc agcgaggagg uggugaagaa gaugaagaac 2640

uacuggcggc agcugcugaa cgccaagcug aucacccagc ggaaguucga caaccugacc 2700

aaggccgagc ggggcggccu gagcgagcug gacaaggccg gcuucaucaa gcggcagcug 2760

guggagacac ggcagaucac caagcacgug gcccagaucc uggacagccg gaugaacacc 2820

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gagcugcugg gcaucaccau cauggagcgg agcagcuucg agaagaaccc caucgacuuc 3540

cuggaggcca agggcuacaa ggaggugaag aaggaccuga ucaucaagcu gcccaaguac 3600

agccuguucg agcuggagaa cggccggaag cggaugcugg ccagcgccgg cgagcugcag 3660

aagggcaacg agcuggcccu gcccagcaag uacgugaacu uccuguaccu ggccagccac 3720

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cacaagcacu accuggacga gaucaucgag cagaucagcg aguucagcaa gcgggugauc 3840

cuggccgacg ccaaccugga caaggugcug agcgccuaca acaagcaccg ggacaagccc 3900

auccgggagc aggccgagaa caucauccac cuguucaccc ugaccaaccu gggcgccccc 3960

gccgccuuca aguacuucga caccaccauc gaccggaagc gguacaccag caccaaggag 4020

gugcuggacg ccacccugau ccaccagagc aucaccggcc uguacgagac acggaucgac 4080

cugagccagc ugggcggcga c 4101

<210> 2160
<211> 1367
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 2160
Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly Thr Asn Ser Val Gly
1 5 10 15

Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe Lys
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
    210                 215                 220

Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
225                 230                 235                 240

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

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

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

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

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

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

Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe Asp
            340                 345                 350
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Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser Gln
        355                 360                 365

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
675 680 685

Asn Ala Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
690 695 700

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

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

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

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

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

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

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

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

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

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

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

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

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

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Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925

His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
    930                 935                 940

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Lys  Glu Leu Leu Gly Ile  Thr Ile Met Glu Arg  Ser Ser Phe
    1160                1165                1170
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Glu Lys  Asn Pro Ile Asp Phe  Leu Glu Ala Lys Gly  Tyr Lys Glu
    1175                1180                1185

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

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

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

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

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

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

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

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

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

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

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

Leu Tyr  Glu Thr Arg Ile Asp  Leu Ser Gln Leu Gly  Gly Asp
    1355                1360                1365
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<210> 2161
<211> 4929
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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agagggaagu gccaguggga gcugugcugg ugcucaacaa cagggucauu ggggaaggau 180

ggaacagggc cauuggacuu cacgauccga cggcucaugc ggaaaucaug gcacugagac 240

agggcggucu ugugaugcag aacuaucgcc ugauugaugc cacucuguac gugaccuucg 300

aaccuugcgu gaugugcgcc ggugccauga uccacucacg caucggucgg gugguguucg 360

gcgugcgaaa cgcuaagacu ggagccgccg gaucacugau ggaugugcuc caucaccccg 420

ggaugaacca caggguggag aucaccgaag gcauucuggc cgacgaaugc gcagcccugu 480

ugugucgcuu cuuccggaug ccucgaagag uguucaacgc gcagaagaag gcgcagagcu 540

ccacugacuc uggagguucc ucgggcggau cgucaggguc cgaaacuccu ggaaccucgg 600

agucagcaac uccggaaucc ucaggaggcu ccagcggagg cuccgauaag aaguacagca 660

ucgggcuugc caucggaacc aacucggucg gcugggcugu gaucacugac gaguacaagg 720

ucccuuccaa aaaguucaaa gugcucggca acacugaucg gcacucgauu aagaagaacc 780

ugaucggugc acugcuguuc gacucugggg agacugcgga agcaacucgc cugaagagga 840

cugcgcgcag acgguacacc aggcgcaaga accggaucug cuacuugcaa gagauuuuca 900

gcaacgagau ggccaagguc gacgacucgu uuuuccaccg gcucgaggaa agcuuccugg 960

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ccuaccauga gaaguacccg accaucuacc aucugcgcaa gaagcucgug gacagcacug 1080

acaaagccga cuugcgccug aucuaccuug cccuggccca caugaucaag uucagagggc 1140

acuuccugau cgagggcgac cugaacccgg acaauuccga cguggauaag cuguucaucc 1200

aacugguaca aacuuacaac cagcuguuug aggagaaccc gaucaacgcu uccggcgugg 1260

acgcgaaggc cauucugagc gcacggcugu ccaagucccg gagauuagaa aaccugauug 1320

cccaacugcc uggagaaaag aagaauggcc uguucggaaa ccugaucgcc cucucgcucg 1380

gucugacccc caacuuuaag agcaacuucg accuggcuga ggacgcgaag cuccagcugu 1440

ccaaggacac cuacgaugau gaccucgaua aucuccucgc ccaaaucggc gaccaauaug 1500

cggaccuguu ucuggccgcc aagaaucugu ccgacgccau ccuccugagc gauauccugc 1560

gcgugaacac ugaaaucacc aaggccccac ugagcgcuag caugauuaag cgcuacgacg 1620

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acaaggagau cuucuucgac caaucgaaga augguuacgc cggcuacauu gacggaggag 1740

cgucacagga ggaguucuac aaguucauua agccaauccu ggagaagaug gacggaaccg 1800

aggaacugcu cgugaagcug aacagagaag aucuacugcg caagcagcgc acuuucgaca 1860

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aagauuucua cccguuccug aaggacaacc gcgagaagau cgaaaagauc cugaccuucc 1980

gcauuccgua cuacguggga ccccucgcaa gaggaaacuc gcgguucgcc uggaugacca 2040

ggaagucgga agaaaccauu acuccgugga acuucgagga agugguggac aagggcgccu 2100

cagcgcaauc cuucaucgaa cggaugacca acuucgacaa gaacuugccu aacgagaaag 2160

ugcuuccuaa gcauucccuc cuuuacgaau acuucacugu guacaacgag cuuaccaagg 2220

ucaaauaugu gaccgagggc augcgcaagc cggccuuucu uuccggggag caaaagaagg 2280

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acuacuuuaa gaaaaucgag ugcuuugauu ccgucgaaau cuccggagug gaagauagau 2400

ucaacgccag ccuaggcacc uaccacgauc ugcucaagau cauuaaggau aaggauuucc 2460

uggacaacga ggagaacgag gauauccugg aggacauugu gcugacccug acacuguucg 2520

aagaucgcga aaugaucgag gagcggcuga aaacauacgc ccaccuguuc gacgacaagg 2580

ucaugaagca gcucaagcgg aggagguaca cgggaugggg aaggcugucc cggaagcuga 2640

ucaacgggau uagagacaag caguccggaa agaccauucu ggacuuccuc aagucggacg 2700

gcuucgcgaa ccggaacuuc augcaacuga uccacgacga cucccugacg uucaaggagg 2760

acauucagaa ggcccaagug uccggacagg gagauucacu gcacgaacac aucgccaauc 2820

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ucgugaaggu caugggccgc cacaagccug agaacaucgu gaucgaaaug gcccgggaga 2940

accagaccac gcagaaaggg cagaagaaca gccgcgagag gaugaagaga aucgaggaag 3000

gaaucaagga acuuggaagc cagauccuga aggaacaccc cguggaaaac acucagcuuc 3060

aaaacgaaaa gcuguaccuc uacuaucugc aaaacggacg ggauauguac guggaccagg 3120

aauuggacau caaucgccug uccgacuacg auguggauca cauugugccg cagagcuuuc 3180

ugaaggacga uucaauugau aacaaggugc ucacccgguc cgacaagaac cggggcaaaa 3240

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ugaacgccaa acugaucacc cagcggaagu ucgacaaccu gaccaaggcc gaaaggggcg 3360

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acaagcugau ucgcgaaguc aaagucauua cccugaaauc caagcucgug uccgacuucc 3540

ggaaggacuu ccaguucuau aagguucgcg aaaucaacaa cuaccaccac gcccaugacg 3600

cguaccugaa cgccgucgug gguaccgccc ugauuaagaa guacccuaag cucgaguccg 3660

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gagaaaccgg cgaaauugug ugggauaagg gcagagacuu ugcgacugug cgcaaagucu 3900

ugucaaugcc ccaagucaac auugucaaaa agaccgaagu gcaaaccggc ggcuucagca 3960

aggaaagcau ccugcccaag cgcaauuccg acaagcucau cgcccggaag aaggacuggg 4020

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cgaaagugga aaagggaaag ucgaagaagc ucaaguccgu gaaggagcuc cuggggauca 4140

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acaaggaggu caagaaggau cugauuauua agcugccgaa guauucccuc uucgaacucg 4260

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agaacauuau ccaccuguuc acccucacua accuuggagc gccugccgca uucaaguacu 4620

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ugauccacca guccaucacu gggcucuaug agacucgcau ugaccugucc caguuugggag 4740

gggacgaagg agccgauaag agaaccgccg augguccga auucgagucg cccaagaaga 4800

agcggaaagu guaagcggcc gcuuaauuaa gcugccuucu gcggggcuug ccuucuggcc 4860

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aagucuaga 4929

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<211> 501
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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agagcucggg augagaggga agugccagug ggagcugugc uggugcucaa caacaggguc 120

auuggggaag gauggaacag ggccauugga cuucacgauc cgacggcuca ugcggaaauc 180

auggcacuga gacagggcgg ucuugugaug cagaacuauc gccugauuga ugccacucug 240

uacgugaccu ucgaaccuug cgugaugugc gccggugcca ugauccacuc acgcaucggu 300

cggguggugu ucggcgugcg aaacgcuaag acuggagccg ccggaucacu gauggaugug 360

cuccaucacc ccgggaugaa ccacagggug gagaucaccg aaggcauucu ggccgacgaa 420

ugcgcagccc uguugugucg cuucuuccgg augccucgaa gaguguucaa cgcgcagaag 480

aaggcgcaga gcuccacuga c 501

<210> 2163
<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2163
ucuggagguu ccucgggcgg aucgucaggg uccgaaacuc cuggaaccuc ggagucagca 60

acuccggaau ccucaggagg cuccagcgga ggcucc 96

<210> 2164
<211> 4101

<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2164
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acugacgagu acaaggcccc uuccaaaaag uucaaagugc ucggcaacac ugaucggcac 120

ucgauuaaga agaaccugau cggugcacug cuguucgacu cuggggagac ugcggaagca 180

acucgccuga agaggacugc gcgcagacgg uacaccaggc gcaagaaccg gaucugcuac 240

uugcaagaga uuuucagcaa cgagauggcc aaggucgacg acucguuuuu ccaccggcuc 300

gaggaaagcu uccuggugga ggaagauaag aagcaugagc gccaucccau cuucggaaac 360

aucguggacg aaguggccua ccaugagaag uacccgacca ucuaccaucu gcgcaagaag 420

cucguggaca gcacugacaa agccgacuug cgccugaucu accuugcccu ggcccacaug 480

aucaaguuca gagggcacuu ccugaucgag ggcgaccuga acccggacaa uuccgacgug 540

gauaagcugu ucauccaacu gguacaaacu uacaaccagc uguuugagga gaacccgauc 600

aacgcuuccg gcguggacgc gaaggccauu cugagcgcac ggcuguccaa gucccggaga 660

uuagaaaacc ugauugccca acugccugga gaaaagaaga auggccuguu cggaaaccug 720

aucgcccucu cgcucggucu gacccccaac uuuaagagca acuucgaccu ggcugaggac 780

gcgaagcucc agcuguccaa ggacaccuac gaugaugacc ucgauaaucu ccucgcccaa 840

aucggcgacc aauaugcgga ccuguuucug gccgccaaga aucuguccga cgccauccuc 900

cugagcgaua uccugcgcgu gaacacugaa aucaccaagg ccccacugag cgcuagcaug 960

auuaagcgcu acgacgaaca ccaucaggac cucacccugc ugaaggcucu ugugcggcag 1020

cagcucccag agaaguacaa ggagaucuuc uucgaccaau cgaagaaugg uuacgccggc 1080

uacauugacg gaggagcguc acaggaggag uucuacaagu ucauuaagcc aauccuggag 1140

aagauggacg gaaccgagga acugcucgug aagcugaaca gagaagaucu acugcgcaag 1200

cagcgcacuu ucgacaacgg aucgauccca caucagauuc accugggaga gcugcacgcg 1260

auccugcgga gacaggaaga uuucuacccg uuccugaagg acaaccgcga gaagaucgaa 1320

aagauccuga ccuuccgcau uccguacuac gugggacccc ucgcaagagg aaacucgcgg 1380

uucgccugga ugaccaggaa gucggaagaa accauuacuc cguggaacuu cgaggaagug 1440

guggacaagg gcgccucagc gcaauccuuc aucgaacgga ugaccaacuu cgacaagaac 1500

uugccuaacg agaaagugcu uccuaagcau ucccuccuuu acgaauacuu cacuguguac 1560

aacgagcuua ccaaggucaa auaugugacc gagggcaugc gcaagccggc cuuucuuucc 1620

ggggagcaaa agaaggccau cguggaccug uuguucaaga ccaaccggaa ggucaccguc 1680

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ggaguggaag auagauucaa cgccagccua ggcaccuacc acgaucugcu caagaucauu 1800

aaggauaagg auuuccugga caacgaggag aacgaggaua uccuggagga cauugugcug 1860

acccugacac uguucgaaga ucgcgaaaug aucgaggagc ggcugaaaac auacgcccac 1920

cuguucgacg acaaggucau gaagcagcuc aagcggagga gguacacggg auggggaagg 1980

cugucccgga agcugaucaa cgggauuaga gacaagcagu ccggaaagac cauucuggac 2040

uuccucaagu cggacggcuu cgcgaaccgg aacuucaugc aacugaucca cgacgacucc 2100

cugacguuca aggaggacau ucagaaggcc caaguguccg gacagggaga uucacugcac 2160

gaacacaucg ccaaucuggc uggaaguccg gccaucaaga aaggcauccu gcaaaccgug 2220

aaggucgugg acgagcucgu gaaggucaug ggccgccaca agccugagaa caucgugauc 2280

gaaauggccc gggagaacca gaccacgcag aaagggcaga agaacagccg cgagaggaug 2340

aagagaaucg aggaaggaau caaggaacuu ggaagccaga uccugaagga acaccccgug 2400

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auguacgugg accaggaauu ggacaucaau cgccuguccg acuacgaugu ggaucacauu 2520

gugccgcaga gcuuucugaa ggacgauuca auugauaaca aggugcucac ccgguccgac 2580

aagaaccggg gcaaaagcga uaacgugccg agcgaagagg uggucaagaa gaugaagaau 2640

uacuggcggc agcucuugaa cgccaaacug aucacccagc ggaaguucga caaccugacc 2700

aaggccgaaa ggggcggucu uuccgaacug gacaaggccg gguuuaucaa gcgccaacug 2760

guggaaaccc ggcagaucac uaagcacgug gcccagauac uggacucuag gaugaauacc 2820

aaauacgacg agaacgacaa gcugauucgc gaagucaaag ucauuacccu gaaauccaag 2880

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ccuaagcucg aguccgaguu cgucuacgga gacuacaaag uguacgacgu gcggaagaug 3060

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aucaugaacu ucuucaagac cgagaucacc cuugccaacg gggagauucg gaagcgcccg 3180

uugauugaga cuaacggaga aaccggcgaa auuguguggg auaagggcag agacuuugcg 3240

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accggcggcu ucagcaagga aagcauccug cccaagcgca auuccgacaa gcucaucgcc 3360

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uccguccugg uggucgcgaa aguggaaaag ggaaagucga agaagcucaa guccgugaag 3480

gagcuccugg ggaucaccau uauggaacgg uccagcuucg agaagaaccc gauugacuuc 3540

cuggaagcca aggguuacaa ggaggucaag aaggaucuga uuauuaagcu gccgaaguau 3600

ucccucuucg aacucgaaaa uggccgcaag cgaauguugg caucggcggg agagcuccag 3660

aagggaaacg aacuggccuu gccuuccaaa uacgugaacu uucuguaccu ggccagccac 3720

uacgagaagc ugaaggguuc ccccgaggac aacgagcaga agcagcuguu cguggagcag 3780

cacaagcacu accuggauga gaucaucgaa cagaucucgg aauucuccaa gagagugauc 3840

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auccgggagc aggcugagaa cauuauccac cuguucaccc ucacuaaccu uggagcgccu 3960

gccgcauuca aguacuucga cacaaccauc gacagaaagc gcuacacuuc caccaaggag 4020

gugcuggacg ccacccugau ccaccagucc aucacugggc ucuaugagac ucgcauugac 4080

cugucccagu ugggagggga c 4101

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<211> 1367
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide

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20 25 30

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

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

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

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

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

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

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

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

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

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

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

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Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
    210                 215                 220

Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
225                 230                 235                 240

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu Val
465                 470                 475                 480
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Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr Asn
                485                 490                 495

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

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

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

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

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

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

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

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

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

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

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

Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
        675                 680                 685

Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
    690                 695                 700

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

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

Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly Arg
            740                 745                 750
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His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln Thr
        755                 760                 765

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

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

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

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

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

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

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

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

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

Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
        915                 920                 925

His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
    930                 935                 940

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Ile  Leu Ala Asp Ala Asn  Leu Asp Lys Val Leu  Ser Ala Tyr
    1280                1285                1290
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Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn Ile
1295 1300 1305

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

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

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

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

<210> 2166
<211> 12
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2166
gaaggagccg au 12

<210> 2167
<211> 57
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 2167
aagagaaccg ccgauggguc cgaauucgag ucgcccaaga agaagcggaa aguguaa 57

<210> 2168
<211> 4929
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

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aauucuccca cgaguauugg augagacacg cucucacacu cgccaagcga gcuagggaug 120

aaagggaagu accagugggg gccguacugg uacucaacaa uagggucaua ggagaggggu 180

ggaaucgagc aauugggcug caugauccca cugcacacgc ggagauuaug gcucuuagac 240

aaggggccu ggugaugcag aauuaccgcc ucauugacgc aacccuuuac gugacauuug 300

agccaugcgu uaugugcgcg ggcgcaauga uacacucuag gauaggccgc guaguuuucg 360

gaguccgaaa ugcgaagacu ggggcggccg gaucucugau ggacgugcuc caccauccag 420

gcaugaacca ccgaguggag auaacggaag gcaucuuggc ggacgaaugu gcugcgcucc 480

uuugcagguu cuuccggaug ccaagacggg uauucaacgc gcagaagaag gcacagucaa 540

gcacugauag uggcggcagu uccggaggau cuaguggguc cgaaacgcca gggaccuccg 600

aauccgcaac ucccgaaagu ucaggaggcu ccuccggcgg cagcgacaag aaguacucca 660

uuggucuggc gaucgguacg aauaguguug ggugggcugu aauaacugac gaguauaagg 720

ugcccaguaa gaaguucaaa guccuggggа acacagaccg acauagcauc aagaagaacc 780

ugauaggugc gcucuuguuu gacuccggag agacagcaga agccacacga cuuaaacgaa 840

ccgcucgaag gcgguacaca cggcgaaaga auaggauuug uuaccugcag gagauauuua 900

gcaacgagau ggcaaagguu gacgauuccu ucuuccaccg gcuugaagag ucuuuccugg 960

uggaggagga caagaaacau gaacgccacc ccauauuugg caauauagug gacgaaguag 1020

cauaccauga gaaauacccu accauauauc aucuucgaaa gaagcuugua gauucaacgg 1080

auaaagcaga ucucagguug auauaucugg cacuggcaca caugaucaag uuucgagguc 1140

acuuucuuau cgagggcgau cuuaauccgg acaacuccga cguggauaag cuguucaucc 1200

agcucgucca aacguauaac caacucuucg aggagaaucc gaucaaugcc ucuggagugg 1260

acgcgaaagc gauacucuca gcaaggcuua guaagucucg ccggcuugag aaccucaucg 1320

cacaguugcc aggagagaag aagaauggcu uguuugguaa ccuuauugca cucagucucg 1380

gccuuacacc uaacuucaag uccaacuucg aucuugccga ggacgccaag cuccagcuua 1440

gcaaggauac cuacgaugac gaucuugaua accugcuggc ccagauaggc gaccaguacg 1500

cggaccuuuu cuuggcagca aagaauuugu ccgacgccau ccucuugagc gacauccucc 1560

ggguaaacac ugaaauuacu aaggcgccac uuuccgccag caugaucaag agauacgaug 1620

agcaucauca ggaucugacc cugcuuaaag cgcuuguacg ccagcaauug ccugagaagu 1680

auaaagaaau cuuuuucgac caaagcaaga acgguuaugc uggcuacaua gacggcgggg 1740

cuucucagga ggaauucuac aaguuuauca agccgauucu cgagaagaug gauggaacag 1800

aggagcuguu ggugaaacug aaccgggagg accugcucag aaagcagcgg accuucgaua 1860

augggagcau cccgcaccag auucauuugg gugagcugca ugcaaucuug cgcaggcaag 1920

aagauuuuua ccccuuccuc aaggacaaua gagagaagau ugagaagauc cuuacguuua 1980

ggauuccgua uuacguaggc ccgcucgcac gcgguaauuc ucgcuuugcg uggaugacac 2040

gaaagagcga ggaaaccaua acacccugga acuuugaaga ggucgucgau aagggugcca 2100

gcgcacaauc auuuaucgaa cgaaugacua auuucgauaa gaaucuccca aaugagaagg 2160

uguugccaaa gcauagccuu uuguaugagu auuuuacugu auacaacgag cucaccaagg 2220

ugaaauaugu cacugaaggg augcgcaagc cggccuuuuu gagcggagaa cagaagaaag 2280

cuauuguaga cuugcuuuuu aagacgaaua gaaagguuac ggucaagcag cucaaagaag 2340

acuacuuuaa gaagauagaa ugcuuugacu cugucgagau uagugggggua gaggaucgau 2400

ucaaugcaag ccuggggaca uaccacgauc ucuugaagau uaucaaggau aaggauuuuc 2460

uggacaacga agagaaugaa gacaucuugg aagauauugu uuugacuuug acucuuuucg 2520

aagaucgcga gaugauagag gaaagguuga agacuuaugc ccaucuuuuu gaugacaagg 2580

uuaugaaaca acugaagaga cggcgauaua cugguugggg gagacucuca cgaaagcuca 2640

uuaacggcau ccgggacaaa cagaguggua agacgauuuu ggacuuccuu aagagcgacg 2700

gguuugcgaa uaggaacuuc augcaguuga uccaugauga uucuuugacc uuuaaggagg 2760

auauacagaa ggcacaaguc aguggacaag gagauagucu gcaugagcac auugccaacc 2820

uugcgggcuc cccagccauc aagaagggua uccugcaaac cgucaaagua guagaugaac 2880

uugugaaagu caugggacga cauaagccug agaauauugu gaucgaaaug gcuagggaga 2940

aucagacgac ucagaagggu cagaagaauu ccagggaacg gaugaagaga auagaggagg 3000

gaauuaagga acucggguca caaauauuga aggagcaucc uguagagaac acacagcuuc 3060

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aacuggauau caaucgcuug uccgauuaug auguagauca cauaguccca caauccuucu 3180

ugaaagacga uaguauugac aauaagguac uuacgagauc cgacaagaac cgcggaaagu 3240

ccgauaacgu accgagugaa gaagugguaa agaagaugaa gaauuauugg aggcagcucc 3300

ucaacgccaa acuuauuacu cagagaaagu ucgauaaccu uacgaaagcu gagcgaggcg 3360

gguugucuga gcucgauaaa gcuggauuca uaaagcggca gcuuguggaa acuagacaga 3420

ucacaaagca cguugcacag auccuugauu ccagaaugaa cacuaaauau gaugagaacg 3480

auaagcugau acgcgaggug aaaguaauaa cacuuaaguc aaagcuggua agcgauuuuc 3540

gcaaagacuu ccaauuuuau aaggucagag agauaaacaa uuaucaucac gcgcaugacg 3600

cuuaccugaa cgcaguugug gggacagcac uuauaaagaa auacccaaag uuggaaagug 3660

aauuugucua uggagacuau aagguauacg auguacggaa gaugauugcg aagucagagc 3720

aagaaaucgg uaaggcaacu gcuaaguacu ucuuuuacuc aaauauuaug aacuuuuuca 3780

agacggaaau cacucuggcu aacggagaaa uucggaagag gcccuugaua gagacgaaug 3840

gggagacugg ugagaucguu ugggacaaag ggcgagauuu cgcaacgguc cgaaaggugc 3900

ucucaaugcc acaagucaau auagucaaga agacagaggu acaaacagga gguuucucca 3960

aggaaucaau acucccaaag cggaauuccg acaaacugau agcuagaaag aaggacuggg 4020

auccgaagaa guauggaggg uuugauuccc caacaguagc guauucagua cuggugguag 4080

cuaaggugga gaaaggcaag ucuaagaagc uuaagucugu caaagagcug cucggcauca 4140

ccauuaugga gcgcaguagc uucgagaaga acccuauaga uuuucuggaa gccaaaggau 4200

auaaggaggu uaagaaggau cucaucauca aacucccgaa guauagucuu uuugaguugg 4260

agaacggacg aaagcgcaug cuugcgucug cgggugaauu gcagaaagga aaugagcucg 4320

ccuugccguc aaaguauguc aauuucuugu accuugcgag ucacuaugag aagcugaaag 4380

gaagcccaga agauaaugaa cagaagcaau uguucguuga acaacauaag cauuauuugg 4440

acgagaucau cgagcaaauc agcgaguuca gcaagcgcgu cauacuugcg gacgccaauc 4500

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agaauauaau acaucucuuc acacuuacua aucuuggagc uccagccgca uucaaguauu 4620

uugacacgac uauagaucgc aagcgauaua ccucuacgaa agaaguucug gacgcuacuc 4680

uuauacauca auccauuacg ggccuguacg agacgaggau ugacuuguca cagcuuggug 4740

gugacgaggg ugcagacaag cgaacagcgg acgggucaga auucgaaagc cccaagaaga 4800

agcggaaagu uuaagcggcc gcuuaauuaa gcugccuucu gcggggcuug ccuucuggcc 4860

augcccuucu ucucucccuu gcaccuguac cucuuggucu uugaauaaag ccugaguagg 4920

aagucuaga 4929

<210> 2169
<211> 501
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2169
augucagaag uagaauucuc ccacgaguau uggaugagac acgcucucac acucgccaag 60

cgagcuaggg augaaaggga aguaccagug ggggccguac ugguacucaa caauaggguc 120

auaggagagg gguggaaucg agcaauuggg cugcaugauc ccacugcaca cgcggagauu 180

auggcucuua gacaaggggg ccuggugaug cagaauuacc gccucauuga cgcaacccuu 240

uacgugacau uugagccaug cguuaugugc gcgggcgcaa ugauacacuc uaggauaggc 300

cgcguaguuu ucggaguccg aaaugcgaag acuggggcgg ccggaucucu gauggacgug 360

cuccaccauc caggcaugaa ccaccgagug gagauaacgg aaggcaucuu ggcggacgaa 420

ugugcugcgc uccuuugcag guucuuccgg augccaagac ggguauucaa cgcgcagaag 480

aaggcacagu caagcacuga u 501

<210> 2170
<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2170
aguggcggca guuccggagg aucuaguggg uccgaaacgc cagggaccuc cgaauccgca 60

acucccgaaa guucaggagg cuccuccggc ggcagc 96

<210> 2171
<211> 4101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 2171

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agcaucaaga agaaccugau aggugcgcuc uuguuugacu ccggagagac agcagaagcc 180

acacgacuua aacgaaccgc ucgaaggcgg uacacacggc gaaagaauag gauuuguuac 240

cugcaggaga uauuuagcaa cgagauggca aagguugacg auuccuucuu ccaccggcuu 300

gaagagucuu uccuggugga ggaggacaag aaacaugaac gccaccccau auuuggcaau 360

auaguggacg aaguagcaua ccaugagaaa uacccuacca uauaucaucu ucgaaagaag 420

cuuguagauu caacggauaa agcagaucuc agguugauau aucuggcacu ggcacacaug 480

aucaaguuuc gaggucacuu ucuuaucgag ggcgaucuua auccggacaa cuccgacgug 540

gauaagcugu ucauccagcu cguccaaacg uauaaccaac ucuucgagga gaauccgauc 600

aaugccucug gaguggacgc gaaagcgaua cucucagcaa ggcuuaguaa gucucgccgg 660

cuugagaacc ucaucgcaca guugccagga gagaagaaga auggcuuguu ugguaaccuu 720

auugcacuca gucucggccu uacaccuaac uucaagucca acuucgaucu ugccgaggac 780

gccaagcucc agcuuagcaa ggauaccuac gaugacgauc uugauaaccu gcuggcccag 840

auaggcgacc aguacgcgga ccuuuucuug gcagcaaaga auuuguccga cgccauccuc 900

uugagcgaca uccuccgggu aaacacugaa auuacuaagg cgccacuuuc cgccagcaug 960

aucaagagau acgaugagca ucaucaggau cugacccugc uuaaagcgcu uguacgccag 1020

caauugccug agaaguauaa agaaaucuuu uucgaccaaa gcaagaacgg uuaugcuggc 1080

uacauagacg gcggggcuuc ucaggaggaa uucuacaagu uuaucaagcc gauucucgag 1140

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cagcggaccu ucgauaaugg gagcaucccg caccagauuc auuuggguga gcugcaugca 1260

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aagauccuua cguuuaggau uccguauuac guaggcccgc ucgcacgcgg uaauucucgc 1380

uuugcgugga ugacacgaaa gagcgaggaa accauaacac ccuggaacuu ugaagagguc 1440

gucgauaagg gugccagcgc acaaucauuu aucgaacgaa ugacuaauuu cgauaagaau 1500

cucccaaaug agaagguguu gccaaagcau agccuuuugu augaguauuu uacuguauac 1560

aacgagcuca ccaaggugaa auaugucacu gaagggaugc gcaagccggc cuuuuugagc 1620

ggagaacaga agaaagcuau uguagacuug cuuuuuaaga cgaauagaaa gguuacgguc 1680

aagcagcuca aagaagacua cuuuaagaag auagaaugcu uugacucugu cgagauuagu 1740

gggguagagg aucgauucaa ugcaagccug gggacauacc acgaucucuu gaagauuauc 1800

aaggauaagg auuuucugga caacgaagag aaugaagaca ucuuggaaga uauuguuuug 1860

acuuugacuc uuuucgaaga ucgcgagaug auagaggaaa gguugaagac uuaugcccau 1920

cuuuuugaug acaagguuau gaaacaacug aagagacggc gauauacugg uuggggaga 1980

cucucacgaa agcucauuaa cggcauccgg gacaaacaga gugguaagac gauuuuggac 2040

uuccuuaaga gcgacggguu ugcgaauagg aacuucaugc aguugaucca ugaugauucu 2100

uugaccuuua aggaggauau acagaaggca caagucagug gacaaggaga uagucugcau 2160

gagcacauug ccaaccuugc gggcucccca gccaucaaga aggguauccu gcaaaccguc 2220

aaaguaguag augaacuugu gaaagucaug ggacgacaua agccugagaa uauugugauc 2280

gaaauggcua gggagaauca gacgacucag aagggucaga agaauuccag ggaacggaug 2340

aagagaauag aggagggaau uaaggaacuc gggucacaaa uauugaagga gcauccugua 2400

gagaacacac agcuucagaa cgagaagcug uaccuguauu aucuccagaa uggcagagac 2460

auguaugucg accaagaacu ggauaucaau cgcuuguccg auuaugaugu agaucacaua 2520

gucccacaau ccuucuugaa agacgauagu auugacaaua agguacuuac gagauccgac 2580

aagaaccgcg gaaaguccga uaacguaccg agugaagaag ugguaaagaa gaugaagaau 2640

uauuggaggc agcuccucaa cgccaaacuu auuacucaga gaaaguucga uaaccuuacg 2700

aaagcugagc gaggcggguu gucugagcuc gauaaagcug gauucauaaa gcggcagcuu 2760

guggaaacua gacagaucac aaagcacguu gcacagaucc uugauuccag aaugaacacu 2820

aaauaugaug agaacgauaa gcugauacgc gaggugaaag uaauaacacu uaagucaaag 2880

cugguaagcg auuuucgcaa agacuuccaa uuuuauaagg ucagagagau aaacaauuau 2940

caucacgcgc augacgcuua ccugaacgca guugugggga cagcacuuau aaagaaauac 3000

ccaaaguugg aaagugaauu ugucuaugga gacuauaagg uauacgaugu acggaagaug 3060

auugcgaagu cagagcaaga aaucgguaag gcaacugcua aguacuucuu uuacucaaau 3120

auuaugaacu uuuucaagac ggaaaucacu cuggcuaacg gagaaauucg gaagaggccc 3180

uugauagaga cgaaugggga gacuggugag aucguuuggg acaaagggcg agauuucgca 3240

acgguccgaa aggugcucuc aaugccacaa gucaauauag ucaagaagac agagguacaa 3300

acaggagguu ucuccaagga aucaauacuc ccaaagcgga auuccgacaa acugauagcu 3360

agaaagaagg acugggaucc gaagaaguau ggaggguuug auuccccaac aguagcguau 3420

ucaguacugg ugguagcuaa gguggagaaa ggcaagucua agaagcuuaa gucugucaaa 3480

gagcugcucg gcaucaccau uauggagcgc aguagcuucg agaagaaccc uauagauuuu 3540

cuggaagcca aaggauauaa ggagguuaag aaggaucuca ucaucaaacu cccgaaguau 3600

agucuuuuug aguuggagaa cggacgaaag cgcaugcuug cgucugcggg ugaauugcag 3660

aaaggaaaug agcucgccuu gccgucaaag uaugucaauu ucuuguaccu ugcgagucac 3720

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cuugcggacg ccaaucugga caaagugcug uccgccuaua acaaacauag ggacaaaccu 3900

auacgagagc aggcagagaa uauaauacau cucuucacac uuacuaaucu uggagcucca 3960

gccgcauuca aguauuuuga cacgacuaua gaucgcaagc gauauaccuc uacgaaagaa 4020

guucuggacg cuacucuuau acaucaaucc auuacgggcc uguacgagac gaggauugac 4080

uugucacagc uuggugguga c 4101

<210> 2172
<211> 12
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2172
gagggugcag ac 12

<210> 2173
<211> 57
<212> RNA
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2173
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<210> 2174
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2174
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aguucuccca cgaguacugg augcggcaug cucugacuuu ggccaagaga gcccgagaug 120

agcgggaggu cccugugggc gcagugcugg ugcugaacaa cagggugauc ggcgagggcu 180

ggaaccgggc caucggccug cacgacccua cagcucacgc cgagaucaug gcccuuagac 240

agggcggccu ggugaugcag aacuacagac ugaucgacgc cacacuguac gucaccuuug 300

agccuugcgu gaugugcgcc ggagccauga uccauagccg gauaggacgg guggucuuug 360

gcgugcggaa cgcgaagacc ggcgccgccg gcagccuuau ggaugugcug caccauccug 420

gcaugaacca caggguggag aucaccgaag gcauccuggc ugaugaaugu gccgcucugc 480

ugugcagauu cuuucggaug ccuagaagag uguucaacgc ccagaagaaa gcccagagua 540

gcaccgauag cggcggcagc agcggcggca gcagcggaag cgagacaccu ggcaccagcg 600

aauccgccac accugagagc ucuggaggaa gcucaggcgg cucugacaag aaauacucaa 660

ucggacuggc caucggcacc aauagcgugg gcugggccgu gaucacagau gaauauaagg 720

ugccuagcaa gaaguucaag gugcugggca acaccgauag acacagcauc aagaagaacc 780

ugaucggagc ccugcuguuc gacagcggcg aaaccgccga agccaccaga cugaagagaa 840

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ccgaccuguu ccuggcugcc aagaaucugu cugacgccau ccuucugucc gauauccugc 1560

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agcaccacca agaucugacg cuccugaagg cccuggucag acagcagcuc ccugagaaau 1680

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aagucuaga 4929

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<211> 501
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2175
augucugagg uggaguucuc ccacgaguac uggaugcggc augcucugac uuuggccaag 60

agagcccgag augagcggga ggucccugug ggcgcagugc uggugcugaa caacagggug 120

aucggcgagg gcuggaaccg ggccaucggc cugcacgacc cuacagcuca cgccgagauc 180

auggcccuua gacagggcgg ccuggugaug cagaacuaca gacugaucga cgccacacug 240

uacgucaccu uugagccuug cgugaugugc gccggagcca ugauccauag ccggauagga 300

cggguggucu uuggcgugcg gaacgcgaag accggcgccg ccggcagccu uauggaugug 360

cugcaccauc cuggcaugaa ccacagggug gagaucaccg aaggcauccu ggcugaugaa 420

ugugccgcuc ugcugugcag auucuuucgg augccuagaa gaguguucaa cgcccagaag 480

aaagcccaga guagcaccga u 501

<210> 2176
<211> 96
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2176
agcggcggca gcagcggcgg cagcagcgga agcgagacac cuggcaccag cgaauccgcc 60

acaccugaga gcucuggagg aagcucaggc ggcucu 96

<210> 2177
<211> 4101
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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agcaucaaga agaaccugau cggagcccug cuguucgaca gcggcgaaac cgccgaagcc 180

accagacuga agagaaccgc cagaagacgg uacacccggc guaagaacag gaucuguuac 240

cugcaggaga ucuucagcaa cgaaauggcc aagguggacg acucuuucuu ccacagacug 300

gaggagagcu uucuggugga agaagacaag aagcaugagc ggcaccccau cuuuggcaac 360

aucguggacg aaguggccua ccacgagaaa uacccaacaa ucuaucaccu gagaaagaag 420

cugguggaca gcaccgauaa ggccgaccug cggcugaucu accuggcccu ggcacacaug 480

aucaaguuca gaggccacuu ccugaucgag ggcgaccuga accccgauaa uagcgaugug 540

gauaagcugu ucauccagcu ggugcagacc uacaaccagc uguucgagga gaacccgauc 600

aacgccucgg gaguugaugc caaggcaauc cugucugcua gacugaguaa gagcagaaga 660

cuggagaacc ugaucgccca gcugcccgga gagaagaaga augggcuguu uggcaaccug 720

auugcccugu cucugggccu uacaccuaac uucaagagca acuuugaccu ggccgaagac 780

gccaagcugc aacugucuaa ggauaccuac gacgacgauc uggacaaccu gcuggcccaa 840

aucggggauc aauacgccga ccuguuccug gcugccaaga aucugucuga cgccauccuu 900

cuguccgaua uccugcgggu gaacacagag auaaccaaag cuccucuuag ugcgagcaug 960

aucaagagau augaugagca ccaccaagau cugacgcucc ugaaggcccu ggucagacag 1020

cagcucccug agaaauacaa ggaaauuuuc uucgaccaga gcaagaaugg cuacgccggc 1080

uacaucgaug gcggcgccag ccaggaggaa uuuuacaagu uuaucaaacc aauccucgag 1140

aagauggacg gcaccgagga acugcucgug aagcugaaca gagaggaccu acugcggaag 1200

cagcggacgu ucgacaacgg cagcaucccu caccagaucc accuggguga gcugcacgca 1260

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acccugacac uguuugaaga ucgugaaaug aucgaagaac ggcugaagac auacgcccau 1920

cuguucgacg acaagguuau gaagcagcug aagagaagaa gauauacagg guggggcagg 1980

cuguccagga aacugaucaa cggcauccgg gacaagcaga gcggcaagac aauucuggac 2040

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auguacgugg aucaggagcu ggacaucaau aggcugucag acuacgacgu ggaccacauc 2520

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gcugccuuca aguacuucga caccaccauc gacagaaaga gauacacaag caccaaggag 4020

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2178
gaaggugcug ac 12

<210> 2179

<211> 57
<212> RNA
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oligonucleotide

<400> 2179
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<210> 2180
<211> 4767
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polynucleotide

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atcggcgaag gttggaatag ggcaatcgga ctccacgacc ccactgcaca tgcggaaatc 180

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cgagttgtat tcggtgttcg caacgccaag acgggtgccg caggttcact gatggacgtg 360

ctgcatcatc caggcatgaa ccaccgggta gaaatcacag aaggcatatt ggcggacgaa 420

tgtgcggcgc tgttgtgtcg ttttttttcgc atgcccaggc gggtctttaa cgcccagaaa 480

aaagcacaat cctctactga ctctggtggt tcttctggtg gttctagcgg cagcgagact 540

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aagaagtaca gcatcggcct ggccatcggc accaactctg tgggctgggc cgtgatcacc 660

gacgagtaca aggtgcccag caagaaattc aaggtgctgg gcaacaccga ccggcacagc 720

atcaagaaga acctgatcgg agccctgctg ttcgacagcg gcgaaacagc cgaggccacc 780

cggctgaaga gaaccgccag aagaagatac accagacgga agaaccggat ctgctatctg 840

caagagatct tcagcaacga gatggccaag gtggacgaca gcttcttcca cagactggaa 900

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cagctgaaag aggactactt caagaaaatc gagtgcttcg actccgtgga aatctccggc 2340

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ctgaagtccg acggcttcgc caacagaaac ttcatgcagc tgatccacga cgacagcctg 2700

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tacgtggacc aggaactgga catcaaccgg ctgtccgact acgatgtgga ccatatcgtg 3120

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ctggacgcca ccctgatcca ccagagcatc accggcctgt acgagacacg gatcgacctg 4680

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agccccaaga agaagaggaa agtctaa 4767

<210> 2181
<211> 501
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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atcggcgaag gttggaatag ggcaatcgga ctccacgacc ccactgcaca tgcggaaatc 180

atggcccttc gacagggagg gcttgtgatg cagaattatc gacttatcga tgcgacgctg 240

tacgtcacgt ttgaaccttg cgtaatgtgc gcgggagcta tgattcactc ccgcattgga 300

cgagttgtat tcggtgttcg caacgccaag acgggtgccg caggttcact gatggacgtg 360

ctgcatcatc caggcatgaa ccaccgggta gaaatcacag aaggcatatt ggcggacgaa 420

tgtgcggcgc tgttgtgtcg ttttttttcgc atgcccaggc gggtctttaa cgcccagaaa 480

aaagcacaat cctctactga c 501

<210> 2182
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2182
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acacccgaaa gttctggtgg ttcttctggt ggttct 96

<210> 2183
<211> 4101
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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accgacgagt acaaggtgcc cagcaagaaa ttcaaggtgc tgggcaacac cgaccggcac 120

agcatcaaga agaacctgat cggagccctg ctgttcgaca gcggcgaaac agccgaggcc 180

acccggctga agagaaccgc cagaagaaga tacaccagac ggaagaaccg gatctgctat 240

ctgcaagaga tcttcagcaa cgagatggcc aaggtggacg acagcttctt ccacagactg 300

gaagagtcct tcctggtgga agaggataag aagcacgagc ggcaccccat cttcggcaac 360

atcgtggacg aggtggccta ccacgagaag taccccacca tctaccacct gagaaagaaa 420

ctggtggaca gcaccgacaa ggccgacctg cggctgatct atctggccct ggcccacatg 480

atcaagttcc ggggccactt cctgatcgag ggcgacctga accccgacaa cagcgacgtg 540

gacaagctgt tcatccagct ggtgcagacc tacaaccagc tgttcgagga aaaccccatc 600

aacgccagcg gcgtggacgc caaggccatc ctgtctgcca gactgagcaa gagcagacgg 660

ctggaaaatc tgatcgccca gctgcccggc gagaagaaga atggcctgtt cggaaacctg 720

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ctgtctcagc tgggaggtga c 4101

<210> 2184
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2184
gagggagctg at 12

<210> 2185
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 2185
aagcgcaccg ccgatggttc cgagttcgaa agccccaaga agaagaggaa agtctaa 57

<210> 2186
<211> 4380
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 2186
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agaagcggaa ggugggcauc cacggcgugc ccgccgccga caagaaguac agcaucggcc 120

uggacaucgg caccaacagc gugggcuggg ccgugaucac cgacgaguac aaggugccca 180

gcaagaaguu caaggugcug ggcaacaccg accggcacag caucaagaag aaccugaucg 240

gcgcccugcu guucgacagc ggcgagacgg ccgaggccac ccggcugaag cggaccgccc 300

ggcggcggua cacccggcgg aagaaccgga ucugcuaccu gcaggagauc uucagcaacg 360

agauggccaa gguggacgac agcuucuucc accggcugga ggagagcuuc cugguggagg 420

aggacaagaa gcacgagcgg caccccaucu ucggcaacau cguggacgag guggccuacc 480

acgagaagua ccccaccauc uaccaccugc ggaagaagcu gguggacagc accgacaagg 540

ccgaccugcg gcugaucuac cuggcccugg cccacaugau caaguuccgg ggccacuucc 600

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cccccaacuu caagagcaac uucgaccugg ccgaggacgc caagcugcag cugagcaagg 900

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ucaagaagau cgagugcuuc gacagcgugg agaucagcgg cguggaggac cgguucaacg 1860

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<210> 2187
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<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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uuccuggugg aggaggacaa gaagcacgag cggcacccca ucuucggcaa caucguggac 420

gagguggccu accacgagaa guaccccacc aucuaccacc ugcggaagaa gcugguggac 480

agcaccgaca aggccgaccu gcggcugauc uaccuggccc uggcccacau gaucaaguuc 540

cggggccacu uccugaucga gggcgaccug aaccccgaca acagcgacgu ggacaagcug 600

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caggccgaga acaucaucca ccuguucacc cugaccaacc ugggcgcccc cgccgccuuc 4020

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<211> 1403
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

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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

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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
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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
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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 Asn 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
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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
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    1235                1240                1245

Val Asn  Phe Leu Tyr Leu Ala  Ser His Tyr Glu Lys  Leu Lys Gly
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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
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Asp Ser  Gly Gly Lys Arg Pro  Ala Ala Thr Lys Lys  Ala Gly Gln
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Ala Lys  Lys Lys Lys
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<213> Artificial Sequence

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polynucleotide

<400> 2189

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uggacaucgg caccaacagc gugggcuggg ccgugaucac cgacgaguac aaggugccca      180

gcaagaaguu caaggugcug ggcaacaccg accgccacag caucaagaag aaccugaucg      240

gcgcccugcu guucgacagc ggcgagacag ccgaggccac ccgccugaag cgcaccgccc      300

gccgccgcua cacccgccgc aagaaccgca ucugcuaccu gcaggagauc uucagcaacg      360
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<211> 4218
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

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<210> 2215
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<210> 2218
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<210> 2220
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<210> 2222
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<210> 2223
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<210> 2224
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<210> 2225

<211> 22
<212> DNA
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<210> 2226
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oligonucleotide

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<210> 2227
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<210> 2228
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<210> 2229
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<210> 2230
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<212> DNA
<213> Artificial Sequence

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oligonucleotide

<400> 2230
ttagcatctt ggtgcagagg tgg 23

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CLAIMS

What is claimed:

1. A composition for editing a gene target comprising:

(i) an mRNA encoding a base editor protein comprising a DNA binding domain and a deaminase, wherein the mRNA comprises a sequence having at least 95% sequence identity to SEQ ID NO: 2192, and

(ii) a guide RNA comprising a tracr sequence that serves as a binding scaffold for the base editor protein, and a spacer sequence that corresponds to a protospacer on ANGPTL3.

2. A composition for editing a gene target comprising:

(i) an mRNA encoding a base editor protein comprising a DNA binding domain and a deaminase, wherein the mRNA comprises a sequence having at least 95% sequence identity to the coding sequence of SEQ ID NO: 2192, and

(ii) a guide RNA comprising a tracr sequence that serves as a binding scaffold for the base editor protein, and a spacer sequence that corresponds to a protospacer ANGPTL3.

3. The composition of claim 1 or 2, wherein the mRNA comprises a sequence having at least 99% sequence identity to SEQ ID NO: 2192.

4. The composition of any one of claims 1-3, wherein the mRNA comprises a 5'UTR having at least 95% identity to the sequence of AGGAAAu'AAGAGAGAAAAGAAGAGu'AAGAAGAAAu'Au'AAGAGCCACC (SEQ ID NO: 2138).

5. The composition of any one of claims 1-4, wherein the mRNA comprises a 3'UTR having at least 95% identity to the sequence of GCGGCCGCu'u'AAu'u'AAGCu'GCCu'u'Cu'GCGGGGCu'u'GCCu'u'Cu'GGCCAu'GCCCu'u'Cu'u'Cu'Cu'CCCu'u'GCACCu'Gu'ACCu'Cu'u'GGu'Cu'u'u'GAAu'AAAGCCu'GAGu'AGGAAGu'Cu'AGA (SEQ ID NO: 2147).

6. The composition of any one of claims 1-5, wherein the mRNA encoding the base editor protein comprises a GC% content greater than 50%.

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7. The composition of any one of claims 1-6, wherein the base editor protein further comprises an adenine tRNA deaminase (TadA) region, a Cas9 nickase region and a nuclear localization sequence (NLS) region.

8. The composition of claim 7, wherein the GC% content of the mRNA encoding the TadA region of the base editor protein is greater than 60%.

9. The composition of claim 7 or 8, wherein the GC% content of the mRNA encoding the Cas9 nickase region of the base editor protein is greater than 56%.

10. The composition of any one of claims 7-9, wherein the GC% content of the mRNA encoding the NLS region of the base editor protein is greater than 54%.

11. The composition of any one of claims 1-10, wherein the mRNA comprises a sequence selected from the group consisting of MA004, MA040, MA041, and MA045.

12. The composition of claim 11, wherein the mRNA comprises MA004.

13. The composition of any one of claims 1-12, wherein the ratio of the guide RNA and the mRNA encoding the base editor protein is from about 1:10 to about 10:1 by weight.

14. The composition of any one of claims 1-13, wherein the guide RNA further comprises a chemical modification on one or more nucleotides.

15. The composition of claim 14, wherein the chemical modification is selected from the group consisting of 2'-O-methyl modifications, 2'-O-(2-methoxyethyl) modifications, 2'-fluoro modifications, phosphonothioate modifications, inverted abasic modifications, deoxyribonucleotides, bicylic ribose analog (e.g., locked nucleic acid (LNA), C-ethylene-bridged nucleic acid (ENA), bridged nucleic acid (BNA), unlocked nucleic acid (UNA)), base or nucleobase modifications, intemucleoside linkage modifications, ribonebularine, 2'-O-methylnebularine, and 2'-deoxynebularine.

16. The composition of any one of claims 1-15, wherein the guide RNA directs the base editor protein to effect a nucleobase alteration in the ANGPTL3 gene.

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17. The composition of claim 16, wherein the nucleobase alteration results in a frame shift, a premature stop codon, an insertion or deletion in a transcript encoded by the ANGPTL3 gene.

18. The composition of claim 16, wherein the nucleobase alteration results in an aberrant transcript encoded by the ANGPTL3 gene.

19. The composition of claim 16, wherein the nucleobase alteration is at a splice donor site of the ANGPTL3 gene.

20. The composition of claim 19, wherein the splice donor site is at 5' end of ANGPTL3 intron 6 as referenced in SEQ ID NO: 7.

21. The composition of any one of claims 1-20, wherein the protospacer comprises a sequence having at least 80% sequence identity to the sequences of
5'-AAGATACCTGAATAACTCTC-3' (SEQ ID No: 14),
5'-AAGATACCTGAATAACCCTC-3' (SEQ ID No: 15),
5'-GATACCTGAATAACTCTC-3' (SEQ ID No: 1606),
5'-AGATACCTGAATAACCCTC-3' (SEQ ID No: 248), or
5'-GATACCTGAATAACCCTC-3' (SEQ ID No: 249).

22. The composition of any one of claims 1-21, wherein the guide RNA comprises a spacer sequence having at least 80% sequence identity to a spacer sequence of a guide RNA selected from the group consisting of SEQ ID No: 59, SEQ ID No: 257, SEQ ID No: 438, SEQ ID No: 439, SEQ ID No: 440, SEQ ID No: 441, SEQ ID No: 442, SEQ ID No: 443, SEQ ID No: 1652 and SEQ ID No: 445.

23. A method for treating or preventing a condition in a subject in need thereof, the method comprising administering to the subject a therapeutically effective amount of a pharmaceutical composition comprising the composition of any one of claims 1-24.

24. The method of claim 23, wherein the condition is hypercholesterolemia, elevated total cholesterol levels, elevated low-density lipoprotein (LDL) levels, elevated blood LDL-

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cholesterol levels, reduced blood high-density lipoprotein cholesterol level, liver steatosis, coronary heart disease, vascular disease, ischemia, stroke, peripheral vascular disease, thrombosis, type 2 diabetes, hypertriglyceridemia, high elevated blood pressure, atherosclerosis, obesity, Alzheimer's disease, or neurodegeneration.

25. The method of claim 23, wherein the condition is homozygous familial hypercholesterolemia.

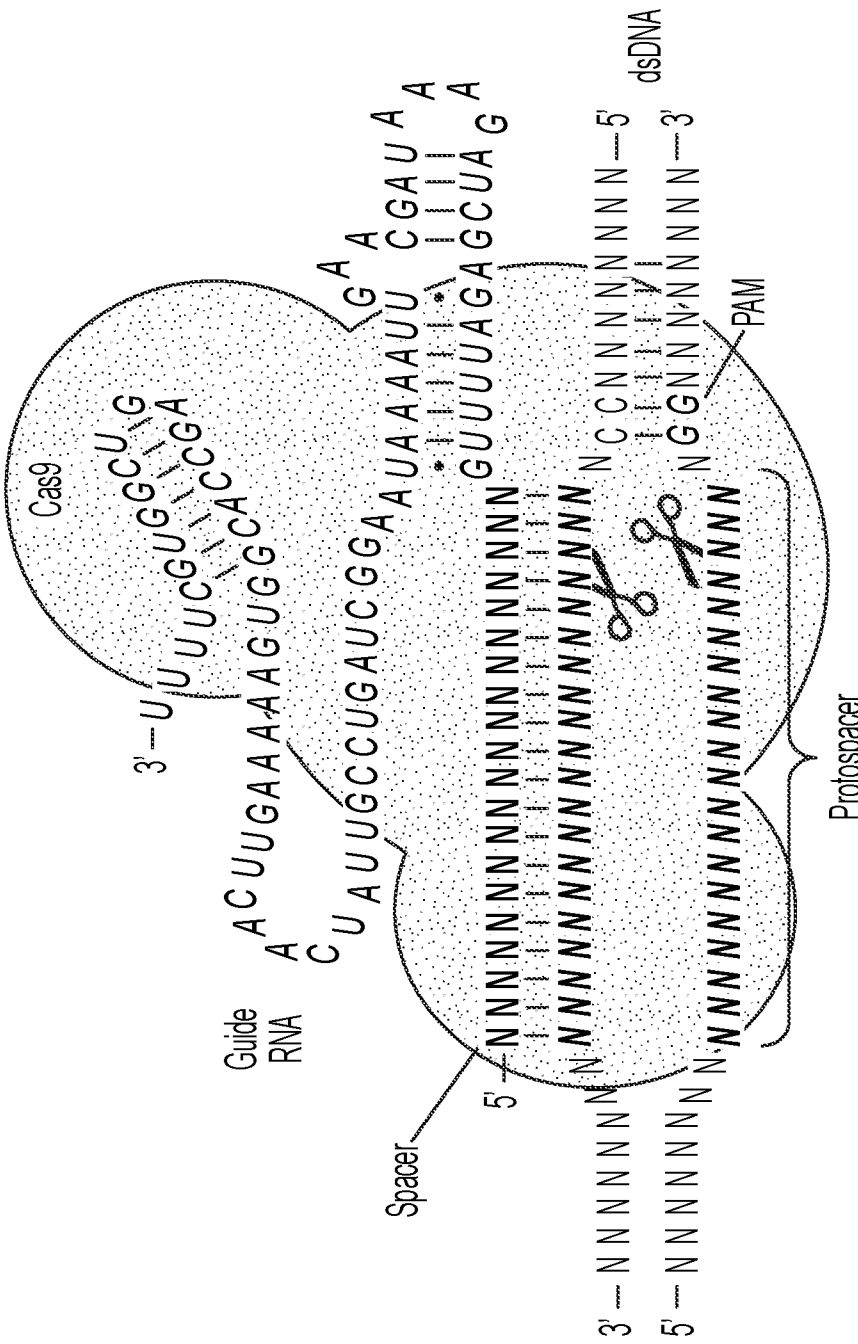


FIG. 1A

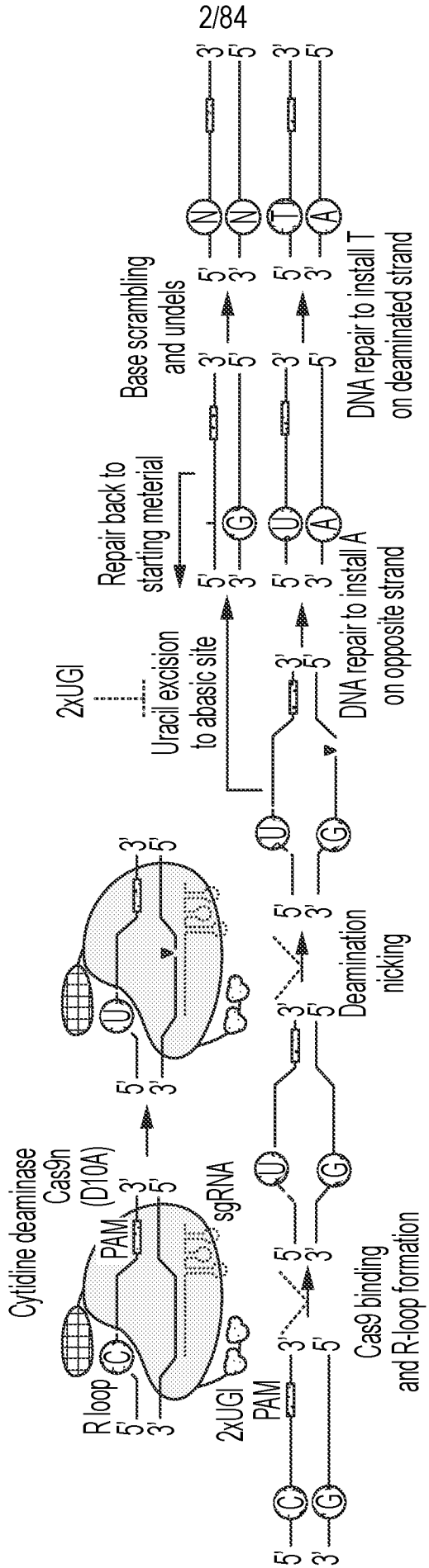

Cytidine deaminase
Cas9n
(D10A)
PAM
sgRNA
R loop
2xUGI
PAM
Cas9 binding
and R-loop formation
Deamination
nicking
2xUGI
Uracil excision
to abasic site
DNA repair to install A
on opposite strand
Repair back to
starting meterial
Base scrambling
and undels
DNA repair to install T
on deaminated strand

FIG. 1B

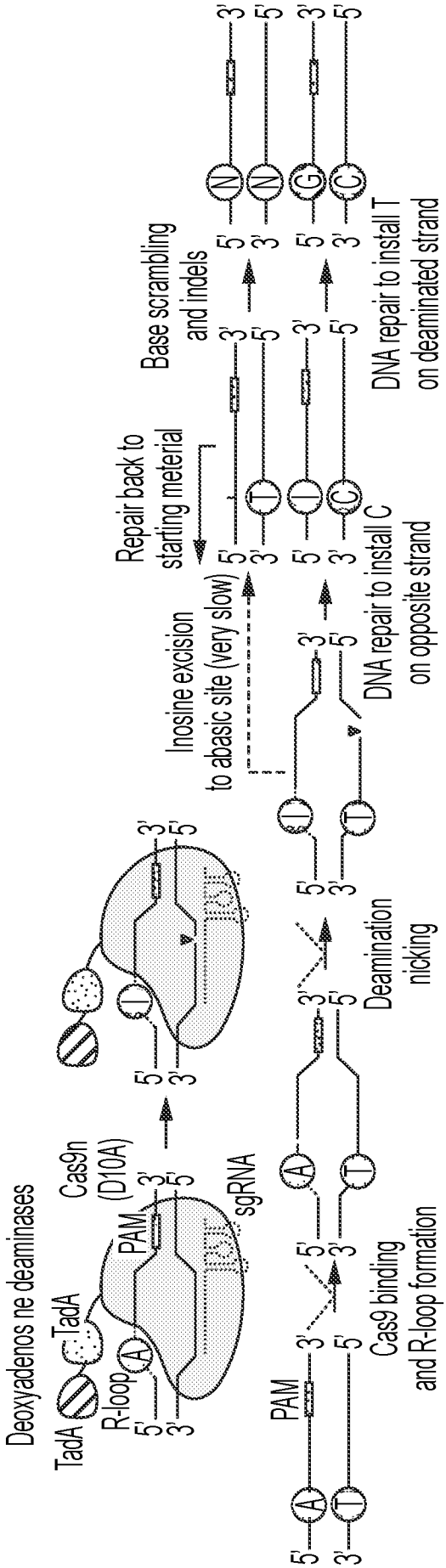

Deoxyadenos ne deaminases
TadA
TadA
R-loop
PAM
Cas9n
(D10A)
sgRNA
Cas9 binding
and R-loop formation
Deamination
nicking
Inosine excision
to abasic site (very slow)
DNA repair to install C
on opposite strand
Repair back to
starting meterial
Base scrambling
and indels
DNA repair to install T
on deaminated strand

FIG. 1C

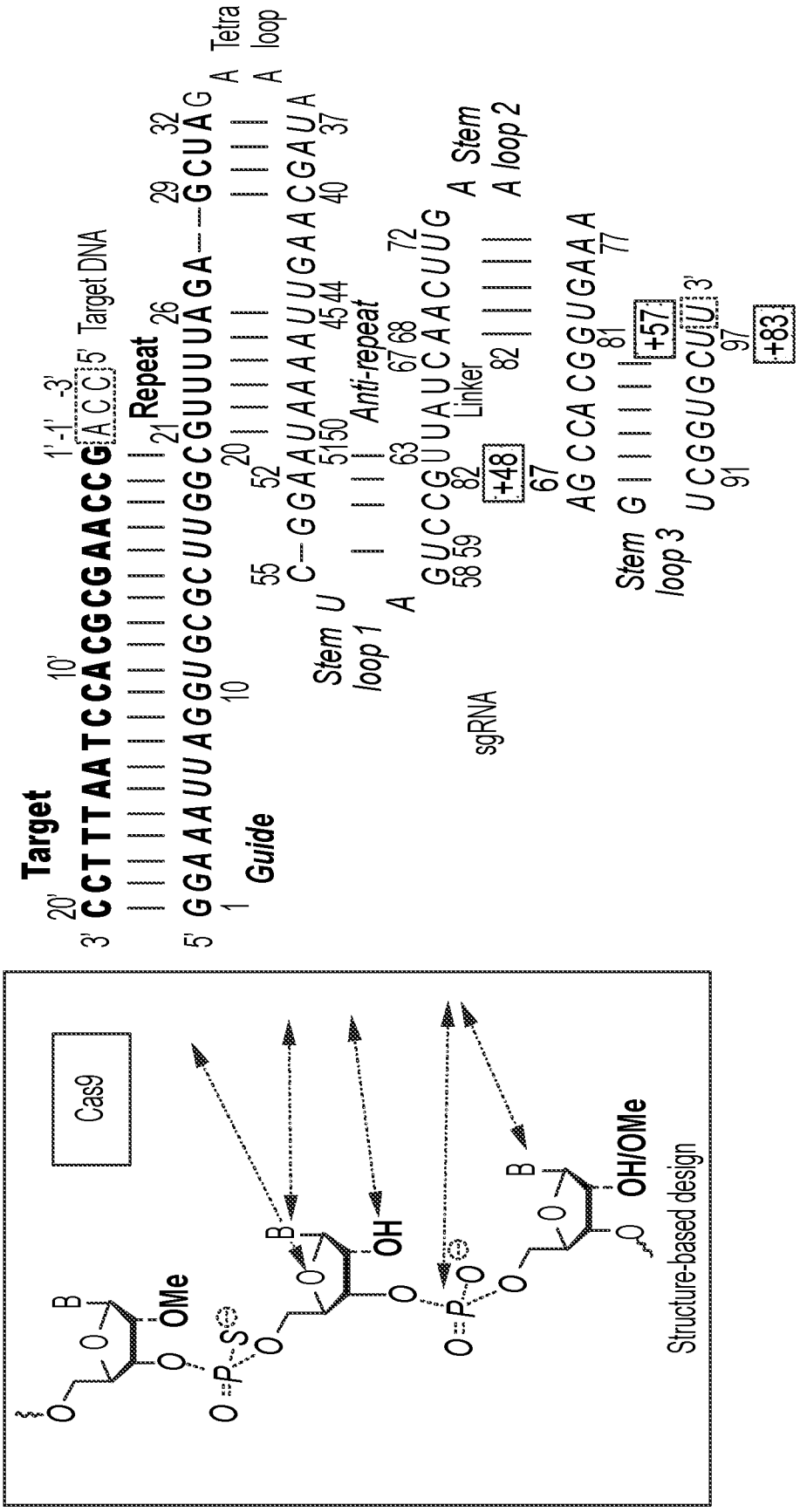

Target
Guide
Repeat
Target DNA
Tetra loop
Stem loop 1
Anti-repeat
sgRNA
Linker
Stem loop 2
Stem loop 3
+48
+57
+83
Cas9
OMe
OH
OH/OMe
Structure-based design

FIG. 1D

PDB ID	Components	State
4CMP	SpCas9 protein	Apo (pre-RNP formation)
4ZT0	SpCas9 protein + gRNA	RNP (forms in cytosol)
5F9R	SpCas9 protein + gRNA + target/non-target DNA	Pre-catalytic ternary complex
4UN3	SpCas9 protein + gRNA + target/non-target DNA	Post-catalytic ternary complex

	4CMP	4ZT0	5F9R	4UN3
4CMP		15	20	20
4ZT0	15		4	3
5F9R	20	4		2
4UN3	20	3	2	

FIG. 2

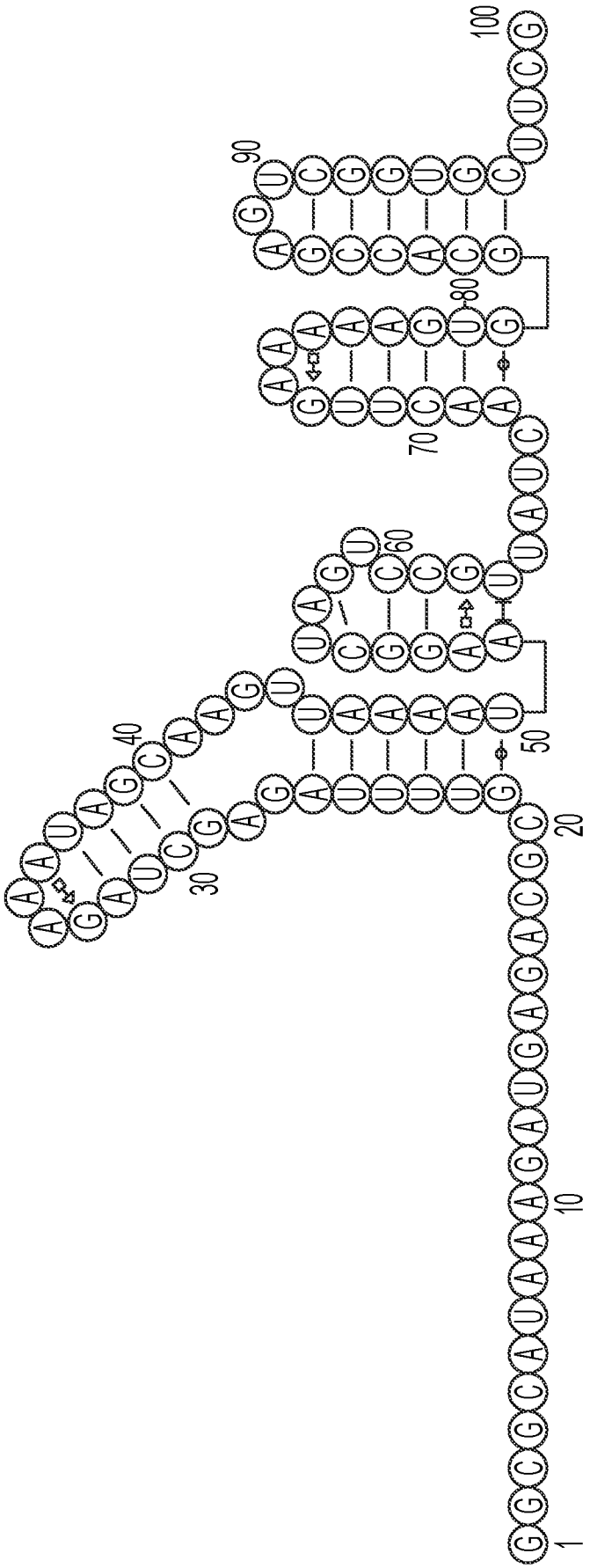


FIG. 3

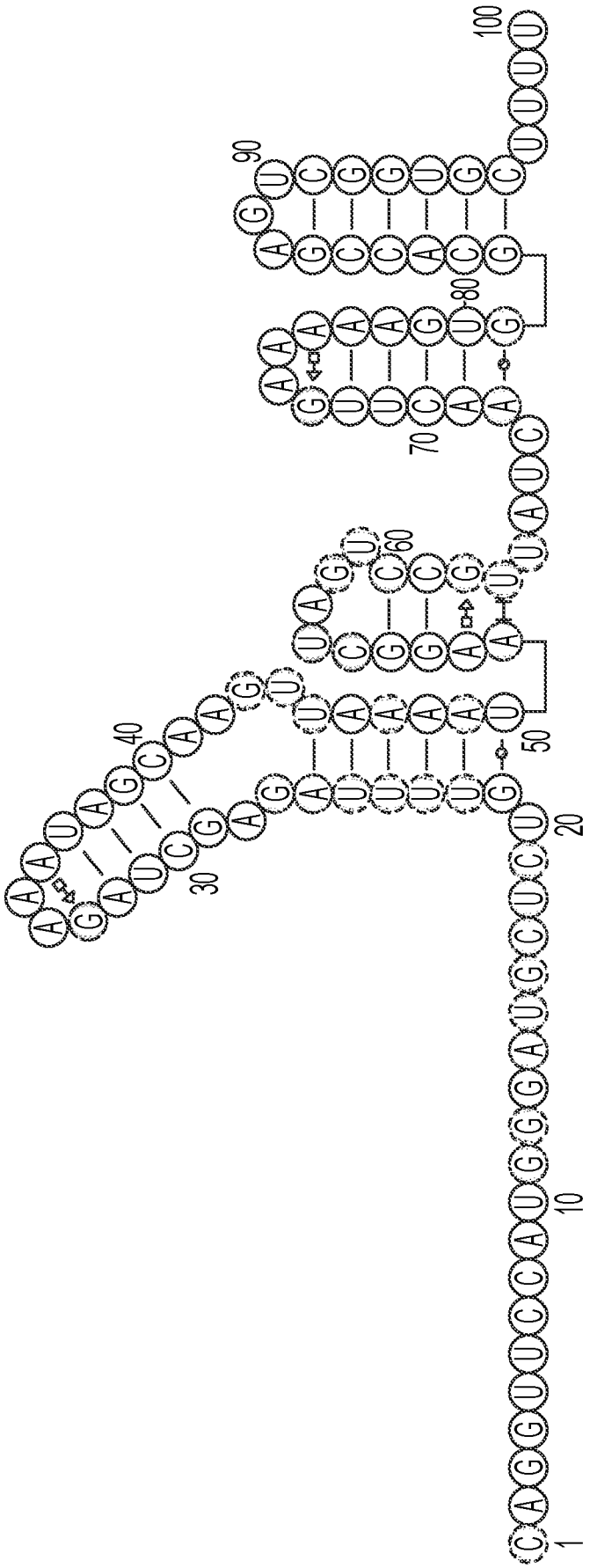


FIG. 4

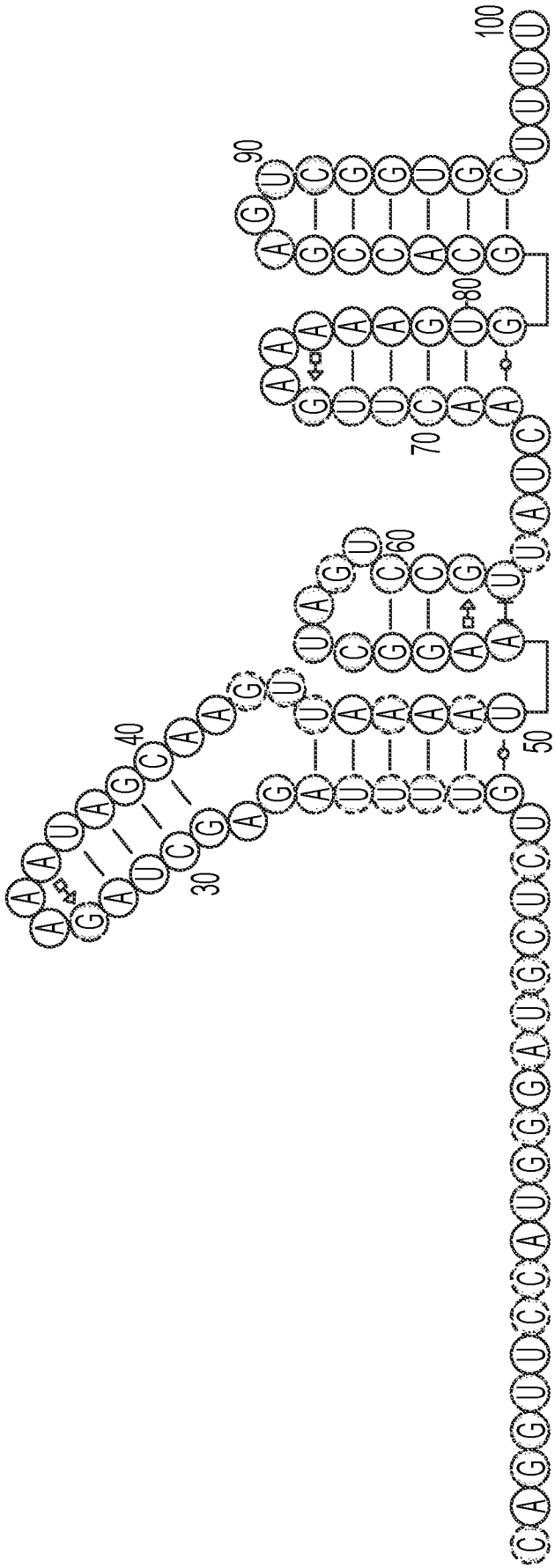


FIG. 5

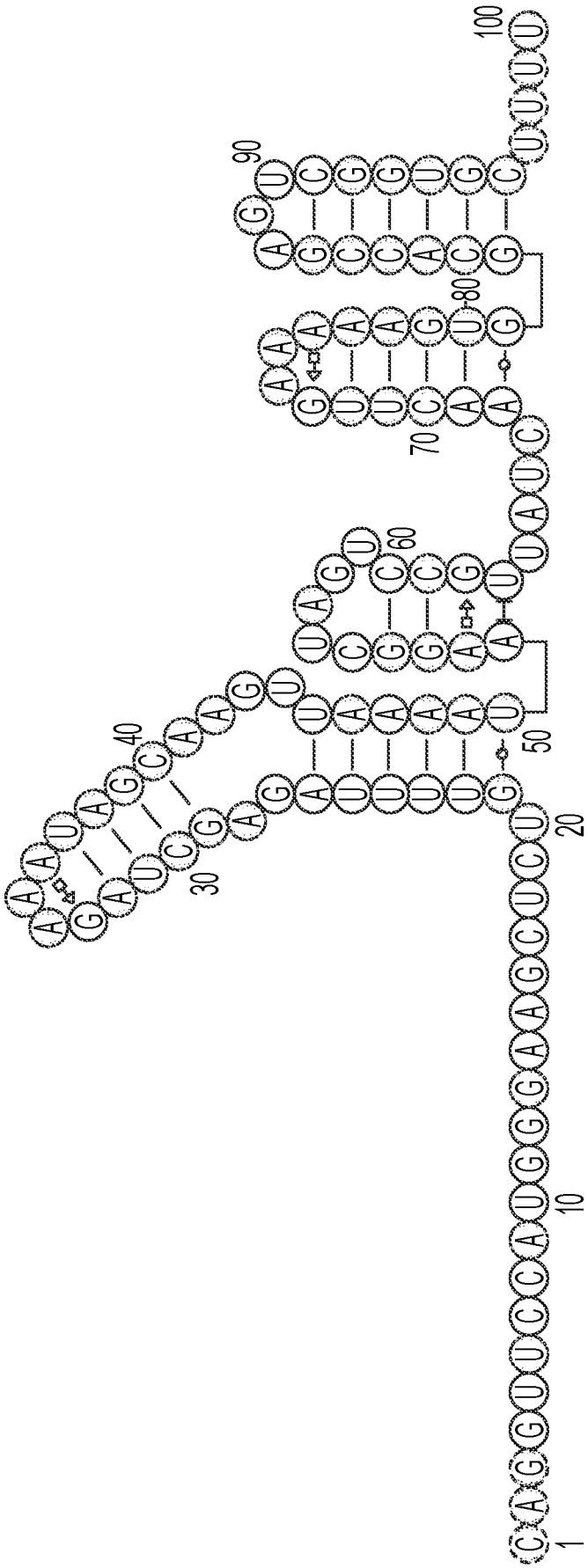


FIG. 6

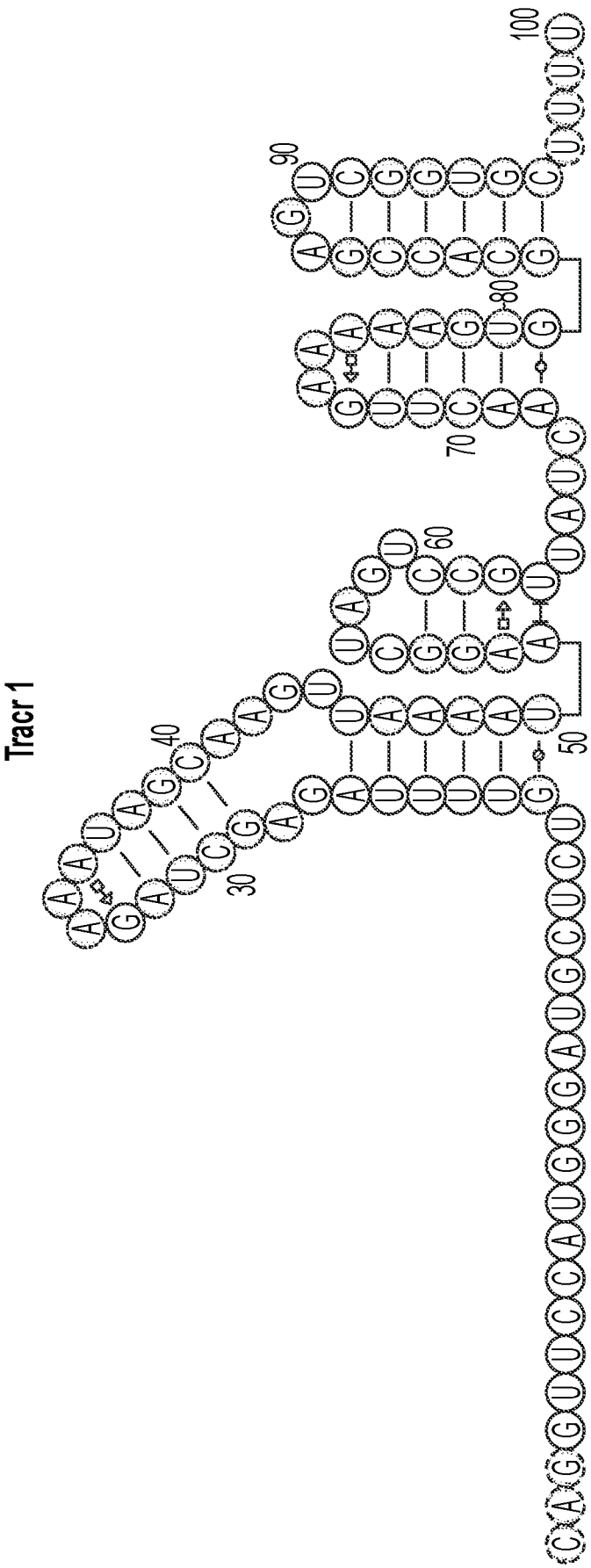


FIG. 7A

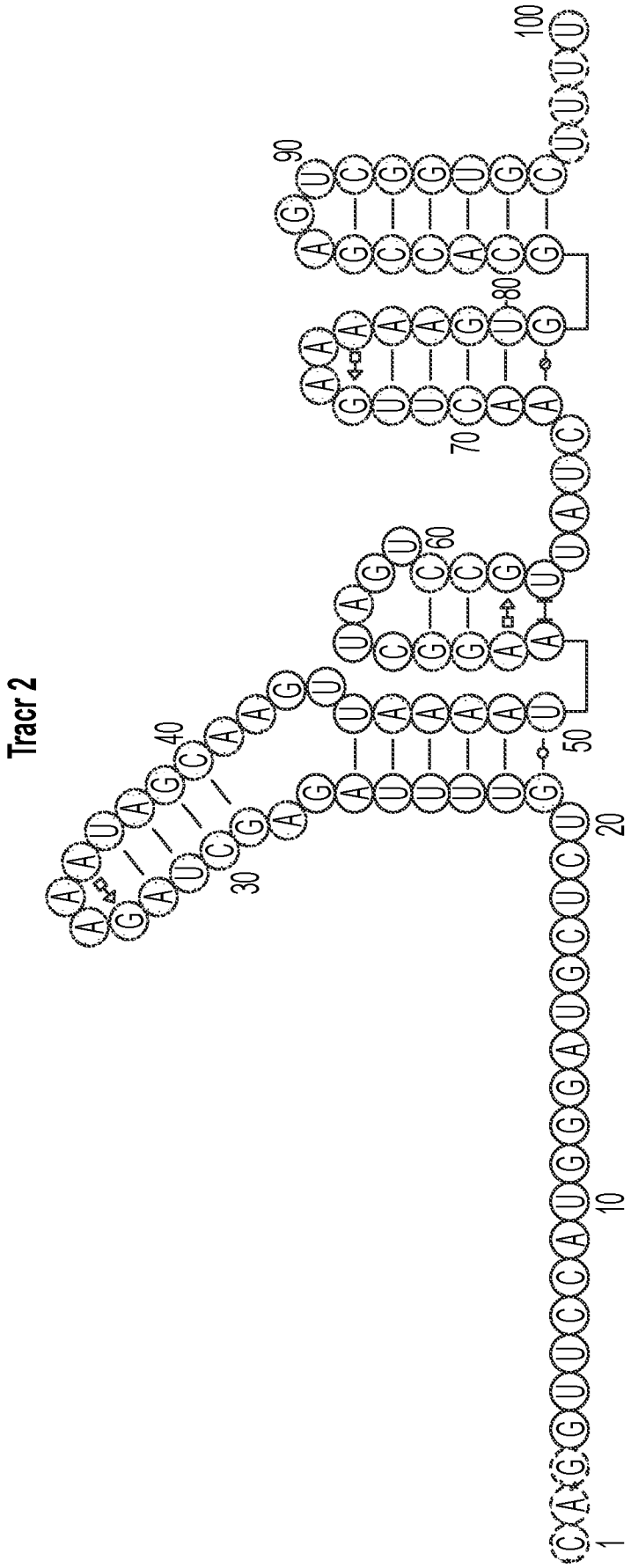


FIG. 7A
(Continued)

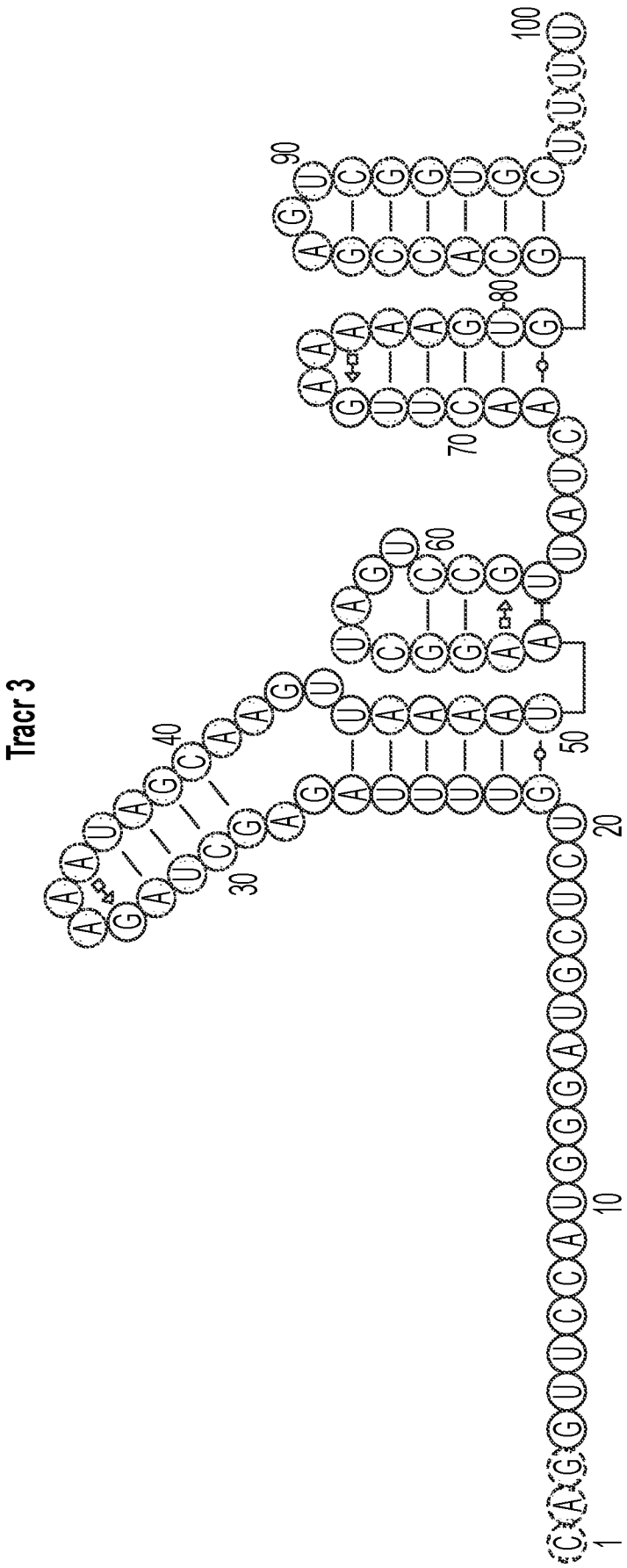


FIG. 7A
(Continued)

```
                                10        20        30        40        50        60        70        80
                       123456789X 123456789X 123456789X 123456789X 123456789X 123456789X 123456789X 123456789X
SEQ ID NO: 61 GUUUUAGAGC UAGAAAUAGC AAGUUAAAAU AAGGCUAGUC CGUUAUCAAC UUGAAAAAGU GGCACCGAGU CGGUGCUUUU
Lit Tracr     GUUUUAGAgc uagaaauagc AAGUUAAAAU AAGGCUAGUC CGUUAUCAac uugaaaaagu ggcaccgagu cggugcusususu
Tracr1        gUUUUAGagc uaGaaauagc aaGUUaAaAu AaggCUaGUC cGUUAucAAc uuGaaaaagu GgcaccgAgU Cggugcusususu
Tracr2        gUUUUAGagc uagaaauagc aaGUUaAaAu AaggcuaGUc cGUUAucAAc uugaaaaagu gGcaccgagu cggugcusususu
Tracr3        gUUUUAGagc uaGaaauagc aaGUUaAaAu AaggcuaGUc cGUUAucAAc uuGaaaaagu gGcaccgagu cggugcusususu
```

FIG. 7B

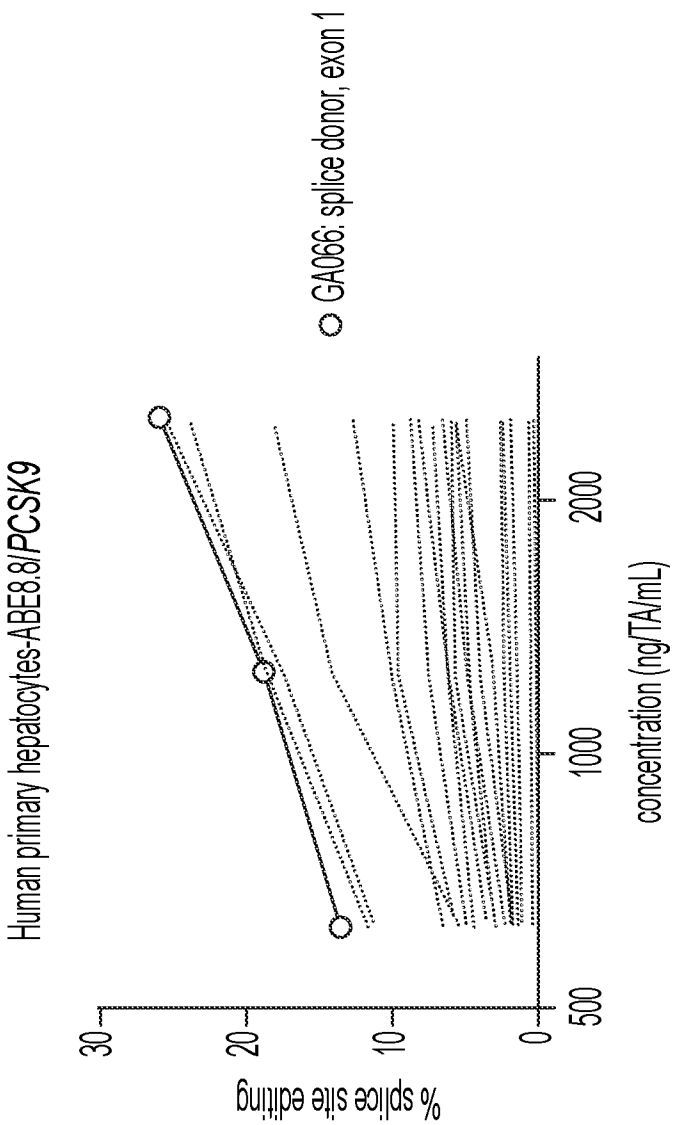

Human primary hepatocytes-ABE8.8/PCSK9
GA066: splice donor, exon 1
% splice site editing
30
20
10
0
500
1000
2000
concentration (ng/TA/mL)

FIG. 8

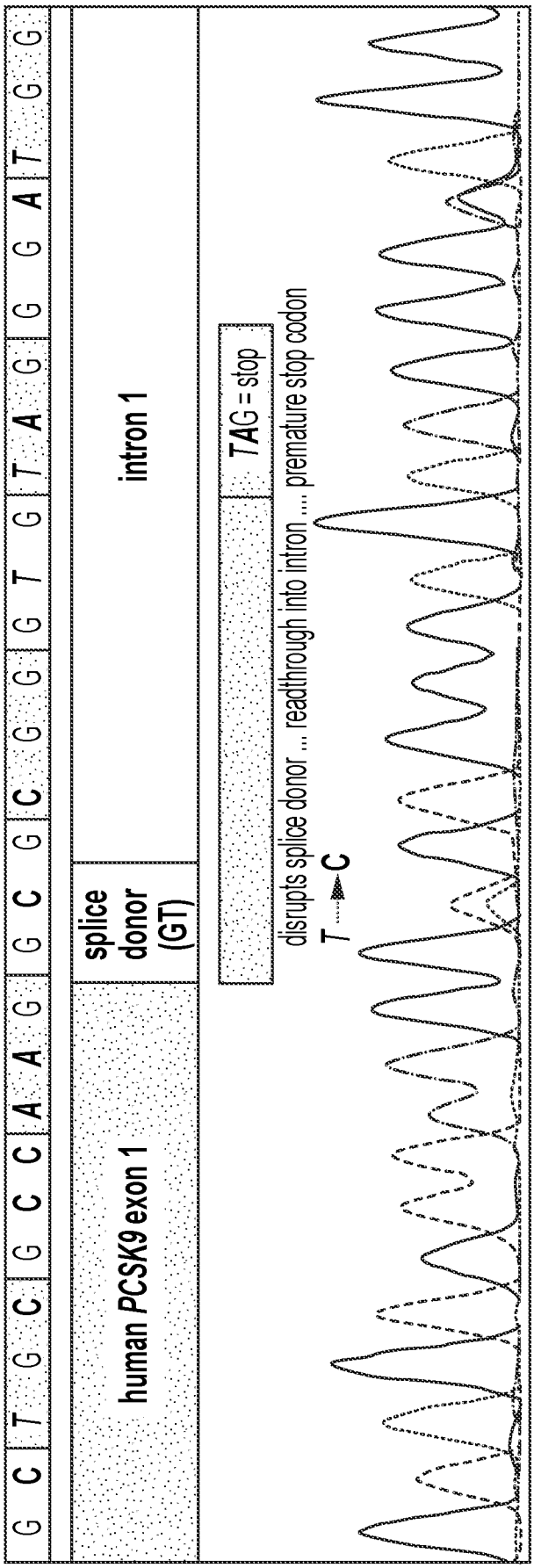

G C T G C G C C A A G G C G G C G G T G T A G G G A T G G
human PCSK9 exon 1
splice donor (GT)
intron 1
TAG = stop
disrupts splice donor ... readthrough into intron .... premature stop codon
T → C
≈ 60% adenine base editing
(editing of A in opposite strand)
natural SNP

FIG. 9

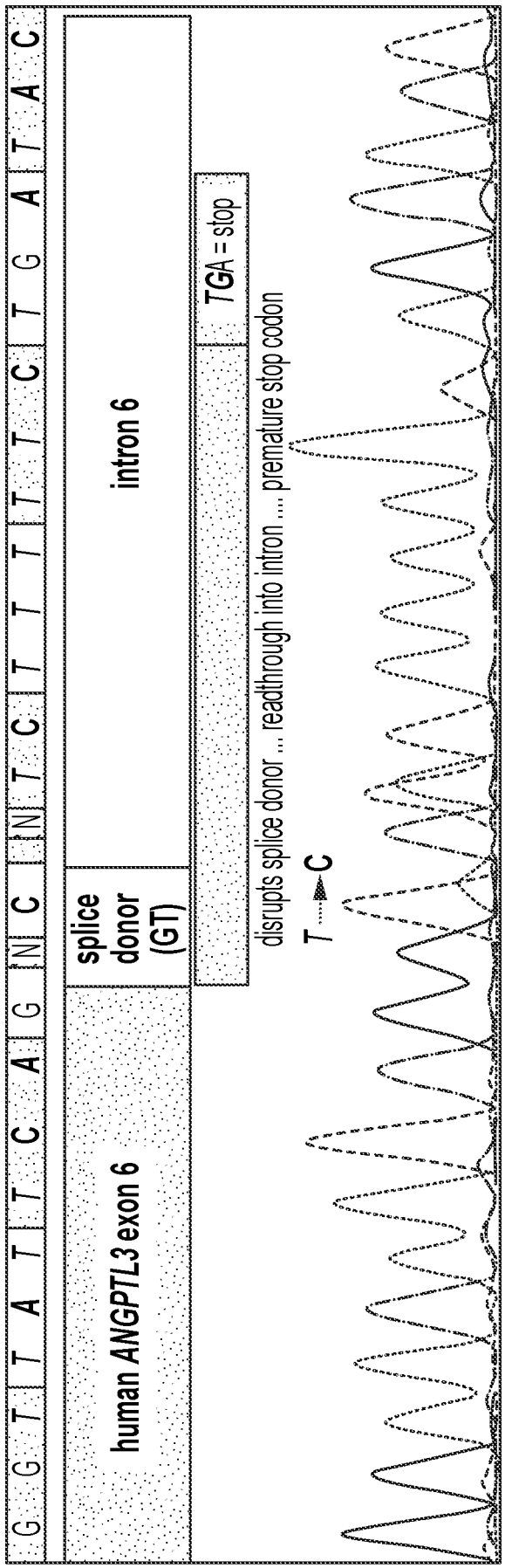

G G T A T T C A G N C N T C T T T T C T G A T A C
human ANGPTL3 exon 6
splice donor (GT)
intron 6
TGA = stop
disrupts splice donor ... readthrough into intron .... premature stop codon
T ---> C
site of natural rare variant (rs398122985, G ---> T) that disrupts splice donor and in homozygous state causes combined hypolipidemia (TG 33, LDL-C 42, HDL-C 24)
T ---> C (additional base edit of no consequence)
≈ 70% adenine base editing (editing of A in opposite strand)

FIG. 10

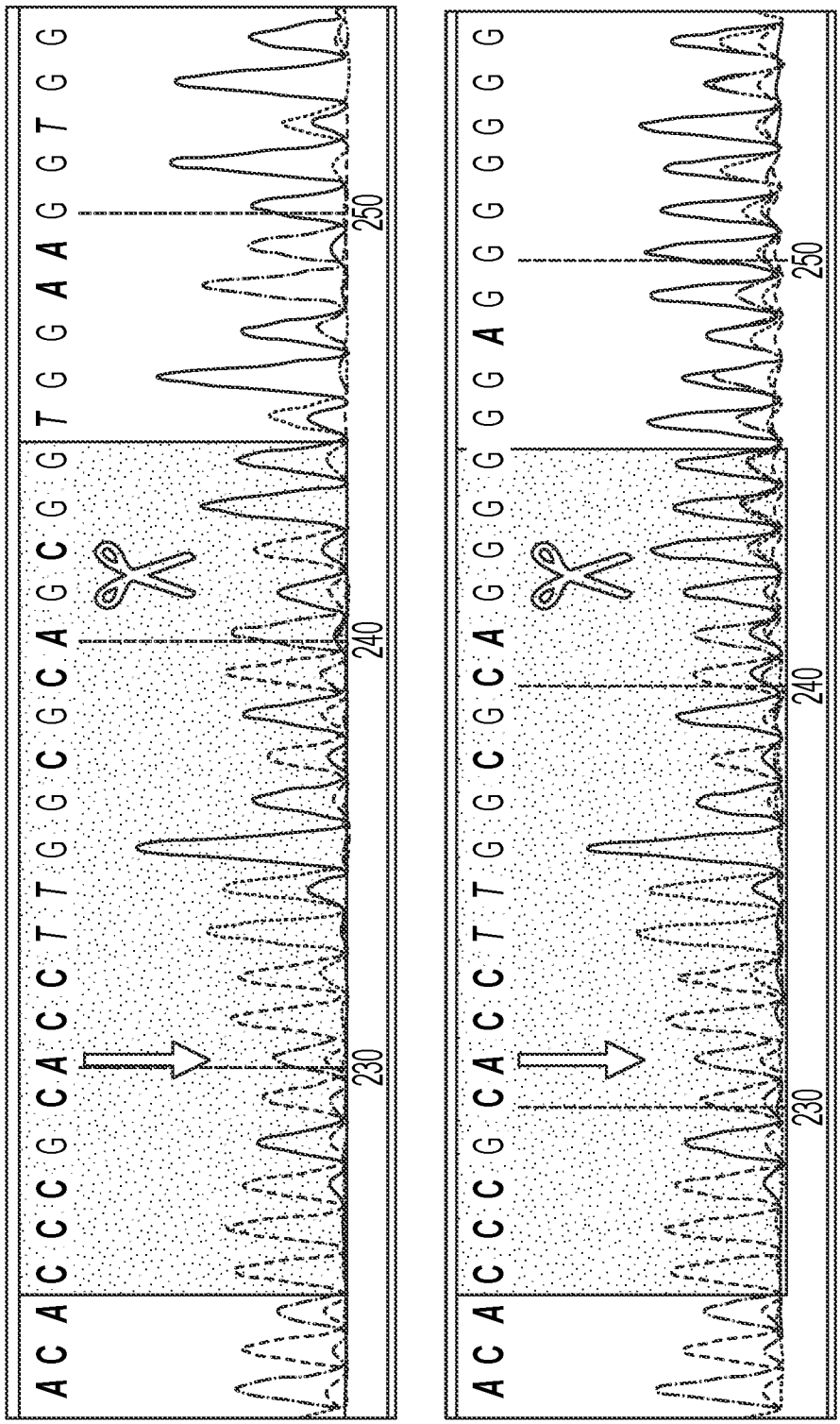


FIG. 11

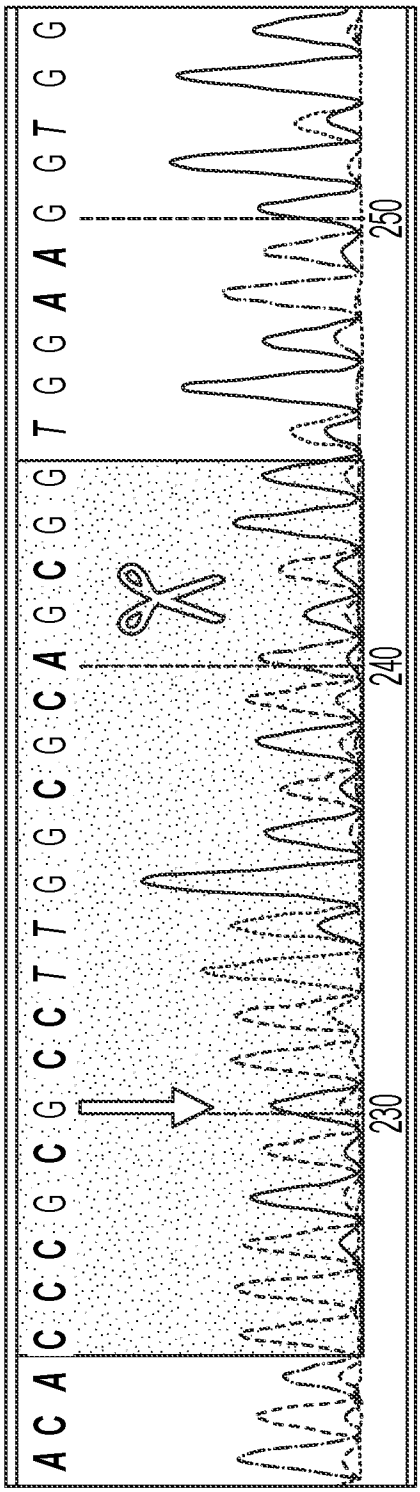

A C A C C C C G C C C C T T G G C G C A G C C G G T G G G A A G G T G G
230
240
250
ABE + Guide

FIG. 11 CONT.

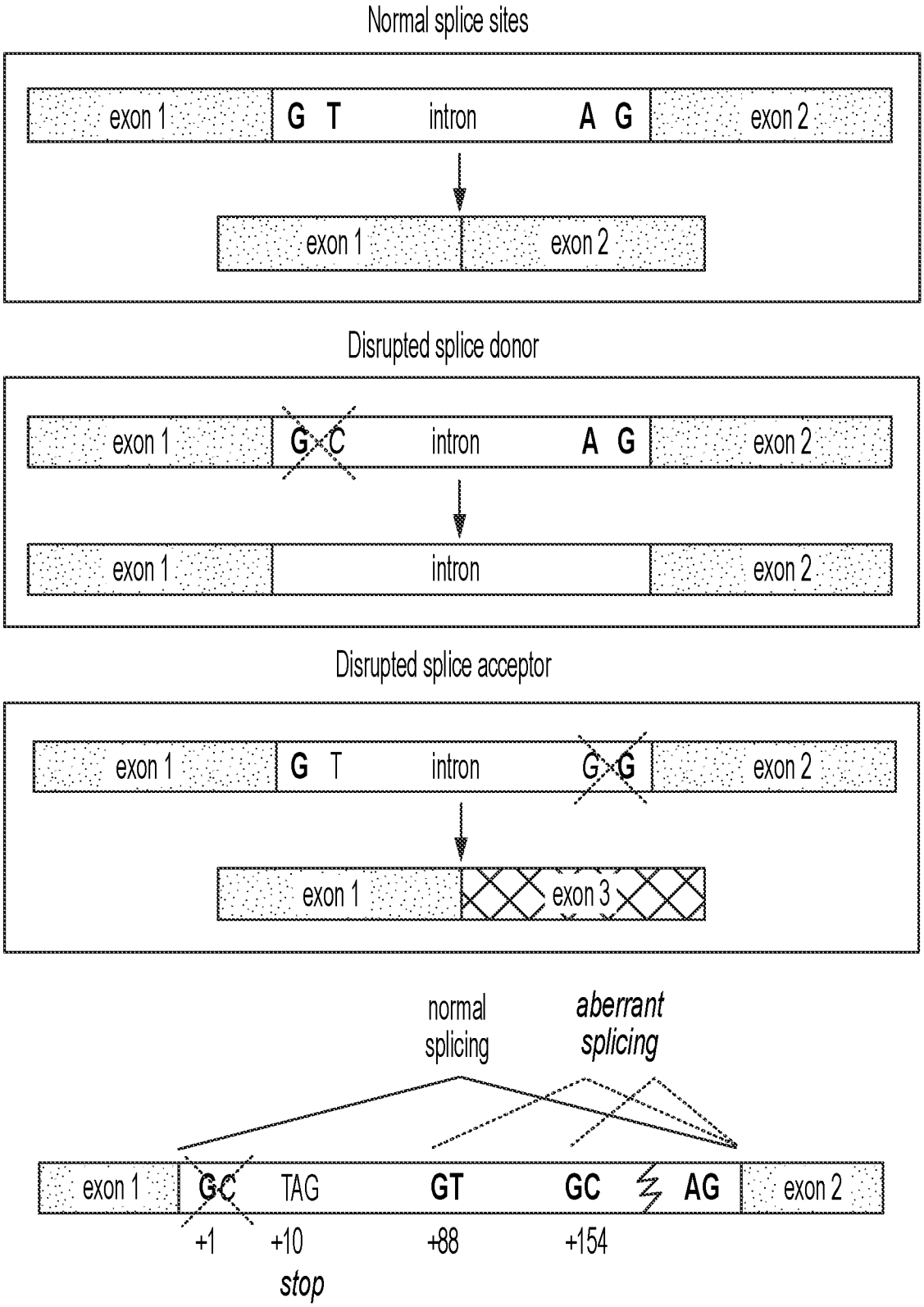

Normal splice sites
exon 1
G T
intron
A G
exon 2
exon 1
exon 2
Disrupted splice donor
exon 1
G C
intron
A G
exon 2
exon 1
intron
exon 2
Disrupted splice acceptor
exon 1
G T
intron
G G
exon 2
exon 1
exon 3
normal splicing
aberrant splicing
exon 1
GC
TAG
GT
GC
AG
exon 2
+1
+10
+88
+154
stop

FIG. 12

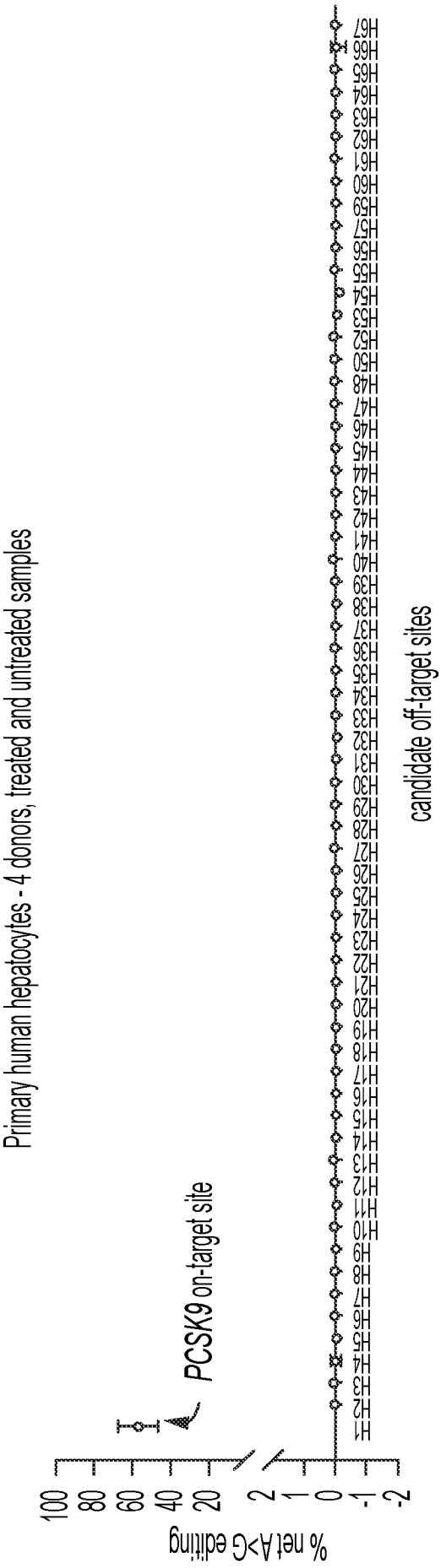

Primary human hepatocytes - 4 donors, treated and untreated samples
% net A>G editing
100
80
60
40
20
2
1
0
-1
-2
PCSK9 on-target site
candidate off-target sites

FIG. 13

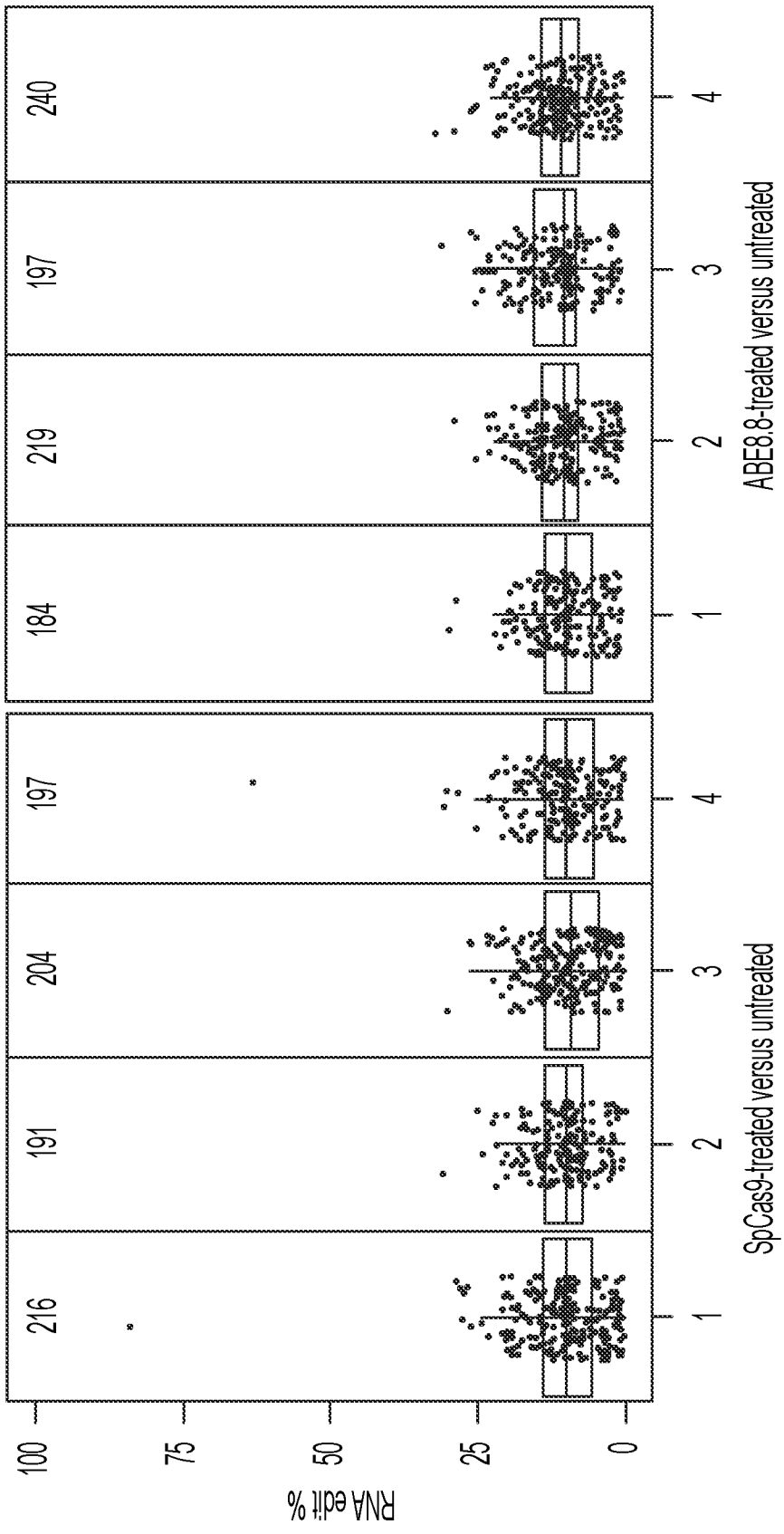

RNA edit %
100
75
50
25
0
216
191
204
197
184
219
197
240
1
2
3
4
1
2
3
4
SpCas9-treated versus untreated
ABE8.8-treated versus untreated

FIG. 14

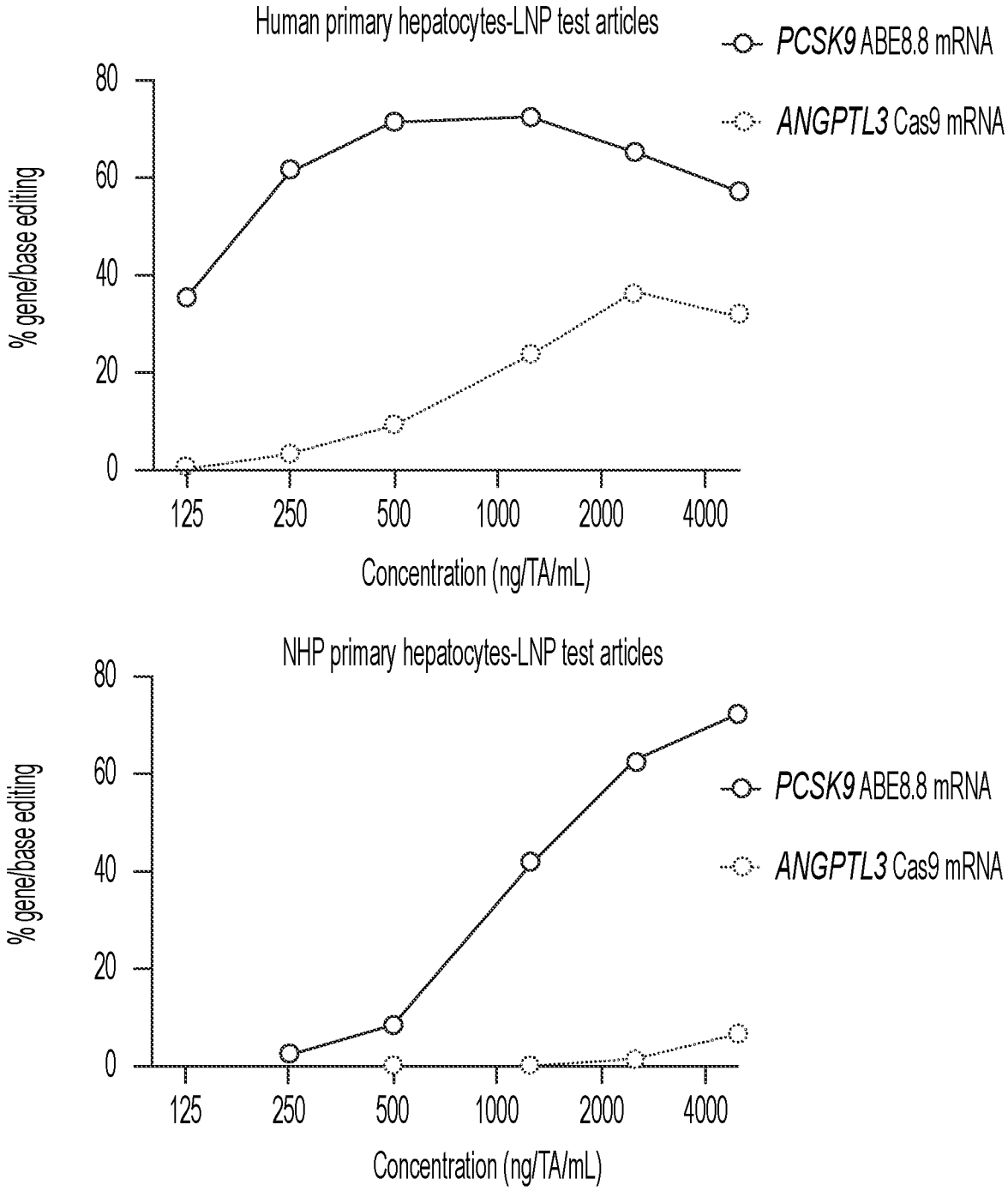

Human primary hepatocytes-LNP test articles
PCSK9 ABE8.8 mRNA
ANGPTL3 Cas9 mRNA
% gene/base editing
0
20
40
60
80
125
250
500
1000
2000
4000
Concentration (ng/TA/mL)
NHP primary hepatocytes-LNP test articles
PCSK9 ABE8.8 mRNA
ANGPTL3 Cas9 mRNA
% gene/base editing
0
20
40
60
80
125
250
500
1000
2000
4000
Concentration (ng/TA/mL)

FIG. 15

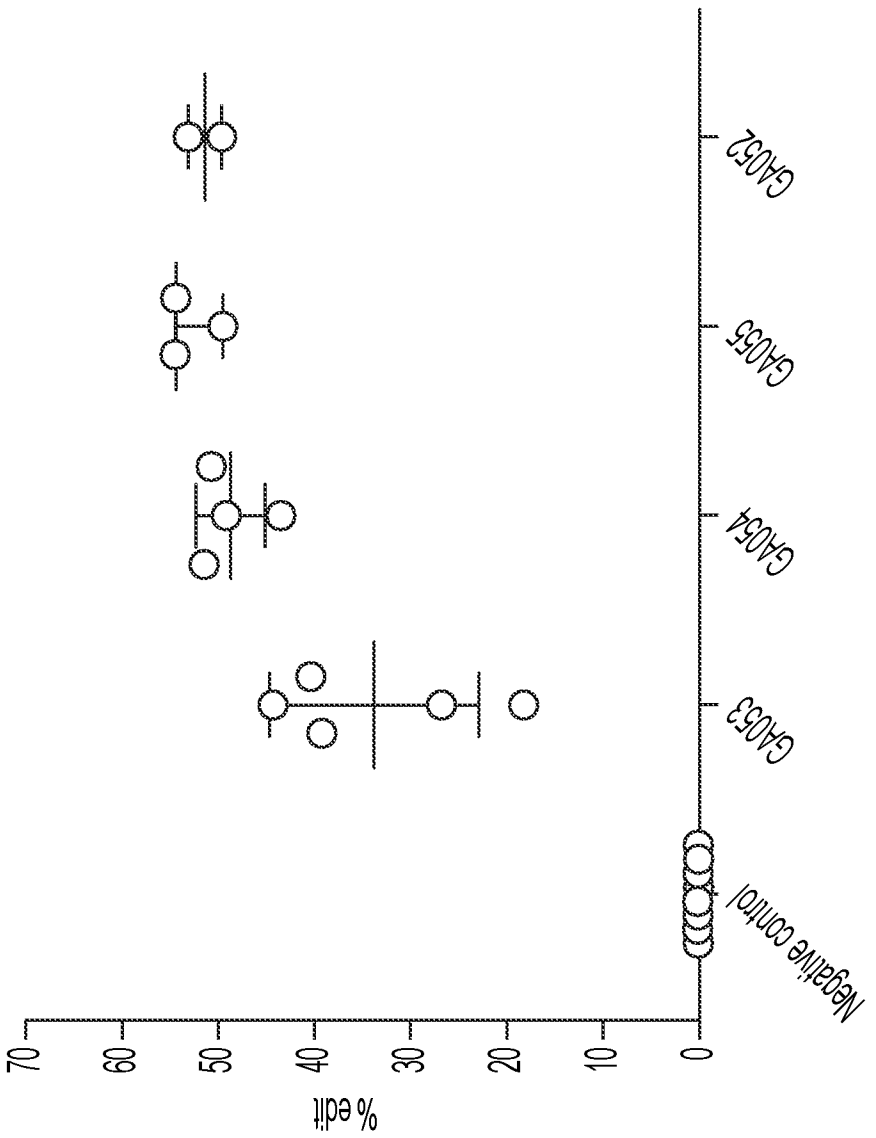

% edit
70
60
50
40
30
20
10
0
Negative control
GA053
GA054
GA055
GA052

FIG. 16

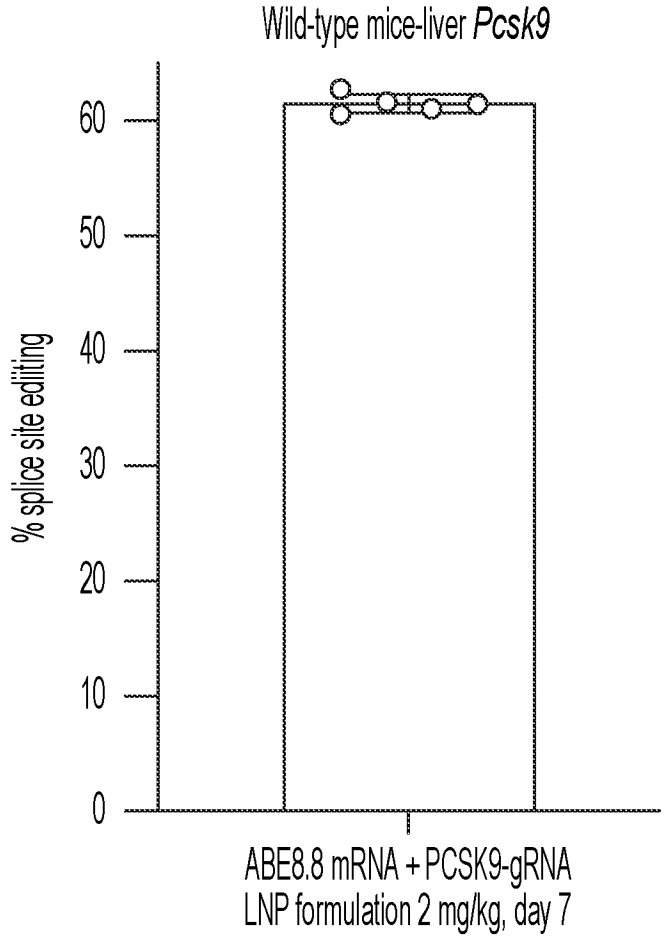

Wild-type mice-liver *Pcsk9*
% splice site editing
0
10
20
30
40
50
60
ABE8.8 mRNA + PCSK9-gRNA
LNP formulation 2 mg/kg, day 7

FIG. 17

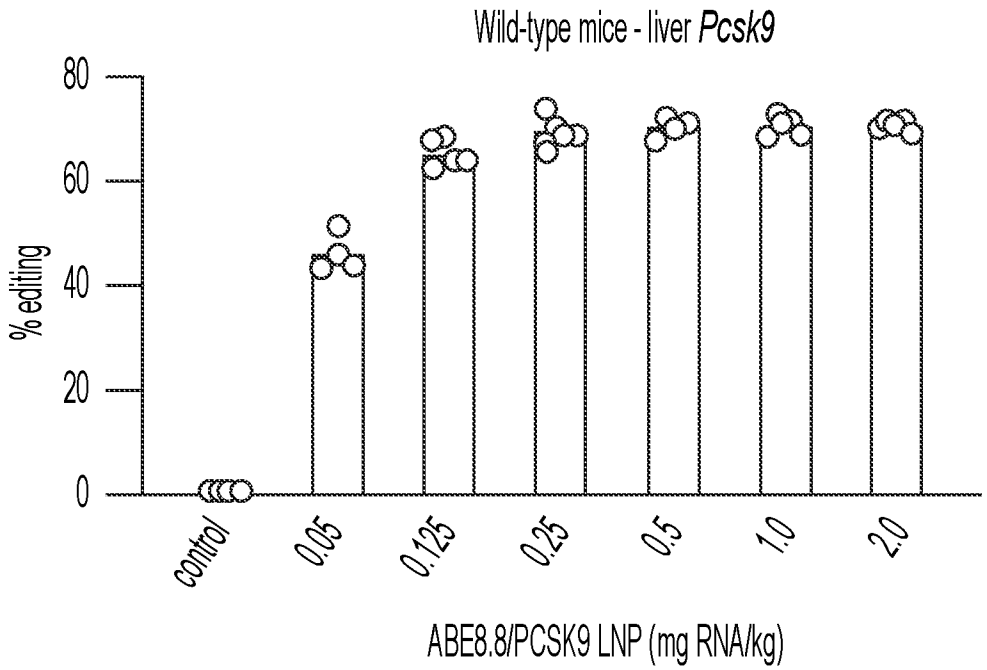

Wild-type mice - liver *Pcsk9*
% editing
0
20
40
60
80
control
0.05
0.125
0.25
0.5
1.0
2.0
ABE8.8/PCSK9 LNP (mg RNA/kg)

FIG. 18

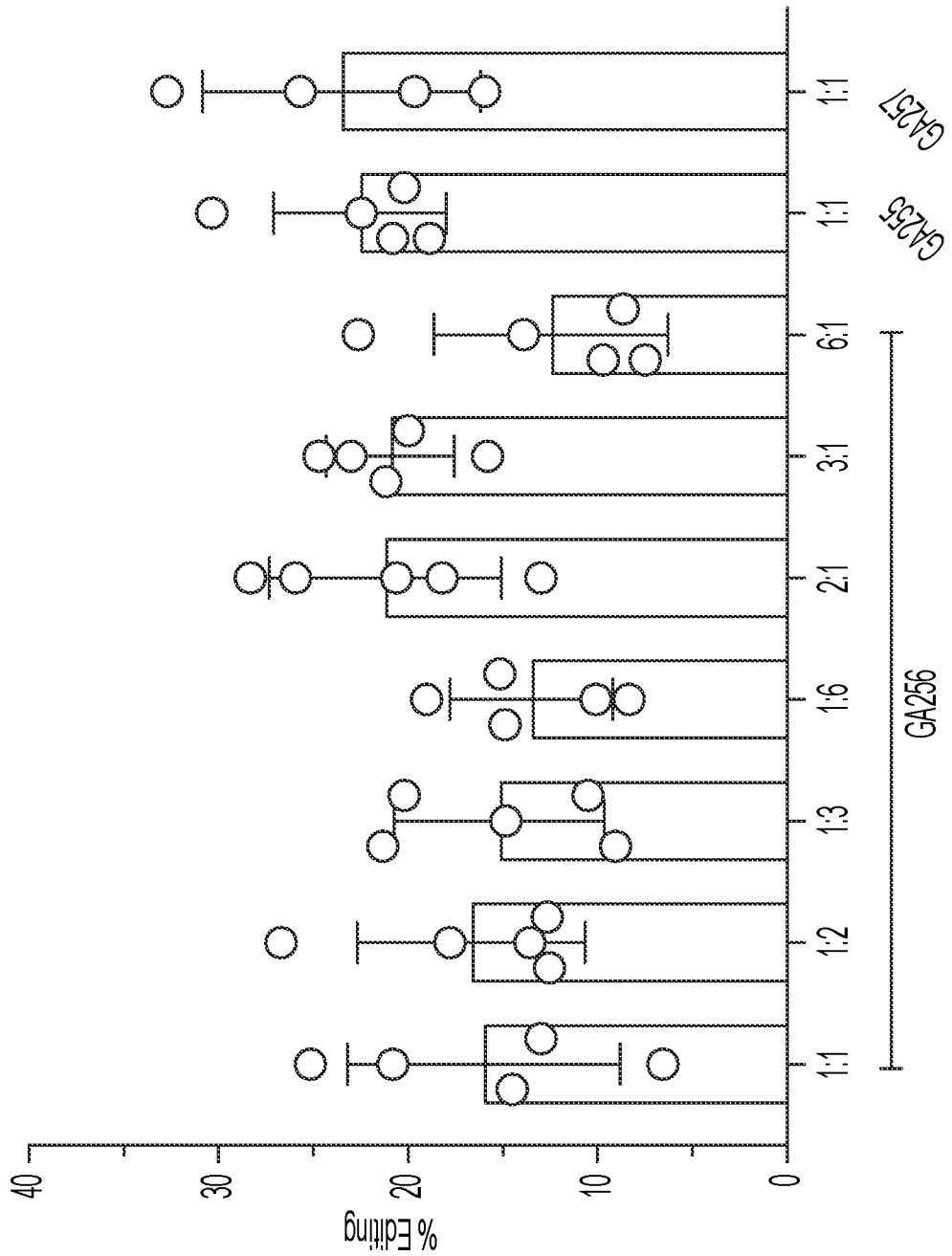

% Editing
0
10
20
30
40
1:1
1:2
1:3
1:6
2:1
3:1
6:1
1:1
1:1
GA256
GA255
GA257
Ratio of gRNA:mRNA

FIG. 19

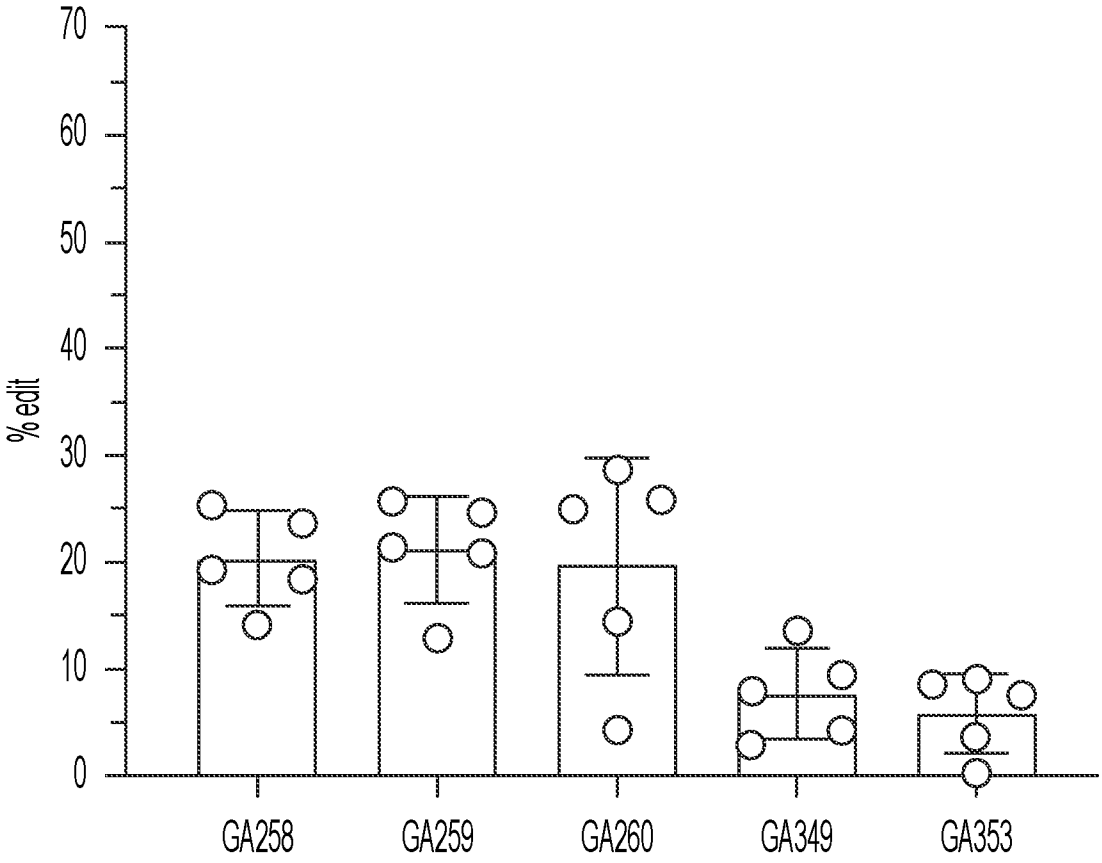


FIG. 20

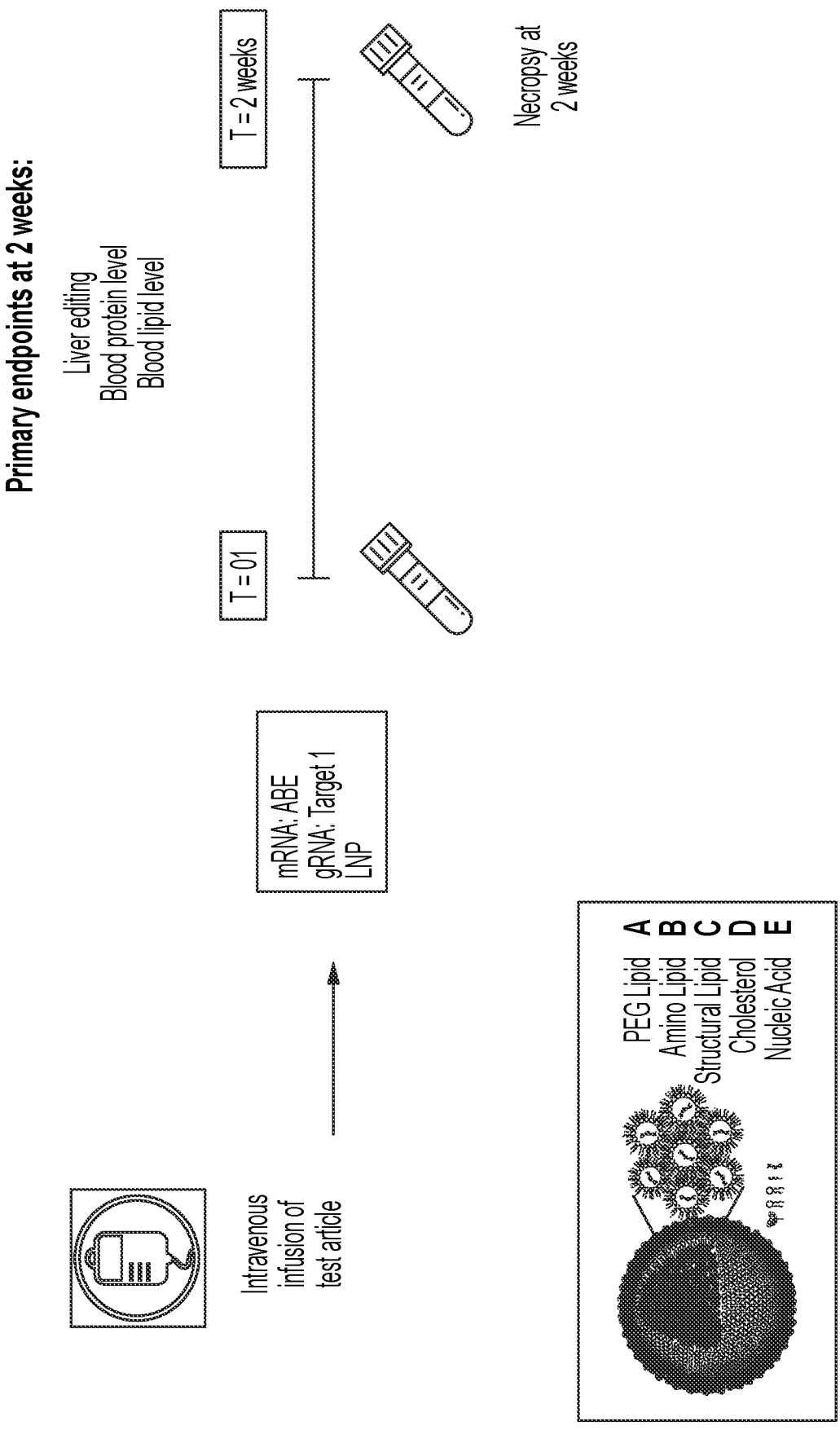

Primary endpoints at 2 weeks:
Liver editing
Blood protein level
Blood lipid level
T = 01
T = 2 weeks
Necropsy at 2 weeks
mRNA: ABE
gRNA: Target 1
LNP
Intravenous infusion of test article
PEG Lipid A
Amino Lipid B
Structural Lipid C
Cholesterol D
Nucleic Acid E

FIG. 21

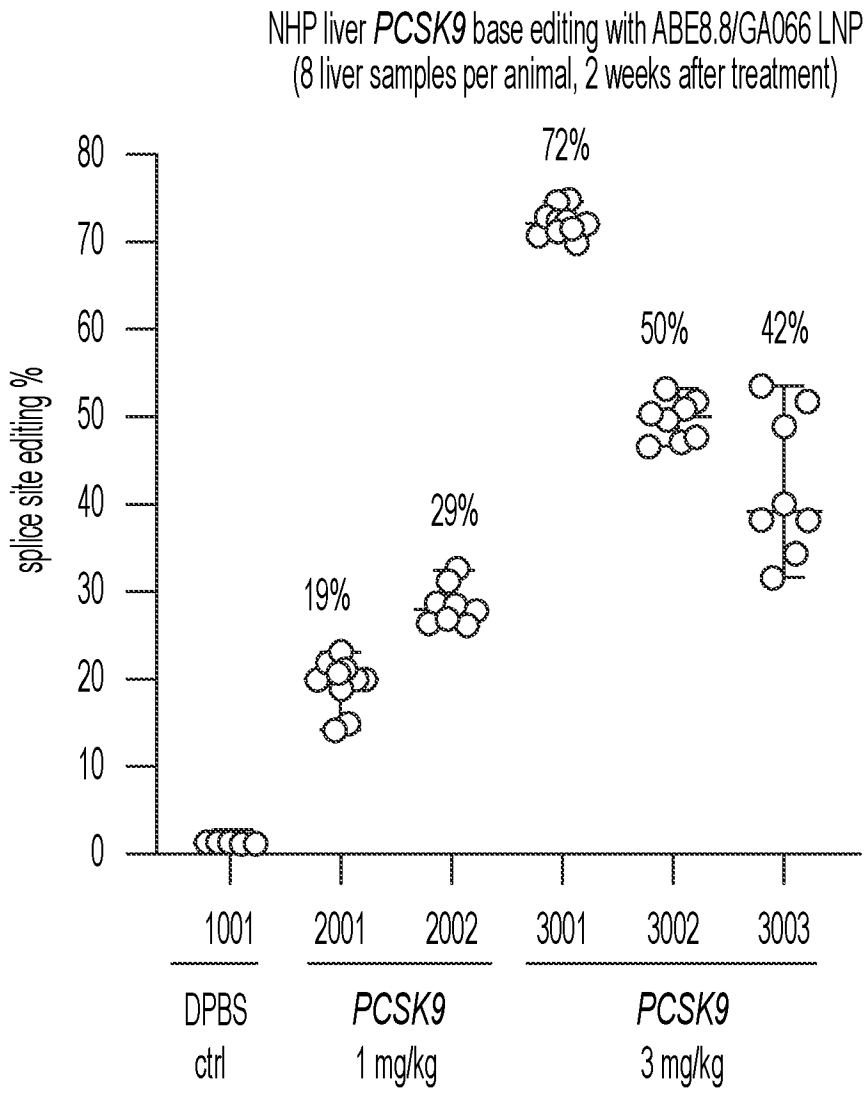

NHP liver PCSK9 base editing with ABE8.8/GA066 LNP
(8 liver samples per animal, 2 weeks after treatment)
splice site editing %
80
70
60
50
40
30
20
10
0
72%
50%
42%
29%
19%
1001
2001
2002
3001
3002
3003
DPBS
ctrl
PCSK9
1 mg/kg
PCSK9
3 mg/kg

FIG. 22

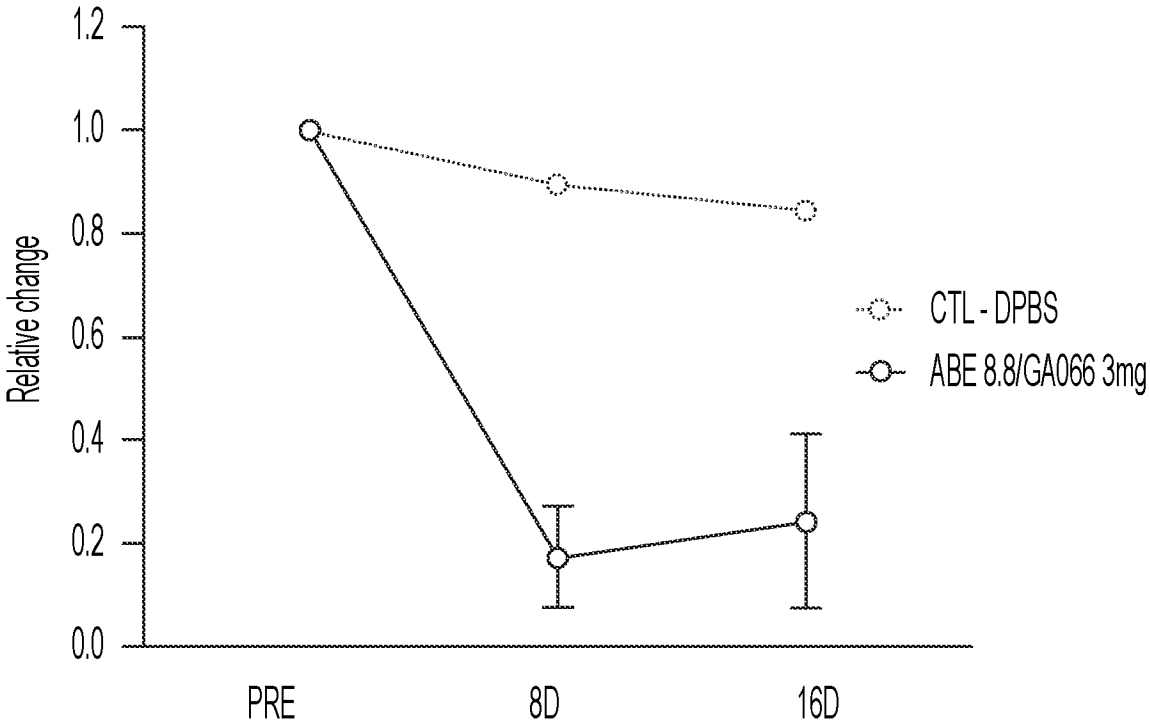

1.2
1.0
0.8
0.6
0.4
0.2
0.0
Relative change
PRE
8D
16D
CTL - DPBS
ABE 8.8/GA066 3mg

FIG. 23

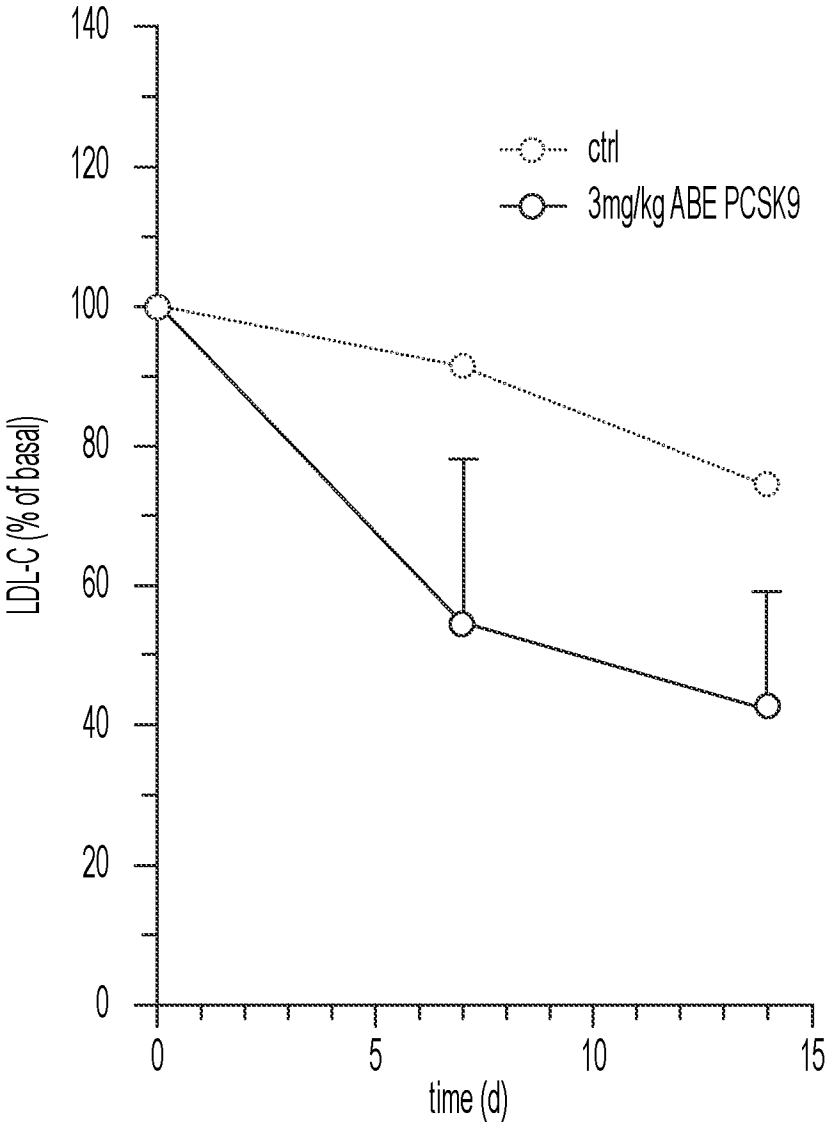

140
120
100
80
60
40
20
0
LDL-C (% of basal)
0
5
10
15
time (d)
ctrl
3mg/kg ABE PCSK9

FIG. 24

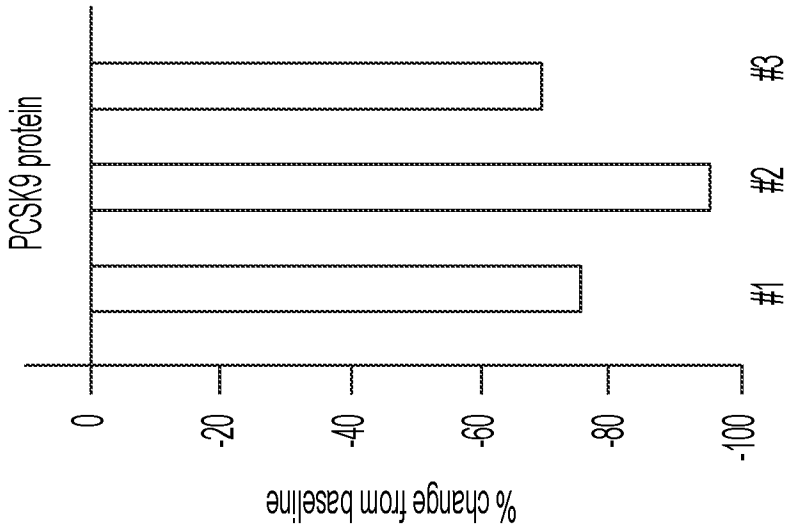


FIG. 25B

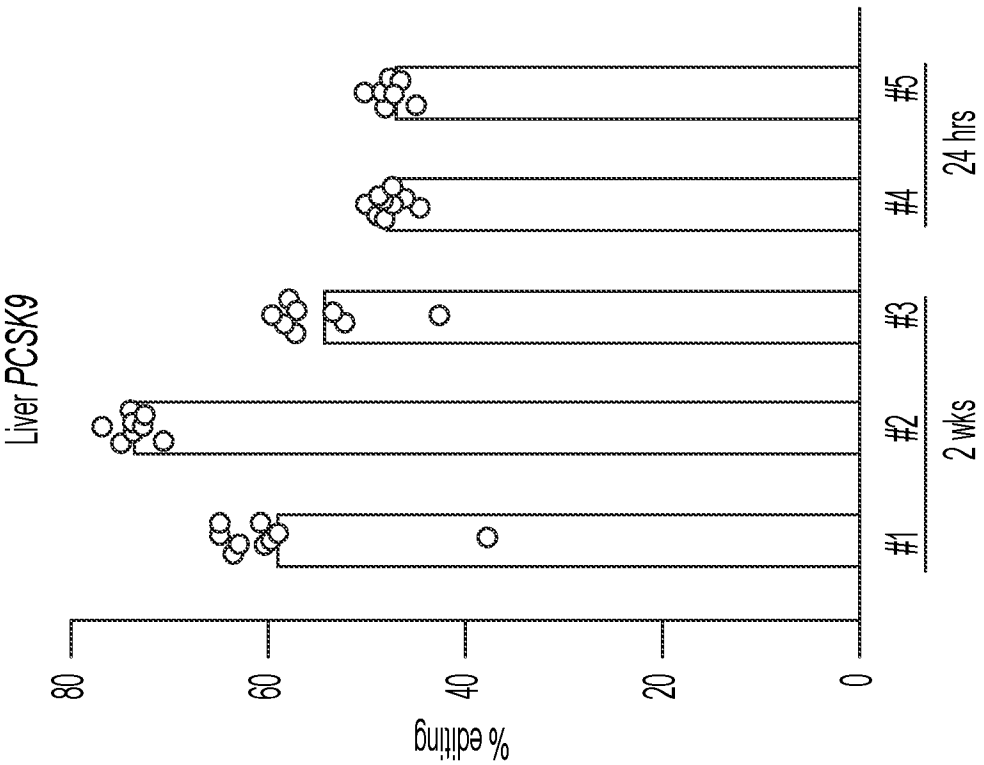


FIG. 25A

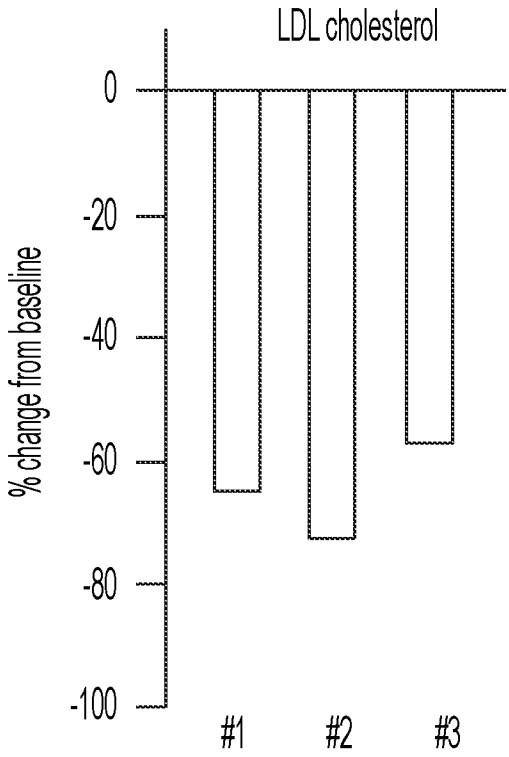


FIG. 25C

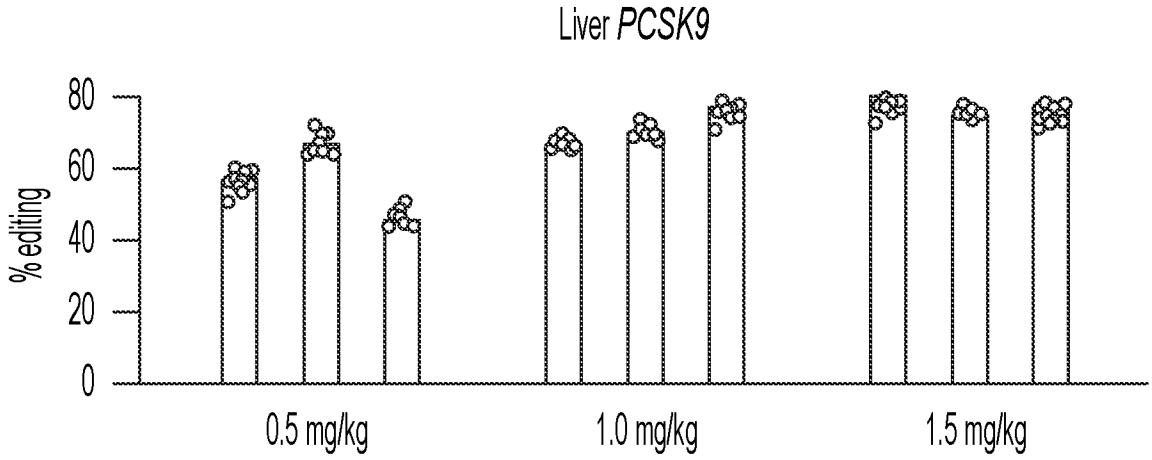


FIG. 26A

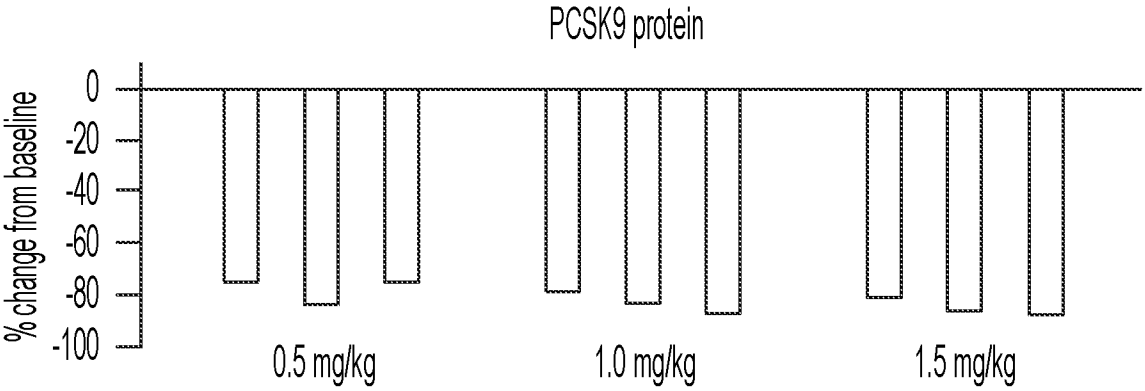


FIG. 26B

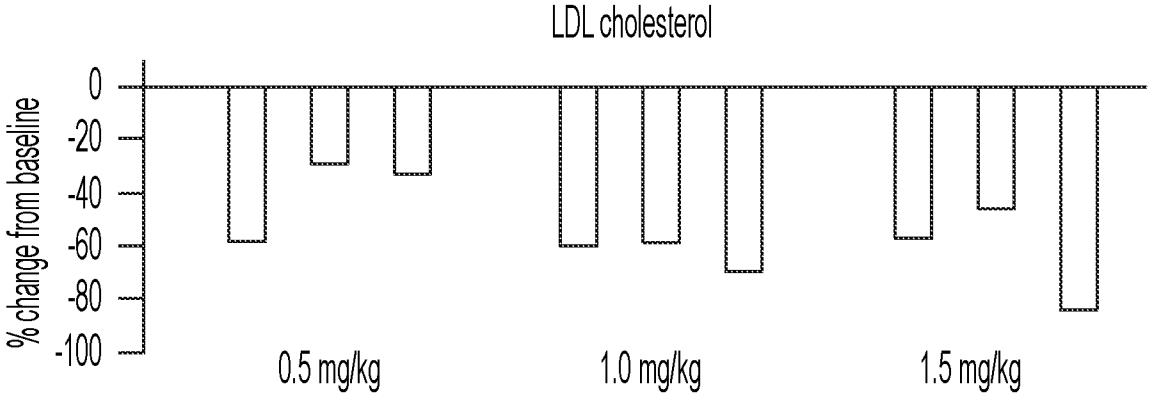


FIG. 26C

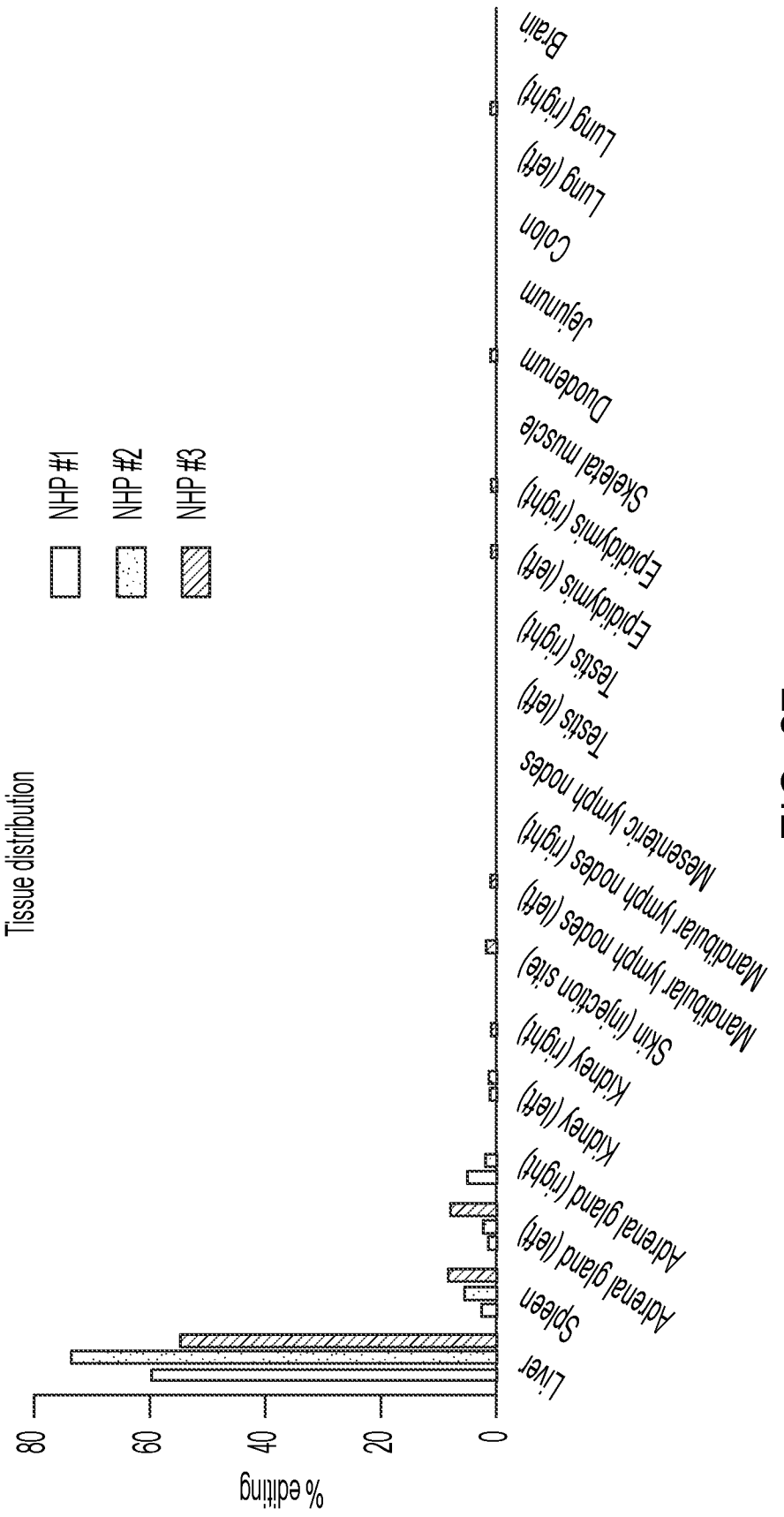

Tissue distribution
NHP #1
NHP #2
NHP #3
% editing
0
20
40
60
80
Liver
Spleen
Adrenal gland (left)
Adrenal gland (right)
Kidney (left)
Kidney (right)
Skin (injection site)
Mandibular lymph nodes (left)
Mandibular lymph nodes (right)
Mesenteric lymph nodes
Testis (left)
Testis (right)
Epididymis (left)
Epididymis (right)
Skeletal muscle
Duodenum
Jejunum
Colon
Lung (left)
Lung (right)
Brain

FIG. 27

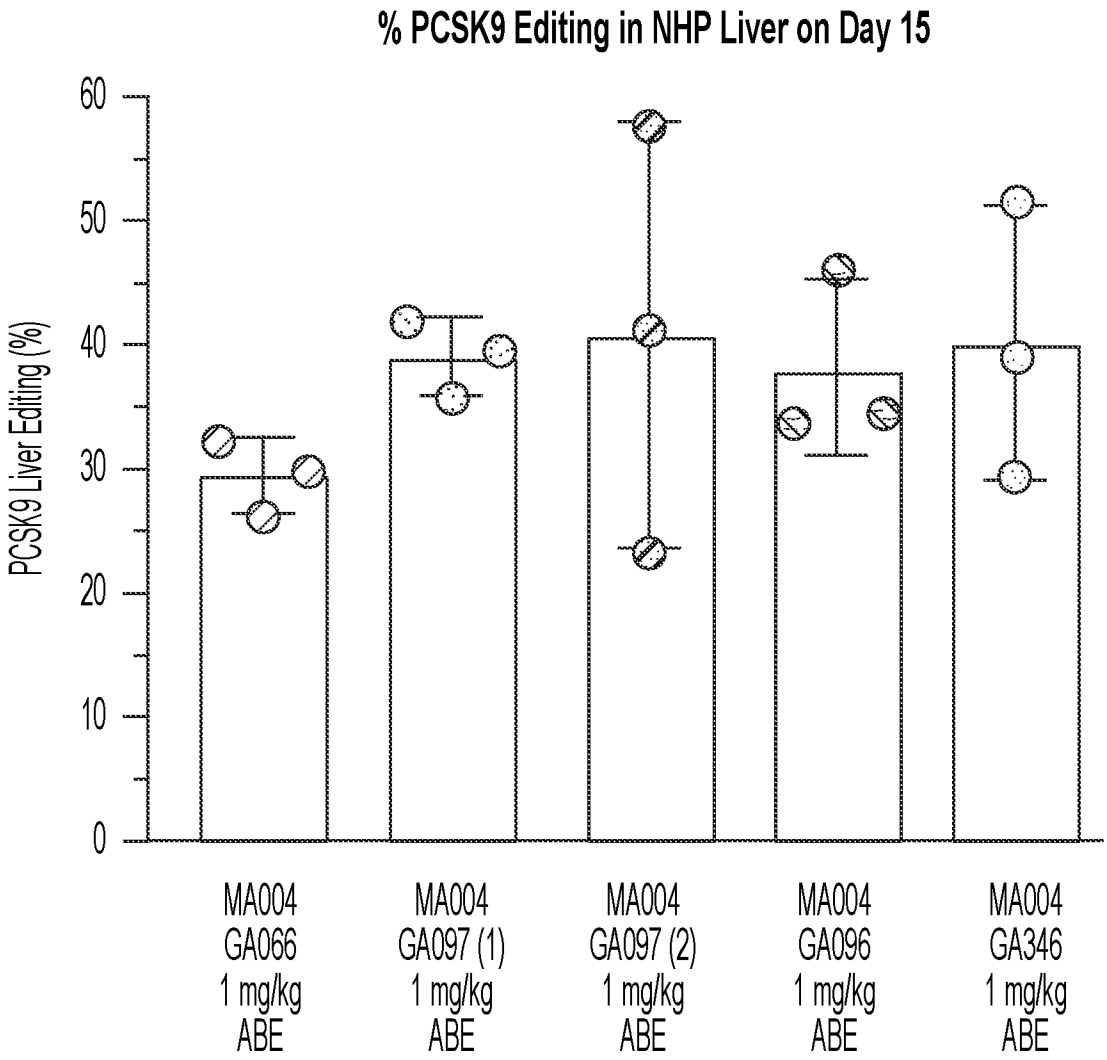

% PCSK9 Editing in NHP Liver on Day 15
PCSK9 Liver Editing (%)
60
50
40
30
20
10
0
MA004 GA066 1 mg/kg ABE
MA004 GA097 (1) 1 mg/kg ABE
MA004 GA097 (2) 1 mg/kg ABE
MA004 GA096 1 mg/kg ABE
MA004 GA346 1 mg/kg ABE

FIG. 28

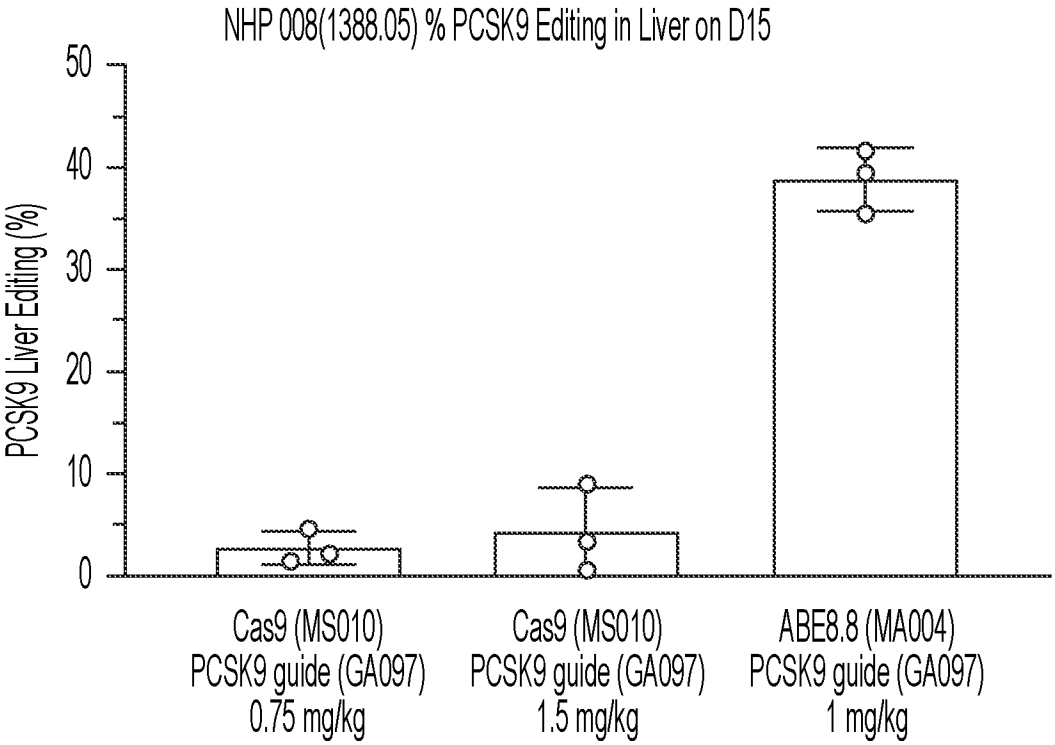

NHP 008(1388.05) % PCSK9 Editing in Liver on D15
PCSK9 Liver Editing (%)
50
40
30
20
10
0
Cas9 (MS010)
PCSK9 guide (GA097)
0.75 mg/kg
Cas9 (MS010)
PCSK9 guide (GA097)
1.5 mg/kg
ABE8.8 (MA004)
PCSK9 guide (GA097)
1 mg/kg

FIG. 29

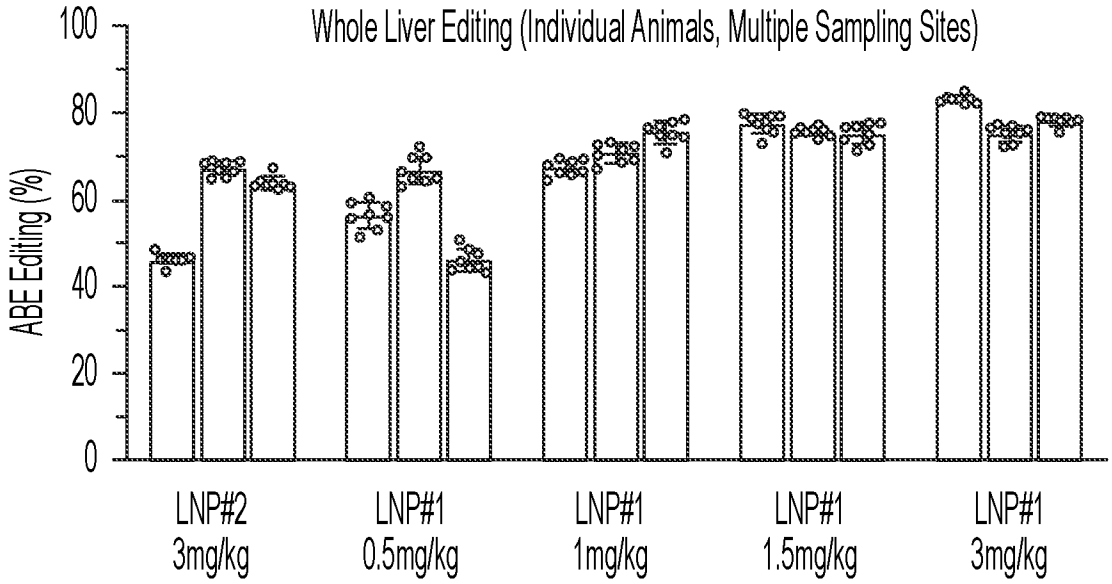

Whole Liver Editing (Individual Animals, Multiple Sampling Sites)
ABE Editing (%)
100
80
60
40
20
0
LNP#2
3mg/kg
LNP#1
0.5mg/kg
LNP#1
1mg/kg
LNP#1
1.5mg/kg
LNP#1
3mg/kg

FIG. 30

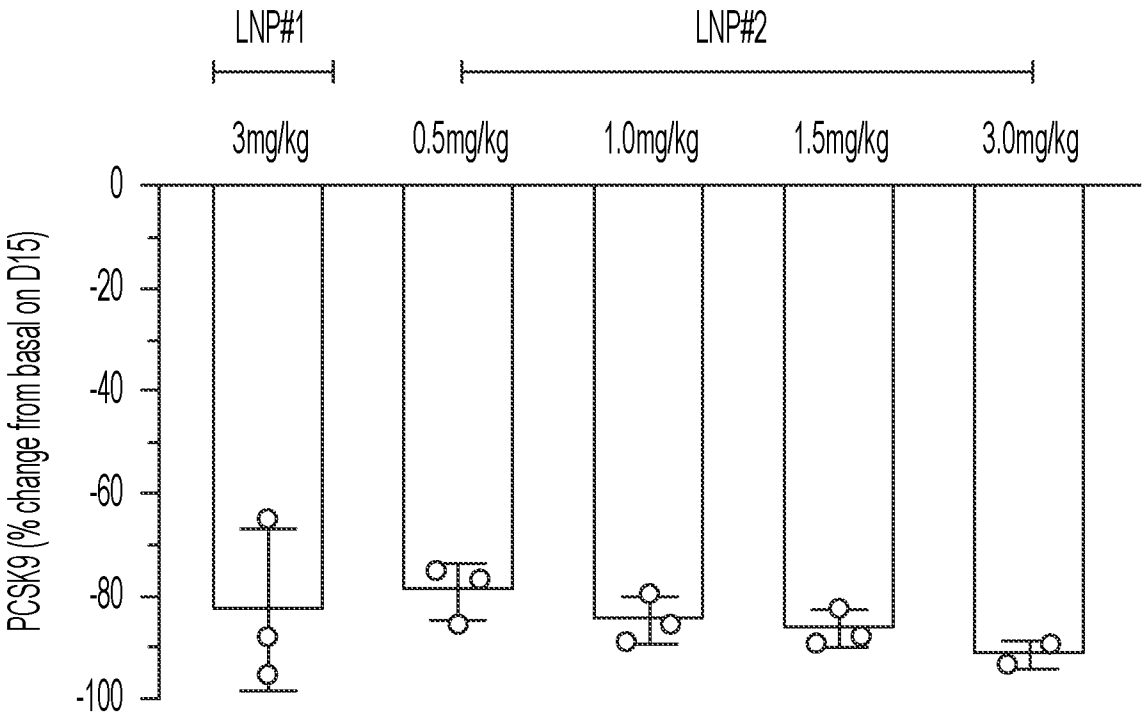

LNP#1
LNP#2
3mg/kg
0.5mg/kg
1.0mg/kg
1.5mg/kg
3.0mg/kg
PCSK9 (% change from basal on D15)
0
-20
-40
-60
-80
-100

FIG. 31

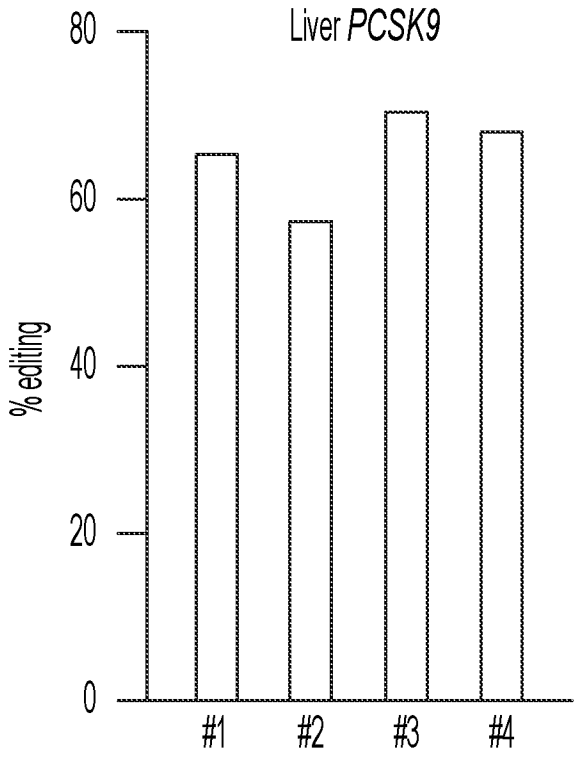

Liver PCSK9
% editing
80
60
40
20
0
#1
#2
#3
#4

FIG. 32

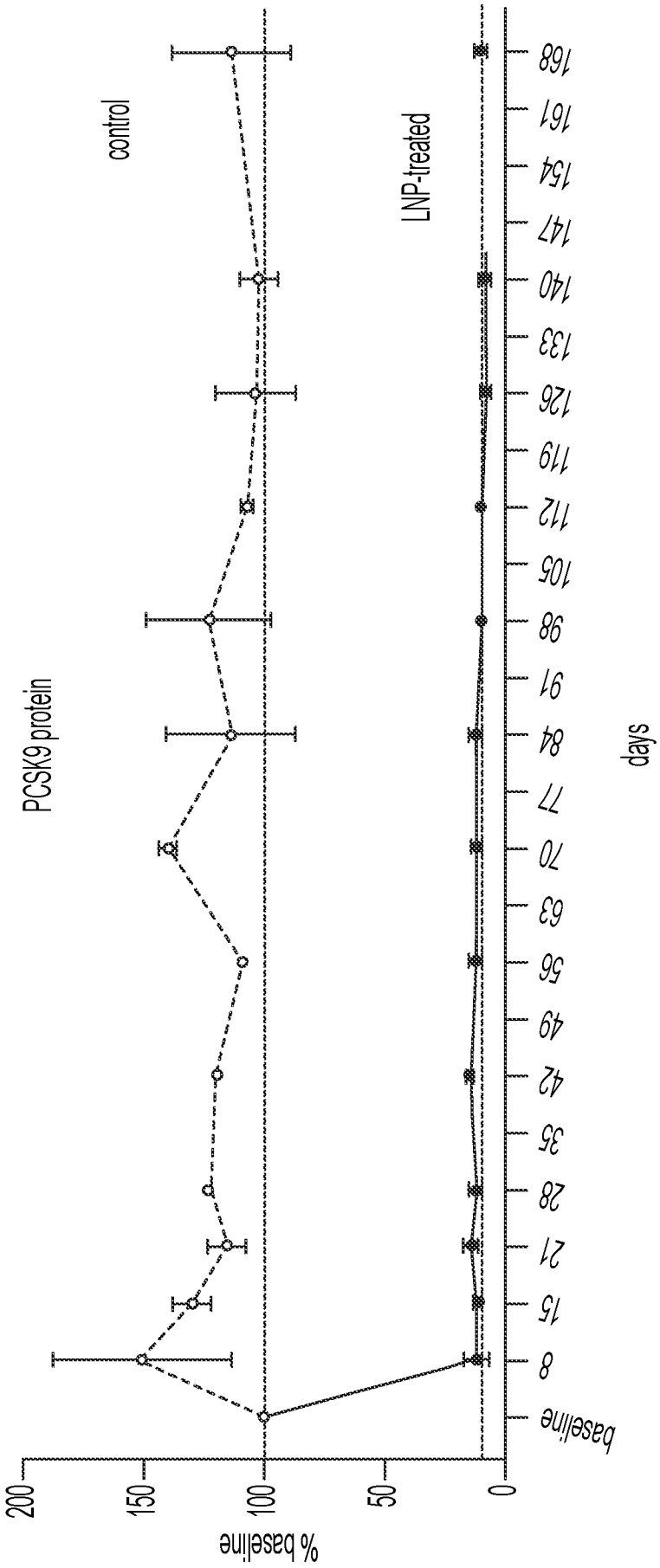

PCSK9 protein
% baseline
200
150
100
50
0
control
LNP-treated
baseline
8
15
21
28
35
42
49
56
63
70
77
84
91
98
105
112
119
126
133
140
147
154
161
168
days

FIG. 33

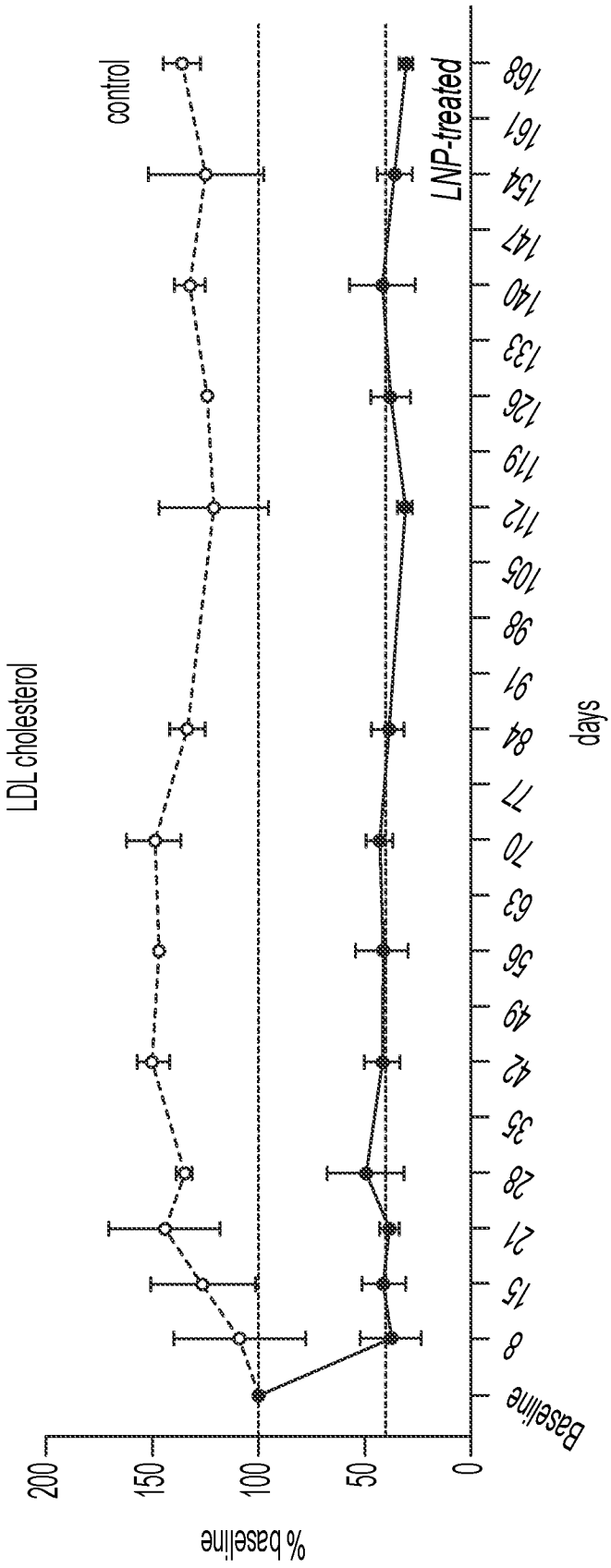

LDL cholesterol
% baseline
200
150
100
50
0
control
LNP-treated
Baseline
8
15
21
28
35
42
49
56
63
70
77
84
91
98
105
112
119
126
133
140
147
154
161
168
days

FIG. 34

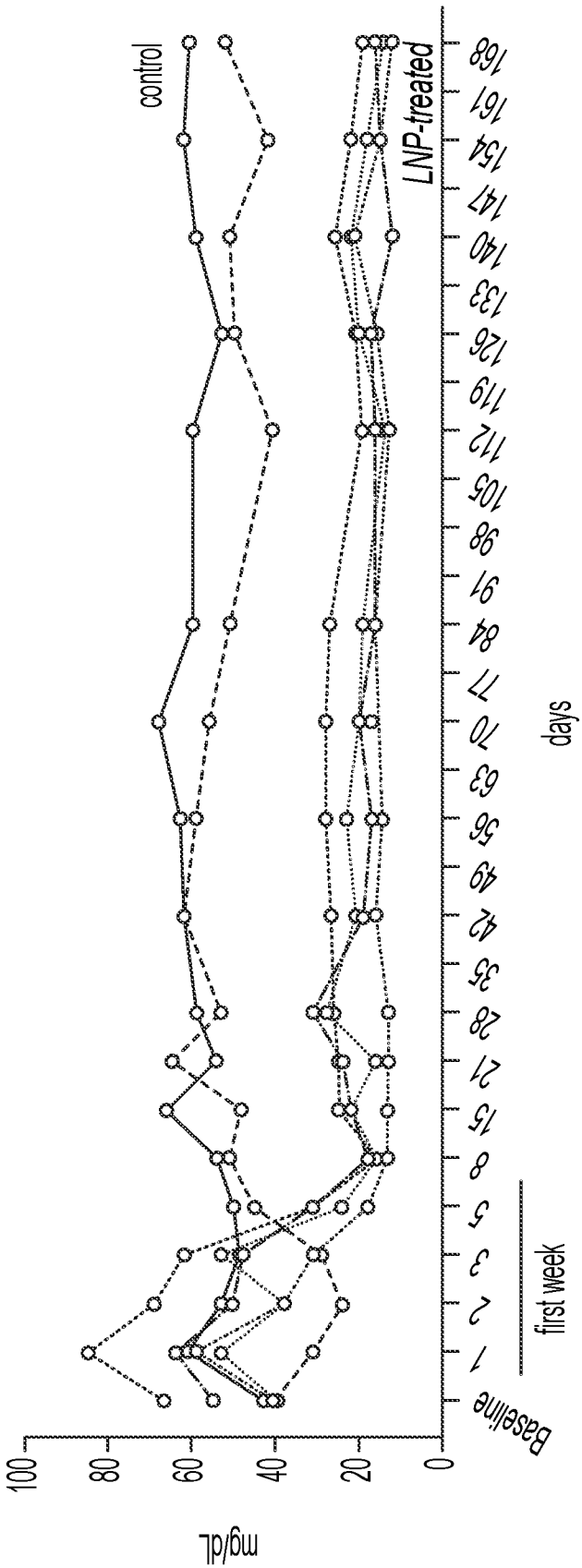


FIG. 34
(Continued)

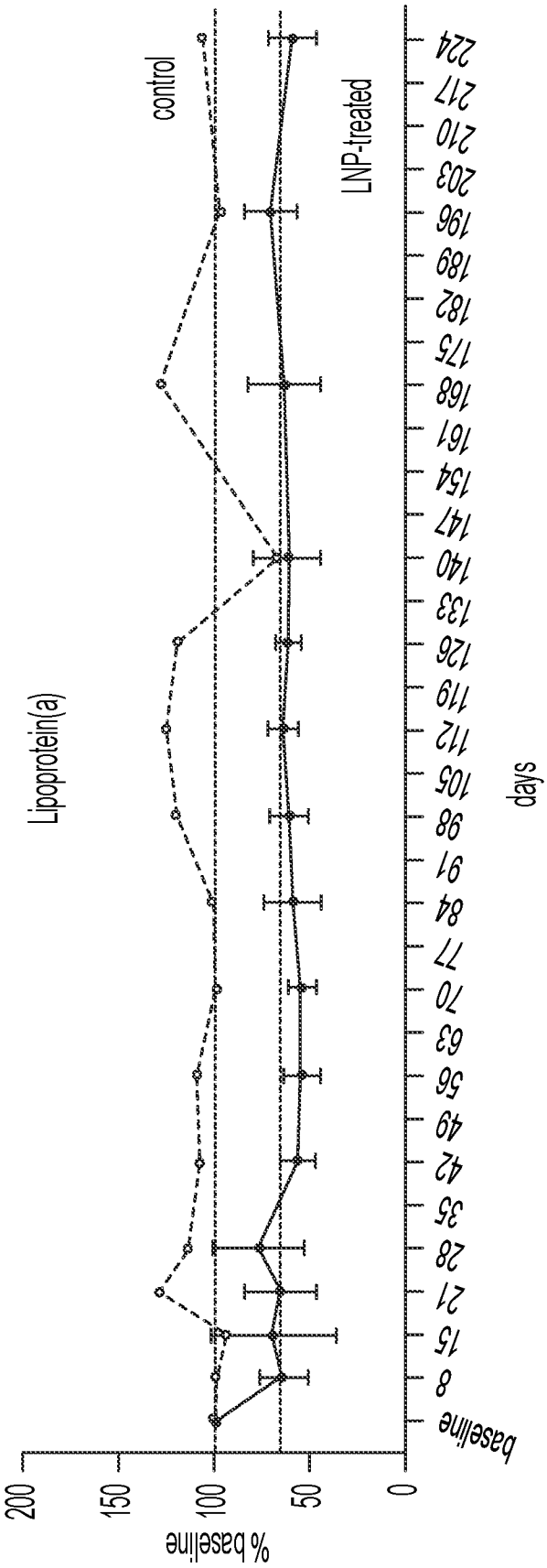

Lipoprotein(a)
% baseline
200
150
100
50
0
control
LNP-treated
baseline
8
15
21
28
35
42
49
56
63
70
77
84
91
98
105
112
119
126
133
140
147
154
161
168
175
182
189
196
203
210
217
224
days

FIG. 35

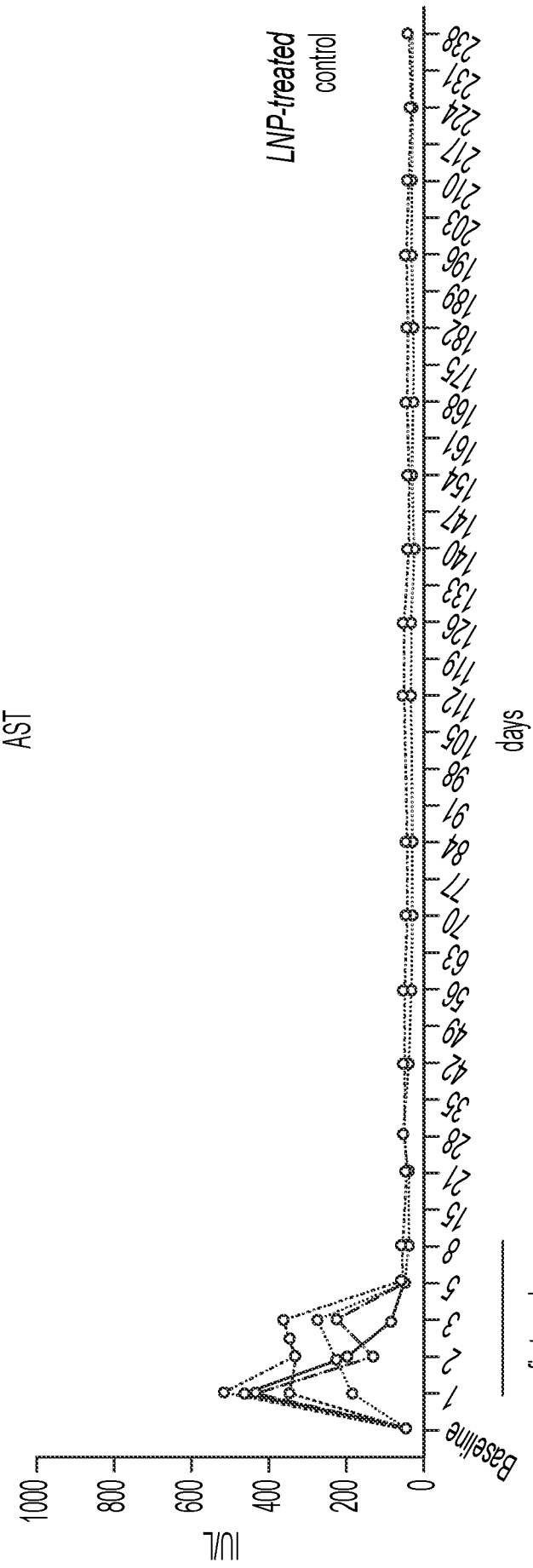

AST
IU/L
1000
800
600
400
200
0
Baseline
1
2
3
5
8
15
21
28
35
42
49
56
63
70
77
84
91
98
105
112
119
126
133
140
147
154
161
168
175
182
189
196
203
210
217
224
231
238
days
first week
LNP-treated
control

FIG. 36

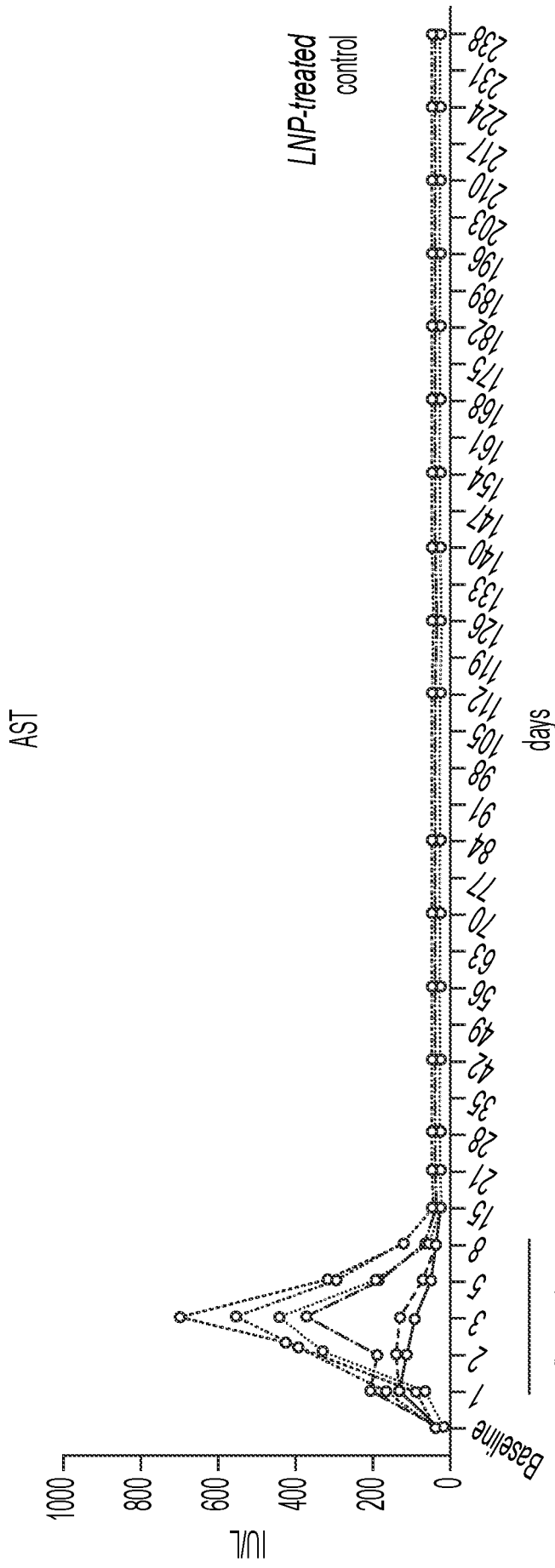


FIG. 36
(Continued)

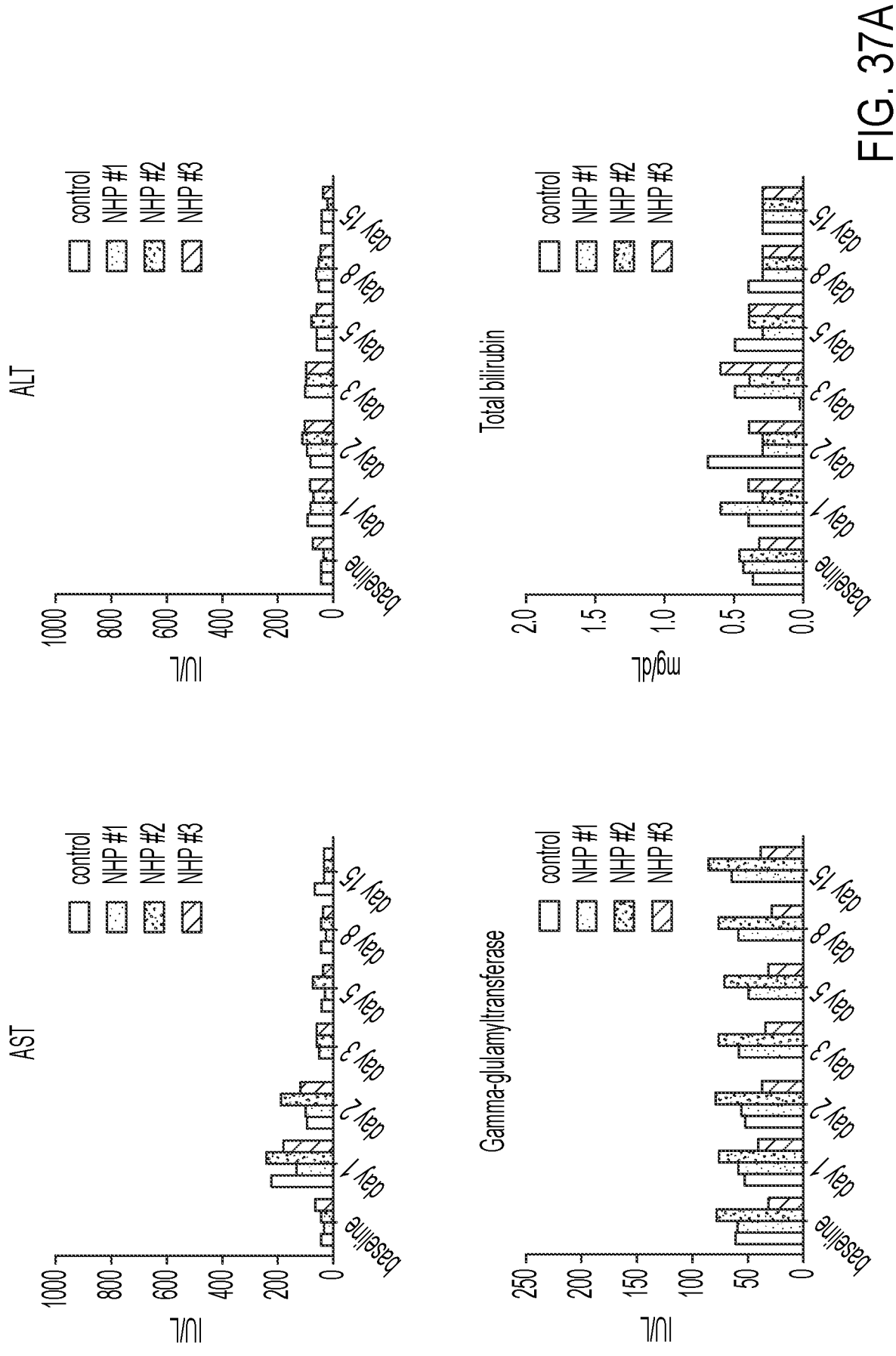

ALT
control
NHP #1
NHP #2
NHP #3
IU/L
1000
800
600
400
200
0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
Total bilirubin
mg/dL
2.0
1.5
1.0
0.5
0.0
AST
Gamma-glulamyltransferase
250
200
150
100
50

FIG. 37A

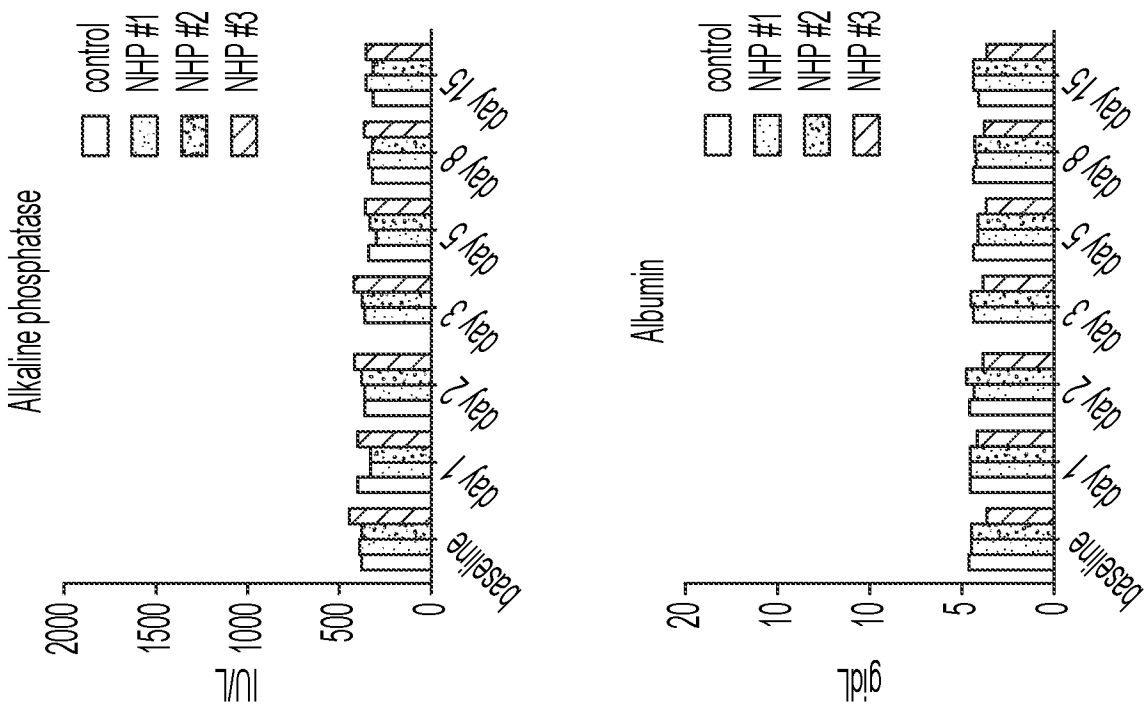


FIG. 37A
(Continued)

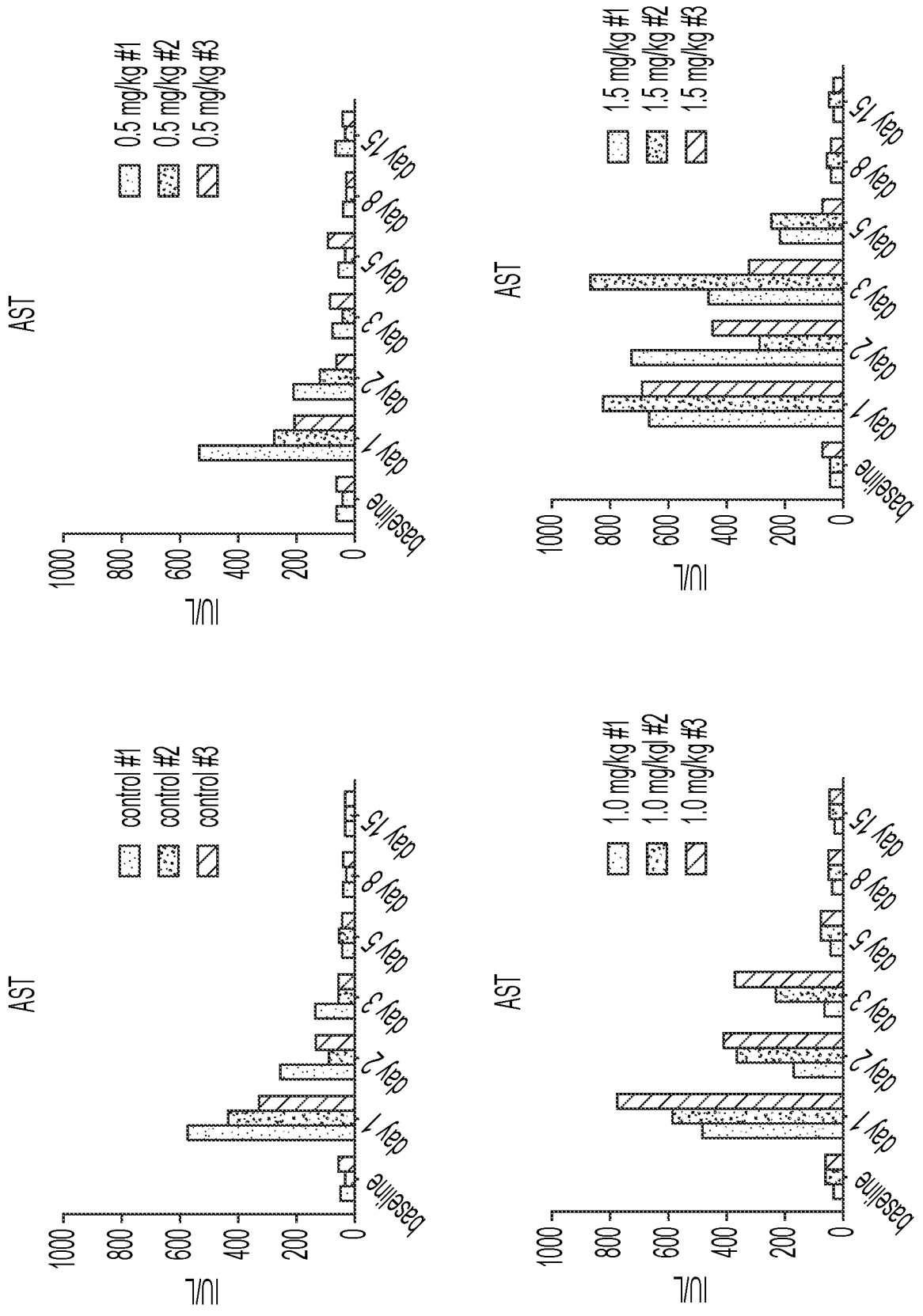

AST
IU/L
1000
800
600
400
200
0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
0.5 mg/kg #1
0.5 mg/kg #2
0.5 mg/kg #3
1.5 mg/kg #1
1.5 mg/kg #2
1.5 mg/kg #3
control #1
control #2
control #3
1.0 mg/kg #1
1.0 mg/kg #2
1.0 mg/kg #3

FIG. 37B

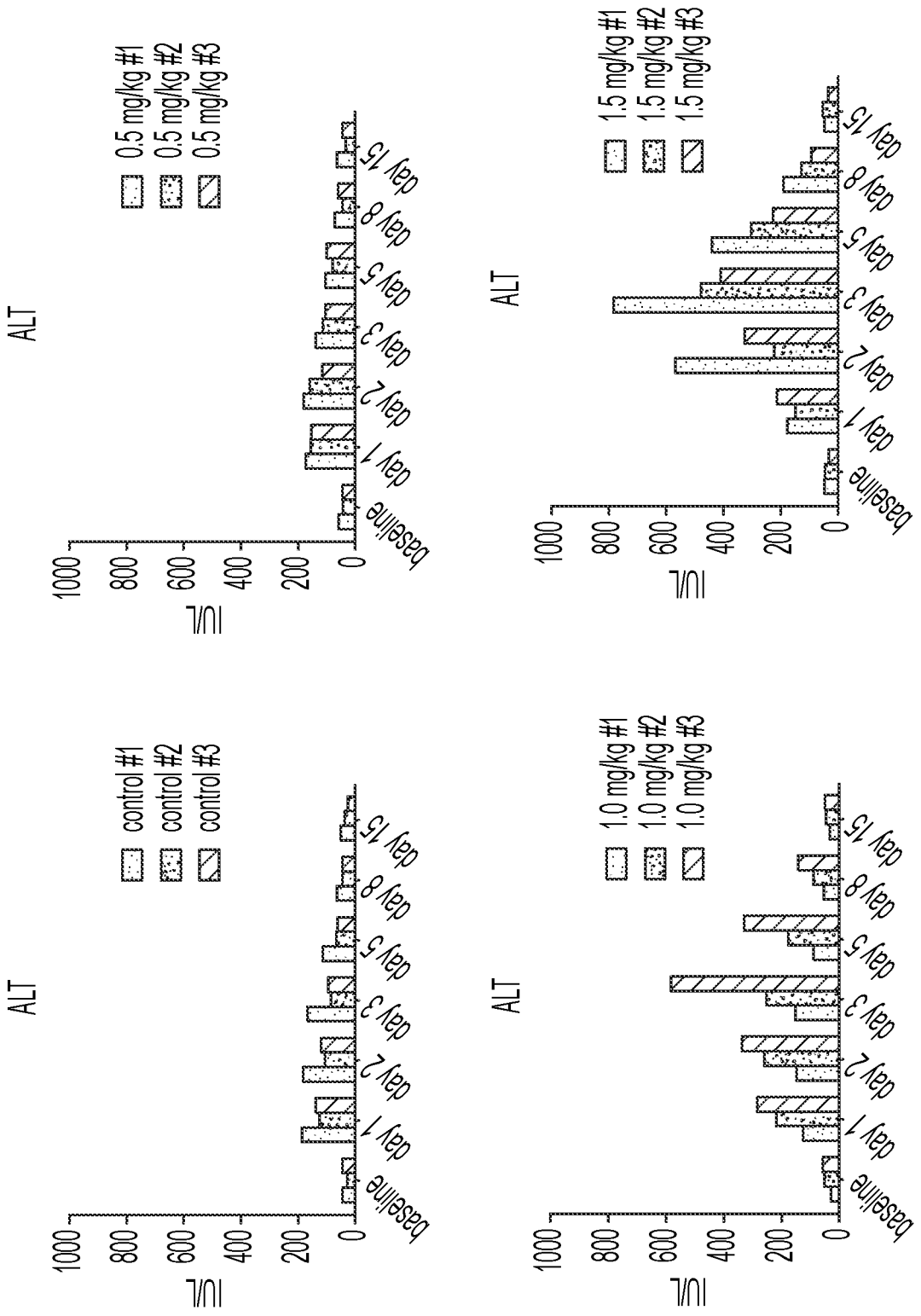

ALT
IU/L
1000
800
600
400
200
0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
control #1
control #2
control #3
0.5 mg/kg #1
0.5 mg/kg #2
0.5 mg/kg #3
1.0 mg/kg #1
1.0 mg/kg #2
1.0 mg/kg #3
1.5 mg/kg #1
1.5 mg/kg #2
1.5 mg/kg #3

FIG. 37C

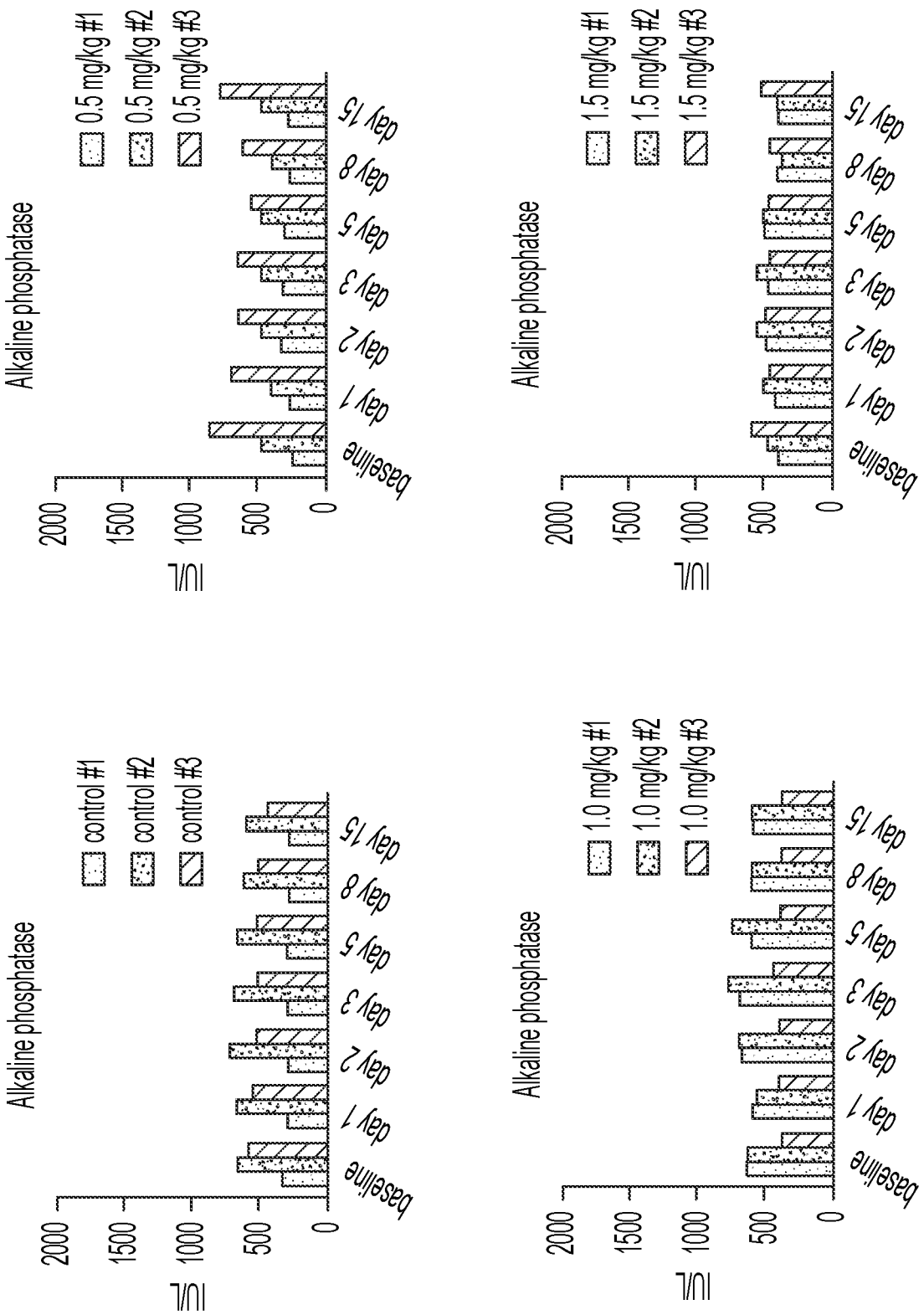

Alkaline phosphatase
IU/L
2000
1500
1000
500
0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
control #1
control #2
control #3
0.5 mg/kg #1
0.5 mg/kg #2
0.5 mg/kg #3
1.5 mg/kg #1
1.5 mg/kg #2
1.5 mg/kg #3
1.0 mg/kg #1
1.0 mg/kg #2
1.0 mg/kg #3

FIG. 37D

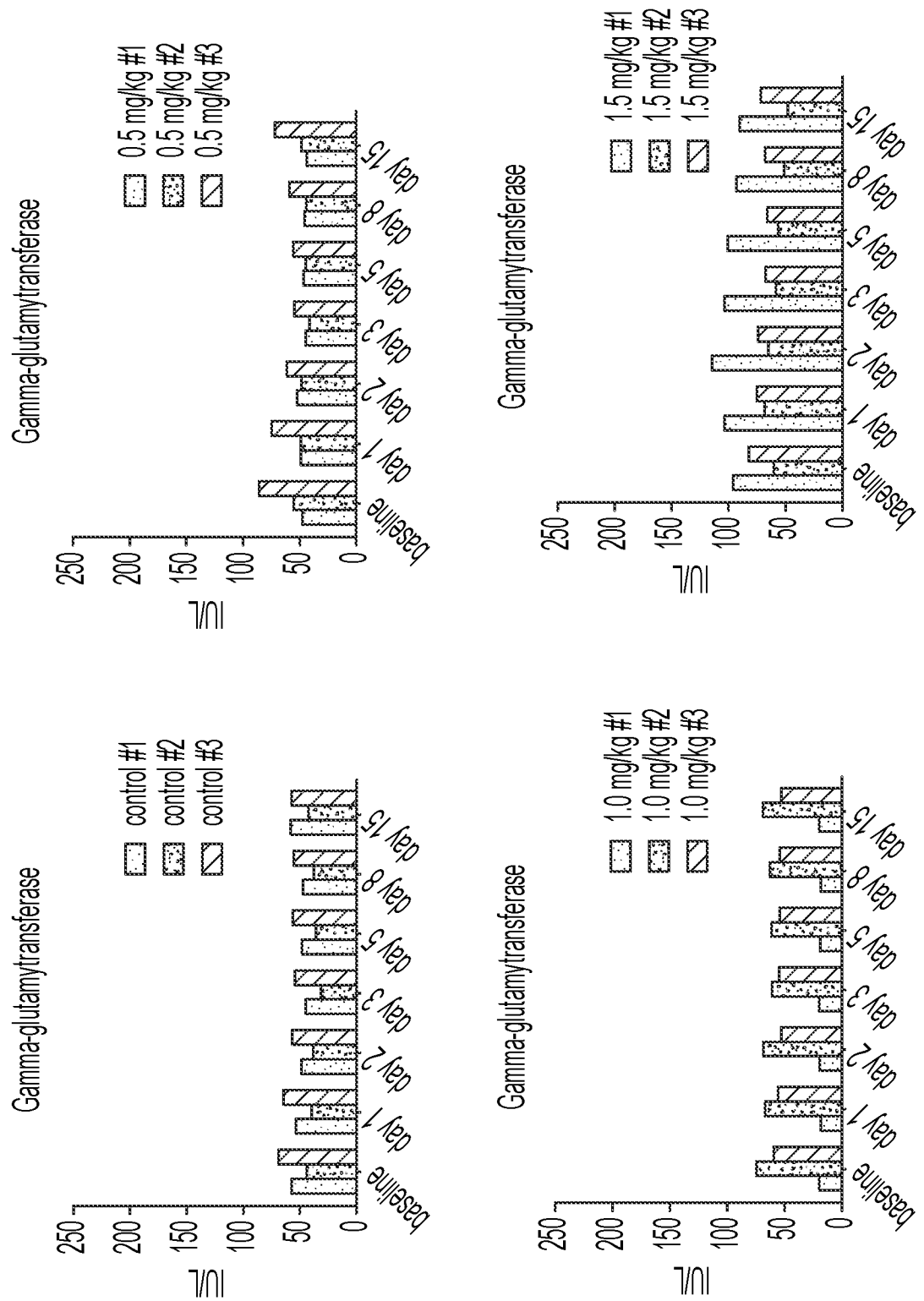

Gamma-glutamytransferase
IU/L
250
200
150
100
50
0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
0.5 mg/kg #1
0.5 mg/kg #2
0.5 mg/kg #3
1.5 mg/kg #1
1.5 mg/kg #2
1.5 mg/kg #3
control #1
control #2
control #3
1.0 mg/kg #1
1.0 mg/kg #2
1.0 mg/kg #3

FIG. 37E

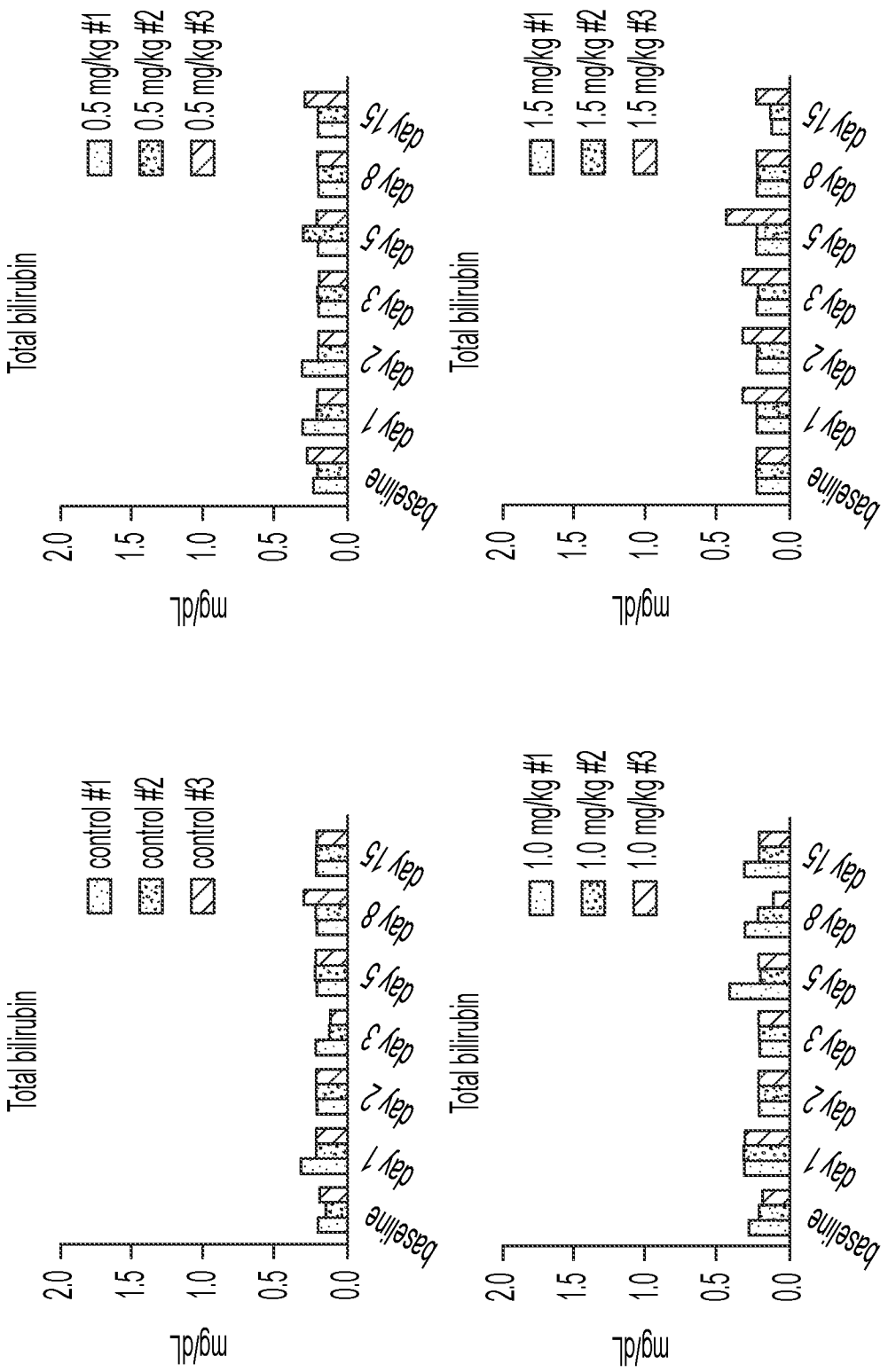

Total bilirubin
0.5 mg/kg #1
0.5 mg/kg #2
0.5 mg/kg #3
mg/dL
2.0
1.5
1.0
0.5
0.0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
Total bilirubin
1.5 mg/kg #1
1.5 mg/kg #2
1.5 mg/kg #3
mg/dL
Total bilirubin
control #1
control #2
control #3
mg/dL
Total bilirubin
1.0 mg/kg #1
1.0 mg/kg #2
1.0 mg/kg #3
mg/dL

FIG. 37F

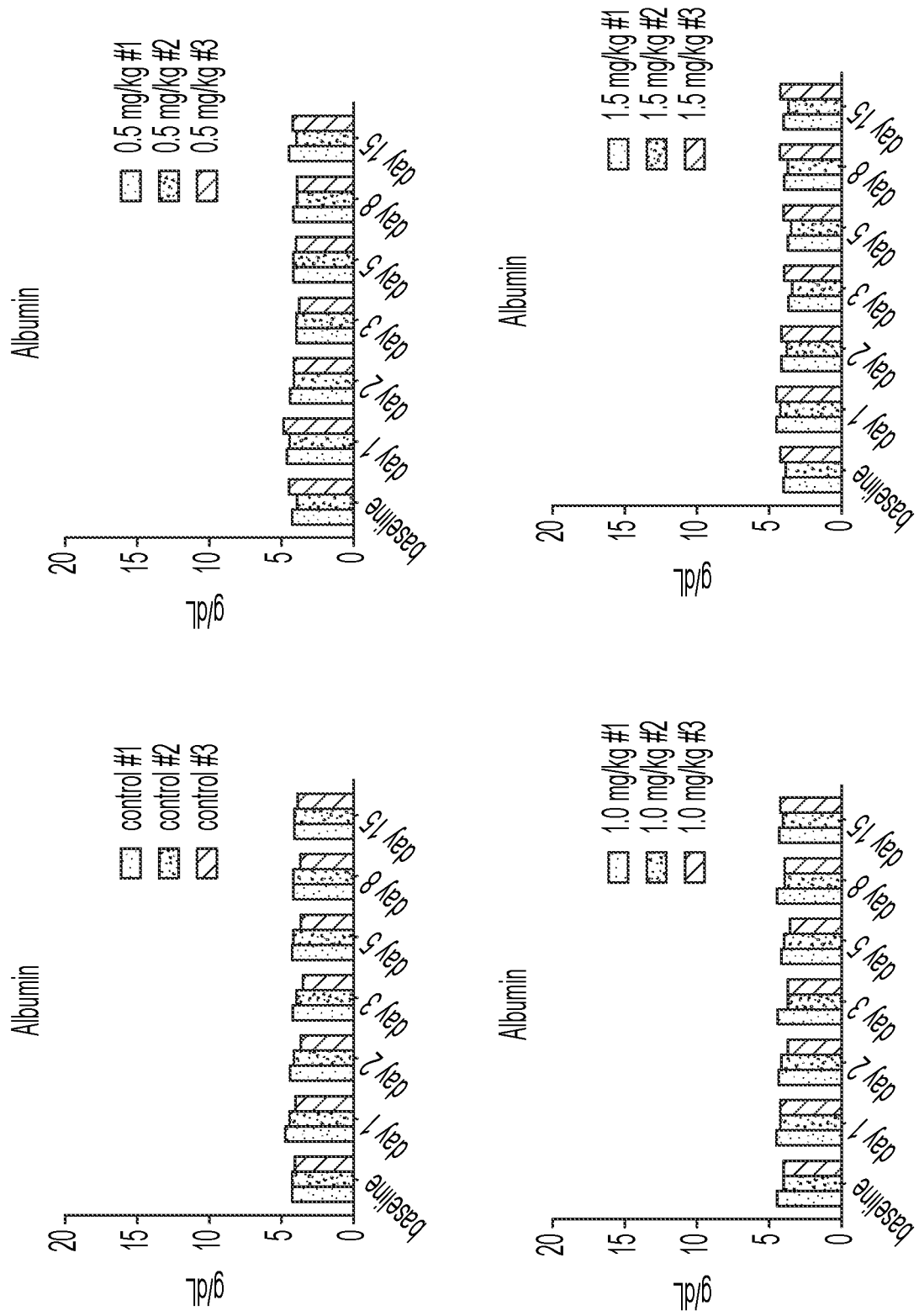

Albumin
g/dL
20
15
10
5
0
baseline
day 1
day 2
day 3
day 5
day 8
day 15
control #1
control #2
control #3
0.5 mg/kg #1
0.5 mg/kg #2
0.5 mg/kg #3
1.0 mg/kg #1
1.0 mg/kg #2
1.0 mg/kg #3
1.5 mg/kg #1
1.5 mg/kg #2
1.5 mg/kg #3

FIG. 37G

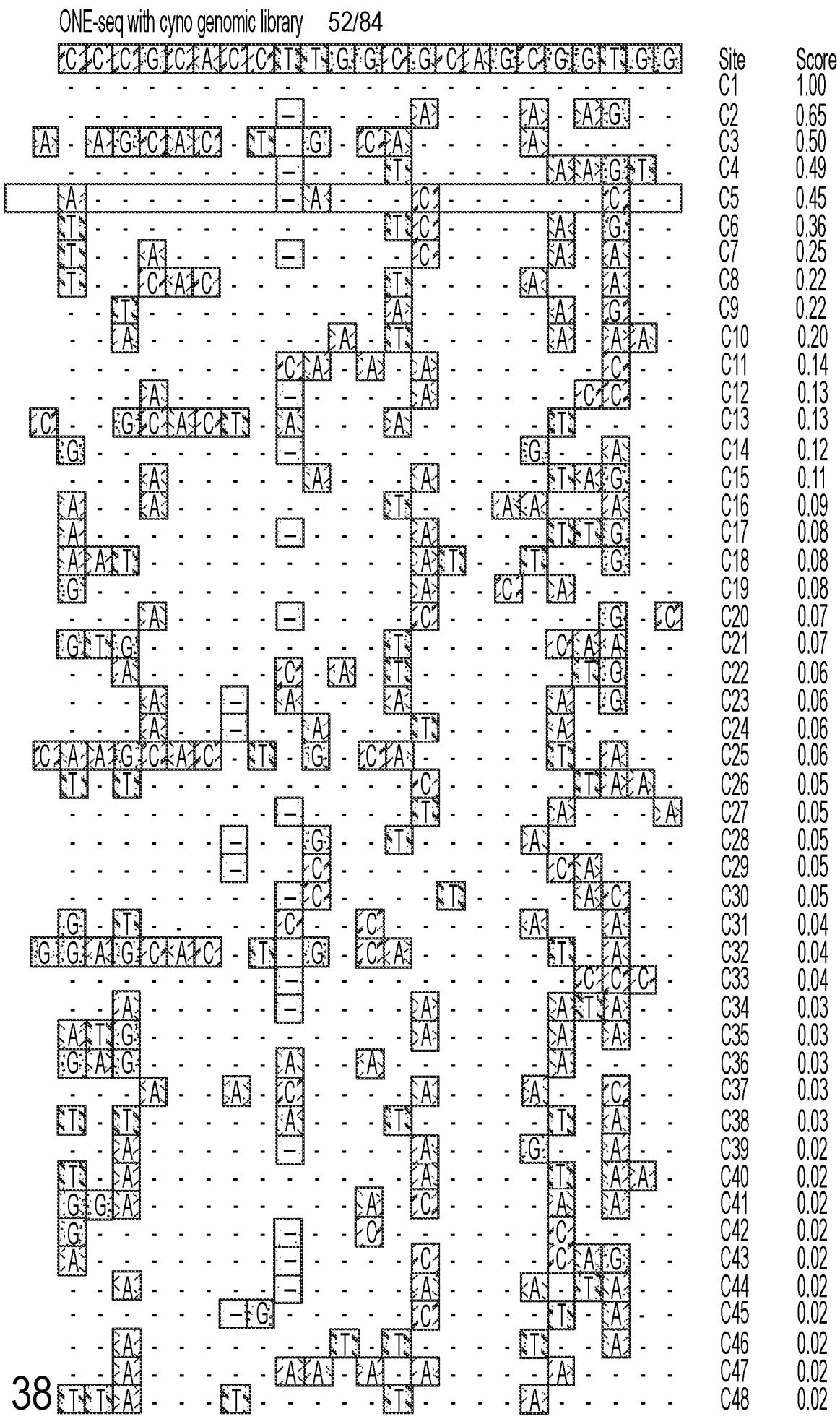

ONE-seq with cyno genomic library 52/84
Site
Score
C1 1.00
C2 0.65
C3 0.50
C4 0.49
C5 0.45
C6 0.36
C7 0.25
C8 0.22
C9 0.22
C10 0.20
C11 0.14
C12 0.13
C13 0.13
C14 0.12
C15 0.11
C16 0.09
C17 0.08
C18 0.08
C19 0.08
C20 0.07
C21 0.07
C22 0.06
C23 0.06
C24 0.06
C25 0.06
C26 0.05
C27 0.05
C28 0.05
C29 0.05
C30 0.05
C31 0.04
C32 0.04
C33 0.04
C34 0.03
C35 0.03
C36 0.03
C37 0.03
C38 0.03
C39 0.02
C40 0.02
C41 0.02
C42 0.02
C43 0.02
C44 0.02
C45 0.02
C46 0.02
C47 0.02
C48 0.02

FIG. 38

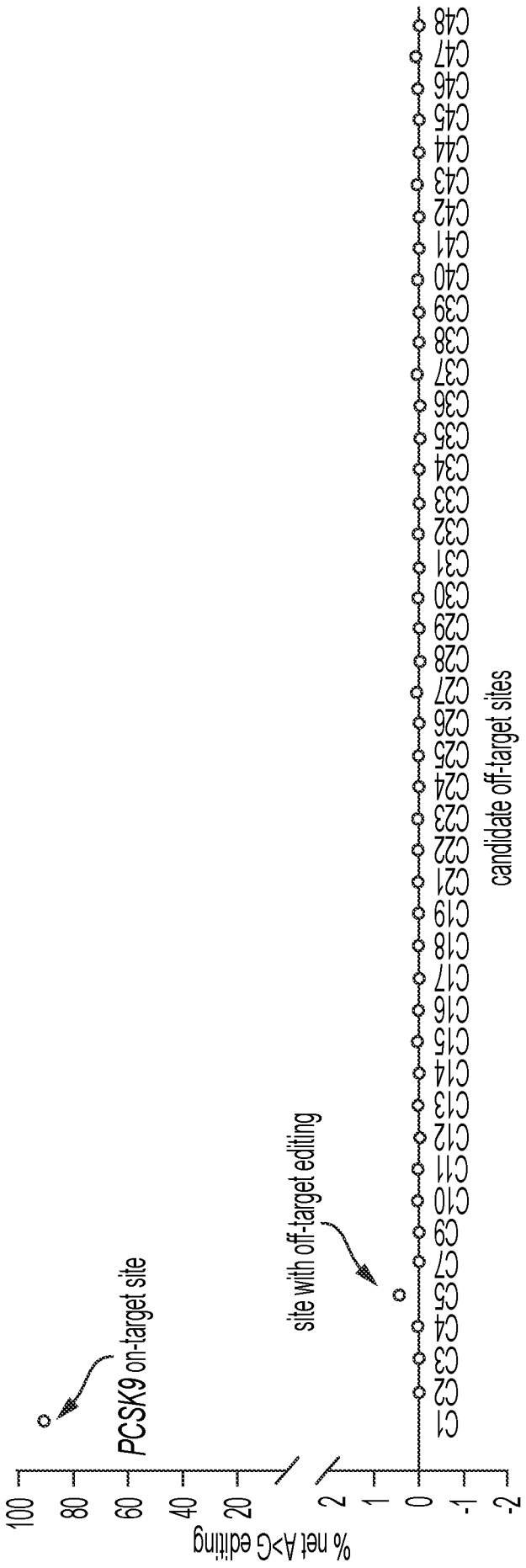

Primary cyno hepatocytes - 3 treated samples, 3 untreated samples
PCSK9 on-target site
site with off-target editing
% net A>G editing
100
80
60
40
20
2
1
0
-1
-2
candidate off-target sites
C1 C2 C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 C13 C14 C15 C16 C17 C18 C19 C21 C22 C23 C24 C25 C26 C27 C28 C29 C30 C31 C32 C33 C34 C35 C36 C37 C38 C39 C40 C41 C42 C43 C44 C45 C46 C47 C48

FIG. 39

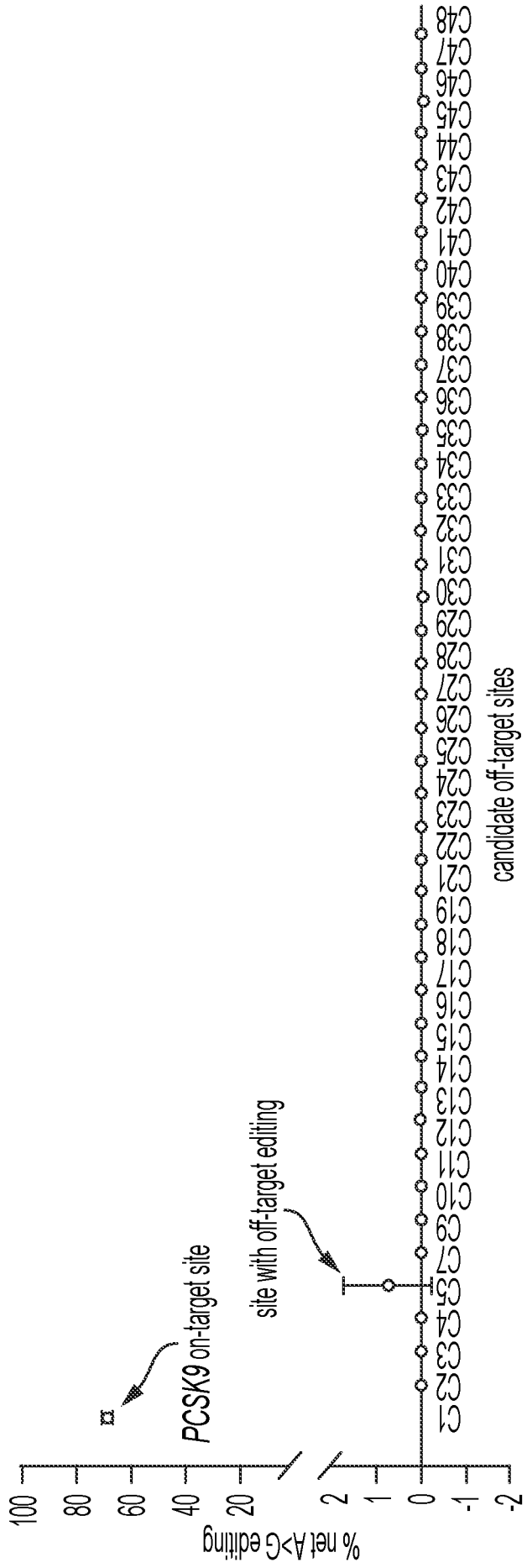


FIG. 39
(Continued)

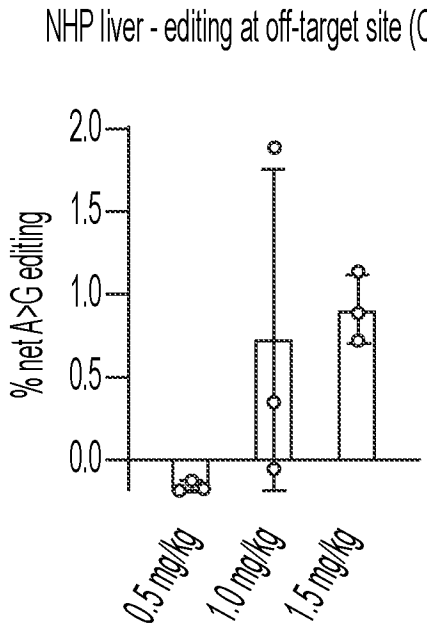

NHP liver - editing at off-target site (C5)
% net A>G editing
2.0
1.5
1.0
0.5
0.0
0.5 mg/kg
1.0 mg/kg
1.5 mg/kg

FIG. 40

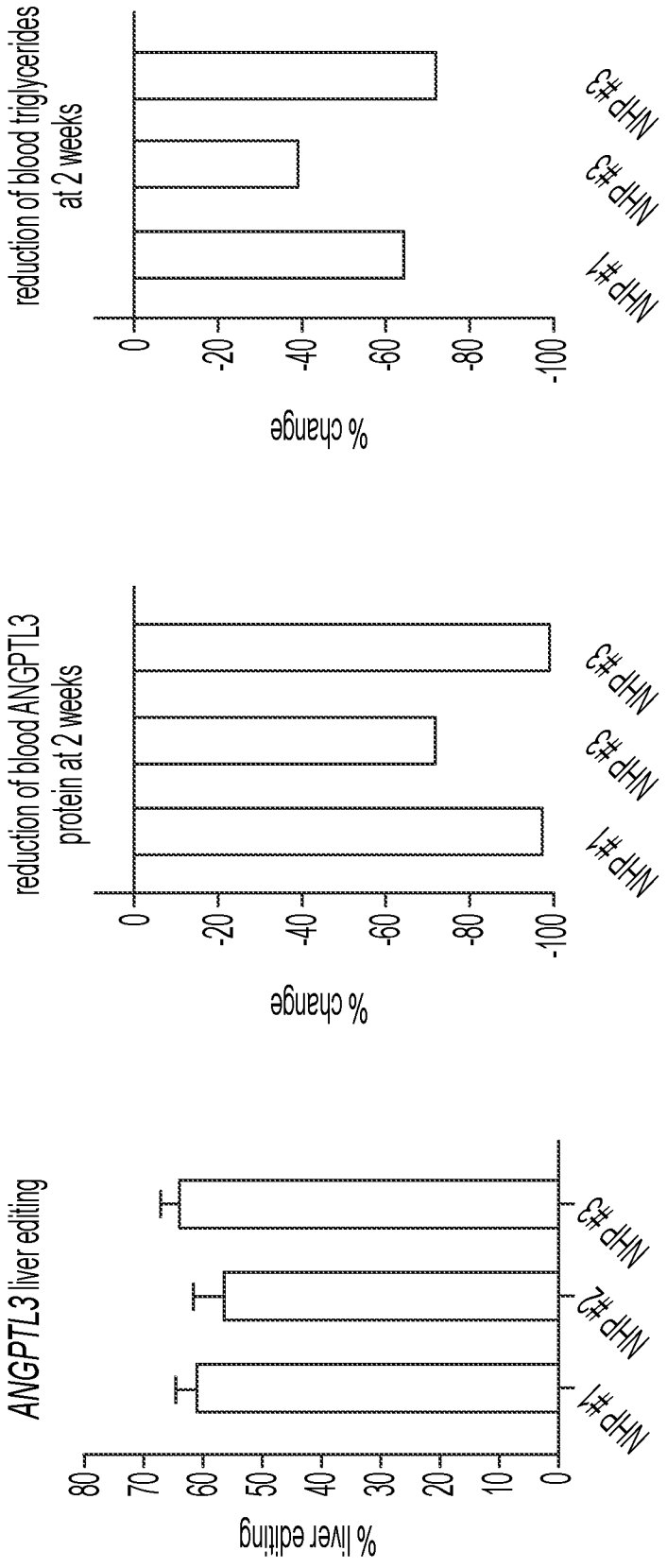

reduction of blood triglycerides at 2 weeks
% change
0
-20
-40
-60
-80
-100
NHP #1
NHP #3
NHP #3
reduction of blood ANGPTL3 protein at 2 weeks
% change
0
-20
-40
-60
-80
-100
NHP #1
NHP #3
NHP #3
ANGPTL3 liver editing
% liver editing
0
10
20
30
40
50
60
70
80
NHP #1
NHP #2
NHP #3

FIG. 41

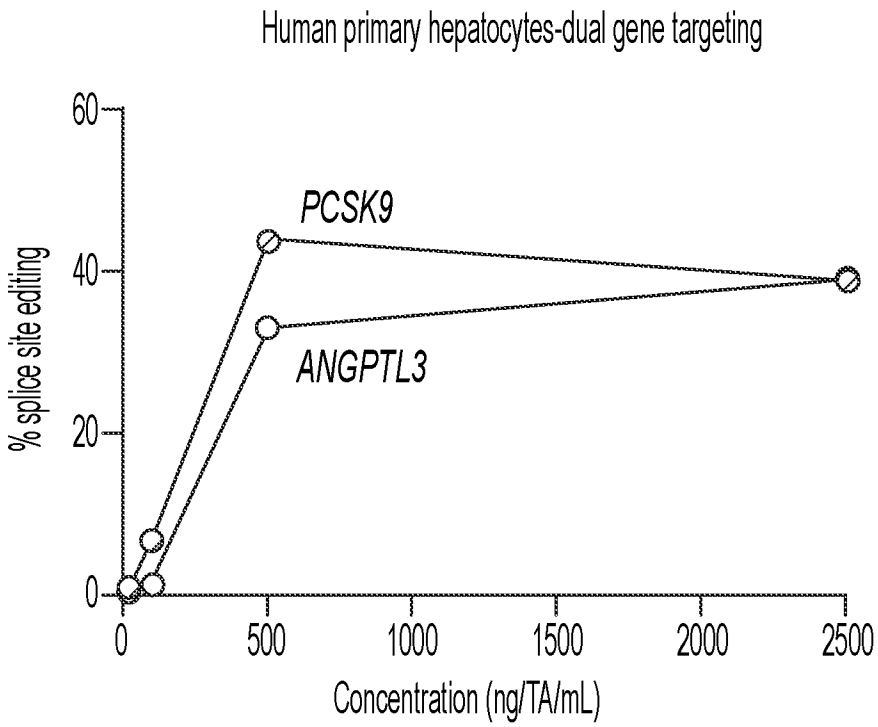

Human primary hepatocytes-dual gene targeting
% splice site editing
60
40
20
0
PCSK9
ANGPTL3
0
500
1000
1500
2000
2500
Concentration (ng/TA/mL)

FIG. 42

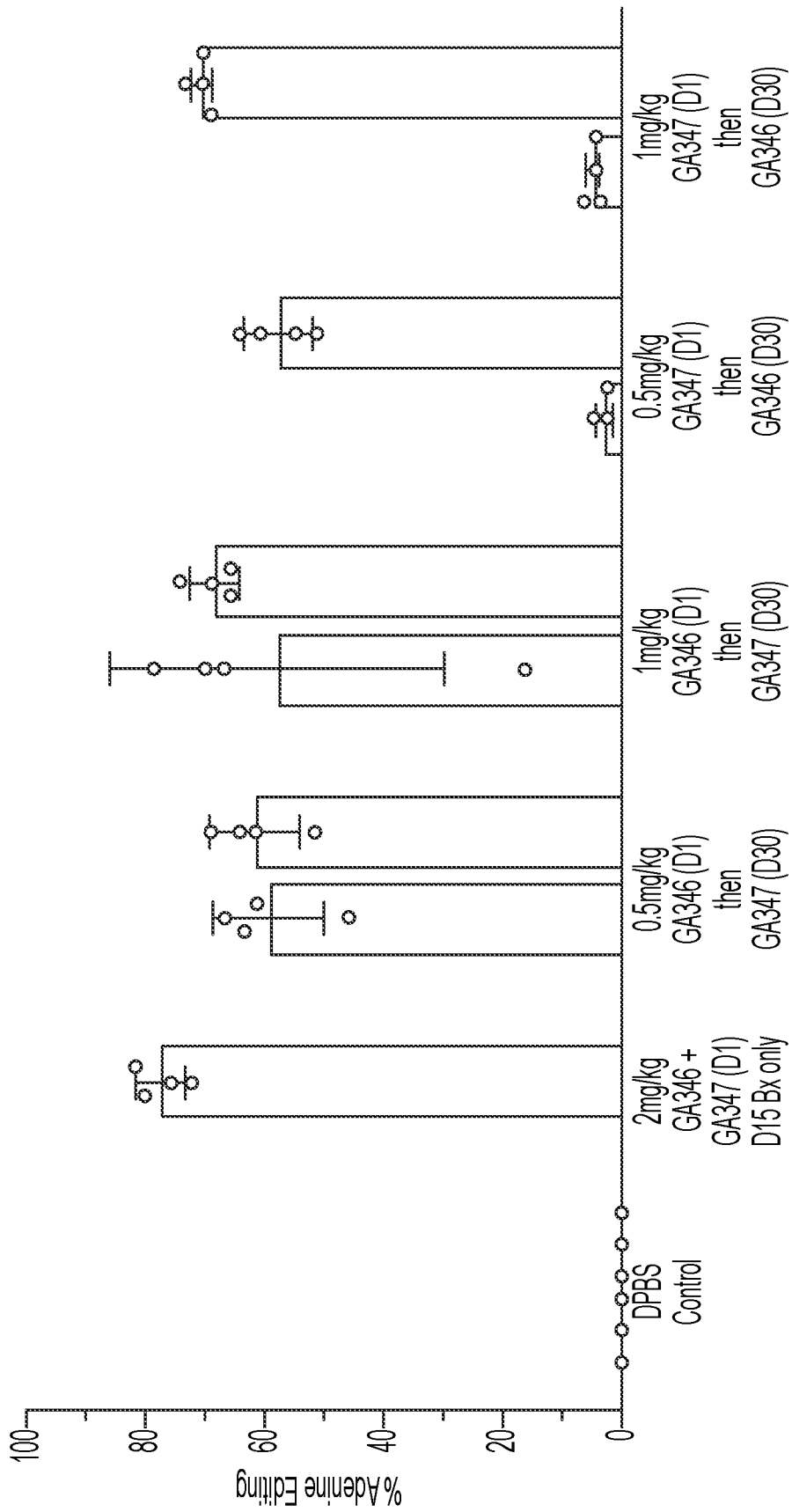

PCSK9 (GA346)
Day 15 & D44 Liver Biopsy
% Adenine Editing
100
80
60
40
20
0
DPBS
Control
2mg/kg
GA346 +
GA347 (D1)
D15 Bx only
0.5mg/kg
GA346 (D1)
then
GA347 (D30)
1mg/kg
GA346 (D1)
then
GA347 (D30)
0.5mg/kg
GA347 (D1)
then
GA346 (D30)
1mg/kg
GA347 (D1)
then
GA346 (D30)

FIG. 43

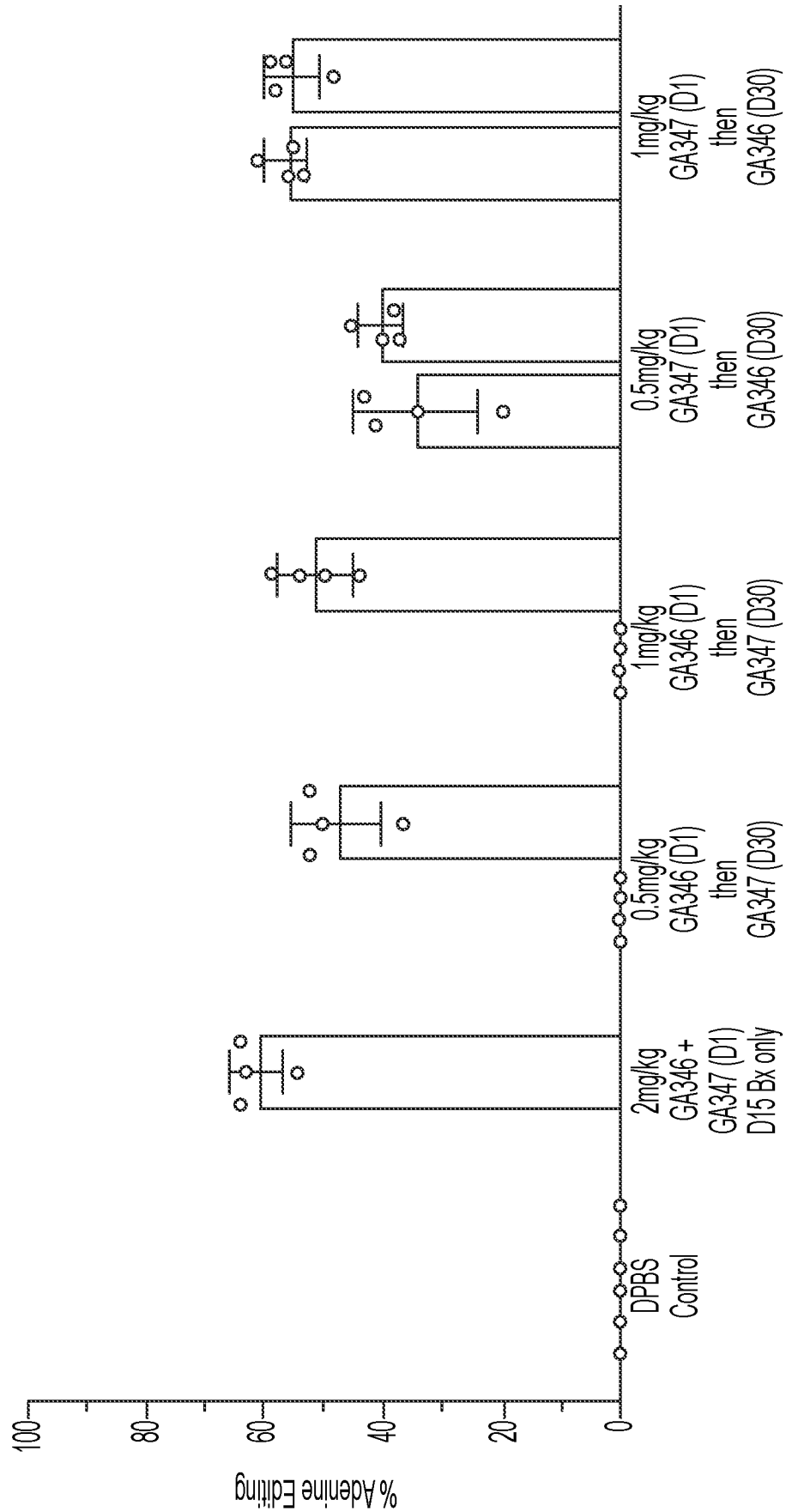


FIG. 43
(Continued)

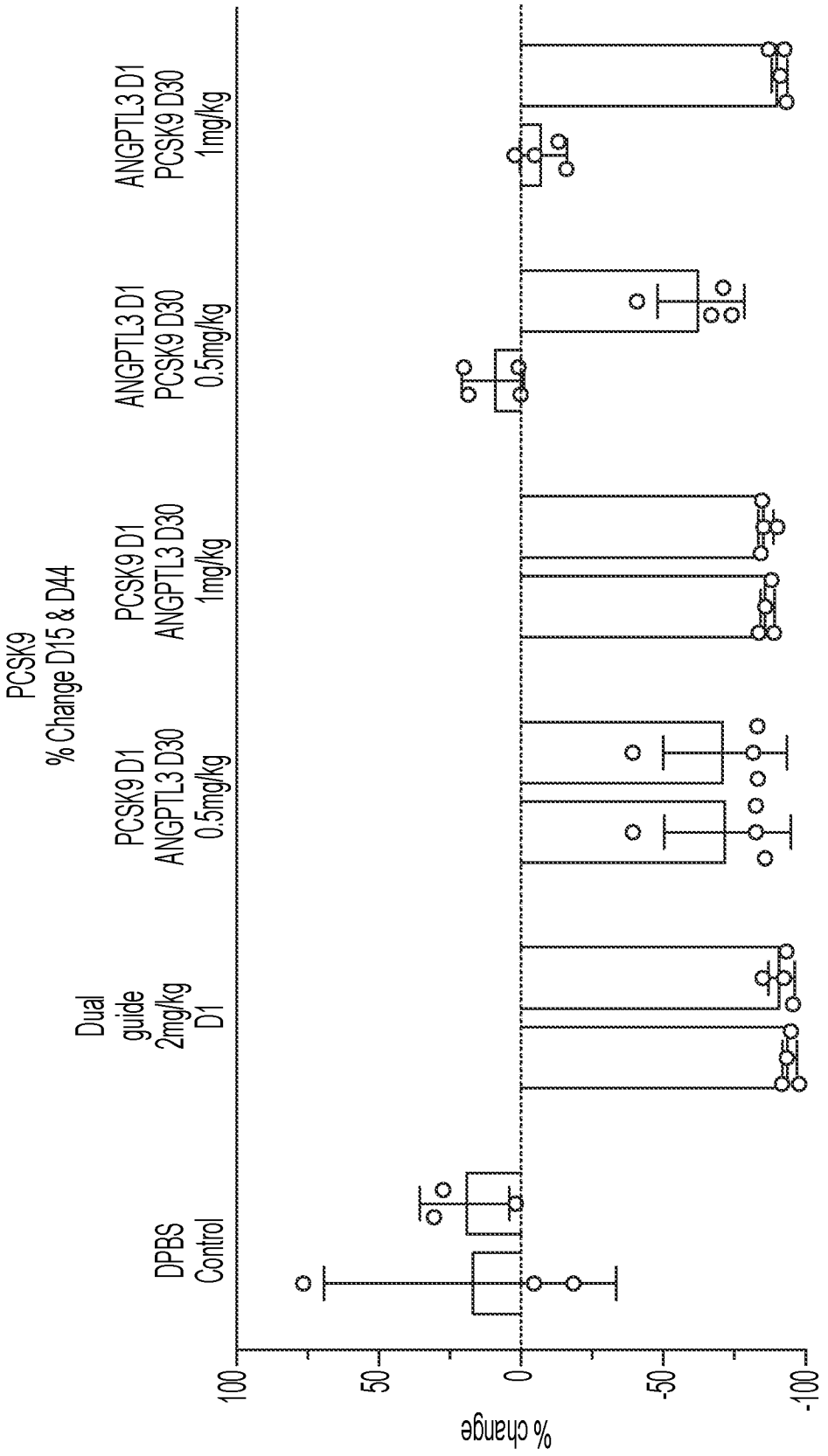

PCSK9
% Change D15 & D44
% change
100
50
0
-50
-100
DPBS Control
Dual guide 2mg/kg D1
PCSK9 D1 ANGPTL3 D30 0.5mg/kg
PCSK9 D1 ANGPTL3 D30 1mg/kg
ANGPTL3 D1 PCSK9 D30 0.5mg/kg
ANGPTL3 D1 PCSK9 D30 1mg/kg

FIG. 44

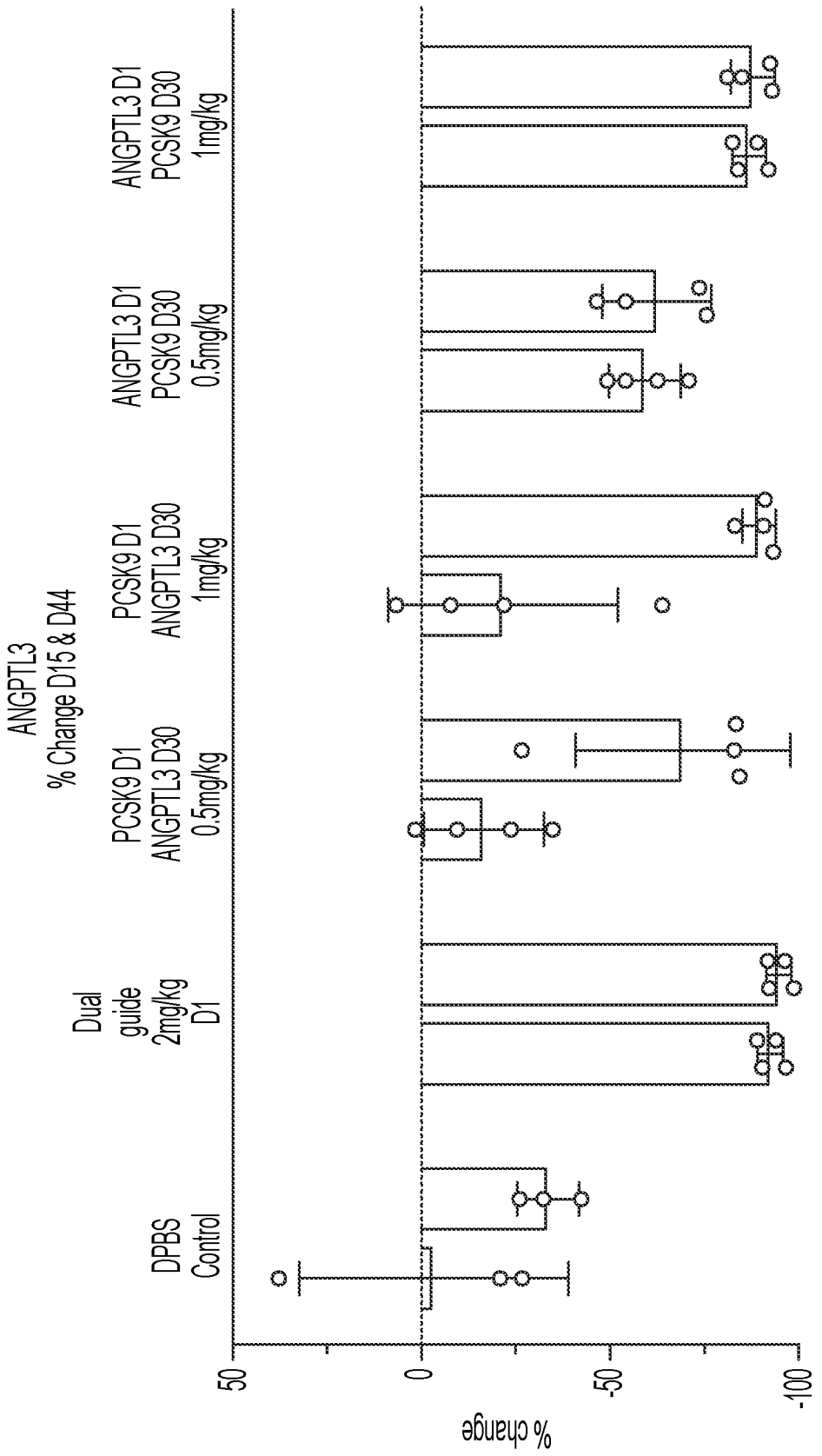


FIG. 44
(Continued)

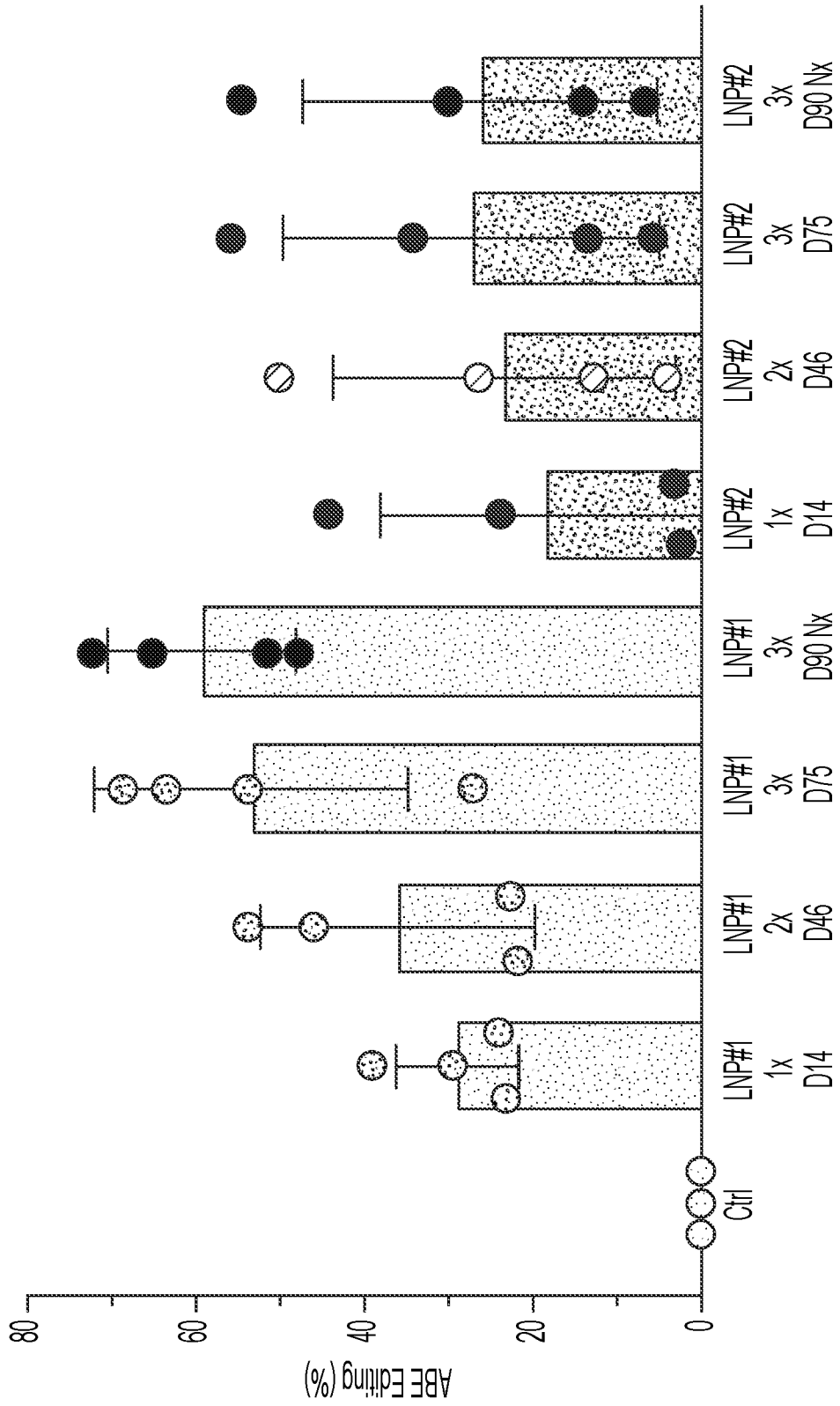

ABE Editing (%)
0
20
40
60
80
Ctrl
LNP#1 1x D14
LNP#1 2x D46
LNP#1 3x D75
LNP#1 3x D90 Nx
LNP#2 1x D14
LNP#2 2x D46
LNP#2 3x D75
LNP#2 3x D90 Nx

FIG. 45

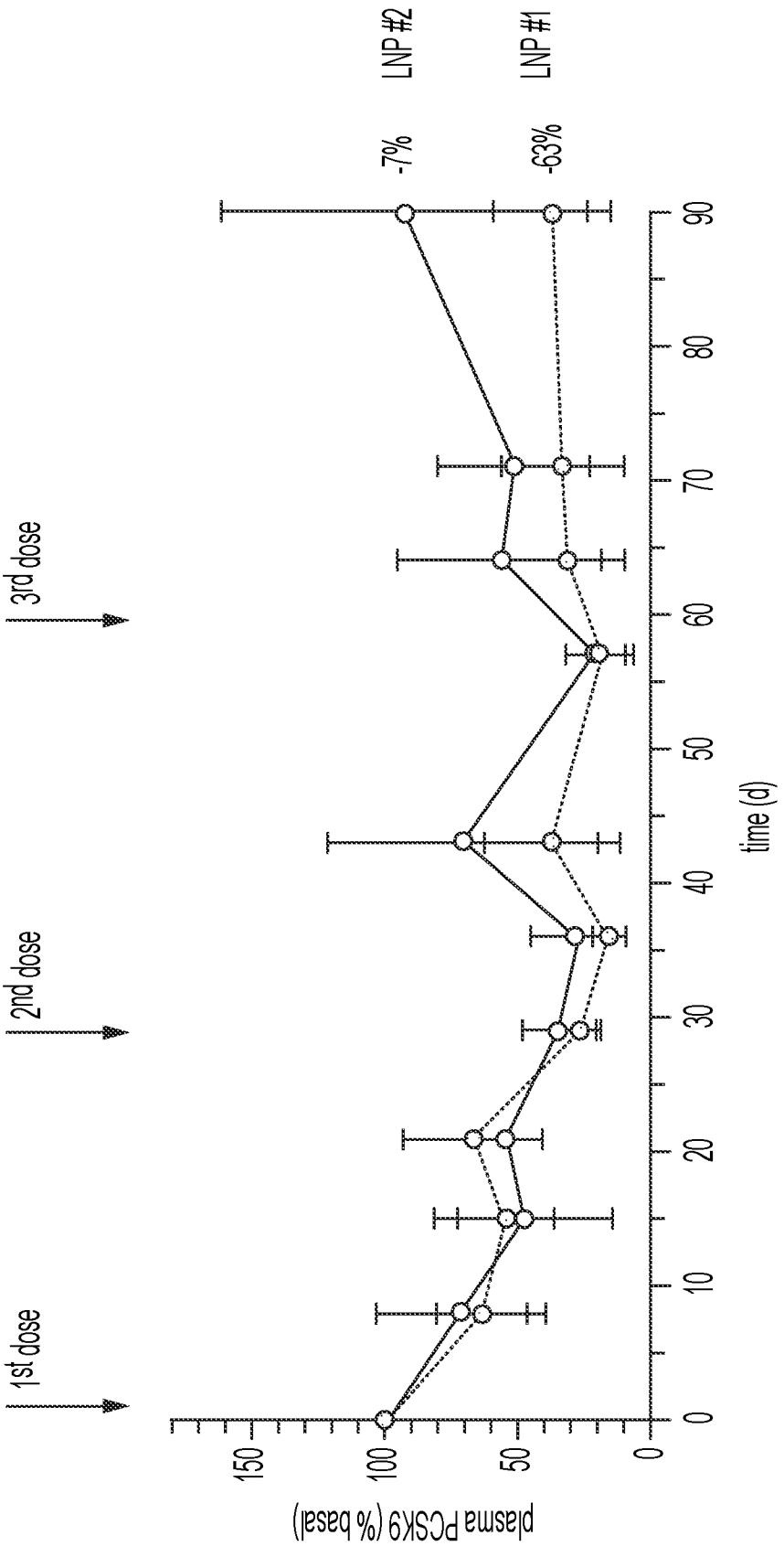

LNP #2
LNP #1
-7%
-63%
1st dose
2nd dose
3rd dose
plasma PCSK9 (% basal)
time (d)
0
50
100
150
0
10
20
30
40
50
60
70
80
90

FIG. 46

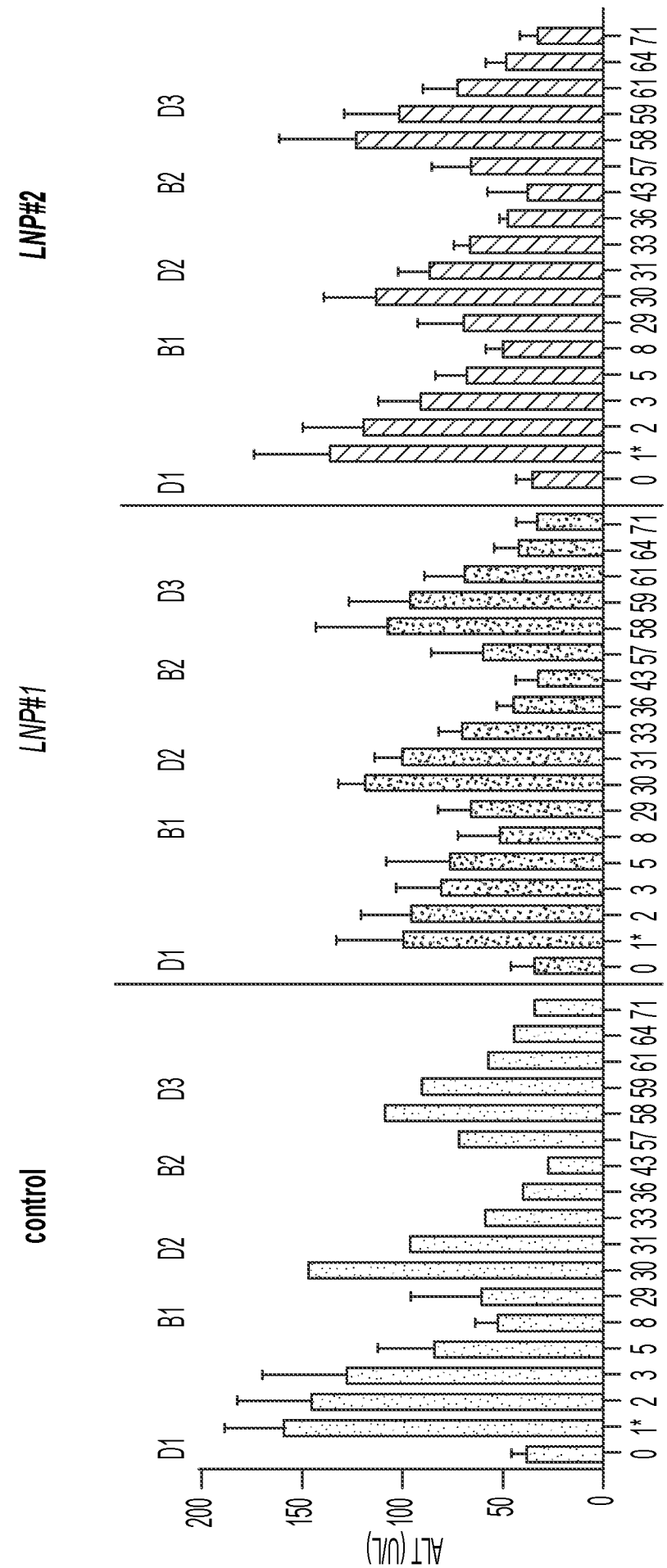

control
LNP#1
LNP#2
ALT (U/L)
200
150
100
50
0
time (d)
D1
B1
D2
B2
D3
0 1* 2 3 5 8 29 30 31 33 36 43 57 58 59 61 64 71

FIG. 47



FIG. 47
(Continued)

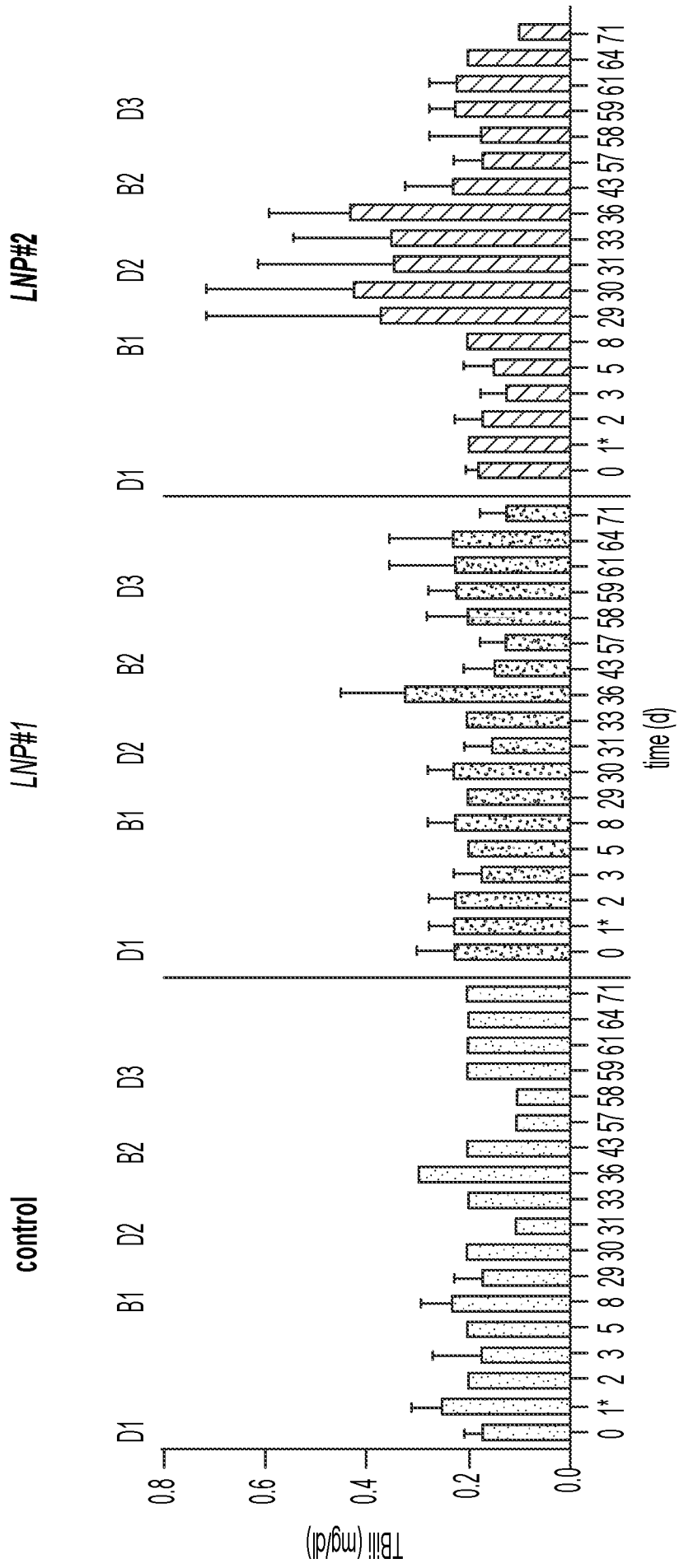


FIG. 47
(Continued)

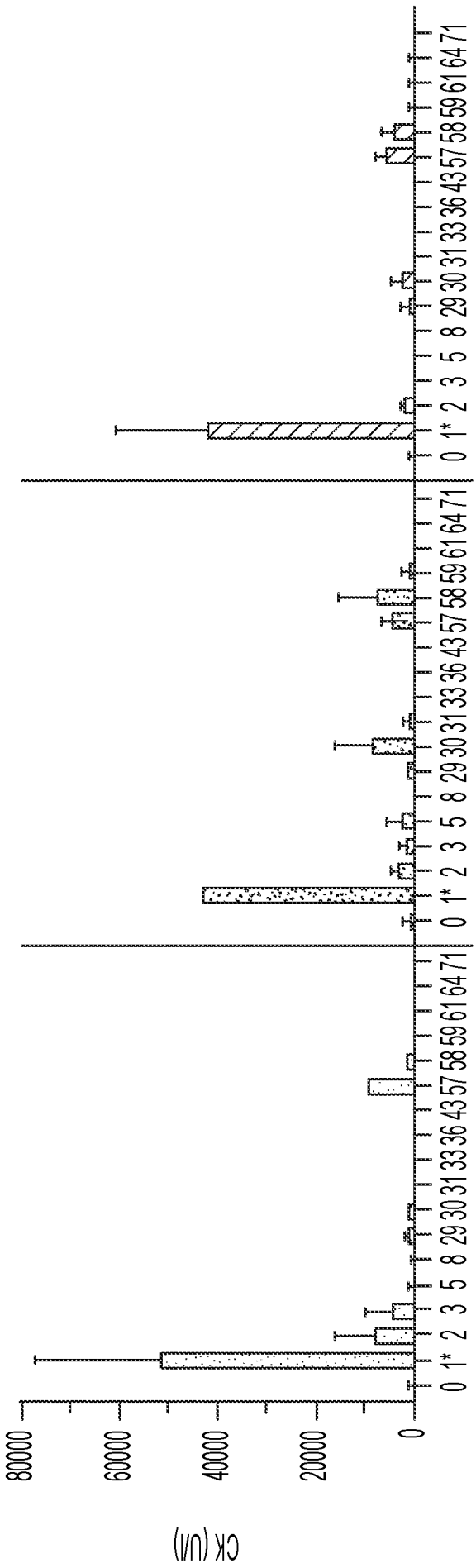


FIG. 47
(Continued)

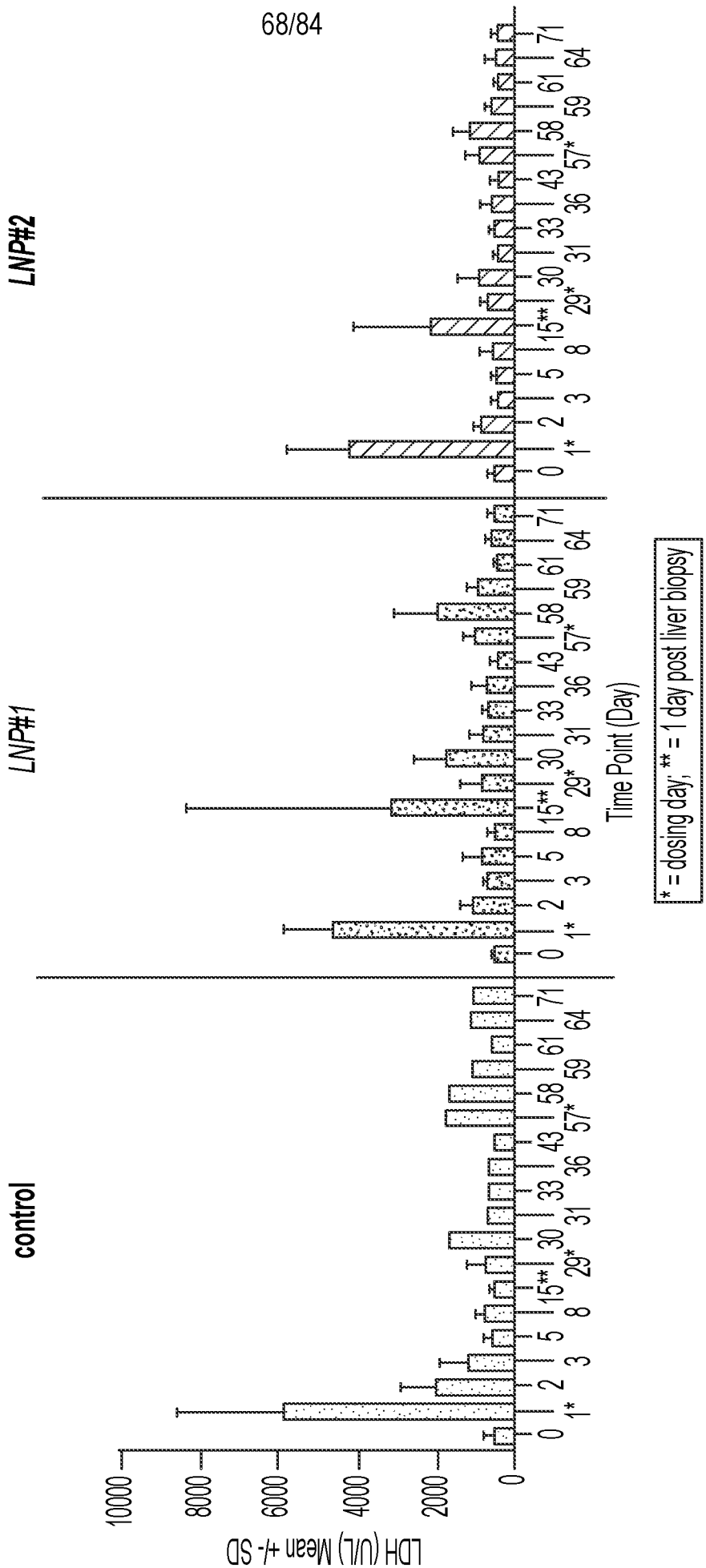

control
LNP#1
LNP#2
LDH (U/L) Mean +/- SD
10000
8000
6000
4000
2000
0
Time Point (Day)
* = dosing day; ** = 1 day post liver biopsy

FIG. 48

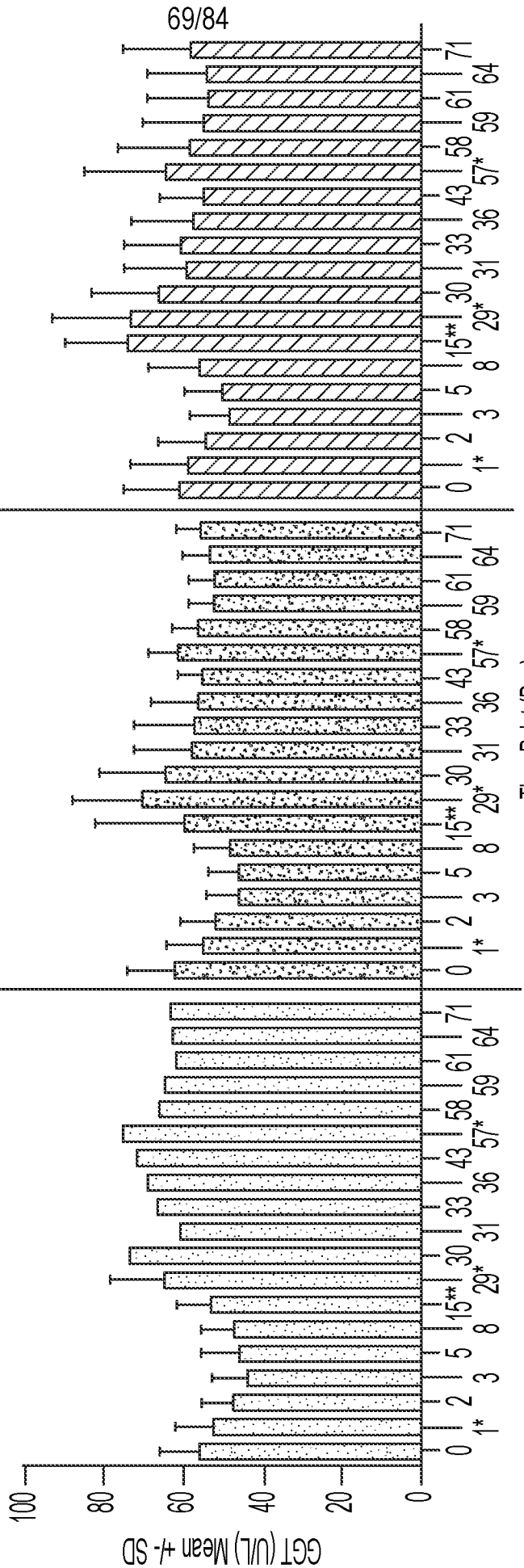


FIG. 48
(Continued)

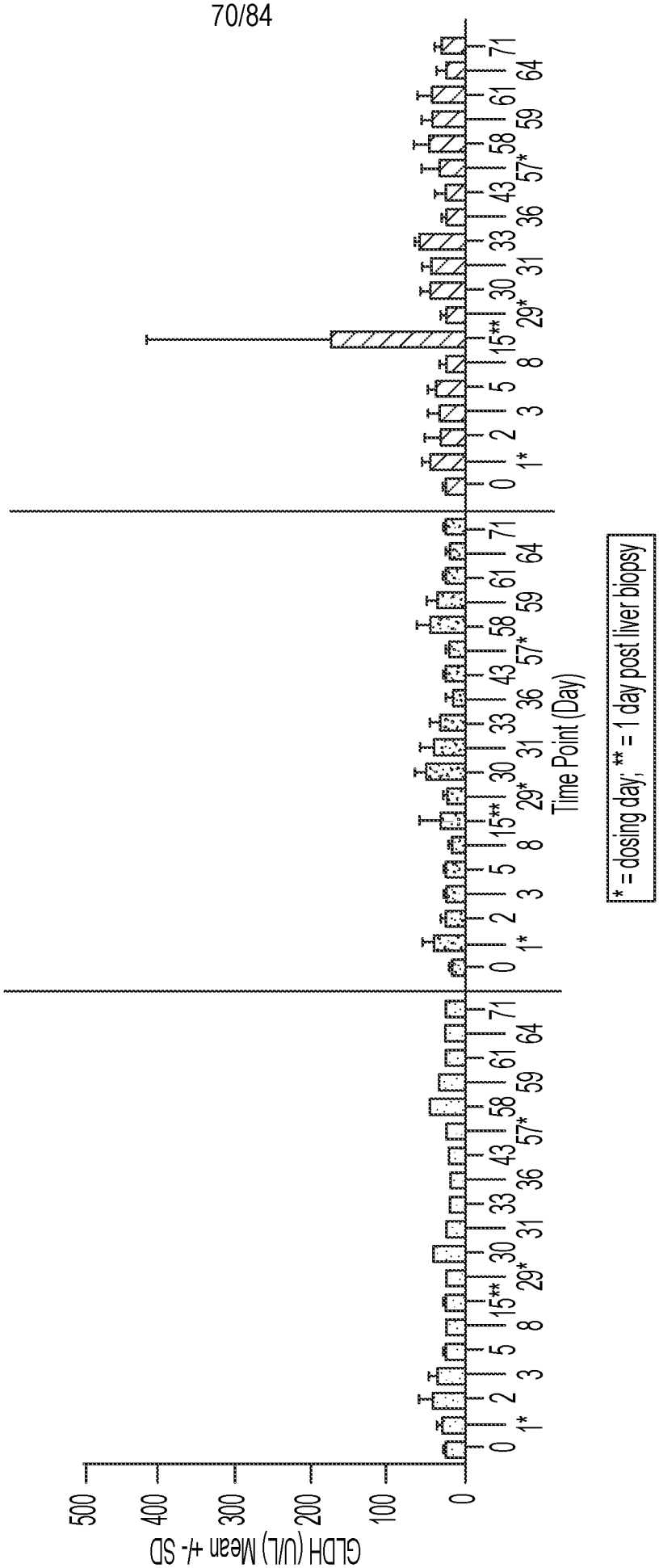


FIG. 48
(Continued)

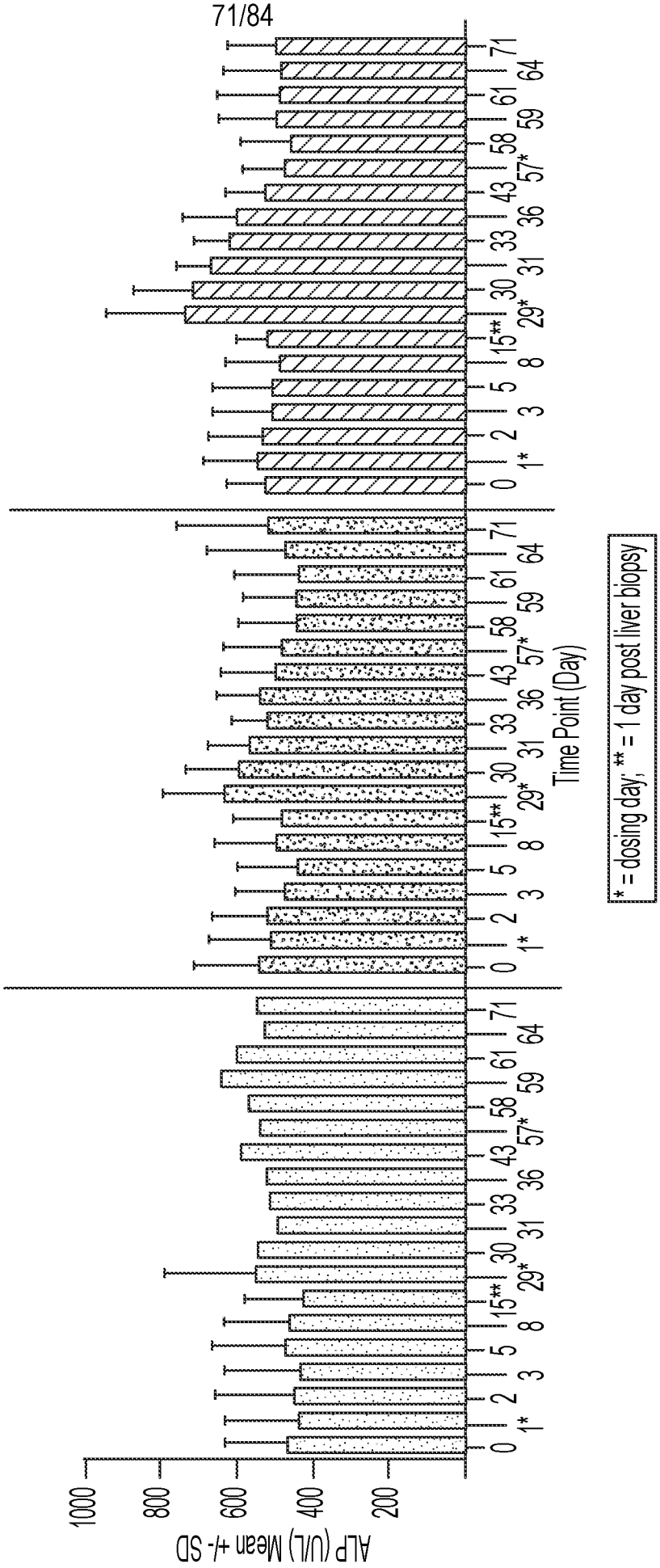


FIG. 48
(Continued)

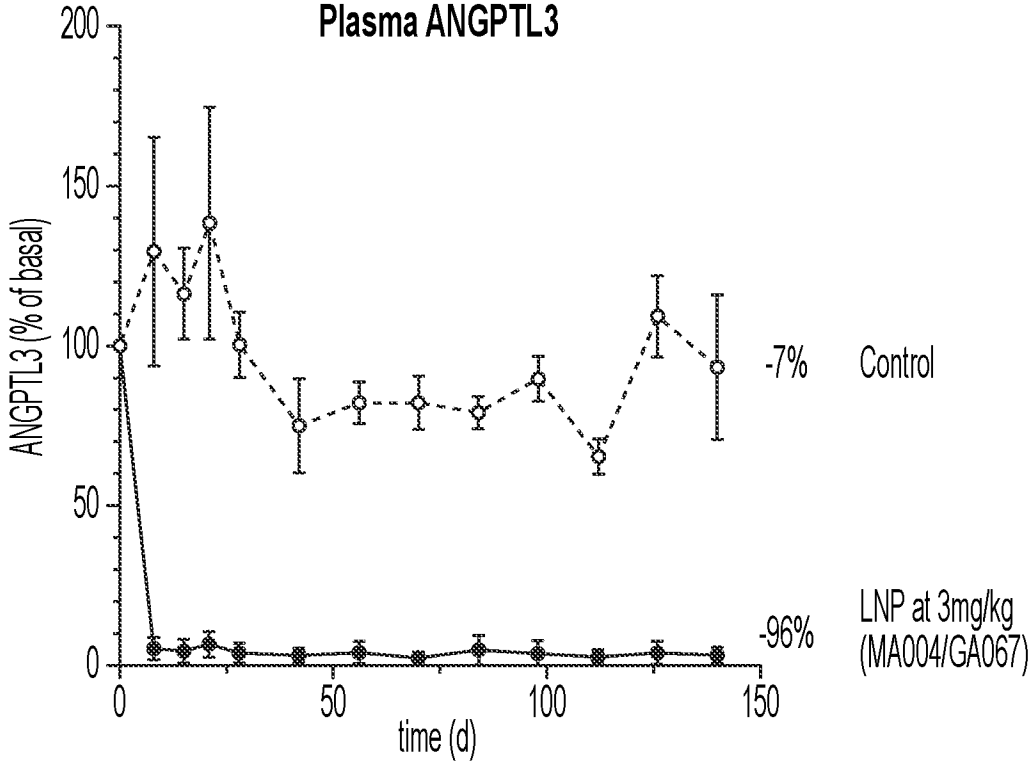


FIG. 49A

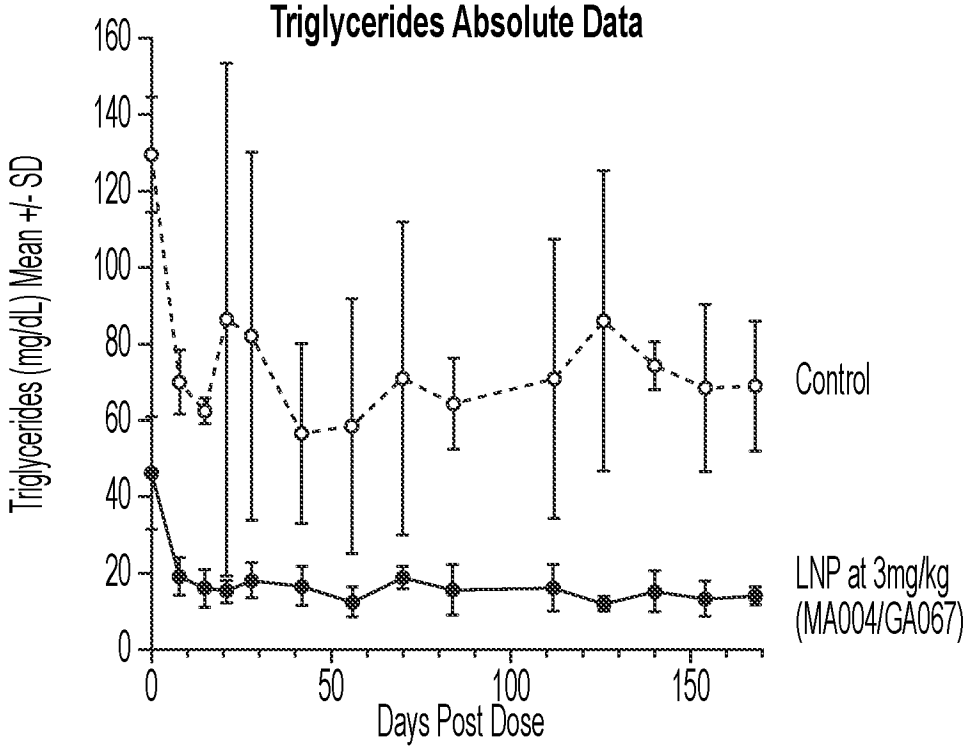


FIG. 49B

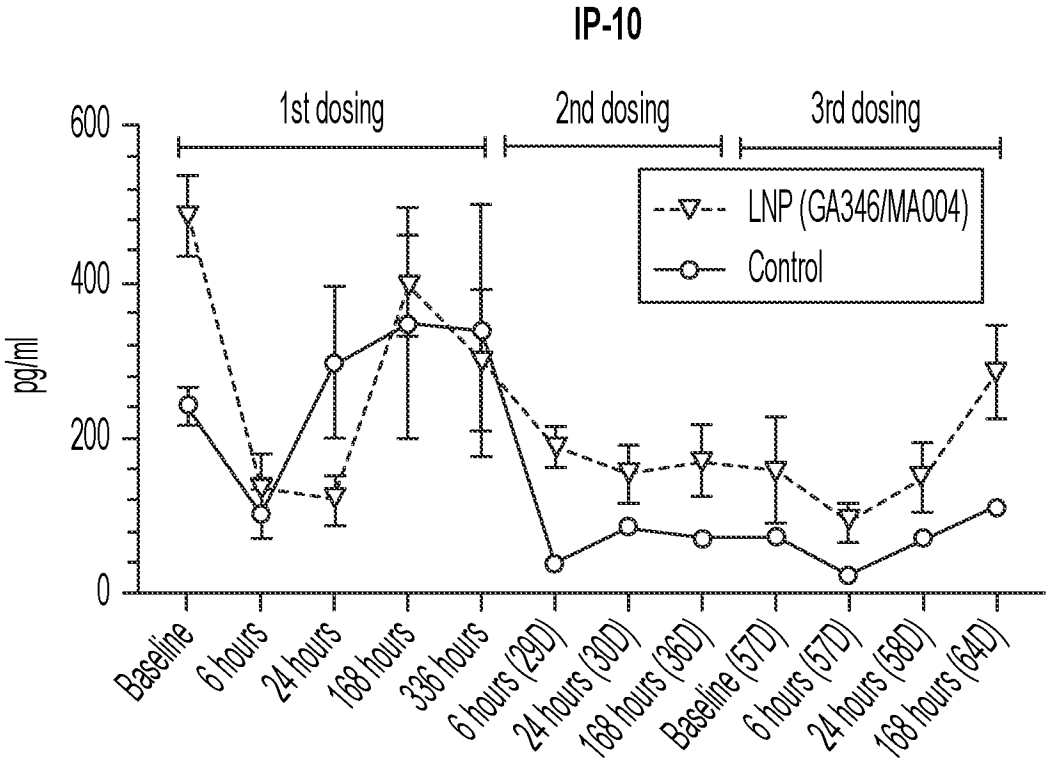


FIG. 50A

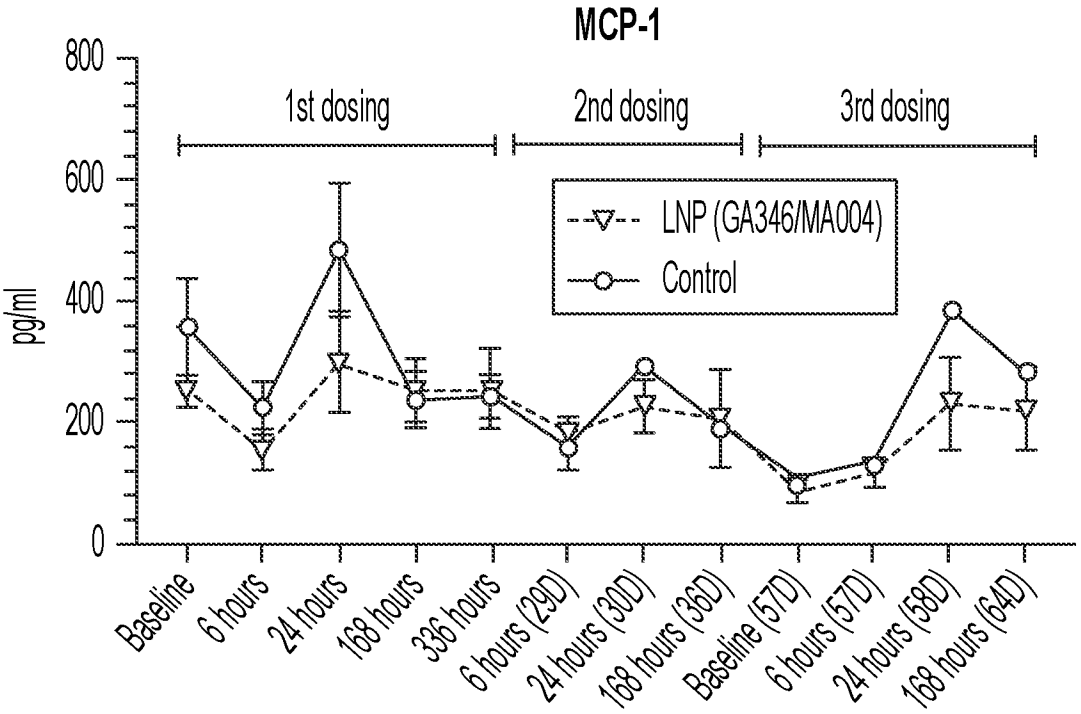


FIG. 50B

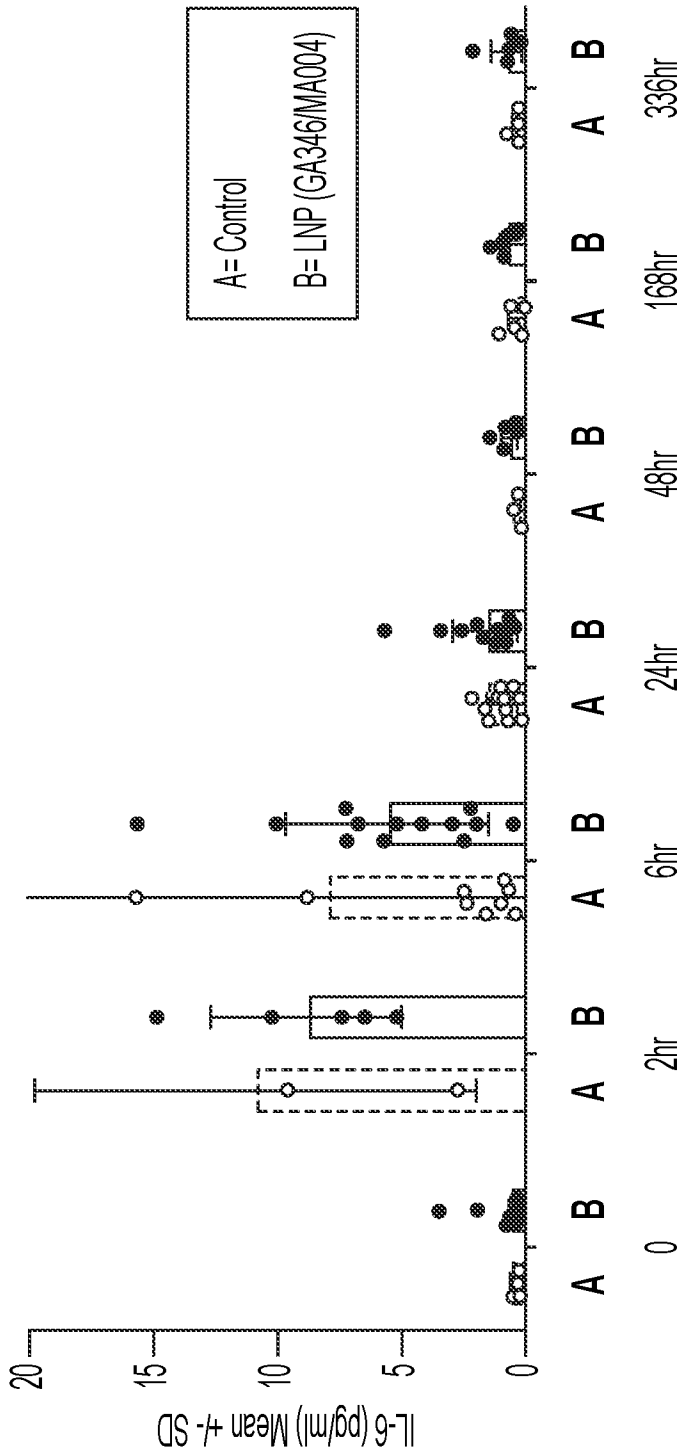

A= Control
B= LNP (GA346/MA004)
IL-6 (pg/ml) Mean +/- SD
20
15
10
5
0
A B A B A B A B A B A B
0
2hr
6hr
24hr
48hr
168hr
336hr
Time Point

FIG. 50C

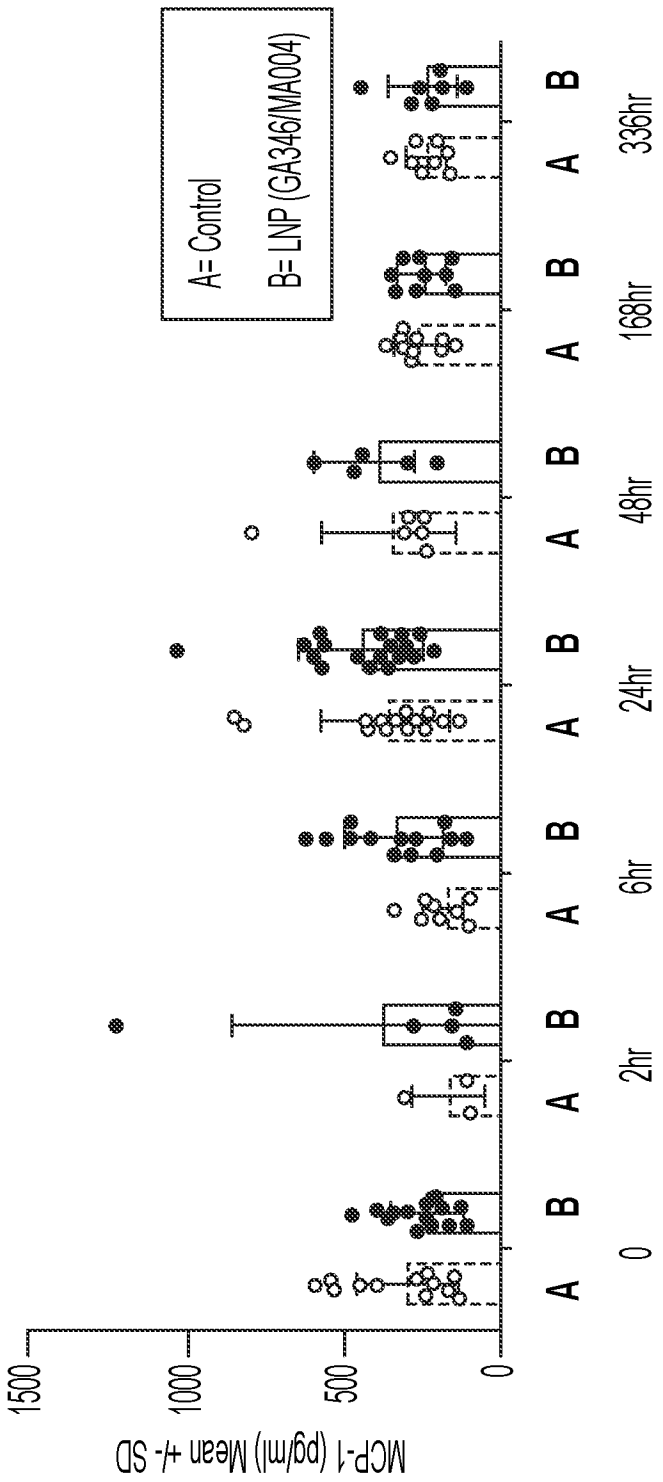

A= Control
B= LNP (GA346/MA004)
MCP-1 (pg/ml) Mean +/- SD
1500
1000
500
0
A B A B A B A B A B A B A B
0
2hr
6hr
24hr
48hr
168hr
336hr
Time Point

FIG. 50D

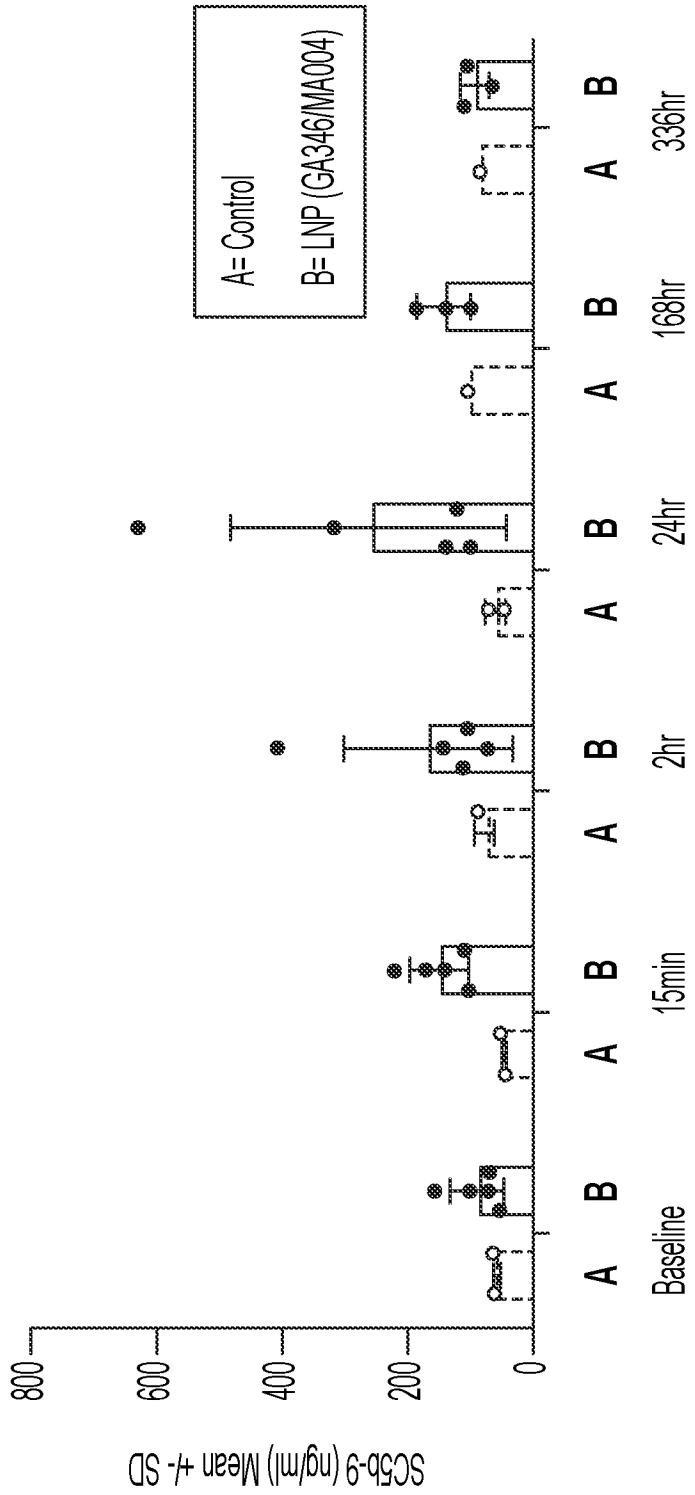

A= Control
B= LNP (GA346/MA004)
SC5b-9 (ng/ml) Mean +/- SD
800
600
400
200
0
A B A B A B A B A B
Baseline
15min
2hr
24hr
168hr
336hr
Time Point

FIG. 50E

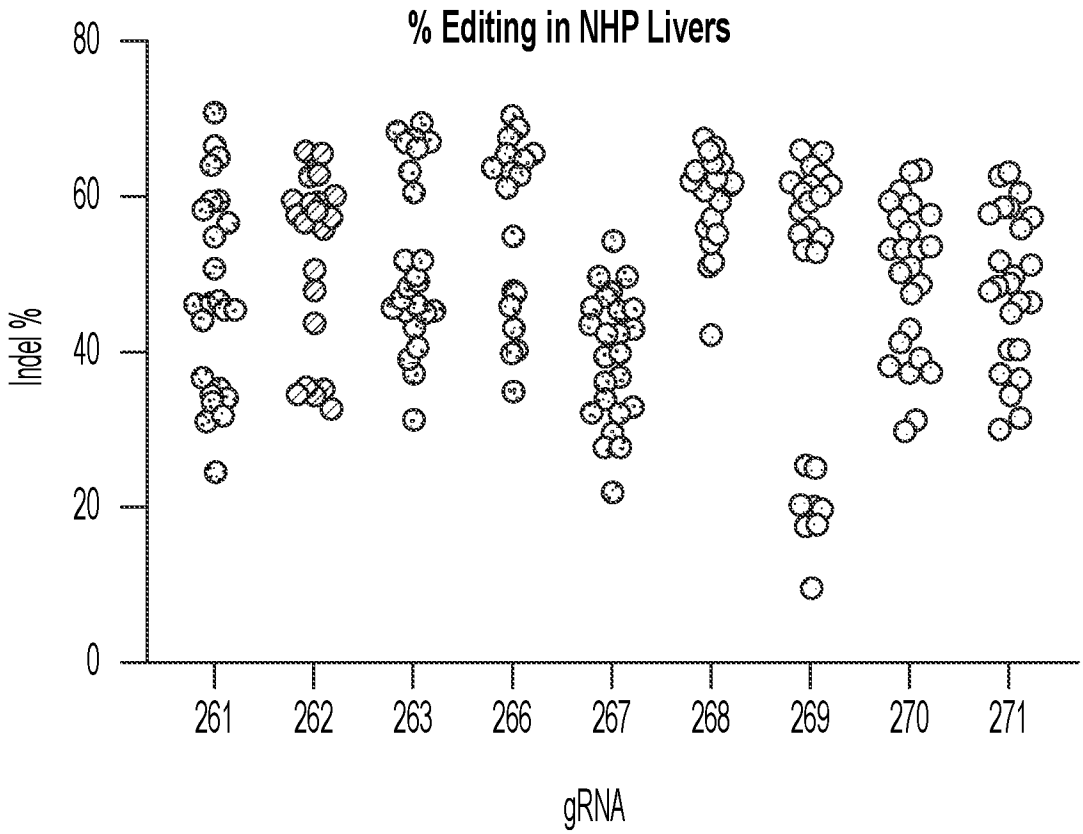

% Editing in NHP Livers
Indel %
80
60
40
20
0
261
262
263
266
267
268
269
270
271
gRNA

FIG. 51

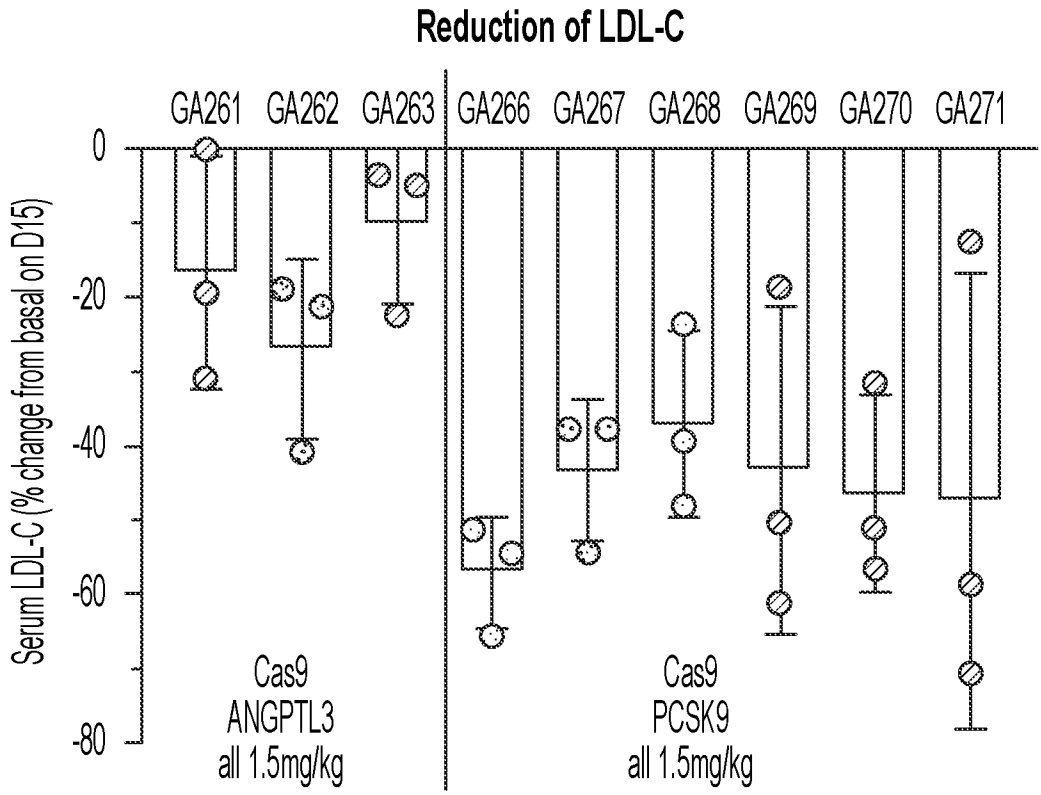

Reduction of LDL-C
GA261
GA262
GA263
GA266
GA267
GA268
GA269
GA270
GA271
0
-20
-40
-60
-80
Serum LDL-C (% change from basal on D15)
Cas9
ANGPTL3
all 1.5mg/kg
Cas9
PCSK9
all 1.5mg/kg

FIG. 52

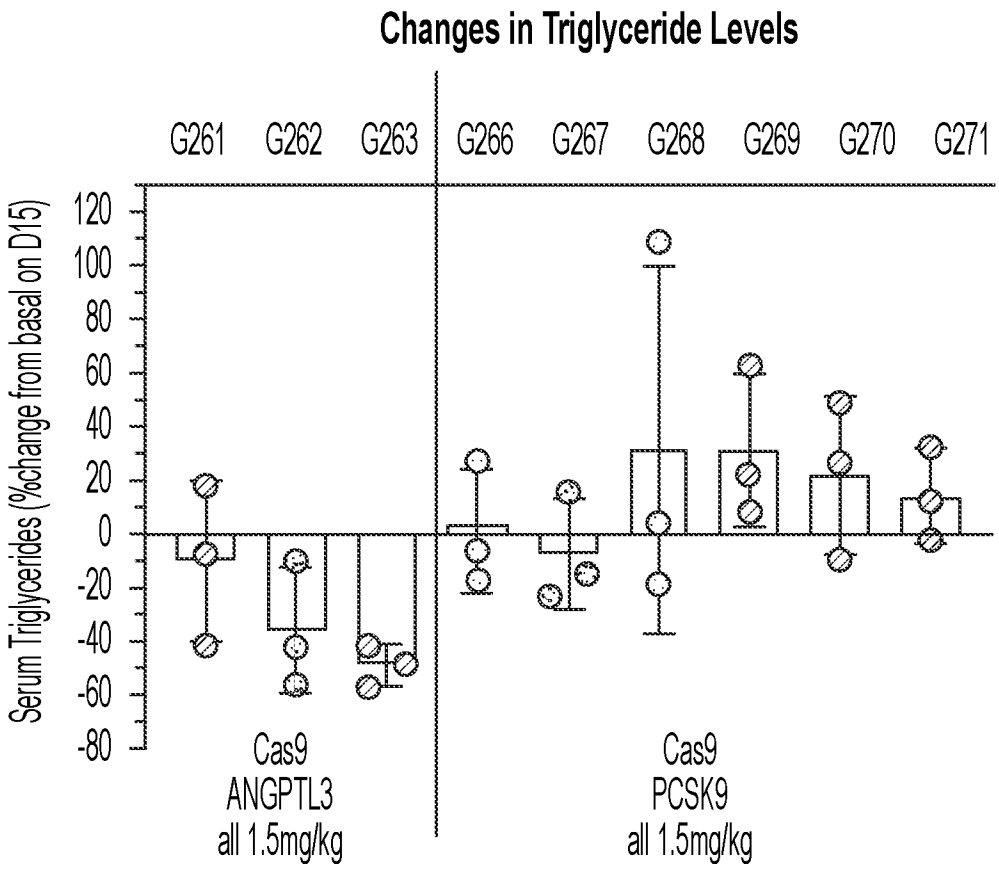

Changes in Triglyceride Levels
G261
G262
G263
G266
G267
G268
G269
G270
G271
Serum Triglycerides (%change from basal on D15)
120
100
80
60
40
20
0
-20
-40
-60
-80
Cas9
ANGPTL3
all 1.5mg/kg
Cas9
PCSK9
all 1.5mg/kg

FIG. 53

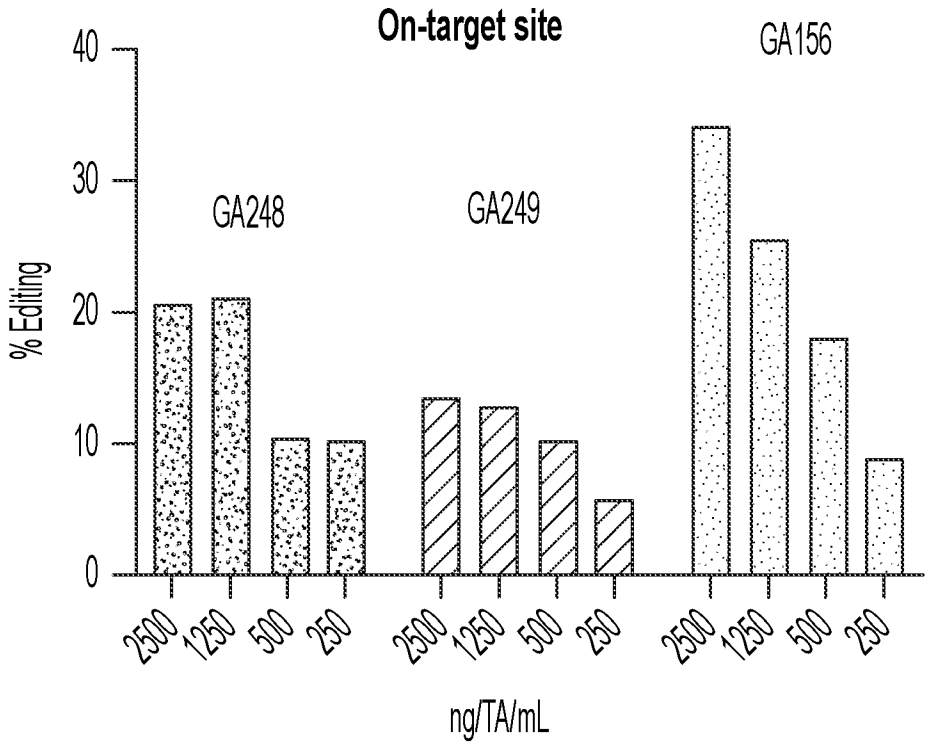


FIG. 54A

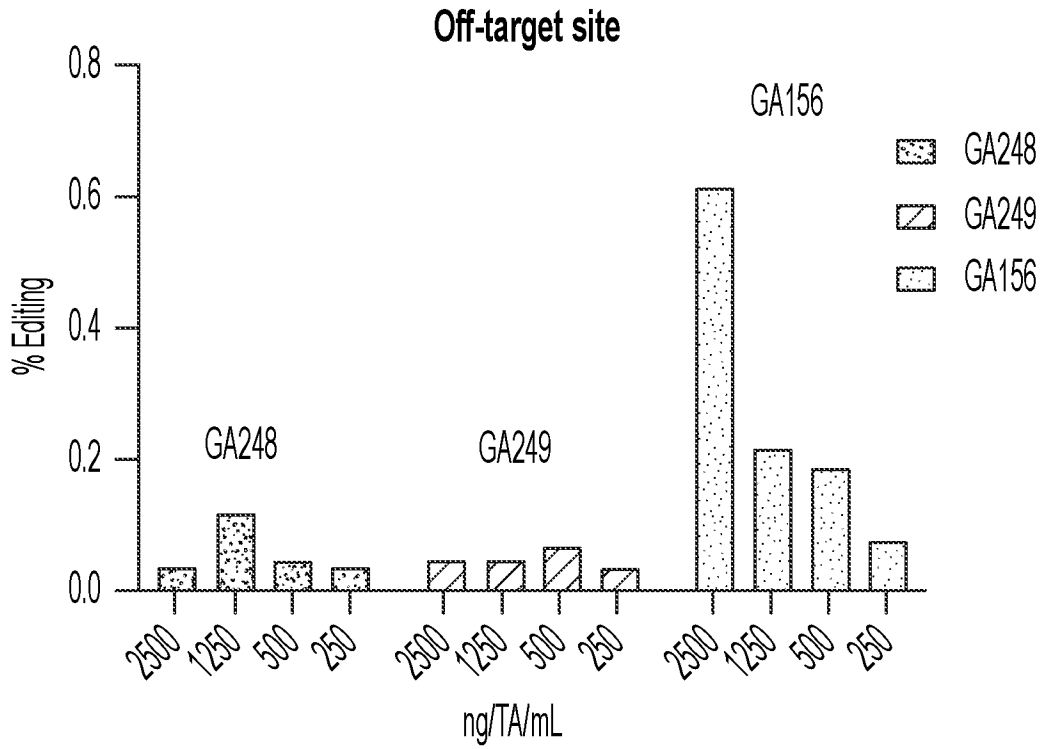


FIG. 54B

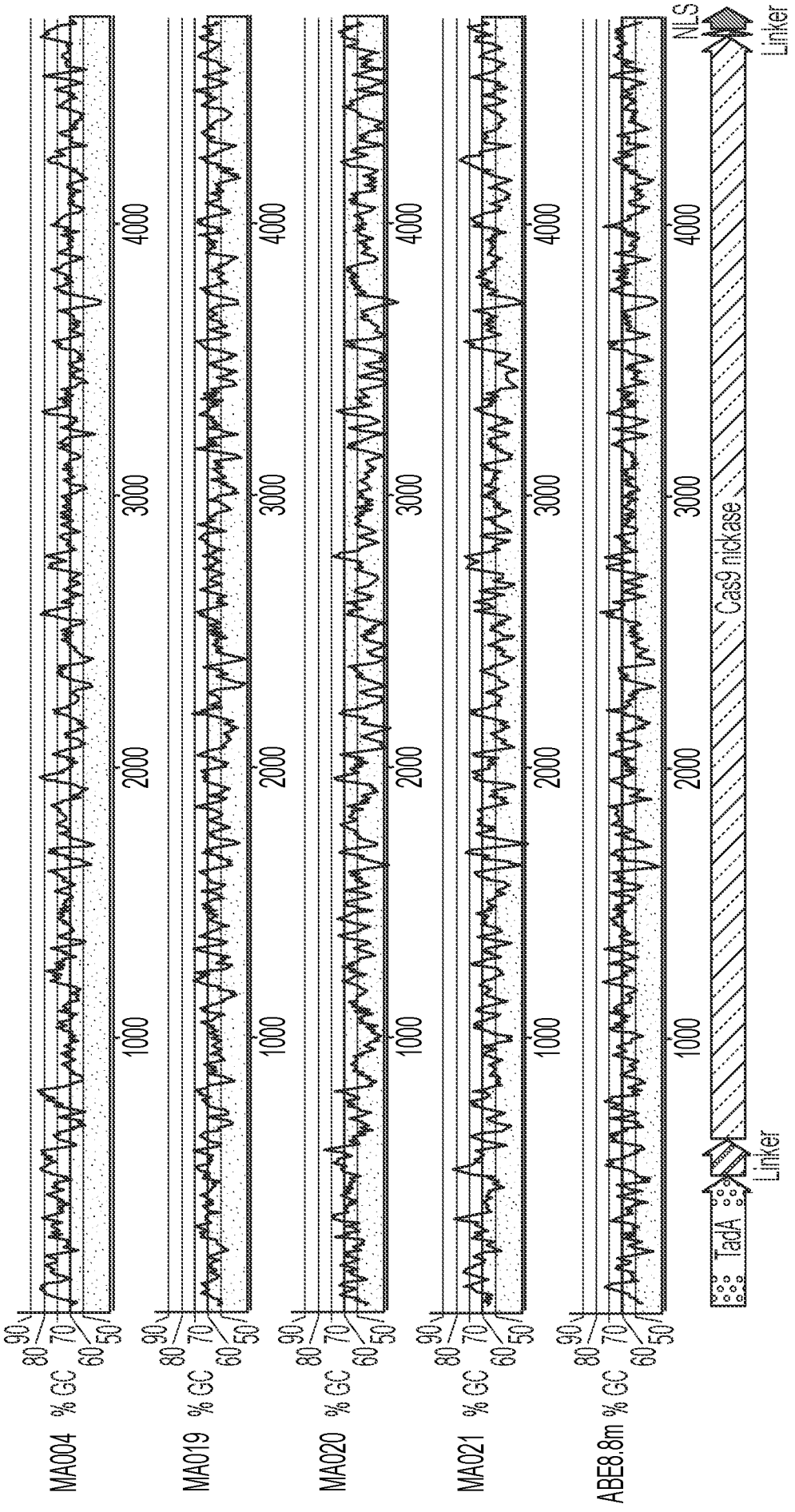

MA004 % GC
MA019 % GC
MA020 % GC
MA021 % GC
ABE8.8m % GC
90
80
70
60
50
1000
2000
3000
4000
TadA
Linker
Cas9 nickase
NLS
Linker

FIG. 55A

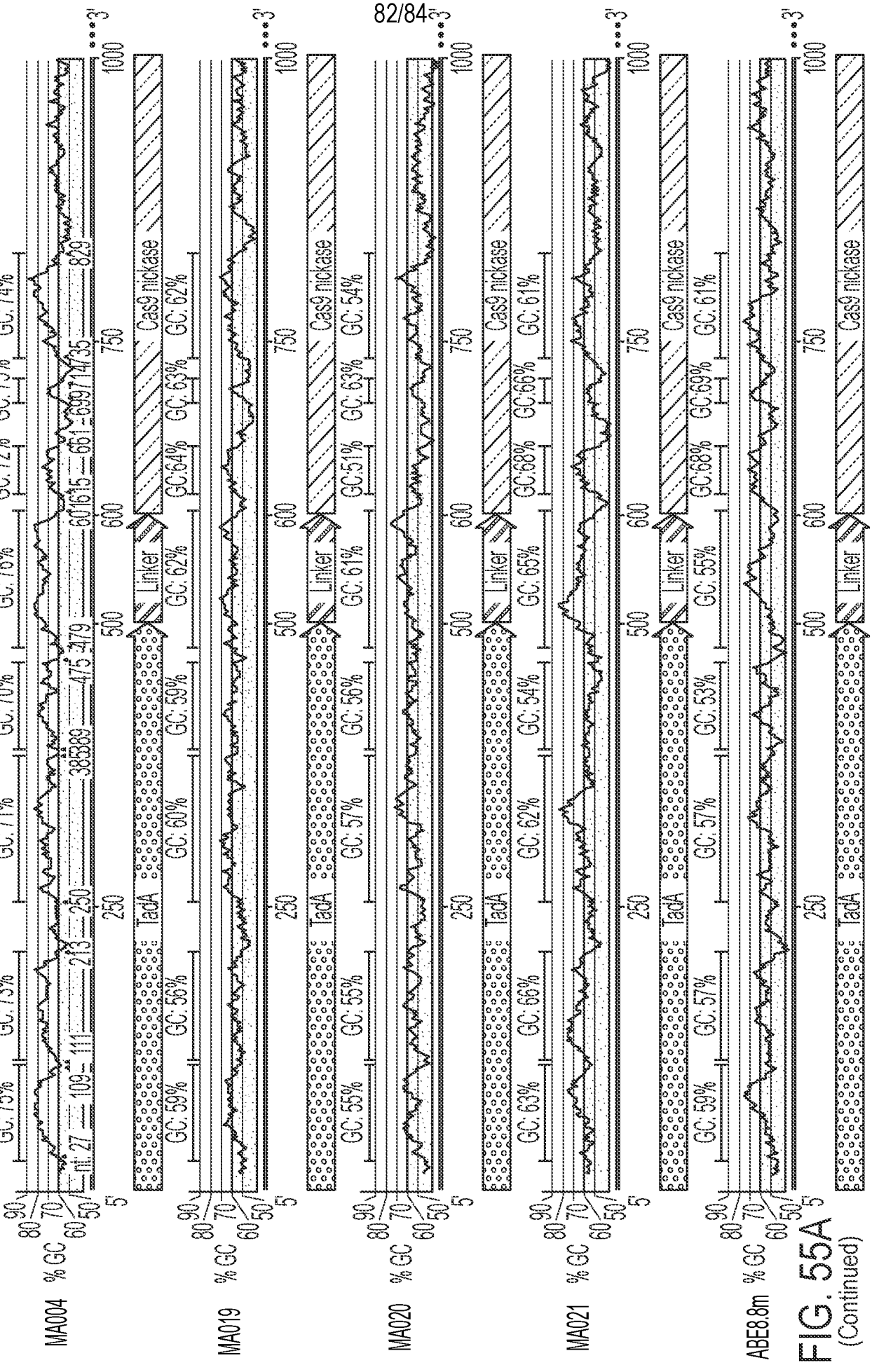


FIG. 55A
(Continued)

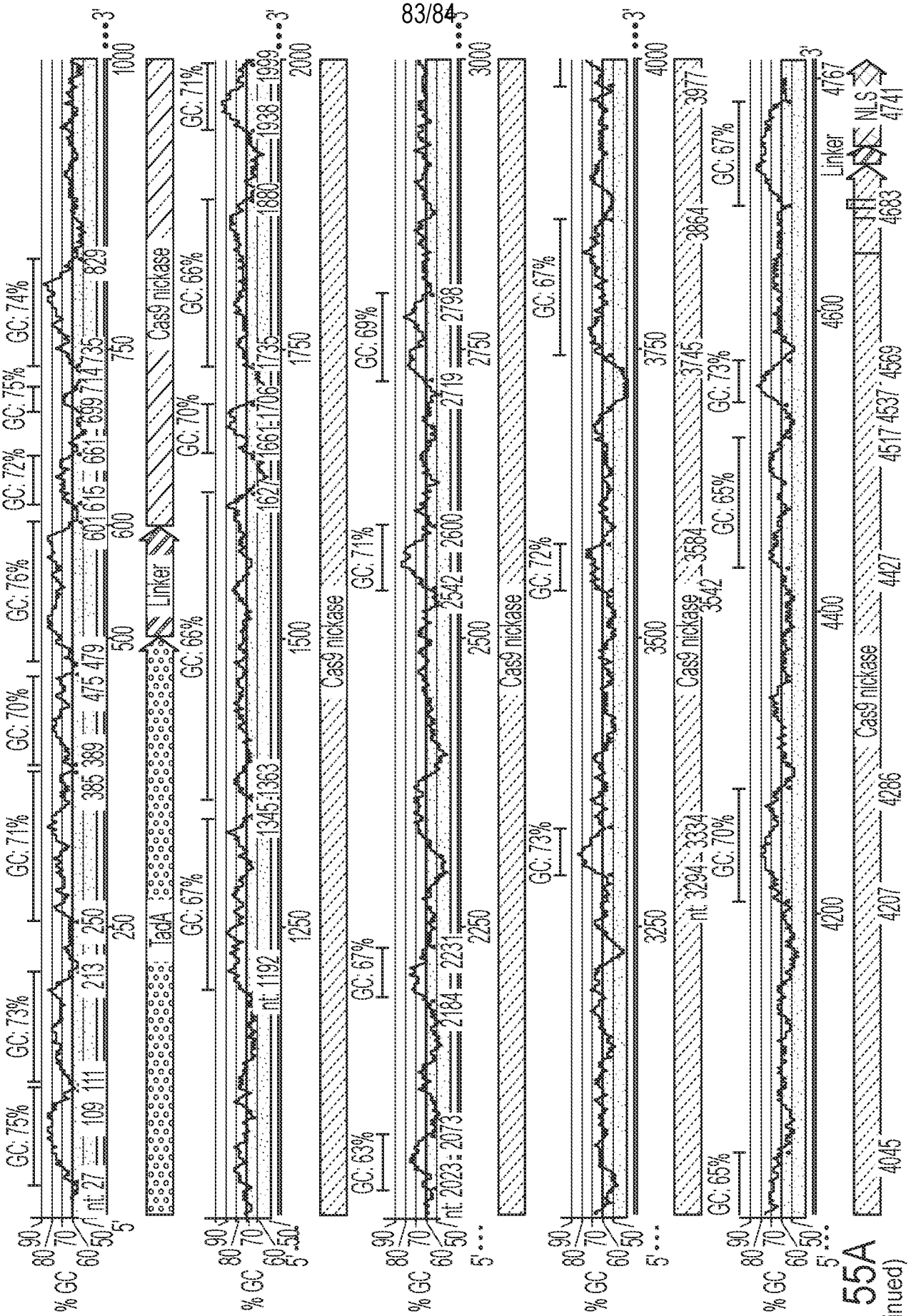


FIG. 55A
(Continued)

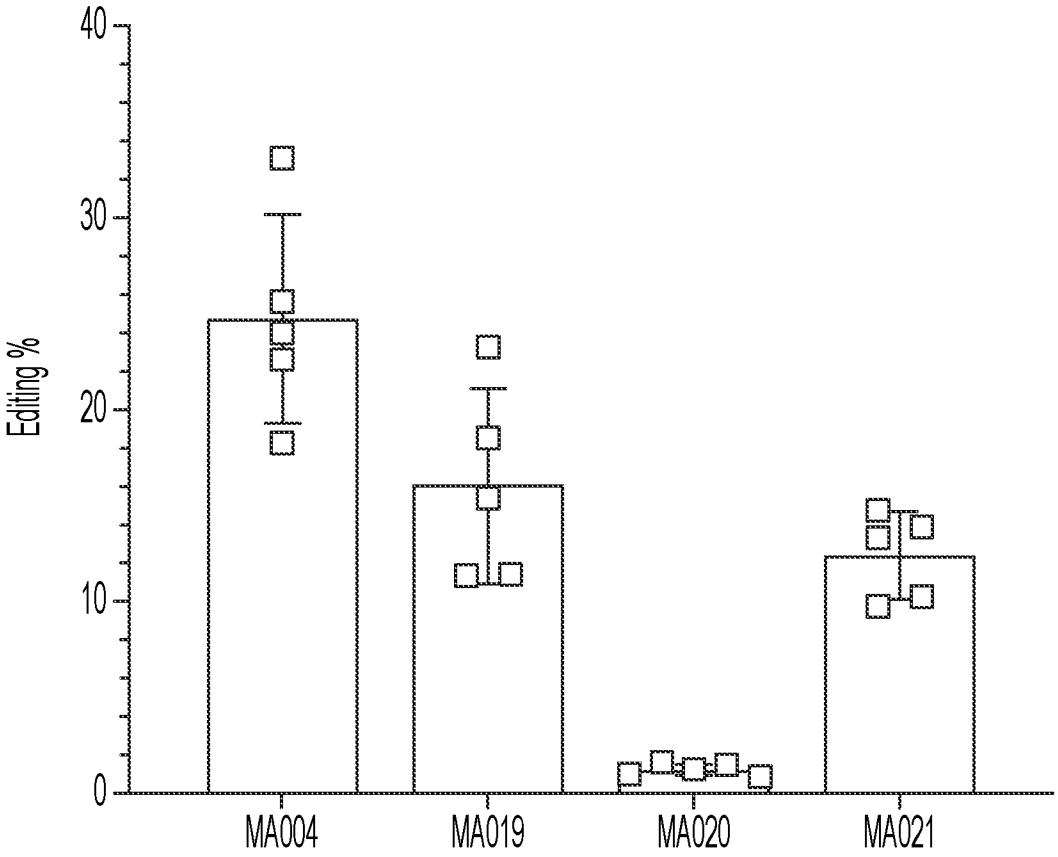


FIG. 55B